# Gretl User's Guide

Gnu Regression, Econometrics and Time-series

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# Contents

Chapter 1

# Introduction

## 1.1 Features at a glance

Gretl is an econometrics package, including a shared library, a command-line client program and a graphical user interface.

**User-friendly** Gretl offers an intuitive user interface; it is very easy to get up and running with econometric analysis. Thanks to its association with the econometrics textbooks by Ramu Ramanathan, Jeffrey Wooldridge, and James Stock and Mark Watson, the package offers many practice data files and command scripts. These are well annotated and accessible. Two other useful resources for gretl users are the available documentation and the gretl-users mailing list.

**Flexible** You can choose your preferred point on the spectrum from interactive point-and-click to batch processing, and can easily combine these approaches.

**Cross-platform** Gretl's "home" platform is Linux but it is also available for MS Windows and Mac OS X, and should work on any unix-like system that has the appropriate basic libraries (see Appendix C).

**Open source** The full source code for gretl is available to anyone who wants to critique it, patch it, or extend it. See Appendix C.

**Sophisticated** Gretl offers a full range of least-squares based estimators, either for single equations and for systems, including vector autoregressions and vector error correction models. Several specific maximum likelihood estimators (e.g. probit, ARIMA, GARCH) are also provided natively; more advanced estimation methods can be implemented by the user via generic maximum likelihood or nonlinear GMM.

**Extensible** Users can enhance gretl by writing their own functions and procedures in gretl's scripting language, which includes a reasonably wide range of matrix functions.

**Accurate** Gretl has been thoroughly tested on several benchmarks, among which the NIST reference datasets. See Appendix D.

**Internet ready** Gretl can access and fetch databases from a server at Wake Forest University. The MS Windows version comes with an updater program which will detect when a new version is available and offer the option of auto-updating.

**International** Gretl will produce its output in English, French, Italian, Spanish, Polish, Portuguese, German or Basque, depending on your computer's native language setting.

## 1.2 Acknowledgements

The gretl code base originally derived from the program ESL ("Econometrics Software Library"), written by Professor Ramu Ramanathan of the University of California, San Diego. We are much in debt to Professor Ramanathan for making this code available under the GNU General Public Licence and for helping to steer gretl's early development.

We are also grateful to the authors of several econometrics textbooks for permission to package for gretl various datasets associated with their texts. This list currently includes William Greene, author of *Econometric Analysis*; Jeffrey Wooldridge (*Introductory Econometrics: A Modern Approach*); James Stock and Mark Watson (*Introduction to Econometrics*); Damodar Gujarati (*Basic Econometrics*); Russell Davidson and James MacKinnon (*Econometric Theory and Methods*); and Marno Verbeek (*A Guide to Modern Econometrics*).

GARCH estimation in gretl is based on code deposited in the archive of the *Journal of Applied Econometrics* by Professors Fiorentini, Calzolari and Panattoni, and the code to generate *p*-values for Dickey–Fuller tests is due to James MacKinnon. In each case we are grateful to the authors for permission to use their work.

With regard to the internationalization of gretl, thanks go to Ignacio Díaz-Emparanza (Spanish), Michel Robitaille and Florent Bresson (French) , Cristian Rigamonti (Italian), Tadeusz Kufel and Pawel Kufel (Polish), Markus Hahn and Sven Schreiber (German), Hélio Guilherme (Portuguese) and Susan Orbe (Basque).

Gretl has benefitted greatly from the work of numerous developers of free, open-source software: for specifics please see Appendix C. Our thanks are due to Richard Stallman of the Free Software Foundation, for his support of free software in general and for agreeing to "adopt" gretl as a GNU program in particular.

Many users of gretl have submitted useful suggestions and bug reports. In this connection particular thanks are due to Ignacio Díaz-Emparanza, Tadeusz Kufel, Pawel Kufel, Alan Isaac, Cri Rigamonti, Sven Schreiber, Talha Yalta, Andreas Rosenblad, and Dirk Eddelbuettel, who maintains the gretl package for Debian GNU/Linux.

## 1.3 Installing the programs

### Linux

On the Linux[1] platform you have the choice of compiling the gretl code yourself or making use of a pre-built package. Building gretl from the source is necessary if you want to access the development version or customize gretl to your needs, but this takes quite a few skills; most users will want to go for a pre-built package.

Some Linux distributions feature gretl as part of their standard offering: Debian, for example, or Ubuntu (in the *universe* repository). If this is the case, all you need to do is install gretl through your package manager of choice (e.g. synaptic).

Ready-to-run packages are available in rpm format (suitable for Red Hat Linux and related systems) on the gretl webpage `http://gretl.sourceforge.net`.

However, we're hopeful that some users with coding skills may consider gretl sufficiently interesting to be worth improving and extending. The documentation of the libgretl API is by no means complete, but you can find some details by following the link "Libgretl API docs" on the gretl homepage. People interested in the gretl development are welcome to subscribe to the gretl-devel mailing list.

If you prefer to compile your own (or are using a unix system for which pre-built packages are not available), instructions on building gretl can be found in Appendix C.

### MS Windows

The MS Windows version comes as a self-extracting executable. Installation is just a matter of downloading `gretl_install.exe` and running this program. You will be prompted for a location to install the package.

[1] In this manual we use "Linux" as shorthand to refer to the GNU/Linux operating system. What is said herein about Linux mostly applies to other unix-type systems too, though some local modifications may be needed.

### Updating

If your computer is connected to the Internet, then on start-up gretl can query its home website at Wake Forest University to see if any program updates are available; if so, a window will open up informing you of that fact. If you want to activate this feature, check the box marked "Tell me about gretl updates" under gretl's "Tools, Preferences, General" menu.

The MS Windows version of the program goes a step further: it tells you that you can update gretl automatically if you wish. To do this, follow the instructions in the popup window: close gretl then run the program titled "gretl updater" (you should find this along with the main gretl program item, under the Programs heading in the Windows Start menu). Once the updater has completed its work you may restart gretl.

# Part I

# Running the program

# Chapter 2

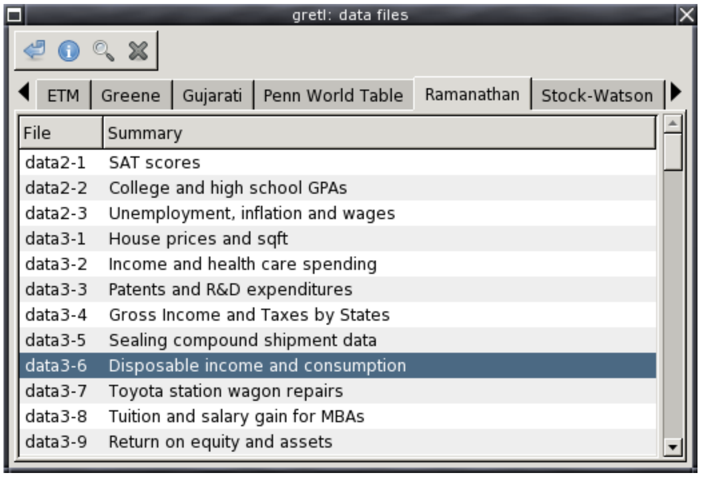
# Getting started

## 2.1 Let’s run a regression

This introduction is mostly angled towards the graphical client program; please see Chapter 27 below and the *Gretl Command Reference* for details on the command-line program, gretlcli.

You can supply the name of a data file to open as an argument to gretl, but for the moment let’s not do that: just fire up the program.[1] You should see a main window (which will hold information on the data set but which is at first blank) and various menus, some of them disabled at first.

What can you do at this point? You can browse the supplied data files (or databases), open a data file, create a new data file, read the help items, or open a command script. For now let’s browse the supplied data files. Under the File menu choose “Open data, Sample file”. A second notebook-type window will open, presenting the sets of data files supplied with the package (see Figure 2.1). Select the first tab, “Ramanathan”. The numbering of the files in this section corresponds to the chapter organization of Ramanathan (2002), which contains discussion of the analysis of these data. The data will be useful for practice purposes even without the text.



| File | Summary |
|---|---|
| data2-1 | SAT scores |
| data2-2 | College and high school GPAs |
| data2-3 | Unemployment, inflation and wages |
| data3-1 | House prices and sqft |
| data3-2 | Income and health care spending |
| data3-3 | Patents and R&D expenditures |
| data3-4 | Gross Income and Taxes by States |
| data3-5 | Sealing compound shipment data |
| data3-6 | Disposable income and consumption |
| data3-7 | Toyota station wagon repairs |
| data3-8 | Tuition and salary gain for MBAs |
| data3-9 | Return on equity and assets |

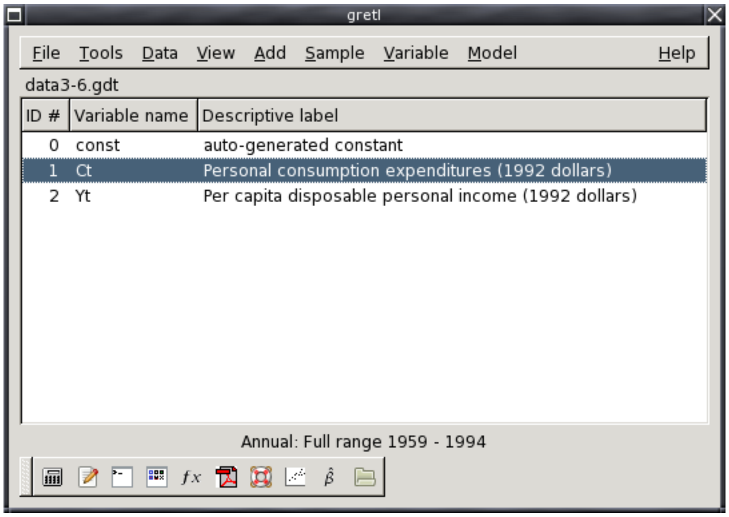
**Figure 2.1**: Practice data files window

If you select a row in this window and click on “Info” this opens a window showing information on the data set in question (for example, on the sources and definitions of the variables). If you find a file that is of interest, you may open it by clicking on “Open”, or just double-clicking on the file name. For the moment let’s open `data3-6`.

☞ In gretl windows containing lists, double-clicking on a line launches a default action for the associated list entry: e.g. displaying the values of a data series, opening a file.

[1] For convenience I will refer to the graphical client program simply as gretl in this manual. Note, however, that the specific name of the program differs according to the computer platform. On Linux it is called `gretl_x11` while on MS Windows it is `gretlw32.exe`. On Linux systems a wrapper script named `gretl` is also installed — see also the *Gretl Command Reference*.

This file contains data pertaining to a classic econometric “chestnut”, the consumption function. The data window should now display the name of the current data file, the overall data range and sample range, and the names of the variables along with brief descriptive tags — see Figure 2.2.



data3-6.gdt

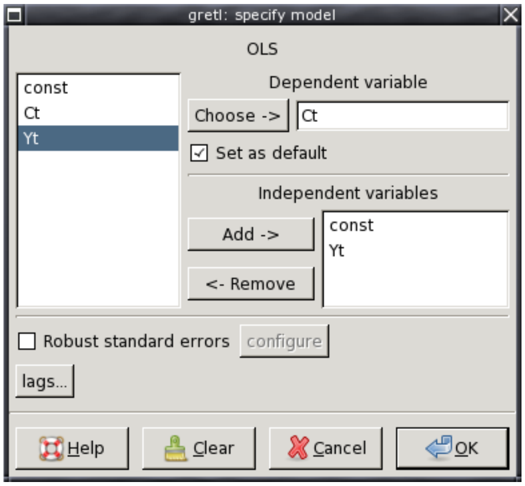
| ID # | Variable name | Descriptive label |
|---|---|---|
| 0 | const | auto-generated constant |
| 1 | Ct | Personal consumption expenditures (1992 dollars) |
| 2 | Yt | Per capita disposable personal income (1992 dollars) |

Annual: Full range 1959 - 1994

**Figure 2.2**: Main window, with a practice data file open

OK, what can we do now? Hopefully the various menu options should be fairly self explanatory. For now we’ll dip into the Model menu; a brief tour of all the main window menus is given in Section 2.3 below.

gretl’s Model menu offers numerous various econometric estimation routines. The simplest and most standard is Ordinary Least Squares (OLS). Selecting OLS pops up a dialog box calling for a *model specification* — see Figure 2.3.



OLS

const
Ct
Yt

Dependent variable: Ct

☑ Set as default

Independent variables:
const
Yt

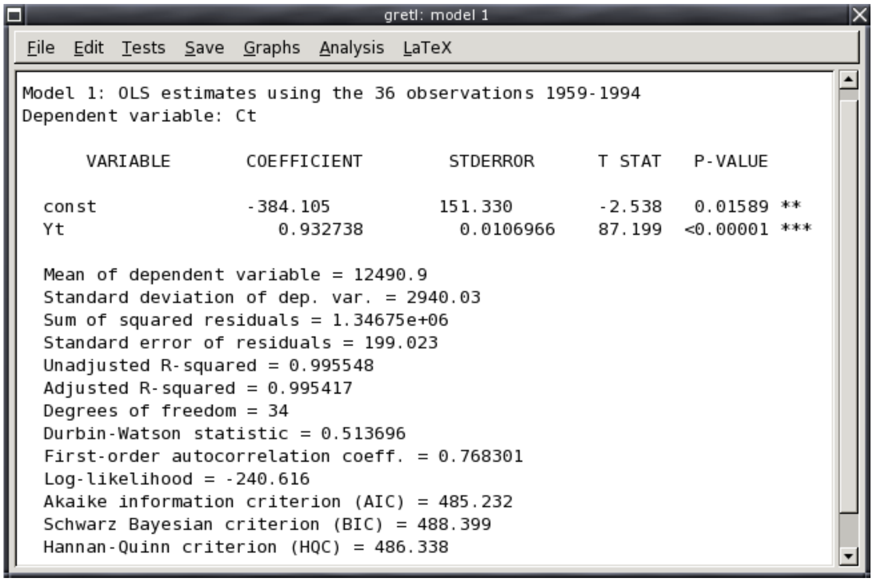
☐ Robust standard errors

**Figure 2.3**: Model specification dialog

To select the dependent variable, highlight the variable you want in the list on the left and click the “Choose” button that points to the Dependent variable slot. If you check the “Set as default” box this variable will be pre-selected as dependent when you next open the model dialog box. Shortcut: double-clicking on a variable on the left selects it as dependent and also sets it as the default. To select independent variables, highlight them on the left and click the “Add” button (or click the right mouse button over the highlighted variable). To select several variable in the list box, drag the mouse over them; to select several non-contiguous variables, hold down the `Ctrl` key and click on the variables you want. To run a regression with consumption as the dependent variable and income as independent, click `Ct` into the Dependent slot and add `Yt` to the Independent variables list.

## 2.2 Estimation output

Once you've specified a model, a window displaying the regression output will appear. The output is reasonably comprehensive and in a standard format (Figure 2.4).



```
Model 1: OLS estimates using the 36 observations 1959-1994
Dependent variable: Ct

      VARIABLE       COEFFICIENT        STDERROR      T STAT   P-VALUE

  const              -384.105          151.330       -2.538    0.01589 **
  Yt                    0.932738         0.0106966    87.199  <0.00001 ***

  Mean of dependent variable = 12490.9
  Standard deviation of dep. var. = 2940.03
  Sum of squared residuals = 1.34675e+06
  Standard error of residuals = 199.023
  Unadjusted R-squared = 0.995548
  Adjusted R-squared = 0.995417
  Degrees of freedom = 34
  Durbin-Watson statistic = 0.513696
  First-order autocorrelation coeff. = 0.768301
  Log-likelihood = -240.616
  Akaike information criterion (AIC) = 485.232
  Schwarz Bayesian criterion (BIC) = 488.399
  Hannan-Quinn criterion (HQC) = 486.338
```

**Figure 2.4**: Model output window

The output window contains menus that allow you to inspect or graph the residuals and fitted values, and to run various diagnostic tests on the model.

For most models there is also an option to print the regression output in LaTeX format. See Chapter 24 for details.

To import gretl output into a word processor, you may copy and paste from an output window, using its Edit menu (or Copy button, in some contexts) to the target program. Many (not all) gretl windows offer the option of copying in RTF (Microsoft's "Rich Text Format") or as LaTeX. If you are pasting into a word processor, RTF may be a good option because the tabular formatting of the output is preserved.[2] Alternatively, you can save the output to a (plain text) file then import the file into the target program. When you finish a gretl session you are given the option of saving all the output from the session to a single file.

Note that on the gnome desktop and under MS Windows, the File menu includes a command to send the output directly to a printer.

☞ When pasting or importing plain text gretl output into a word processor, select a monospaced or typewriter-style font (e.g. Courier) to preserve the output's tabular formatting. Select a small font (10-point Courier should do) to prevent the output lines from being broken in the wrong place.

[2] Note that when you copy as RTF under MS Windows, Windows will only allow you to paste the material into applications that "understand" RTF. Thus you will be able to paste into MS Word, but not into notepad. Note also that there appears to be a bug in some versions of Windows, whereby the paste will not work properly unless the "target" application (e.g. MS Word) is already running prior to copying the material in question.

## 2.3 The main window menus

Reading left to right along the main window's menu bar, we find the File, Tools, Data, View, Add, Sample, Variable, Model and Help menus.

- File menu
  - Open data: Open a native gretl data file or import from other formats. See Chapter 4.
  - Append data: Add data to the current working data set, from a gretl data file, a comma-separated values file or a spreadsheet file.
  - Save data: Save the currently open native gretl data file.
  - Save data as: Write out the current data set in native format, with the option of using gzip data compression. See Chapter 4.
  - Export data: Write out the current data set in Comma Separated Values (CSV) format, or the formats of GNU R or GNU Octave. See Chapter 4 and also Appendix E.
  - Send to: Send the current data set as an e-mail attachment.
  - New data set: Allows you to create a blank data set, ready for typing in values or for importing series from a database. See below for more on databases.
  - Clear data set: Clear the current data set out of memory. Generally you don't have to do this (since opening a new data file automatically clears the old one) but sometimes it's useful.
  - Script files: A "script" is a file containing a sequence of gretl commands. This item contains entries that let you open a script you have created previously ("User file"), open a sample script, or open an editor window in which you can create a new script.
  - Session files: A "session" file contains a snapshot of a previous gretl session, including the data set used and any models or graphs that you saved. Under this item you can open a saved session or save the current session.
  - Databases: Allows you to browse various large databases, either on your own computer or, if you are connected to the internet, on the gretl database server. See Section 4.3 for details.
  - Function files: Handles "function packages" (see Section 10.5), which allow you to access functions written by other users and share the ones written by you.
  - Exit: Quit the program. You'll be prompted to save any unsaved work.
- Tools menu
  - Statistical tables: Look up critical values for commonly used distributions (normal or Gaussian, *t*, chi-square, *F* and Durbin–Watson).
  - P-value finder: Look up p-values from the Gaussian, *t*, chi-square, *F*, gamma, binomial or Poisson distributions. See also the `pvalue` command in the *Gretl Command Reference*.
  - Distribution graphs: Produce graphs of various probability distributions. In the resulting graph window, the pop-up menu includes an item "Add another curve", which enables you to superimpose a further plot (for example, you can draw the *t* distribution with various different degrees of freedom).
  - Test statistic calculator: Calculate test statistics and p-values for a range of common hypothesis tests (population mean, variance and proportion; difference of means, variances and proportions).
  - Nonparametric tests: Calculate test statistics for various nonparametric tests (Sign test, Wilcoxon rank sum test, Wilcoxon signed rank test, Runs test).

  - Seed for random numbers: Set the seed for the random number generator (by default this is set based on the system time when the program is started).
  - Command log: Open a window containing a record of the commands executed so far.
  - Gretl console: Open a "console" window into which you can type commands as you would using the command-line program, gretlcli (as opposed to using point-and-click).
  - Start Gnu R: Start R (if it is installed on your system), and load a copy of the data set currently open in gretl. See Appendix E.
  - Sort variables: Rearrange the listing of variables in the main window, either by ID number or alphabetically by name.
  - NIST test suite: Check the numerical accuracy of gretl against the reference results for linear regression made available by the (US) National Institute of Standards and Technology.
  - Preferences: Set the paths to various files gretl needs to access. Choose the font in which gretl displays text output. Activate or suppress gretl's messaging about the availability of program updates, and so on. See the *Gretl Command Reference* for further details.

- Data menu
  - Select all: Several menu items act upon those variables that are currently selected in the main window. This item lets you select all the variables.
  - Display values: Pops up a window with a simple (not editable) printout of the values of the selected variable or variables.
  - Edit values: Opens a spreadsheet window where you can edit the values of the selected variables.
  - Add observations: Gives a dialog box in which you can choose a number of observations to add at the end of the current dataset; for use with forecasting.
  - Remove extra observations: Active only if extra observations have been added automatically in the process of forecasting; deletes these extra observations.
  - Read info, Edit info: "Read info" just displays the summary information for the current data file; "Edit info" allows you to make changes to it (if you have permission to do so).
  - Print description: Opens a window containing a full account of the current dataset, including the summary information and any specific information on each of the variables.
  - Add case markers: Prompts for the name of a text file containing "case markers" (short strings identifying the individual observations) and adds this information to the data set. See Chapter 4.
  - Remove case markers: Active only if the dataset has case markers identifying the observations; removes these case markers.
  - Dataset structure: invokes a series of dialog boxes which allow you to change the structural interpretation of the current dataset. For example, if data were read in as a cross section you can get the program to interpret them as time series or as a panel. See also section 4.5.
  - Compact data: For time-series data of higher than annual frequency, gives you the option of compacting the data to a lower frequency, using one of four compaction methods (average, sum, start of period or end of period).
  - Expand data: For time-series data, gives you the option of expanding the data to a higher frequency.
  - Transpose data: Turn each observation into a variable and vice versa (or in other words, each row of the data matrix becomes a column in the modified data matrix); can be useful with imported data that have been read in "sideways".

- View menu

  - Icon view: Opens a window showing the content of the current session as a set of icons; see section 3.4.
  - Graph specified vars: Gives a choice between a time series plot, a regular X–Y scatter plot, an X–Y plot using impulses (vertical bars), an X–Y plot "with factor separation" (i.e. with the points colored differently depending to the value of a given dummy variable), boxplots, and a 3-D graph. Serves up a dialog box where you specify the variables to graph. See Chapter 7 for details.
  - Multiple graphs: Allows you to compose a set of up to six small graphs, either pairwise scatter-plots or time-series graphs. These are displayed together in a single window.
  - Summary statistics: Shows a full set of descriptive statistics for the variables selected in the main window.
  - Correlation matrix: Shows the pairwise correlation coefficients for the selected variables.
  - Cross Tabulation: Shows a cross-tabulation of the selected variables. This works only if at least two variables in the data set have been marked as discrete (see Chapter 8).
  - Principal components: Produces a Principal Components Analysis for the selected variables.
  - Mahalonobis distances: Computes the Mahalonobis distance of each observation from the centroid of the selected set of variables.
  - Cross-correlogram: Computes and graphs the cross-correlogram for two selected variables.

- Add menu Offers various standard transformations of variables (logs, lags, squares, etc.) that you may wish to add to the data set. Also gives the option of adding random variables, and (for time-series data) adding seasonal dummy variables (e.g. quarterly dummy variables for quarterly data).

- Sample menu

  - Set range: Select a different starting and/or ending point for the current sample, within the range of data available.
  - Restore full range: self-explanatory.
  - Define, based on dummy: Given a dummy (indicator) variable with values 0 or 1, this drops from the current sample all observations for which the dummy variable has value 0.
  - Restrict, based on criterion: Similar to the item above, except that you don't need a predefined variable: you supply a Boolean expression (e.g. `sqft > 1400`) and the sample is restricted to observations satisfying that condition. See the entry for `genr` in the *Gretl Command Reference* for details on the Boolean operators that can be used.
  - Random sub-sample: Draw a random sample from the full dataset.
  - Drop all obs with missing values: Drop from the current sample all observations for which at least one variable has a missing value (see Section 4.6).
  - Count missing values: Give a report on observations where data values are missing. May be useful in examining a panel data set, where it's quite common to encounter missing values.
  - Set missing value code: Set a numerical value that will be interpreted as "missing" or "not available". This is intended for use with imported data, when gretl has not recognized the missing-value code used.

- Variable menu Most items under here operate on a single variable at a time. The "active" variable is set by highlighting it (clicking on its row) in the main data window. Most options will be self-explanatory. Note that you can rename a variable and can edit its descriptive label under "Edit attributes". You can also "Define a new variable" via a formula (e.g. involving some function of one or more existing variables). For the syntax of such formulae, look at the online help for "Generate variable syntax" or see the `genr` command in the *Gretl Command Reference*. One simple example:

```
foo = x1 * x2
```

will create a new variable `foo` as the product of the existing variables `x1` and `x2`. In these formulae, variables must be referenced by name, not number.

- Model menu For details on the various estimators offered under this menu please consult the *Gretl Command Reference*. Also see Chapter 16 regarding the estimation of nonlinear models.
- Help menu Please use this as needed! It gives details on the syntax required in various dialog entries.

## 2.4 Keyboard shortcuts

When working in the main gretl window, some common operations may be performed using the keyboard, as shown in the table below.

`Return` Opens a window displaying the values of the currently selected variables: it is the same as selecting "Data, Display Values".

`Delete` Pressing this key has the effect of deleting the selected variables. A confirmation is required, to prevent accidental deletions.

`e` Has the same effect as selecting "Edit attributes" from the "Variable" menu.

`F2` Same as "e". Included for compatibility with other programs.

`g` Has the same effect as selecting "Define new variable" from the "Variable" menu (which maps onto the `genr` command).

`h` Opens a help window for gretl commands.

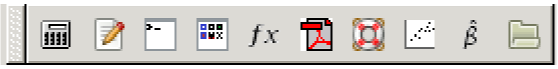
`F1` Same as "h". Included for compatibility with other programs.

`r` Refreshes the variable list in the main window: has the same effect as selecting "Refresh window" from the "Data" menu.

`t` Graphs the selected variable; a line graph is used for time-series datasets, whereas a distribution plot is used for cross-sectional data.

## 2.5 The gretl toolbar

At the bottom left of the main window sits the toolbar.



The icons have the following functions, reading from left to right:

1. Launch a calculator program. A convenience function in case you want quick access to a calculator when you're working in gretl. The default program is `calc.exe` under MS Windows, or `xcalc` under the X window system. You can change the program under the "Tools, Preferences, General" menu, "Programs" tab.
2. Start a new script. Opens an editor window in which you can type a series of commands to be sent to the program as a batch.
3. Open the gretl console. A shortcut to the "Gretl console" menu item (Section 2.3 above).

4. Open the gretl session icon window.
5. Open a window displaying available gretl function packages.
6. Open this manual in PDF format.
7. Open the help item for script commands syntax (i.e. a listing with details of all available commands).
8. Open the dialog box for defining a graph.
9. Open the dialog box for estimating a model using ordinary least squares.
10. Open a window listing the sample datasets supplied with gretl, and any other data file collections that have been installed.

Chapter 3

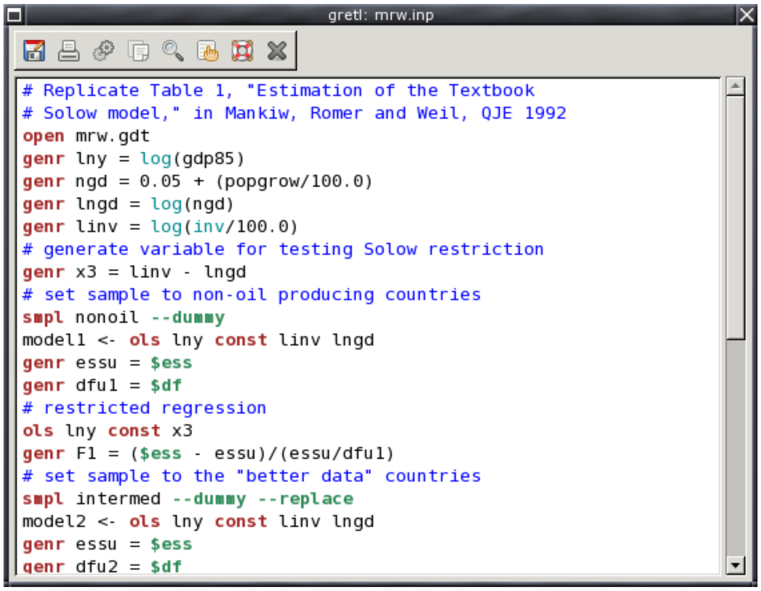
# Modes of working

## 3.1 Command scripts

As you execute commands in gretl, using the GUI and filling in dialog entries, those commands are recorded in the form of a "script" or batch file. Such scripts can be edited and re-run, using either gretl or the command-line client, gretlcli.

To view the current state of the script at any point in a gretl session, choose "Command log" under the Tools menu. This log file is called `session.inp` and it is overwritten whenever you start a new session. To preserve it, save the script under a different name. Script files will be found most easily, using the GUI file selector, if you name them with the extension "`.inp`".

To open a script you have written independently, use the "File, Script files" menu item; to create a script from scratch use the "File, Script files, New script" item or the "new script" toolbar button. In either case a script window will open (see Figure 3.1).



```
# Replicate Table 1, "Estimation of the Textbook
# Solow model," in Mankiw, Romer and Weil, QJE 1992
open mrw.gdt
genr lny = log(gdp85)
genr ngd = 0.05 + (popgrow/100.0)
genr lngd = log(ngd)
genr linv = log(inv/100.0)
# generate variable for testing Solow restriction
genr x3 = linv - lngd
# set sample to non-oil producing countries
smpl nonoil --dummy
model1 <- ols lny const linv lngd
genr essu = $ess
genr dfu1 = $df
# restricted regression
ols lny const x3
genr F1 = ($ess - essu)/(essu/dfu1)
# set sample to the "better data" countries
smpl intermed --dummy --replace
model2 <- ols lny const linv lngd
genr essu = $ess
genr dfu2 = $df
```

**Figure 3.1**: Script window, editing a command file

The toolbar at the top of the script window offers the following functions (left to right): (1) Save the file; (2) Save the file under a specified name; (3) Print the file (this option is not available on all platforms); (4) Execute the commands in the file; (5) Copy selected text; (6) Paste the selected text; (7) Find and replace text; (8) Undo the last Paste or Replace action; (9) Help (if you place the cursor in a command word and press the question mark you will get help on that command); (10) Close the window.

When you execute the script, by clicking on the Execute icon or by pressing Ctrl-r, all output is directed to a single window, where it can be edited, saved or copied to the clipboard. To learn more about the possibilities of scripting, take a look at the gretl Help item "Command reference," or start up the command-line program gretlcli and consult its help, or consult the *Gretl Command Reference*.

If you run the script when part of it is highlighted, gretl will only run that portion. Moreover, if you want to run just the current line, you can do so by pressing Ctrl-Enter.[1]

Clicking the right mouse button in the script editor window produces a pop-up menu. This gives you the option of executing either the line on which the cursor is located, or the selected region of the script if there's a selection in place. If the script is editable, this menu also gives the option of adding or removing comment markers from the start of the line or lines.

The gretl package includes over 70 "practice" scripts. Most of these relate to Ramanathan (2002), but they may also be used as a free-standing introduction to scripting in gretl and to various points of econometric theory. You can explore the practice files under "File, Script files, Practice file" There you will find a listing of the files along with a brief description of the points they illustrate and the data they employ. Open any file and run it to see the output. Note that long commands in a script can be broken over two or more lines, using backslash as a continuation character.

You can, if you wish, use the GUI controls and the scripting approach in tandem, exploiting each method where it offers greater convenience. Here are two suggestions.

- Open a data file in the GUI. Explore the data — generate graphs, run regressions, perform tests. Then open the Command log, edit out any redundant commands, and save it under a specific name. Run the script to generate a single file containing a concise record of your work.
- Start by establishing a new script file. Type in any commands that may be required to set up transformations of the data (see the genr command in the *Gretl Command Reference*). Typically this sort of thing can be accomplished more efficiently via commands assembled with forethought rather than point-and-click. Then save and run the script: the GUI data window will be updated accordingly. Now you can carry out further exploration of the data via the GUI. To revisit the data at a later point, open and rerun the "preparatory" script first.

### Scripts and data files

One common way of doing econometric research with gretl is as follows: compose a script; execute the script; inspect the output; modify the script; run it again — with the last three steps repeated as many times as necessary. In this context, note that when you open a data file this clears out most of gretl's internal state. It's therefore probably a good idea to have your script start with an open command: the data file will be re-opened each time, and you can be confident you're getting "fresh" results.

One further point should be noted. When you go to open a new data file via the graphical interface, you are always prompted: opening a new data file will lose any unsaved work, do you really want to do this? When you execute a script that opens a data file, however, you are *not* prompted. The assumption is that in this case you're not going to lose any work, because the work is embodied in the script itself (and it would be annoying to be prompted at each iteration of the work cycle described above).

This means you should be careful if you've done work using the graphical interface and then decide to run a script: the current data file will be replaced without any questions asked, and it's your responsibility to save any changes to your data first.

[1] This feature is not unique to gretl; other econometric packages offer the same facility. However, experience shows that while this can be remarkably useful, it can also lead to writing dinosaur scripts that are never meant to be executed all at once, but rather used as a chaotic repository to cherry-pick snippets from. Since gretl allows you to have several script windows open at the same time, you may want to keep your scripts tidy and reasonably small.

## 3.2 Saving script objects

When you estimate a model using point-and-click, the model results are displayed in a separate window, offering menus which let you perform tests, draw graphs, save data from the model, and so on. Ordinarily, when you estimate a model using a script you just get a non-interactive printout of the results. You can, however, arrange for models estimated in a script to be "captured", so that you can examine them interactively when the script is finished. Here is an example of the syntax for achieving this effect:

```
Model1 <- ols Ct 0 Yt
```

That is, you type a name for the model to be saved under, then a back-pointing "assignment arrow", then the model command. You may use names that have embedded spaces if you like, but such names must be wrapped in double quotes:

```
"Model 1" <- ols Ct 0 Yt
```

Models saved in this way will appear as icons in the gretl icon view window (see Section 3.4) after the script is executed. In addition, you can arrange to have a named model displayed (in its own window) automatically as follows:

```
Model1.show
```

Again, if the name contains spaces it must be quoted:

```
"Model 1".show
```

The same facility can be used for graphs. For example the following will create a plot of Ct against Yt, save it under the name "CrossPlot" (it will appear under this name in the icon view window), and have it displayed:

```
CrossPlot <- gnuplot Ct Yt
CrossPlot.show
```

You can also save the output from selected commands as named pieces of text (again, these will appear in the session icon window, from where you can open them later). For example this command sends the output from an augmented Dickey–Fuller test to a "text object" named ADF1 and displays it in a window:

```
ADF1 <- adf 2 x1
ADF1.show
```

Objects saved in this way (whether models, graphs or pieces of text output) can be destroyed using the command .free appended to the name of the object, as in ADF1.free.

## 3.3 The gretl console

A further option is available for your computing convenience. Under gretl's "Tools" menu you will find the item "Gretl console" (there is also an "open gretl console" button on the toolbar in the main window). This opens up a window in which you can type commands and execute them one by one (by pressing the Enter key) interactively. This is essentially the same as gretlcli's mode of operation, except that the GUI is updated based on commands executed from the console, enabling you to work back and forth as you wish.

In the console, you have "command history"; that is, you can use the up and down arrow keys to navigate the list of command you have entered to date. You can retrieve, edit and then re-enter a previous command.

In console mode, you can create, display and free objects (models, graphs or text) aa described above for script mode.

## 3.4 The Session concept

gretl offers the idea of a "session" as a way of keeping track of your work and revisiting it later. The basic idea is to provide an iconic space containing various objects pertaining to your current working session (see Figure 3.2). You can add objects (represented by icons) to this space as you go along. If you save the session, these added objects should be available again if you re-open the session later.

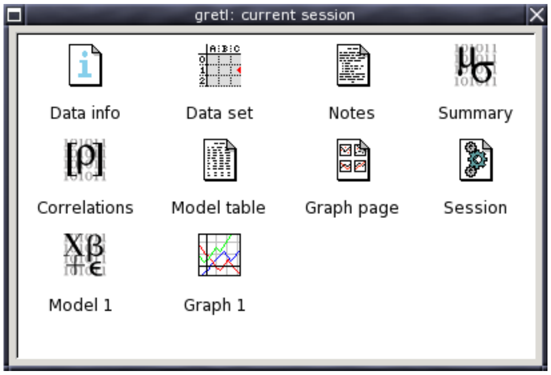


**Figure 3.2**: Icon view: one model and one graph have been added to the default icons

If you start gretl and open a data set, then select "Icon view" from the View menu, you should see the basic default set of icons: these give you quick access to information on the data set (if any), correlation matrix ("Correlations") and descriptive summary statistics ("Summary"). All of these are activated by double-clicking the relevant icon. The "Data set" icon is a little more complex: double-clicking opens up the data in the built-in spreadsheet, but you can also right-click on the icon for a menu of other actions.

To add a model to the Icon view, first estimate it using the Model menu. Then pull down the File menu in the model window and select "Save to session as icon..." or "Save as icon and close". Simply hitting the S key over the model window is a shortcut to the latter action.

To add a graph, first create it (under the View menu, "Graph specified vars", or via one of gretl's other graph-generating commands). Click on the graph window to bring up the graph menu, and select "Save to session as icon".

Once a model or graph is added its icon will appear in the Icon view window. Double-clicking on the icon redisplays the object, while right-clicking brings up a menu which lets you display or delete the object. This popup menu also gives you the option of editing graphs.

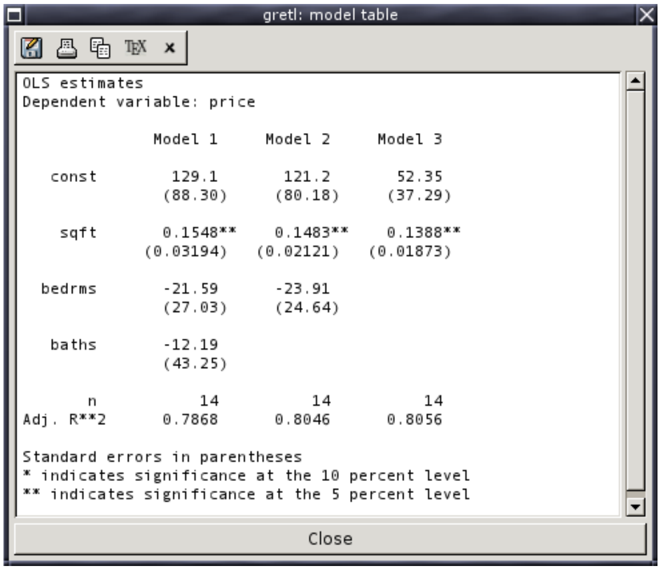
### The model table

In econometric research it is common to estimate several models with a common dependent variable — the models differing in respect of which independent variables are included, or perhaps in respect of the estimator used. In this situation it is convenient to present the regression results in the form of a table, where each column contains the results (coefficient estimates and standard errors) for a given model, and each row contains the estimates for a given variable across the models.

In the Icon view window gretl provides a means of constructing such a table (and copying it in plain text, LaTeX or Rich Text Format). Here is how to do it:[2]

1. Estimate a model which you wish to include in the table, and in the model display window, under the File menu, select “Save to session as icon” or “Save as icon and close”.
2. Repeat step 1 for the other models to be included in the table (up to a total of six models).
3. When you are done estimating the models, open the icon view of your gretl session, by selecting “Icon view” under the View menu in the main gretl window, or by clicking the “session icon view” icon on the gretl toolbar.
4. In the Icon view, there is an icon labeled “Model table”. Decide which model you wish to appear in the left-most column of the model table and add it to the table, either by dragging its icon onto the Model table icon, or by right-clicking on the model icon and selecting “Add to model table” from the pop-up menu.
5. Repeat step 4 for the other models you wish to include in the table. The second model selected will appear in the second column from the left, and so on.
6. When you are finished composing the model table, display it by double-clicking on its icon. Under the Edit menu in the window which appears, you have the option of copying the table to the clipboard in various formats.
7. If the ordering of the models in the table is not what you wanted, right-click on the model table icon and select “Clear table”. Then go back to step 4 above and try again.

A simple instance of gretl’s model table is shown in Figure 3.3.



```
OLS estimates
Dependent variable: price

              Model 1     Model 2     Model 3

   const       129.1       121.2       52.35
              (88.30)     (80.18)     (37.29)

    sqft       0.1548**    0.1483**    0.1388**
            (0.03194)   (0.02121)   (0.01873)

  bedrms      -21.59      -23.91
              (27.03)     (24.64)

   baths      -12.19
              (43.25)

       n          14          14          14
Adj. R**2     0.7868      0.8046      0.8056

Standard errors in parentheses
* indicates significance at the 10 percent level
** indicates significance at the 5 percent level
```

**Figure 3.3**: Example of model table

[2] The model table can also be built non-interactively, in script mode. For details on how to do this, see the entry for `modeltab` in the *Gretl Command Reference*.

### The graph page

The “graph page” icon in the session window offers a means of putting together several graphs for printing on a single page. This facility will work only if you have the LaTeX typesetting system installed, and are able to generate and view either PDF or PostScript output.[3]

In the Icon view window, you can drag up to eight graphs onto the graph page icon. When you double-click on the icon (or right-click and select “Display”), a page containing the selected graphs (in PDF or EPS format) will be composed and opened in your viewer. From there you should be able to print the page.

To clear the graph page, right-click on its icon and select “Clear”.

On systems other than MS Windows, you may have to adjust the setting for the program used to view postscript. Find that under the “Programs” tab in the Preferences dialog box (under the “Tools” menu in the main window). On Windows, you may need to adjust your file associations so that the appropriate viewer is called for the “Open” action on files with the `.ps` extension. FIXME discuss PDF here.

### Saving and re-opening sessions

If you create models or graphs that you think you may wish to re-examine later, then before quitting gretl select “Session files, Save session” from the File menu and give a name under which to save the session. To re-open the session later, either

- Start gretl then re-open the session file by going to the “File, Session files, Open session”, or
- From the command line, type `gretl -r` *sessionfile*, where *sessionfile* is the name under which the session was saved.

[3] For PDF output you need pdflatex and either Adobe’s PDF reader or xpdf on X11. For PostScript, you must have dvips and ghostscript installed, along with a viewer such as gv, ggv or kghostview. The default viewer for systems other than MS Windows is gv.

## Chapter 4

# Data files

## 4.1 Native format

gretl has its own format for data files. Most users will probably not want to read or write such files outside of gretl itself, but occasionally this may be useful and full details on the file formats are given in Appendix A.

## 4.2 Other data file formats

gretl will read various other data formats.

- Plain text (ASCII) files. These can be brought in using gretl's "File, Open Data, Import ASCII..." menu item, or the `import` script command. For details on what gretl expects of such files, see Section 4.4.
- Comma-Separated Values (CSV) files. These can be imported using gretl's "File, Open Data, Import CSV..." menu item, or the `import` script command. See also Section 4.4.
- Spreadsheets: MS Excel, Gnumeric and Open Document (ODS). These are also brought in using gretl's "File, Open Data, Import" menu. The requirements for such files are given in Section 4.4.
- Stata data files (`.dta`).
- SPSS data files (`.sav`).
- Eviews workfiles (`.wf1`).[1]
- JMulTi data files.

When you import data from the ASCII or CSV formats, gretl opens a "diagnostic" window, reporting on its progress in reading the data. If you encounter a problem with ill-formatted data, the messages in this window should give you a handle on fixing the problem.

As of version 1.7.5, gretl also offers ODBC conntictivity. Be warned: this is a recent feature meant for somewhat advanced users; it may still have a few rough edges and there is no GUI interface for this yet. Interested readers will find more info in appendix B.

For the convenience of anyone wanting to carry out more complex data analysis, gretl has a facility for writing out data in the native formats of GNU R, Octave, JMulTi and PcGive (see Appendix E). In the GUI client this option is found under the "File, Export data" menu; in the command-line client use the `store` command with the appropriate option flag.

## 4.3 Binary databases

For working with large amounts of data gretl is supplied with a database-handling routine. A *database*, as opposed to a *data file*, is not read directly into the program's workspace. A database

[1] See `http://www.ecn.wfu.edu/eviews_format/`.

can contain series of mixed frequencies and sample ranges. You open the database and select series to import into the working dataset. You can then save those series in a native format data file if you wish. Databases can be accessed via gretl's menu item "File, Databases".

For details on the format of gretl databases, see Appendix A.

### Online access to databases

As of version 0.40, gretl is able to access databases via the internet. Several databases are available from Wake Forest University. Your computer must be connected to the internet for this option to work. Please see the description of the "data" command under gretl's Help menu.

☞ Visit the gretl data page for details and updates on available data.

### Foreign database formats

Thanks to Thomas Doan of *Estima*, who made available the specification of the database format used by RATS 4 (Regression Analysis of Time Series), gretl can handle such databases — or at least, a subset of same, namely time-series databases containing monthly and quarterly series.

Gretl can also import data from PcGive databases. These take the form of a pair of files, one containing the actual data (with suffix `.bn7`) and one containing supplementary information (`.in7`).

## 4.4 Creating a data file from scratch

There are several ways of doing this:

1. Find, or create using a text editor, a plain text data file and open it with gretl's "Import ASCII" option.
2. Use your favorite spreadsheet to establish the data file, save it in Comma Separated Values format if necessary (this should not be necessary if the spreadsheet format is MS Excel, Gnumeric or Open Document), then use one of gretl's "Import" options.
3. Use gretl's built-in spreadsheet.
4. Select data series from a suitable database.
5. Use your favorite text editor or other software tools to a create data file in gretl format independently.

Here are a few comments and details on these methods.

### Common points on imported data

Options (1) and (2) involve using gretl's "import" mechanism. For gretl to read such data successfully, certain general conditions must be satisfied:

- The first row must contain valid variable names. A valid variable name is of 15 characters maximum; starts with a letter; and contains nothing but letters, numbers and the underscore character, _. (Longer variable names will be truncated to 15 characters.) Qualifications to the above: First, in the case of an ASCII or CSV import, if the file contains no row with variable names the program will automatically add names, v1, v2 and so on. Second, by "the first row" is meant the first *relevant* row. In the case of ASCII and CSV imports, blank rows and rows beginning with a hash mark, #, are ignored. In the case of Excel and Gnumeric imports, you are presented with a dialog box where you can select an offset into the spreadsheet, so that gretl will ignore a specified number of rows and/or columns.

- Data values: these should constitute a rectangular block, with one variable per column (and one observation per row). The number of variables (data columns) must match the number of variable names given. See also section 4.6. Numeric data are expected, but in the case of importing from ASCII/CSV, the program offers limited handling of character (string) data: if a given column contains character data only, consecutive numeric codes are substituted for the strings, and once the import is complete a table is printed showing the correspondence between the strings and the codes.
- Dates (or observation labels): Optionally, the *first* column may contain strings such as dates, or labels for cross-sectional observations. Such strings have a maximum of 8 characters (as with variable names, longer strings will be truncated). A column of this sort should be headed with the string `obs` or `date`, or the first row entry may be left blank.

  For dates to be recognized as such, the date strings must adhere to one or other of a set of specific formats, as follows. For *annual* data: 4-digit years. For *quarterly* data: a 4-digit year, followed by a separator (either a period, a colon, or the letter `Q`), followed by a 1-digit quarter. Examples: `1997.1`, `2002:3`, `1947Q1`. For *monthly* data: a 4-digit year, followed by a period or a colon, followed by a two-digit month. Examples: `1997.01`, `2002:10`.

CSV files can use comma, space or tab as the column separator. When you use the “Import CSV” menu item you are prompted to specify the separator. In the case of “Import ASCII” the program attempts to auto-detect the separator that was used.

If you use a spreadsheet to prepare your data you are able to carry out various transformations of the “raw” data with ease (adding things up, taking percentages or whatever): note, however, that you can also do this sort of thing easily — perhaps more easily — within gretl, by using the tools under the “Add” menu.

### Appending imported data

You may wish to establish a gretl dataset piece by piece, by incremental importation of data from other sources. This is supported via the “File, Append data” menu items: gretl will check the new data for conformability with the existing dataset and, if everything seems OK, will merge the data. You can add new variables in this way, provided the data frequency matches that of the existing dataset. Or you can append new observations for data series that are already present; in this case the variable names must match up correctly. Note that by default (that is, if you choose “Open data” rather than “Append data”), opening a new data file closes the current one.

### Using the built-in spreadsheet

Under gretl’s “File, New data set” menu you can choose the sort of dataset you want to establish (e.g. quarterly time series, cross-sectional). You will then be prompted for starting and ending dates (or observation numbers) and the name of the first variable to add to the dataset. After supplying this information you will be faced with a simple spreadsheet into which you can type data values. In the spreadsheet window, clicking the right mouse button will invoke a popup menu which enables you to add a new variable (column), to add an observation (append a row at the foot of the sheet), or to insert an observation at the selected point (move the data down and insert a blank row.)

Once you have entered data into the spreadsheet you import these into gretl’s workspace using the spreadsheet’s “Apply changes” button.

Please note that gretl’s spreadsheet is quite basic and has no support for functions or formulas. Data transformations are done via the “Add” or “Variable” menus in the main gretl window.

### Selecting from a database

Another alternative is to establish your dataset by selecting variables from a database.

Begin with gretl's "File, Databases" menu item. This has four forks: "Gretl native", "RATS 4", "PcGive" and "On database server". You should be able to find the file `fedstl.bin` in the file selector that opens if you choose the "Gretl native" option — this file, which contains a large collection of US macroeconomic time series, is supplied with the distribution.

You won't find anything under "RATS 4" unless you have purchased RATS data.[2] If you do possess RATS data you should go into gretl's "Tools, Preferences, General" dialog, select the Databases tab, and fill in the correct path to your RATS files.

If your computer is connected to the internet you should find several databases (at Wake Forest University) under "On database server". You can browse these remotely; you also have the option of installing them onto your own computer. The initial remote databases window has an item showing, for each file, whether it is already installed locally (and if so, if the local version is up to date with the version at Wake Forest).

Assuming you have managed to open a database you can import selected series into gretl's workspace by using the "Series, Import" menu item in the database window, or via the popup menu that appears if you click the right mouse button, or by dragging the series into the program's main window.

### Creating a gretl data file independently

It is possible to create a data file in one or other of gretl's own formats using a text editor or software tools such as awk, sed or perl. This may be a good choice if you have large amounts of data already in machine readable form. You will, of course, need to study the gretl data formats (XML format or "traditional" format) as described in Appendix A.

## 4.5 Structuring a dataset

Once your data are read by gretl, it may be necessary to supply some information on the nature of the data. We distinguish between three kinds of datasets:

1. Cross section
2. Time series
3. Panel data

The primary tool for doing this is the "Data, Dataset structure" menu entry in the graphical interface, or the `setobs` command for scripts and the command-line interface.

### Cross sectional data

By a cross section we mean observations on a set of "units" (which may be firms, countries, individuals, or whatever) at a common point in time. This is the default interpretation for a data file: if gretl does not have sufficient information to interpret data as time-series or panel data, they are automatically interpreted as a cross section. In the unlikely event that cross-sectional data are wrongly interpreted as time series, you can correct this by selecting the "Data, Dataset structure" menu item. Click the "cross-sectional" radio button in the dialog box that appears, then click "Forward". Click "OK" to confirm your selection.

### Time series data

When you import data from a spreadsheet or plain text file, gretl will make fairly strenuous efforts to glean time-series information from the first column of the data, if it looks at all plausible that such information may be present. If time-series structure is present but not recognized, again you

[2] See www.estima.com

can use the "Data, Dataset structure" menu item. Select "Time series" and click "Forward"; select the appropriate data frequency and click "Forward" again; then select or enter the starting observation and click "Forward" once more. Finally, click "OK" to confirm the time-series interpretation if it is correct (or click "Back" to make adjustments if need be).

Besides the basic business of getting a data set interpreted as time series, further issues may arise relating to the frequency of time-series data. In a gretl time-series data set, all the series must have the same frequency. Suppose you wish to make a combined dataset using series that, in their original state, are not all of the same frequency. For example, some series are monthly and some are quarterly.

Your first step is to formulate a strategy: Do you want to end up with a quarterly or a monthly data set? A basic point to note here is that "compacting" data from a higher frequency (e.g. monthly) to a lower frequency (e.g. quarterly) is usually unproblematic. You lose information in doing so, but in general it is perfectly legitimate to take (say) the average of three monthly observations to create a quarterly observation. On the other hand, "expanding" data from a lower to a higher frequency is not, in general, a valid operation.

In most cases, then, the best strategy is to start by creating a data set of the *lower* frequency, and then to compact the higher frequency data to match. When you import higher-frequency data from a database into the current data set, you are given a choice of compaction method (average, sum, start of period, or end of period). In most instances "average" is likely to be appropriate.

You *can* also import lower-frequency data into a high-frequency data set, but this is generally not recommended. What gretl does in this case is simply replicate the values of the lower-frequency series as many times as required. For example, suppose we have a quarterly series with the value 35.5 in 1990:1, the first quarter of 1990. On expansion to monthly, the value 35.5 will be assigned to the observations for January, February and March of 1990. The expanded variable is therefore useless for fine-grained time-series analysis, outside of the special case where you know that the variable in question does in fact remain constant over the sub-periods.

When the current data frequency is appropriate, gretl offers both "Compact data" and "Expand data" options under the "Data" menu. These options operate on the whole data set, compacting or exanding all series. They should be considered "expert" options and should be used with caution.

### Panel data

Panel data are inherently three dimensional — the dimensions being variable, cross-sectional unit, and time-period. For example, a particular number in a panel data set might be identified as the observation on capital stock for General Motors in 1980. (A note on terminology: we use the terms "cross-sectional unit", "unit" and "group" interchangeably below to refer to the entities that compose the cross-sectional dimension of the panel. These might, for instance, be firms, countries or persons.)

For representation in a textual computer file (and also for gretl's internal calculations) the three dimensions must somehow be flattened into two. This "flattening" involves taking layers of the data that would naturally stack in a third dimension, and stacking them in the vertical dimension.

Gretl always expects data to be arranged "by observation", that is, such that each row represents an observation (and each variable occupies one and only one column). In this context the flattening of a panel data set can be done in either of two ways:

- Stacked time series: the successive vertical blocks each comprise a time series for a given unit.
- Stacked cross sections: the successive vertical blocks each comprise a cross-section for a given period.

You may input data in whichever arrangement is more convenient. Internally, however, gretl always stores panel data in the form of stacked time series.

When you import panel data into gretl from a spreadsheet or comma separated format, the panel nature of the data will not be recognized automatically (most likely the data will be treated as "undated"). A panel interpretation can be imposed on the data using the graphical interface or via the setobs command.

In the graphical interface, use the menu item "Data, Dataset structure". In the first dialog box that appears, select "Panel". In the next dialog you have a three-way choice. The first two options, "Stacked time series" and "Stacked cross sections" are applicable if the data set is already organized in one of these two ways. If you select either of these options, the next step is to specify the number of cross-sectional units in the data set. The third option, "Use index variables", is applicable if the data set contains two variables that index the units and the time periods respectively; the next step is then to select those variables. For example, a data file might contain a country code variable and a variable representing the year of the observation. In that case gretl can reconstruct the panel structure of the data regardless of how the observation rows are organized.

The setobs command has options that parallel those in the graphical interface. If suitable index variables are available you can do, for example

```
setobs unitvar timevar --panel-vars
```

where unitvar is a variable that indexes the units and timevar is a variable indexing the periods. Alternatively you can use the form setobs *freq* 1:1 *structure*, where *freq* is replaced by the "block size" of the data (that is, the number of periods in the case of stacked time series, or the number of units in the case of stacked cross-sections) and structure is either --stacked-time-series or --stacked-cross-section. Two examples are given below: the first is suitable for a panel in the form of stacked time series with observations from 20 periods; the second for stacked cross sections with 5 units.

```
setobs 20 1:1 --stacked-time-series
setobs 5 1:1 --stacked-cross-section
```

*Panel data arranged by variable*

Publicly available panel data sometimes come arranged "by variable." Suppose we have data on two variables, x1 and x2, for each of 50 states in each of 5 years (giving a total of 250 observations per variable). One textual representation of such a data set would start with a block for x1, with 50 rows corresponding to the states and 5 columns corresponding to the years. This would be followed, vertically, by a block with the same structure for variable x2. A fragment of such a data file is shown below, with quinquennial observations 1965–1985. Imagine the table continued for 48 more states, followed by another 50 rows for variable x2.

| x1 | | | | | |
|---|---|---|---|---|---|
| | 1965 | 1970 | 1975 | 1980 | 1985 |
| AR | 100.0 | 110.5 | 118.7 | 131.2 | 160.4 |
| AZ | 100.0 | 104.3 | 113.8 | 120.9 | 140.6 |

If a datafile with this sort of structure is read into gretl,[3] the program will interpret the columns as distinct variables, so the data will not be usable "as is." But there is a mechanism for correcting the situation, namely the stack function within the genr command.

Consider the first data column in the fragment above: the first 50 rows of this column constitute a cross-section for the variable x1 in the year 1965. If we could create a new variable by stacking the

[3] Note that you will have to modify such a datafile slightly before it can be read at all. The line containing the variable name (in this example x1) will have to be removed, and so will the initial row containing the years, otherwise they will be taken as numerical data.

first 50 entries in the second column underneath the first 50 entries in the first, we would be on the way to making a data set "by observation" (in the first of the two forms mentioned above, stacked cross-sections). That is, we'd have a column comprising a cross-section for x1 in 1965, followed by a cross-section for the same variable in 1970.

The following gretl script illustrates how we can accomplish the stacking, for both x1 and x2. We assume that the original data file is called panel.txt, and that in this file the columns are headed with "variable names" p1, p2, ..., p5. (The columns are not really variables, but in the first instance we "pretend" that they are.)

```
open panel.txt
genr x1 = stack(p1..p5) --length=50
genr x2 = stack(p1..p5) --offset=50 --length=50
setobs 50 1:1 --stacked-cross-section
store panel.gdt x1 x2
```

The second line illustrates the syntax of the stack function. The double dots within the parentheses indicate a range of variables to be stacked: here we want to stack all 5 columns (for all 5 years). The full data set contains 100 rows; in the stacking of variable x1 we wish to read only the first 50 rows from each column: we achieve this by adding --length=50. Note that if you want to stack a non-contiguous set of columns you can put a comma-separated list within the parentheses, as in

```
genr x = stack(p1,p3,p5)
```

On line 3 we do the stacking for variable x2. Again we want a length of 50 for the components of the stacked series, but this time we want gretl to start reading from the 50th row of the original data, and we specify --offset=50. Line 4 imposes a panel interpretation on the data; finally, we save the data in gretl format, with the panel interpretation, discarding the original "variables" p1 through p5.

The illustrative script above is appropriate when the number of variable to be processed is small. When then are many variables in the data set it will be more efficient to use a command loop to accomplish the stacking, as shown in the following script. The setup is presumed to be the same as in the previous section (50 units, 5 periods), but with 20 variables rather than 2.

```
open panel.txt
loop for i=1..20
  genr k = ($i - 1) * 50
  genr x$i = stack(p1..p5) --offset=k --length=50
endloop
setobs 50 1.01 --stacked-cross-section
store panel.gdt x1 x2 x3 x4 x5 x6 x7 x8 x9 x10 \
  x11 x12 x13 x14 x15 x16 x17 x18 x19 x20
```

### *Panel data marker strings*

It can be helpful with panel data to have the observations identified by mnemonic markers. A special function in the genr command is available for this purpose.

In the example above, suppose all the states are identified by two-letter codes in the left-most column of the original datafile. When the stacking operation is performed, these codes will be stacked along with the data values. If the first row is marked AR for Arkansas, then the marker AR will end up being shown on each row containing an observation for Arkansas. That's all very well, but these markers don't tell us anything about the date of the observation. To rectify this we could do:

```
genr time
genr year = 1960 + (5 * time)
genr markers = "%s:%d", marker, year
```

The first line generates a 1-based index representing the period of each observation, and the second line uses the time variable to generate a variable representing the year of the observation. The third line contains this special feature: if (and only if) the name of the new "variable" to generate is markers, the portion of the command following the equals sign is taken as C-style format string (which must be wrapped in double quotes), followed by a comma-separated list of arguments. The arguments will be printed according to the given format to create a new set of observation markers. Valid arguments are either the names of variables in the dataset, or the string marker which denotes the pre-existing observation marker. The format specifiers which are likely to be useful in this context are %s for a string and %d for an integer. Strings can be truncated: for example %.3s will use just the first three characters of the string. To chop initial characters off an existing observation marker when constructing a new one, you can use the syntax marker + n, where n is a positive integer: in the case the first n characters will be skipped.

After the commands above are processed, then, the observation markers will look like, for example, AR:1965, where the two-letter state code and the year of the observation are spliced together with a colon.

## 4.6 Missing data values

These are represented internally as DBL_MAX, the largest floating-point number that can be represented on the system (which is likely to be at least 10 to the power 300, and so should not be confused with legitimate data values). In a native-format data file they should be represented as NA. When importing CSV data gretl accepts several common representations of missing values including −999, the string NA (in upper or lower case), a single dot, or simply a blank cell. Blank cells should, of course, be properly delimited, e.g. 120.6,,5.38, in which the middle value is presumed missing.

As for handling of missing values in the course of statistical analysis, gretl does the following:

- In calculating descriptive statistics (mean, standard deviation, etc.) under the summary command, missing values are simply skipped and the sample size adjusted appropriately.
- In running regressions gretl first adjusts the beginning and end of the sample range, truncating the sample if need be. Missing values at the beginning of the sample are common in time series work due to the inclusion of lags, first differences and so on; missing values at the end of the range are not uncommon due to differential updating of series and possibly the inclusion of leads.

If gretl detects any missing values "inside" the (possibly truncated) sample range for a regression, the result depends on the character of the dataset and the estimator chosen. In many cases, the program will automatically skip the missing observations when calculating the regression results. In this situation a message is printed stating how many observations were dropped. On the other hand, the skipping of missing observations is not supported for all procedures: exceptions include all autoregressive estimators, system estimators such as SUR, and nonlinear least squares. In the case of panel data, the skipping of missing observations is supported only if their omission leaves a balanced panel. If missing observations are found in cases where they are not supported, gretl gives an error message and refuses to produce estimates.

In case missing values in the middle of a dataset present a problem, the misszero function (use with care!) is provided under the genr command. By doing genr foo = misszero(bar) you can produce a series foo which is identical to bar except that any missing values become zeros. Then you can use carefully constructed dummy variables to, in effect, drop the missing observations from the regression while retaining the surrounding sample range.[4]

## 4.7 Maximum size of data sets

Basically, the size of data sets (both the number of variables and the number of observations per variable) is limited only by the characteristics of your computer. Gretl allocates memory dynamically, and will ask the operating system for as much memory as your data require. Obviously, then, you are ultimately limited by the size of RAM.

Aside from the multiple-precision OLS option, gretl uses double-precision floating-point numbers throughout. The size of such numbers in bytes depends on the computer platform, but is typically eight. To give a rough notion of magnitudes, suppose we have a data set with 10,000 observations on 500 variables. That's 5 million floating-point numbers or 40 million bytes. If we define the megabyte (MB) as $1024 \times 1024$ bytes, as is standard in talking about RAM, it's slightly over 38 MB. The program needs additional memory for workspace, but even so, handling a data set of this size should be quite feasible on a current PC, which at the time of writing is likely to have at least 256 MB of RAM.

If RAM is not an issue, there is one further limitation on data size (though it's very unlikely to be a binding constraint). That is, variables and observations are indexed by signed integers, and on a typical PC these will be 32-bit values, capable of representing a maximum positive value of $2^{31} - 1 = 2,147,483,647$.

The limits mentioned above apply to gretl's "native" functionality. There are tighter limits with regard to two third-party programs that are available as add-ons to gretl for certain sorts of time-series analysis including seasonal adjustment, namely TRAMO/SEATS and X-12-ARIMA. These programs employ a fixed-size memory allocation, and can't handle series of more than 600 observations.

## 4.8 Data file collections

If you're using gretl in a teaching context you may be interested in adding a collection of data files and/or scripts that relate specifically to your course, in such a way that students can browse and access them easily.

There are three ways to access such collections of files:

- For data files: select the menu item "File, Open data, Sample file", or click on the folder icon on the gretl toolbar.
- For script files: select the menu item "File, Script files, Practice file".

When a user selects one of the items:

- The data or script files included in the gretl distribution are automatically shown (this includes files relating to Ramanathan's *Introductory Econometrics* and Greene's *Econometric Analysis*).
- The program looks for certain known collections of data files available as optional extras, for instance the datafiles from various econometrics textbooks (Davidson and MacKinnon, Gujarati, Stock and Watson, Verbeek, Wooldridge) and the Penn World Table (PWT 5.6). (See the data page at the gretl website for information on these collections.) If the additional files are found, they are added to the selection windows.

[4] genr also offers the inverse function to misszero, namely zeromiss, which replaces zeros in a given series with the missing observation code.

- The program then searches for valid file collections (not necessarily known in advance) in these places: the "system" data directory, the system script directory, the user directory, and all first-level subdirectories of these. For reference, typical values for these directories are shown in Table 4.1. (Note that PERSONAL is a placeholder that is expanded by Windows, corresponding to "My Documents" on English-language systems.)

| | *Linux* | *MS Windows* |
|---|---|---|
| system data dir | `/usr/share/gretl/data` | `c:\Program Files\gretl\data` |
| system script dir | `/usr/share/gretl/scripts` | `c:\Program Files\gretl\scripts` |
| user dir | `$HOME/gretl` | `PERSONAL\gretl` |

**Table 4.1**: Typical locations for file collections

Any valid collections will be added to the selection windows. So what constitutes a valid file collection? This comprises either a set of data files in gretl XML format (with the `.gdt` suffix) or a set of script files containing gretl commands (with `.inp` suffix), in each case accompanied by a "master file" or catalog. The gretl distribution contains several example catalog files, for instance the file `descriptions` in the `misc` sub-directory of the gretl data directory and `ps_descriptions` in the `misc` sub-directory of the scripts directory.

If you are adding your own collection, data catalogs should be named `descriptions` and script catalogs should be be named `ps_descriptions`. In each case the catalog should be placed (along with the associated data or script files) in its own specific sub-directory (e.g. `/usr/share/gretl/data/mydata` or `c:\userdata\gretl\data\mydata`).

The syntax of the (plain text) description files is straightforward. Here, for example, are the first few lines of gretl's "misc" data catalog:

```
# Gretl: various illustrative datafiles
"arma","artificial data for ARMA script example"
"ects_nls","Nonlinear least squares example"
"hamilton","Prices and exchange rate, U.S. and Italy"
```

The first line, which must start with a hash mark, contains a short name, here "Gretl", which will appear as the label for this collection's tab in the data browser window, followed by a colon, followed by an optional short description of the collection.

Subsequent lines contain two elements, separated by a comma and wrapped in double quotation marks. The first is a datafile name (leave off the `.gdt` suffix here) and the second is a short description of the content of that datafile. There should be one such line for each datafile in the collection.

A script catalog file looks very similar, except that there are three fields in the file lines: a filename (without its `.inp` suffix), a brief description of the econometric point illustrated in the script, and a brief indication of the nature of the data used. Again, here are the first few lines of the supplied "misc" script catalog:

```
# Gretl: various sample scripts
"arma","ARMA modeling","artificial data"
"ects_nls","Nonlinear least squares (Davidson)","artificial data"
"leverage","Influential observations","artificial data"
"longley","Multicollinearity","US employment"
```

If you want to make your own data collection available to users, these are the steps:

1. Assemble the data, in whatever format is convenient.

2. Convert the data to gretl format and save as gdt files. It is probably easiest to convert the data by importing them into the program from plain text, CSV, or a spreadsheet format (MS Excel or Gnumeric) then saving them. You may wish to add descriptions of the individual variables (the “Variable, Edit attributes” menu item), and add information on the source of the data (the “Data, Edit info” menu item).

3. Write a descriptions file for the collection using a text editor.

4. Put the datafiles plus the descriptions file in a subdirectory of the gretl data directory (or user directory).

5. If the collection is to be distributed to other people, package the data files and catalog in some suitable manner, e.g. as a zipfile.

If you assemble such a collection, and the data are not proprietary, we would encourage you to submit the collection for packaging as a gretl optional extra.

Chapter 5

# Special functions in genr

## 5.1 Introduction

The genr command provides a flexible means of defining new variables. It is documented in the *Gretl Command Reference*. This chapter offers a more expansive discussion of some of the special functions available via genr and some of the finer points of the command.

## 5.2 Long-run variance

As is well known, the variance of the average of $T$ random variables $x_1, x_2, \ldots, x_T$ with equal variance $\sigma^2$ equals $\sigma^2/T$ if the data are uncorrelated. In this case, the sample variance of $x_t$ over the sample size provides a consistent estimator.

If, however, there is serial correlation among the $x_t$s, the variance of $\bar{X} = T^{-1}\sum_{t=1}^{T} x_t$ must be estimated differently. One of the most widely used statistics for this purpose is a nonparametric kernel estimator with the Bartlett kernel defined as

$$\hat{\omega}^2(k) = T^{-1}\sum_{t=k}^{T-k}\left[\sum_{i=-k}^{k} w_i (x_t - \bar{X})(x_{t-i} - \bar{X})\right], \tag{5.1}$$

where the integer $k$ is known as the window size and the $w_i$ terms are the so-called *Bartlett weights*, defined as $w_i = 1 - \frac{|i|}{k+1}$. It can be shown that, for $k$ large enough, $\hat{\omega}^2(k)/T$ yields a consistent estimator of the variance of $\bar{X}$.

Gretl implements this estimator by means of the function lrvar(), which takes two arguments: the series whose long-run variance must be estimated and the scalar $k$. If $k$ is negative, the popular choice $T^{1/3}$ is used.

## 5.3 Time-series filters

One sort of specialized function in genr is time-series filtering. In addition to the usual application of lags and differences, gretl provides fractional differencing and two filters commonly used in macroeconomics for trend-cycle decomposition: the Hodrick–Prescott filter (Hodrick and Prescott, 1997) and the Baxter–King bandpass filter (Baxter and King, 1999).

### Fractional differencing

The concept of differencing a time series $d$ times is pretty obvious when $d$ is an integer; it may seem odd when $d$ is fractional. However, this idea has a well-defined mathematical content: consider the function

$$f(z) = (1-z)^{-d},$$

where $z$ and $d$ are real numbers. By taking a Taylor series expansion around $z = 0$, we see that

$$f(z) = 1 + dz + \frac{d(d+1)}{2}z^2 + \cdots$$

or, more compactly,

$$f(z) = 1 + \sum_{i=1}^{\infty} \psi_i z^i$$

with

$$\psi_k = \frac{\prod_{i=1}^{k}(d+i-1)}{k!} = \psi_{k-1}\frac{d+k-1}{k}$$

The same expansion can be used with the lag operator, so that if we defined

$$Y_t = (1-L)^{0.5} X_t$$

this could be considered shorthand for

$$Y_t = X_t - 0.5X_{t-1} - 0.125X_{t-2} - 0.0625X_{t-3} - \cdots$$

In gretl this transformation can be accomplished by the syntax

```
genr Y = fracdiff(X,0.5)
```

### The Hodrick–Prescott filter

This filter is accessed using the `hpfilt()` function, which takes one argument, the name of the variable to be processed.

A time series $y_t$ may be decomposed into a trend or growth component $g_t$ and a cyclical component $c_t$.

$$y_t = g_t + c_t, \quad t = 1, 2, \ldots, T$$

The Hodrick–Prescott filter effects such a decomposition by minimizing the following:

$$\sum_{t=1}^{T} (y_t - g_t)^2 + \lambda \sum_{t=2}^{T-1} \left((g_{t+1} - g_t) - (g_t - g_{t-1})\right)^2 .$$

The first term above is the sum of squared cyclical components $c_t = y_t - g_t$. The second term is a multiple $\lambda$ of the sum of squares of the trend component's second differences. This second term penalizes variations in the growth rate of the trend component: the larger the value of $\lambda$, the higher is the penalty and hence the smoother the trend series.

Note that the `hpfilt` function in gretl produces the cyclical component, $c_t$, of the original series. If you want the smoothed trend you can subtract the cycle from the original:

```
genr ct = hpfilt(yt)
genr gt = yt - ct
```

Hodrick and Prescott (1997) suggest that a value of $\lambda = 1600$ is reasonable for quarterly data. The default value in gretl is 100 times the square of the data frequency (which, of course, yields 1600 for quarterly data). The value can be adjusted using the `set` command, with a parameter of `hp_lambda`. For example, `set hp_lambda 1200`.

### The Baxter and King filter

This filter is accessed using the `bkfilt()` function, which again takes the name of the variable to be processed as its single argument.

Consider the spectral representation of a time series $y_t$:

$$y_t = \int_{-\pi}^{\pi} e^{i\omega} \mathrm{d}Z(\omega)$$

To extract the component of $y_t$ that lies between the frequencies $\underline{\omega}$ and $\overline{\omega}$ one could apply a bandpass filter:

$$c_t^* = \int_{-\pi}^{\pi} F^*(\omega) e^{i\omega} \mathrm{d}Z(\omega)$$

where $F^*(\omega) = 1$ for $\underline{\omega} < |\omega| < \overline{\omega}$ and 0 elsewhere. This would imply, in the time domain, applying to the series a filter with an infinite number of coefficients, which is undesirable. The Baxter and King bandpass filter applies to $y_t$ a finite polynomial in the lag operator $A(L)$:

$$c_t = A(L) y_t$$

where $A(L)$ is defined as

$$A(L) = \sum_{i=-k}^{k} a_i L^i$$

The coefficients $a_i$ are chosen such that $F(\omega) = A(e^{i\omega})A(e^{-i\omega})$ is the best approximation to $F^*(\omega)$ for a given $k$. Clearly, the higher $k$ the better the approximation is, but since $2k$ observations have to be discarded, a compromise is usually sought. Moreover, the filter has also other appealing theoretical properties, among which the property that $A(1) = 0$, so a series with a single unit root is made stationary by application of the filter.

In practice, the filter is normally used with monthly or quarterly data to extract the "business cycle" component, namely the component between 6 and 36 quarters. Usual choices for $k$ are 8 or 12 (maybe higher for monthly series). The default values for the frequency bounds are 8 and 32, and the default value for the approximation order, $k$, is 8. You can adjust these values using the set command. The keyword for setting the frequency limits is bkbp_limits and the keyword for $k$ is bkbp_k. Thus for example if you were using monthly data and wanted to adjust the frequency bounds to 18 and 96, and $k$ to 24, you could do

```
set bkbp_limits 18 96
set bkbp_k 24
```

These values would then remain in force for calls to the bkfilt function until changed by a further use of set.

## 5.4 Panel data specifics

### Dummy variables

In a panel study you may wish to construct dummy variables of one or both of the following sorts: (a) dummies as unique identifiers for the units or groups, and (b) dummies as unique identifiers for the time periods. The former may be used to allow the intercept of the regression to differ across the units, the latter to allow the intercept to differ across periods.

Two special functions are available to create such dummies. These are found under the "Add" menu in the GUI, or under the genr command in script mode or gretlcli.

1. "unit dummies" (script command genr unitdum). This command creates a set of dummy variables identifying the cross-sectional units. The variable du_1 will have value 1 in each row corresponding to a unit 1 observation, 0 otherwise; du_2 will have value 1 in each row corresponding to a unit 2 observation, 0 otherwise; and so on.

2. "time dummies" (script command genr timedum). This command creates a set of dummy variables identifying the periods. The variable dt_1 will have value 1 in each row corresponding to a period 1 observation, 0 otherwise; dt_2 will have value 1 in each row corresponding to a period 2 observation, 0 otherwise; and so on.

If a panel data set has the YEAR of the observation entered as one of the variables you can create a periodic dummy to pick out a particular year, e.g. genr dum = (YEAR=1960). You can also create periodic dummy variables using the modulus operator, %. For instance, to create a dummy with value 1 for the first observation and every thirtieth observation thereafter, 0 otherwise, do

```
genr index
genr dum = ((index-1) % 30) = 0
```

### Lags, differences, trends

If the time periods are evenly spaced you may want to use lagged values of variables in a panel regression (but see section 15.2 below); you may also wish to construct first differences of variables of interest.

Once a dataset is identified as a panel, gretl will handle the generation of such variables correctly. For example the command genr x1_1 = x1(-1) will create a variable that contains the first lag of x1 where available, and the missing value code where the lag is not available (e.g. at the start of the time series for each group). When you run a regression using such variables, the program will automatically skip the missing observations.

When a panel data set has a fairly substantial time dimension, you may wish to include a trend in the analysis. The command genr time creates a variable named time which runs from 1 to $T$ for each unit, where $T$ is the length of the time-series dimension of the panel. If you want to create an index that runs consecutively from 1 to $m \times T$, where $m$ is the number of units in the panel, use genr index.

### Basic statistics by unit

Gretl contains functions which can be used to generate basic descriptive statistics for a given variable, on a per-unit basis; these are pnobs() (number of valid cases), pmin() and pmax() (minimum and maximum) and pmean() and psd() (mean and standard deviation).

As a brief illustration, suppose we have a panel data set comprising 8 time-series observations on each of $N$ units or groups. Then the command

```
genr pmx = pmean(x)
```

creates a series of this form: the first 8 values (corresponding to unit 1) contain the mean of x for unit 1, the next 8 values contain the mean for unit 2, and so on. The psd() function works in a similar manner. The sample standard deviation for group $i$ is computed as

$$s_i = \sqrt{\frac{\sum(x - \bar{x}_i)^2}{T_i - 1}}$$

where $T_i$ denotes the number of valid observations on x for the given unit, $\bar{x}_i$ denotes the group mean, and the summation is across valid observations for the group. If $T_i < 2$, however, the standard deviation is recorded as 0.

One particular use of psd() may be worth noting. If you want to form a sub-sample of a panel that contains only those units for which the variable x is time-varying, you can either use

```
smpl (pmin(x) < pmax(x)) --restrict
```

or

```
smpl (psd(x) > 0) --restrict
```

### Special functions for data manipulation

Besides the functions discussed above, there are some facilities in `genr` designed specifically for manipulating panel data — in particular, for the case where the data have been read into the program from a third-party source and they are not in the correct form for panel analysis. These facilities are explained in Chapter 4.

## 5.5 Resampling and bootstrapping

Another specialized function is the resampling, with replacement, of a series. Given an original data series `x`, the command

```
genr xr = resample(x)
```

creates a new series each of whose elements is drawn at random from the elements of `x`. If the original series has 100 observations, each element of `x` is selected with probability 1/100 at each drawing. Thus the effect is to "shuffle" the elements of `x`, with the twist that each element of `x` may appear more than once, or not at all, in `xr`.

The primary use of this function is in the construction of bootstrap confidence intervals or p-values. Here is a simple example. Suppose we estimate a simple regression of $y$ on $x$ via OLS and find that the slope coefficient has a reported $t$-ratio of 2.5 with 40 degrees of freedom. The two-tailed p-value for the null hypothesis that the slope parameter equals zero is then 0.0166, using the $t(40)$ distribution. Depending on the context, however, we may doubt whether the ratio of coefficient to standard error truly follows the $t(40)$ distribution. In that case we could derive a bootstrap p-value as shown in Example 5.1.

Under the null hypothesis that the slope with respect to $x$ is zero, $y$ is simply equal to its mean plus an error term. We simulate $y$ by resampling the residuals from the initial OLS and re-estimate the model. We repeat this procedure a large number of times, and record the number of cases where the absolute value of the $t$-ratio is greater than 2.5: the proportion of such cases is our bootstrap p-value. For a good discussion of simulation-based tests and bootstrapping, see Davidson and MacKinnon (2004, chapter 4).

**Example 5.1**: Calculation of bootstrap p-value

```
ols y 0 x
# save the residuals
genr ui = $uhat
scalar ybar = mean(y)
# number of replications for bootstrap
scalar replics = 10000
scalar tcount = 0
series ysim = 0
loop replics --quiet
  # generate simulated y by resampling
  ysim = ybar + resample(ui)
  ols ysim 0 x
  scalar tsim = abs($coeff(x) / $stderr(x))
  tcount += (tsim > 2.5)
endloop
printf "proportion of cases with |t| > 2.5 = %g\n", tcount / replics
```

## 5.6 Cumulative densities and p-values

The two functions `cdf` and `pvalue` provide complementary means of examining values from several probability distributions: the standard normal, Student's $t$, $\chi^2$, $F$, gamma, and binomial. The syntax of these functions is set out in the *Gretl Command Reference*; here we expand on some subtleties.

The cumulative density function or CDF for a random variable is the integral of the variable's density from its lower limit (typically either $-\infty$ or 0) to any specified value $x$. The p-value (at least the one-tailed, right-hand p-value as returned by the `pvalue` function) is the complementary probability, the integral from $x$ to the upper limit of the distribution, typically $+\infty$.

In principle, therefore, there is no need for two distinct functions: given a CDF value $p_0$ you could easily find the corresponding p-value as $1 - p_0$ (or vice versa). In practice, with finite-precision computer arithmetic, the two functions are not redundant. This requires a little explanation. In gretl, as in most statistical programs, floating point numbers are represented as "doubles" — double-precision values that typically have a storage size of eight bytes or 64 bits. Since there are only so many bits available, only so many floating-point numbers can be represented: *doubles do not model the real line.* Typically doubles can represent numbers over the range (roughly) $\pm 1.7977 \times 10^{308}$, but only to about 15 digits of precision.

Suppose you're interested in the left tail of the $\chi^2$ distribution with 50 degrees of freedom: you'd like to know the CDF value for $x = 0.9$. Take a look at the following interactive session:

```
? genr p1 = cdf(X, 50, 0.9)
Generated scalar p1 (ID 2) = 8.94977e-35
? genr p2 = pvalue(X, 50, 0.9)
Generated scalar p2 (ID 3) = 1
? genr test = 1 - p2
Generated scalar test (ID 4) = 0
```

The `cdf` function has produced an accurate value, but the `pvalue` function gives an answer of 1, from which it is not possible to retrieve the answer to the CDF question. This may seem surprising at first, but consider: if the value of `p1` above is correct, then the correct value for `p2` is $1 - 8.94977 \times 10^{-35}$. But there's no way that value can be represented as a double: that would require over 30 digits of precision.

Of course this is an extreme example. If the $x$ in question is not too far off into one or other tail of the distribution, the `cdf` and `pvalue` functions will in fact produce complementary answers, as shown below:

```
? genr p1 = cdf(X, 50, 30)
Generated scalar p1 (ID 2) = 0.0111648
? genr p2 = pvalue(X, 50, 30)
Generated scalar p2 (ID 3) = 0.988835
? genr test = 1 - p2
Generated scalar test (ID 4) = 0.0111648
```

But the moral is that if you want to examine extreme values you should be careful in selecting the function you need, in the knowledge that values very close to zero can be represented as doubles while values very close to 1 cannot.

## 5.7 Handling missing values

Four special functions are available for the handling of missing values. The boolean function `missing()` takes the name of a variable as its single argument; it returns a series with value 1 for each observation at which the given variable has a missing value, and value 0 otherwise (that is, if the given variable has a valid value at that observation). The function `ok()` is complementary to `missing`; it is just a shorthand for `!missing` (where `!` is the boolean NOT operator). For example, one can count the missing values for variable `x` using

```
genr nmiss_x = sum(missing(x))
```

The function `zeromiss()`, which again takes a single series as its argument, returns a series where all zero values are set to the missing code. This should be used with caution — one does not want to confuse missing values and zeros — but it can be useful in some contexts. For example, one can determine the first valid observation for a variable `x` using

```
genr time
genr x0 = min(zeromiss(time * ok(x)))
```

The function `misszero()` does the opposite of `zeromiss`, that is, it converts all missing values to zero.

It may be worth commenting on the propagation of missing values within `genr` formulae. The general rule is that in arithmetical operations involving two variables, if either of the variables has a missing value at observation $t$ then the resulting series will also have a missing value at $t$. The one exception to this rule is multiplication by zero: zero times a missing value produces zero (since this is mathematically valid regardless of the unknown value).

## 5.8 Retrieving internal variables

The `genr` command provides a means of retrieving various values calculated by the program in the course of estimating models or testing hypotheses. The variables that can be retrieved in this way are listed in the *Gretl Command Reference*; here we say a bit more about the special variables `$test` and `$pvalue`.

These variables hold, respectively, the value of the last test statistic calculated using an explicit testing command and the p-value for that test statistic. If no such test has been performed at the time when these variables are referenced, they will produce the missing value code. The "explicit testing commands" that work in this way are as follows: `add` (joint test for the significance of variables added to a model); `adf` (Augmented Dickey–Fuller test, see below); `arch` (test for ARCH); `chow` (Chow test for a structural break); `coeffsum` (test for the sum of specified coefficients); `cusum` (the Harvey–Collier $t$-statistic); `kpss` (KPSS stationarity test, no p-value available); `lmtest` (see below); `meantest` (test for difference of means); `omit` (joint test for the significance of variables omitted from a model); `reset` (Ramsey's RESET); `restrict` (general linear restriction); `runs` (runs test for randomness); `testuhat` (test for normality of residual); and `vartest` (test for difference of variances). In most cases both a `$test` and a `$pvalue` are stored; the exception is the KPSS test, for which a p-value is not currently available.

An important point to notice about this mechanism is that the internal variables `$test` and `$pvalue` are over-written each time one of the tests listed above is performed. If you want to reference these values, you must do so at the correct point in the sequence of gretl commands.

A related point is that some of the test commands generate, by default, more than one test statistic and p-value; in these cases only the last values are stored. To get proper control over the retrieval of values via `$test` and `$pvalue` you should formulate the test command in such a way that the result is unambiguous. This comment applies in particular to the `adf` and `lmtest` commands.

- By default, the `adf` command generates three variants of the Dickey–Fuller test: one based on a regression including a constant, one using a constant and linear trend, and one using a constant and a quadratic trend. When you wish to reference `$test` or `$pvalue` in connection with this command, you can control the variant that is recorded by using one of the flags `--nc`, `--c`, `--ct` or `--ctt` with `adf`.
- By default, the `lmtest` command (which must follow an OLS regression) performs several diagnostic tests on the regression in question. To control what is recorded in `$test` and `$pvalue` you should limit the test using one of the flags `--logs`, `--autocorr`, `--squares` or `--white`.

As an aid in working with values retrieved using `$test` and `$pvalue`, the nature of the test to which these values relate is written into the descriptive label for the generated variable. You can read the label for the variable using the `label` command (with just one argument, the name of the variable), to check that you have retrieved the right value. The following interactive session illustrates this point.

```
? adf 4 x1 --c
Augmented Dickey-Fuller tests, order 4, for x1
sample size 59
unit-root null hypothesis: a = 1
  test with constant
  model: (1 - L)y = b0 + (a-1)*y(-1) + ... + e
  estimated value of (a - 1): -0.216889
  test statistic: t = -1.83491
  asymptotic p-value 0.3638
P-values based on MacKinnon (JAE, 1996)
? genr pv = $pvalue
Generated scalar pv (ID 13) = 0.363844
? label pv
  pv=Dickey-Fuller pvalue (scalar)
```

## 5.9 Numerical procedures

Two special functions are available to aid in the construction of special-purpose estimators, namely `BFGSmax` (the BFGS maximizer, discussed in Chapter 17) and `fdjac`, which produces a forward-difference approximation to the Jacobian.

### The BFGS maximizer

The `BFGSmax` function takes two arguments: a vector holding the initial values of a set of parameters, and a call to a function that calculates the (scalar) criterion to be maximized, given the current parameter values and any other relevant data. If the object is in fact minimization, this function should return the negative of the criterion. On successful completion, `BFGSmax` returns the maximized value of the criterion and the matrix given via the first argument holds the parameter values which produce the maximum. Here is an example:

```
matrix X = { dataset }
matrix theta = { 1, 100 }'
scalar J = BFGSmax(theta, ObjFunc(&theta, &X))
```

It is assumed here that `ObjFunc` is a user-defined function (see Chapter 10) with the following general set-up:

```
function ObjFunc (matrix *theta, matrix *X)
  scalar val = ...  # do some computation
  return scalar val
end function
```

The operation of the BFGS maximizer can be adjusted using the `set` variables `bfgs_maxiter` and `bfgs_toler` (see Chapter 17). In addition you can provoke verbose output from the maximizer by assigning a positive value to `max_verbose`, again via the `set` command.

The Rosenbrock function is often used as a test problem for optimization algorithms. It is also known as "Rosenbrock's Valley" or "Rosenbrock's Banana Function", on account of the fact that its contour lines are banana-shaped. It is defined by:

$$f(x, y) = (1 - x)^2 + 100(y - x^2)^2$$

**Example 5.2**: Finding the minimum of the Rosenbrock function

```
function Rosenbrock(matrix *param)
  scalar x = param[1]
  scalar y = param[2]
  scalar f = -(1-x)^2 - 100 * (y - x^2)^2
  return scalar f
end function

nulldata 10

matrix theta = { 0 , 0 }

set max_verbose 1
M = BFGSmax(theta, Rosenbrock(&theta))

print theta
```

The function has a global minimum at $(x, y) = (1, 1)$ where $f(x, y) = 0$. Example 5.2 shows a gretl script that discovers the minimum using BFGSmax (giving a verbose account of progress).

### Computing a Jacobian

Gretl offers the possibility of differentiating numerically a user-defined function via the fdjac function.

This function again takes two arguments: an $n \times 1$ matrix holding initial parameter values and a function call that calculates and returns an $m \times 1$ matrix, given the current parameter values and any other relevant data. On successful completion it returns an $m \times n$ matrix holding the Jacobian. For example,

```
  matrix Jac = fdjac(theta, SumOC(&theta, &X))
```

where we assume that SumOC is a user-defined function with the following structure:

```
  function SumOC (matrix *theta, matrix *X)
    matrix V = ...  # do some computation
    return matrix V
  end function
```

This may come in handy in several cases: for example, if you use BFGSmax to estimate a model, you may wish to calculate a numerical approximation to the relevant Jacobian to construct a covariance matrix for your estimates.

Another example is the delta method: if you have a consistent estimator of a vector of parameters $\hat\theta$, and a consistent estimate of its covariance matrix $\Sigma$, you may need to compute estimates for a nonlinear continuous transformation $\psi = g(\theta)$. In this case, a standard result in asymptotic theory is that

$$\left\{ \begin{array}{c} \hat\theta \xrightarrow{\text{p}} \theta \\ \sqrt{T}\left(\hat\theta - \theta\right) \xrightarrow{\text{d}} N(0,\Sigma) \end{array} \right\} \Longrightarrow \left\{ \begin{array}{c} \hat\psi = g(\hat\theta) \xrightarrow{\text{p}} \psi = g(\theta) \\ \sqrt{T}\left(\hat\psi - \psi\right) \xrightarrow{\text{d}} N(0, J\Sigma J') \end{array} \right\}$$

where $T$ is the sample size and $J$ is the Jacobian $\left.\frac{\partial g(x)}{\partial x}\right|_{x=\theta}$.

Script 5.3 exemplifies such a case: the example is taken from Greene (2003), section 9.3.1. The slight differences between the results reported in the original source and what gretl returns are due to the fact that the Jacobian is computed numerically, rather than analytically as in the book.

## 5.10 The discrete Fourier transform

The discrete Fourier transform can be best thought of as a linear, invertible transform of a complex vector. Hence, if $\mathbf{x}$ is an $n$-dimensional vector whose $k$-th element is $x_k = a_k + ib_k$, then the output of the discrete Fourier transform is a vector $\mathbf{f} = \mathcal{F}(\mathbf{x})$ whose $k$-th element is

$$f_k = \sum_{j=0}^{n-1} e^{-i\omega(j,k)} x_j$$

where $\omega(j,k) = 2\pi i \frac{jk}{n}$. Since the transformation is invertible, the vector $\mathbf{x}$ can be recovered from $\mathbf{f}$ via the so-called inverse transform

$$x_k = \frac{1}{n} \sum_{j=0}^{n-1} e^{i\omega(j,k)} f_j.$$

The Fourier transform is used in many diverse situations on account of this key property: the convolution of two vectors can be performed efficiently by multiplying the elements of their Fourier transforms and inverting the result. If

$$z_k = \sum_{j=1}^{n} x_j y_{k-j},$$

then

$$\mathcal{F}(\mathbf{z}) = \mathcal{F}(\mathbf{x}) \odot \mathcal{F}(\mathbf{y}).$$

That is, $\mathcal{F}(\mathbf{z})_k = \mathcal{F}(\mathbf{x})_k \mathcal{F}(\mathbf{y})_k$.

For computing the Fourier transform, gretl uses the external library `fftw3`: see Frigo and Johnson (2003). This guarantees extreme speed and accuracy. In fact, the CPU time needed to perform the transform is $O(n \log n)$ for any $n$. This is why the array of numerical techniques employed in `fftw3` is commonly known as the *Fast* Fourier Transform.

Gretl provides two matrix functions[1] for performing the Fourier transform and its inverse: `fft` and `ffti`. In fact, gretl's implementation of the Fourier transform is somewhat more specialized: the input to the `fft` function is understood to be real. Conversely, `ffti` takes a complex argument and delivers a real result. For example:

```
x1 = { 1 ; 2 ; 3 }
# perform the transform
f = fft(a)
# perform the inverse transform
x2 = ffti(f)
```

yields

$$x_1 = \begin{bmatrix} 1 \\ 2 \\ 3 \end{bmatrix} \qquad f = \begin{bmatrix} 6 & 0 \\ -1.5 & 0.866 \\ -1.5 & -0.866 \end{bmatrix} \qquad x_2 = \begin{bmatrix} 1 \\ 2 \\ 3 \end{bmatrix}$$

where the first column of $f$ holds the real part and the second holds the complex part. In general, if the input to `fft` has $n$ columns, the output has $2n$ columns, where the real parts are stored in

[1] See chapter 12.

the odd columns and the complex parts in the even ones. Should it be necessary to compute the Fourier transform on several vectors with the same number of elements, it is numerically more efficient to group them into a matrix rather than invoking `fft` for each vector separately.

As an example, consider the multiplication of two polynomals:

$$\begin{aligned} a(x) &= 1 + 0.5x \\ b(x) &= 1 + 0.3x - 0.8x^2 \\ c(x) = a(x) \cdot b(x) &= 1 + 0.8x - 0.65x^2 - 0.4x^3 \end{aligned}$$

The coefficients of the polynomial $c(x)$ are the convolution of the coefficents of $a(x)$ and $b(x)$; the following gretl code fragment illustrates how to compute the coefficients of $c(x)$:

```
# define the two polynomials
a = { 1, 0.5, 0, 0 }'
b = { 1, 0.3, -0.8, 0 }'
# perform the transforms
fa = fft(a)
fb = fft(b)
# complex-multiply the two transforms
fc = cmult(fa, fb)
# compute the coefficients of c via the inverse transform
c = ffti(fc)
```

Maximum efficiency would have been achieved by grouping `a` and `b` into a matrix. The computational advantage is so little in this case that the exercise is a bit silly, but the following alternative may be preferable for a large number of rows/columns:

```
# define the two polynomials
a = { 1 ; 0.5; 0 ; 0 }
b = { 1 ; 0.3 ; -0.8 ; 0 }
# perform the transforms jointly
f = fft(a ~ b)
# complex-multiply the two transforms
fc = cmult(f[,1:2], f[,3:4])
# compute the coefficients of c via the inverse transform
c = ffti(fc)
```

Traditionally, the Fourier tranform in econometrics has been mostly used in time-series analysis, the periodogram being the best known example. Example script 5.4 shows how to compute the periodogram of a time series via the `fft` function.

**Example 5.3**: Delta Method

```
function MPC(matrix *param, matrix *Y)
  beta = param[2]
  gamma = param[3]
  y = Y[1]
  matrix ret = beta*gamma*y^(gamma-1)
  return matrix ret
end function

# William Greene, Econometric Analysis, 5e, Chapter 9
set echo off
set messages off
open greene5_1.gdt

# Use OLS to initialize the parameters
ols realcons 0 realdpi --quiet
genr a = $coeff(0)
genr b = $coeff(realdpi)
genr g = 1.0

# Run NLS with analytical derivatives
nls realcons = a + b * (realdpi^g)
  deriv a = 1
  deriv b = realdpi^g
  deriv g = b * realdpi^g * log(realdpi)
end nls

matrix Y = realdpi[2000:4]
matrix theta = $coeff
matrix V = $vcv

mpc = MPC(&theta, &Y)
matrix Jac = fdjac(theta, MPC(&theta, &Y))
Sigma = qform(Jac, V)

printf "\nmpc = %g, std.err = %g\n", mpc, sqrt(Sigma)
scalar teststat = (mpc-1)/sqrt(Sigma)
printf "\nTest for MPC = 1: %g (p-value = %g)\n", \
        teststat, pvalue(n,abs(teststat))
```

**Example 5.4**: Periodogram via the Fourier transform

```
nulldata 50
# generate an AR(1) process
series e = normal()
series x = 0
x = 0.9*x(-1) + e
# compute the periodogram
scale = 2*pi*$nobs
X = { x }
F = fft(X)
S = sumr(F.^2)
S = S[2:($nobs/2)+1]/scale
omega = seq(1,($nobs/2))’ .* (2*pi/$nobs)
omega = omega ~ S
# compare the built-in command
pergm x
print omega
```

Chapter 6

# Sub-sampling a dataset

## 6.1 Introduction

Some subtle issues can arise here. This chapter attempts to explain the issues.

A sub-sample may be defined in relation to a full data set in two different ways: we will refer to these as "setting" the sample and "restricting" the sample respectively.

## 6.2 Setting the sample

By "setting" the sample we mean defining a sub-sample simply by means of adjusting the starting and/or ending point of the current sample range. This is likely to be most relevant for time-series data. For example, one has quarterly data from 1960:1 to 2003:4, and one wants to run a regression using only data from the 1970s. A suitable command is then

```
smpl 1970:1 1979:4
```

Or one wishes to set aside a block of observations at the end of the data period for out-of-sample forecasting. In that case one might do

```
smpl ; 2000:4
```

where the semicolon is shorthand for "leave the starting observation unchanged". (The semicolon may also be used in place of the second parameter, to mean that the ending observation should be unchanged.) By "unchanged" here, we mean unchanged relative to the last `smpl` setting, or relative to the full dataset if no sub-sample has been defined up to this point. For example, after

```
smpl 1970:1 2003:4
smpl ; 2000:4
```

the sample range will be 1970:1 to 2000:4.

An incremental or relative form of setting the sample range is also supported. In this case a relative offset should be given, in the form of a signed integer (or a semicolon to indicate no change), for both the starting and ending point. For example

```
smpl +1 ;
```

will advance the starting observation by one while preserving the ending observation, and

```
smpl +2 -1
```

will both advance the starting observation by two and retard the ending observation by one.

An important feature of "setting" the sample as described above is that it necessarily results in the selection of a subset of observations that are contiguous in the full dataset. The structure of the dataset is therefore unaffected (for example, if it is a quarterly time series before setting the sample, it remains a quarterly time series afterwards).

## 6.3 Restricting the sample

By "restricting" the sample we mean selecting observations on the basis of some Boolean (logical) criterion, or by means of a random number generator. This is likely to be most relevant for cross-sectional or panel data.

Suppose we have data on a cross-section of individuals, recording their gender, income and other characteristics. We wish to select for analysis only the women. If we have a `gender` dummy variable with value 1 for men and 0 for women we could do

```
smpl gender=0 --restrict
```

to this effect. Or suppose we want to restrict the sample to respondents with incomes over $50,000. Then we could use

```
smpl income>50000 --restrict
```

A question arises here. If we issue the two commands above in sequence, what do we end up with in our sub-sample: all cases with income over 50000, or just women with income over 50000? By default, in a gretl script, the answer is the latter: women with income over 50000. The second restriction augments the first, or in other words the final restriction is the logical product of the new restriction and any restriction that is already in place. If you want a new restriction to replace any existing restrictions you can first recreate the full dataset using

```
smpl --full
```

Alternatively, you can add the `replace` option to the `smpl` command:

```
smpl income>50000 --restrict --replace
```

This option has the effect of automatically re-establishing the full dataset before applying the new restriction.

Unlike a simple "setting" of the sample, "restricting" the sample may result in selection of non-contiguous observations from the full data set. It may also change the structure of the data set.

This can be seen in the case of panel data. Say we have a panel of five firms (indexed by the variable `firm`) observed in each of several years (identified by the variable `year`). Then the restriction

```
smpl year=1995 --restrict
```

produces a dataset that is not a panel, but a cross-section for the year 1995. Similarly

```
smpl firm=3 --restrict
```

produces a time-series dataset for firm number 3.

For these reasons (possible non-contiguity in the observations, possible change in the structure of the data), gretl acts differently when you "restrict" the sample as opposed to simply "setting" it. In the case of setting, the program merely records the starting and ending observations and uses these as parameters to the various commands calling for the estimation of models, the computation of statistics, and so on. In the case of restriction, the program makes a reduced copy of the dataset and by default treats this reduced copy as a simple, undated cross-section.[1]

If you wish to re-impose a time-series or panel interpretation of the reduced dataset you can do so using the `setobs` command, or the GUI menu item "Data, Dataset structure".

[1] With one exception: if you start with a balanced panel dataset and the restriction is such that it preserves a balanced panel — for example, it results in the deletion of all the observations for one cross-sectional unit — then the reduced dataset is still, by default, treated as a panel.

The fact that "restricting" the sample results in the creation of a reduced copy of the original dataset may raise an issue when the dataset is very large (say, several thousands of observations). With such a dataset in memory, the creation of a copy may lead to a situation where the computer runs low on memory for calculating regression results. You can work around this as follows:

1. Open the full data set, and impose the sample restriction.
2. Save a copy of the reduced data set to disk.
3. Close the full dataset and open the reduced one.
4. Proceed with your analysis.

## 6.4 Random sampling

With very large datasets (or perhaps to study the properties of an estimator) you may wish to draw a random sample from the full dataset. This can be done using, for example,

```
smpl 100 --random
```

to select 100 cases. If you want the sample to be reproducible, you should set the seed for the random number generator first, using `set`. This sort of sampling falls under the "restriction" category: a reduced copy of the dataset is made.

## 6.5 The Sample menu items

The discussion above has focused on the script command `smpl`. You can also use the items under the Sample menu in the GUI program to select a sub-sample.

The menu items work in the same way as the corresponding `smpl` variants. When you use the item "Sample, Restrict based on criterion", and the dataset is already sub-sampled, you are given the option of preserving or replacing the current restriction. Replacing the current restriction means, in effect, invoking the `replace` option described above (Section 6.3).

Chapter 7

# Graphs and plots

## 7.1 Gnuplot graphs

A separate program, gnuplot, is called to generate graphs. Gnuplot is a very full-featured graphing program with myriad options. It is available from www.gnuplot.info (but note that a suitable copy of gnuplot is bundled with the packaged versions of gretl for MS Windows and Mac OS X). gretl gives you direct access, via a graphical interface, to a subset of gnuplot's options and it tries to choose sensible values for you; it also allows you to take complete control over graph details if you wish.

With a graph displayed, you can click on the graph window for a pop-up menu with the following options.

- Save as PNG: Save the graph in Portable Network Graphics format.
- Save as postscript: Save in encapsulated postscript (EPS) format.
- Save as Windows metafile: Save in Enhanced Metafile (EMF) format.
- Save to session as icon: The graph will appear in iconic form when you select "Icon view" from the View menu.
- Zoom: Lets you select an area within the graph for closer inspection (not available for all graphs).
- Print: (Gnome desktop or MS Windows only) lets you print the graph directly.
- Copy to clipboard: MS Windows only, lets you paste the graph into Windows applications such as MS Word.
- Edit: Opens a controller for the plot which lets you adjust many aspects of its appearance.
- Close: Closes the graph window.

### Displaying data labels

In the case of a simple X-Y scatterplot (with or without a line of best fit displayed), some further options are available if the dataset includes "case markers" (that is, labels identifying each observation).[1] With a scatter plot displayed, when you move the mouse pointer over a data point its label is shown on the graph. By default these labels are transient: they do not appear in the printed or copied version of the graph. They can be removed by selecting "Clear data labels" from the graph pop-up menu. If you want the labels to be affixed permanently (so they will show up when the graph is printed or copied), you have two options.

- To affix the labels currently shown on the graph, select "Freeze data labels" from the graph pop-up menu.

[1] For an example of such a dataset, see the Ramanathan file data4-10: this contains data on private school enrollment for the 50 states of the USA plus Washington, DC; the case markers are the two-letter codes for the states.

- To affix labels for all points in the graph, select “Edit” from the graph pop-up and check the box titled “Show all data labels”. This option is available only if there are less than 55 data points, and it is unlikely to produce good results if the points are tightly clustered since the labels will tend to overlap.

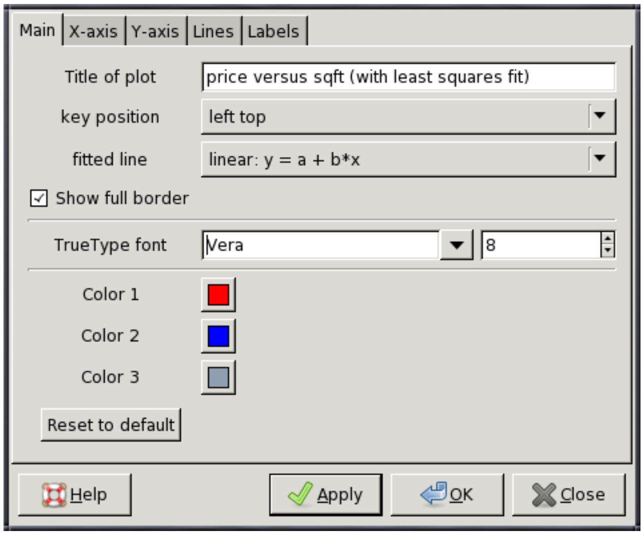
To remove labels that have been affixed in either of these ways, select “Edit” from the graph pop-up and uncheck “Show all data labels”.

### Advanced options

If you know something about gnuplot and wish to get finer control over the appearance of a graph than is available via the graphical controller (“Edit” option), here’s what to do. In the graph display window, right-click and choose “Save to session as icon”. Then open the icon view window — either via the menu item View/Icon view, or by clicking the “session icon view” button on the main-window toolbar. You should see an icon representing your graph. Right-click on that and select “Edit plot commands” from the pop-up menu. This opens an editing window with the actual gnuplot commands displayed. You can edit these commands and either save them for future processing or send them to gnuplot directly, using the Execute (cogwheel) button on the toolbar in the plot commands editing window.

To find out more about gnuplot visit www.gnuplot.info. This site has documentation for the current version of the program in various formats.

See also the entry for `gnuplot` in the *Gretl Command Reference* — and the `graph` and `plot` commands for “quick and dirty” ASCII graphs.



Title of plot: price versus sqft (with least squares fit)

key position: left top

fitted line: linear: y = a + b*x

☑ Show full border

TrueType font: Vera 8

Color 1 🟥

Color 2 🟦

Color 3 ▨

**Figure 7.1**: gretl’s gnuplot controller

## 7.2 Boxplots

These plots (after Tukey and Chambers) display the distribution of a variable. The central box encloses the middle 50 percent of the data, i.e. it is bounded by the first and third quartiles. The “whiskers” extend to the minimum and maximum values. A line is drawn across the box at the median and a “+” sign identifies the mean.

In the case of boxplots with confidence intervals, dotted lines show the limits of an approximate 90 percent confidence interval for the median. This is obtained by the bootstrap method, which can take a while if the data series is very long.

After each variable specified in the boxplot command, a parenthesized boolean expression may be added, to limit the sample for the variable in question. A space must be inserted between the variable name or number and the expression. Suppose you have salary figures for men and women, and you have a dummy variable GENDER with value 1 for men and 0 for women. In that case you could draw comparative boxplots with the following line in the boxplots dialog:

```
salary (GENDER=1) salary (GENDER=0)
```

## Chapter 8

# Discrete variables

When a variable can take only a finite, typically small, number of values, then the variable is said to be *discrete*. Some gretl commands act in a slightly different way when applied to discrete variables; moreover, gretl provides a few commands that only apply to discrete variables. Specifically, the dummify and xtab commands (see below) are available only for discrete variables, while the freq (frequency distribution) command produces different output for discrete variables.

## 8.1 Declaring variables as discrete

Gretl uses a simple heuristic to judge whether a given variable should be treated as discrete, but you also have the option of explicitly marking a variable as discrete, in which case the heuristic check is bypassed.

The heuristic is as follows: First, are all the values of the variable "reasonably round", where this is taken to mean that they are all integer multiples of 0.25? If this criterion is met, we then ask whether the variable takes on a "fairly small" set of distinct values, where "fairly small" is defined as less than or equal to 8. If both conditions are satisfied, the variable is automatically considered discrete.

To mark a variable as discrete you have two options.

1. From the graphical interface, select "Variable, Edit Attributes" from the menu. A dialog box will appear and, if the variable seems suitable, you will see a tick box labeled "Treat this variable as discrete". This dialog box can also be invoked via the context menu (right-click on a variable) or by pressing the F2 key.

2. From the command-line interface, via the discrete command. The command takes one or more arguments, which can be either variables or list of variables. For example:

   ```
   list xlist = x1 x2 x3
   discrete z1 xlist z2
   ```

   This syntax makes it possible to declare as discrete many variables at once, which cannot presently be done via the graphical interface. The switch --reverse reverses the declaration of a variable as discrete, or in other words marks it as continuous. For example:

   ```
   discrete foo
   # now foo is discrete
   discrete foo --reverse
   # now foo is continuous
   ```

The command-line variant is more powerful, in that you can mark a variable as discrete even if it does not seem to be suitable for this treatment.

Note that marking a variable as discrete does not affect its content. It is the user's responsibility to make sure that marking a variable as discrete is a sensible thing to do. Note that if you want to recode a continuous variable into classes, you can use the genr command and its arithmetic functions, as in the following example:

```
nulldata 100
# generate a variable with mean 2 and variance 1
genr x = normal() + 2
# split into 4 classes
genr z = (x>0) + (x>2) + (x>4)
# now declare z as discrete
discrete z
```

Once a variable is marked as discrete, this setting is remembered when you save the file.

## 8.2 Commands for discrete variables

### The dummify command

The dummify command takes as argument a series $x$ and creates dummy variables for each distinct value present in $x$, which must have already been declared as discrete. Example:

```
open greene22_2
discrete Z5 # mark Z5 as discrete
dummify Z5
```

The effect of the above command is to generate 5 new dummy variables, labeled DZ5_1 through DZ5_5, which correspond to the different values in Z5. Hence, the variable DZ5_4 is 1 if Z5 equals 4 and 0 otherwise. This functionality is also available through the graphical interface by selecting the menu item "Add, Dummies for selected discrete variables".

The dummify command can also be used with the following syntax:

```
list dlist = dummify(x)
```

This not only creates the dummy variables, but also a named list (see section 11.1) that can be used afterwards. The following example computes summary statistics for the variable Y for each value of Z5:

```
open greene22_2
discrete Z5 # mark Z5 as discrete
list foo = dummify(Z5)
loop foreach i foo
  smpl $i --restrict --replace
  summary Y
end loop
smpl full
```

Since dummify generates a list, it can be used directly in commands that call for a list as input, such as ols. For example:

```
open greene22_2
discrete Z5 # mark Z5 as discrete
ols Y 0 dummify(Z5)
```

### The freq command

The freq command displays absolute and relative frequencies for a given variable. The way frequencies are counted depends on whether the variable is continuous or discrete. This command is also available via the graphical interface by selecting the "Variable, Frequency distribution" menu entry.

For discrete variables, frequencies are counted for each distinct value that the variable takes. For continuous variables, values are grouped into “bins” and then the frequencies are counted for each bin. The number of bins, by default, is computed as a function of the number of valid observations in the currently selected sample via the rule shown in Table 8.1. However, when the command is invoked through the menu item “Variable, Frequency Plot”, this default can be overridden by the user.

| Observations | Bins |
|---|---|
| $8 \le n < 16$ | 5 |
| $16 \le n < 50$ | 7 |
| $50 \le n \le 850$ | $\lceil \sqrt{n} \rceil$ |
| $n > 850$ | 29 |

**Table 8.1**: Number of bins for various sample sizes

For example, the following code

```
open greene19_1
freq TUCE
discrete TUCE # mark TUCE as discrete
freq TUCE
```

yields

```
Read datafile /usr/local/share/gretl/data/greene/greene19_1.gdt
periodicity: 1, maxobs: 32,
observations range: 1-32

Listing 5 variables:
  0) const     1) GPA       2) TUCE      3) PSI       4) GRADE

? freq TUCE

Frequency distribution for TUCE, obs 1-32
number of bins = 7, mean = 21.9375, sd = 3.90151

       interval          midpt   frequency    rel.     cum.

          <  13.417     12.000        1      3.12%    3.12% *
    13.417 - 16.250     14.833        1      3.12%    6.25% *
    16.250 - 19.083     17.667        6     18.75%   25.00% ******
    19.083 - 21.917     20.500        6     18.75%   43.75% ******
    21.917 - 24.750     23.333        9     28.12%   71.88% **********
    24.750 - 27.583     26.167        7     21.88%   93.75% *******
          >= 27.583     29.000        2      6.25%  100.00% **

Test for null hypothesis of normal distribution:
Chi-square(2) = 1.872 with p-value 0.39211
? discrete TUCE # mark TUCE as discrete
? freq TUCE

Frequency distribution for TUCE, obs 1-32

          frequency    rel.     cum.

  12           1      3.12%    3.12% *
  14           1      3.12%    6.25% *
```

```
   17           3      9.38%   15.62% ***
   19           3      9.38%   25.00% ***
   20           2      6.25%   31.25% **
   21           4     12.50%   43.75% ****
   22           2      6.25%   50.00% **
   23           4     12.50%   62.50% ****
   24           3      9.38%   71.88% ***
   25           4     12.50%   84.38% ****
   26           2      6.25%   90.62% **
   27           1      3.12%   93.75% *
   28           1      3.12%   96.88% *
   29           1      3.12%  100.00% *

Test for null hypothesis of normal distribution:
Chi-square(2) = 1.872 with p-value 0.39211
```

As can be seen from the sample output, a Doornik-Hansen test for normality is computed automatically. This test is suppressed for discrete variables where the number of distinct values is less than 10.

This command accepts two options: `--quiet`, to avoid generation of the histogram when invoked from the command line and `--gamma`, for replacing the normality test with Locke's nonparametric test, whose null hypothesis is that the data follow a Gamma distribution.

If the distinct values of a discrete variable need to be saved, the `values()` matrix construct can be used (see chapter 12).

### The `xtab` command

The `xtab` command cab be invoked in either of the following ways. First,

```
xtab ylist ; xlist
```

where `ylist` and `xlist` are lists of discrete variables. This produces cross-tabulations (two-way frequencies) of each of the variables in `ylist` (by row) against each of the variables in `xlist` (by column). Or second,

```
xtab xlist
```

In the second case a full set of cross-tabulations is generated; that is, each variable in `xlist` is tabulated against each other variable in the list. In the graphical interface, this command is represented by the "Cross Tabulation" item under the View menu, which is active if at least two variables are selected.

Here is an example of use:

```
open greene22_2
discrete Z* # mark Z1-Z8 as discrete
xtab Z1 Z4 ; Z5 Z6
```

which produces

```
Cross-tabulation of Z1 (rows) against Z5 (columns)

       [   1][   2][   3][   4][   5]  TOT.

[   0]    20    91    75    93    36    315
[   1]    28    73    54    97    34    286
```

```
  TOTAL     48   164   129   190    70    601

  Pearson chi-square test = 5.48233 (4 df, p-value = 0.241287)

  Cross-tabulation of Z1 (rows) against Z6 (columns)

         [   9][  12][  14][  16][  17][  18][  20]  TOT.

  [   0]     4    36   106    70    52    45     2    315
  [   1]     3     8    48    45    37    67    78    286

  TOTAL      7    44   154   115    89   112    80    601

  Pearson chi-square test = 123.177 (6 df, p-value = 3.50375e-24)

  Cross-tabulation of Z4 (rows) against Z5 (columns)

         [   1][   2][   3][   4][   5]  TOT.

  [   0]    17    60    35    45    14    171
  [   1]    31   104    94   145    56    430

  TOTAL     48   164   129   190    70    601

  Pearson chi-square test = 11.1615 (4 df, p-value = 0.0248074)

  Cross-tabulation of Z4 (rows) against Z6 (columns)

         [   9][  12][  14][  16][  17][  18][  20]  TOT.

  [   0]     1     8    39    47    30    32    14    171
  [   1]     6    36   115    68    59    80    66    430

  TOTAL      7    44   154   115    89   112    80    601

  Pearson chi-square test = 18.3426 (6 df, p-value = 0.0054306)
```

Pearson's $\chi^2$ test for independence is automatically displayed, provided that all cells have expected frequencies under independence greater than $10^{-7}$. However, a common rule of thumb states that this statistic is valid only if the expected frequency is 5 or greater for at least 80 percent of the cells. If this condition is not met a warning is printed.

Additionally, the `--row` or `--column` options can be given: in this case, the output displays row or column percentages, respectively.

If you want to cut and paste the output of `xtab` to some other program, e.g. a spreadsheet, you may want to use the `--zeros` option; this option causes cells with zero frequency to display the number 0 instead of being empty.

Chapter 9

# Loop constructs

## 9.1 Introduction

The command `loop` opens a special mode in which gretl accepts a block of commands to be repeated zero or more times. This feature may be useful for, among other things, Monte Carlo simulations, bootstrapping of test statistics and iterative estimation procedures. The general form of a loop is:

```
loop control-expression [ --progressive | --verbose | --quiet ]
   loop body
endloop
```

Five forms of control-expression are available, as explained in section 9.2.

Not all gretl commands are available within loops. The commands that are not presently accepted in this context are shown in Table 9.1.

**Table 9.1**: Commands not usable in loops

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| boxplot | corrgm | cusum | data | delete | eqnprint | function | hurst |
| include | leverage | modeltab | nulldata | open | qlrtest | rmplot | run |
| scatters | setmiss | setobs | tabprint | vif | xcorrgm | | |

By default, the `genr` command operates quietly in the context of a loop (without printing information on the variable generated). To force the printing of feedback from `genr` you may specify the `--verbose` option to `loop`. The `--quiet` option suppresses the usual printout of the number of iterations performed, which may be desirable when loops are nested.

The `--progressive` option to `loop` modifies the behavior of the commands `print` and `store`, and certain estimation commands, in a manner that may be useful with Monte Carlo analyses (see Section 9.3).

The following sections explain the various forms of the loop control expression and provide some examples of use of loops.

☞ If you are carrying out a substantial Monte Carlo analysis with many thousands of repetitions, memory capacity and processing time may be an issue. To minimize the use of computer resources, run your script using the command-line program, gretlcli, with output redirected to a file.

## 9.2 Loop control variants

### Count loop

The simplest form of loop control is a direct specification of the number of times the loop should be repeated. We refer to this as a "count loop". The number of repetitions may be a numerical constant, as in `loop 1000`, or may be read from a scalar variable, as in `loop replics`.

In the case where the loop count is given by a variable, say replics, in concept replics is an integer; if the value is not integral, it is converted to an integer by truncation. Note that replics is evaluated only once, when the loop is initially compiled.

### While loop

A second sort of control expression takes the form of the keyword while followed by a boolean expression. For example,

```
loop while essdiff > .00001
```

Execution of the commands within the loop will continue so long as (a) the specified condition evaluates as true and (b) the number of iterations does not exceed the value of the internal variable loop_maxiter. By default this equals 250, but you can specify a different value via the set command (see the *Gretl Command Reference*).

### Index loop

A third form of loop control uses an index variable, for example i.[1] In this case you specify starting and ending values for the index, which is incremented by one each time round the loop. The syntax looks like this: loop i=1..20.

The index variable may be a pre-existing scalar; if this is not the case, the variable is created automatically and is destroyed on exit from the loop.

The index may be used within the loop body in either of two ways: you can access the integer value of i (see Example 9.4) or you can use its string representation, $i (see Example 9.5).

The starting and ending values for the index can be given in numerical form, or by reference to predefined scalar variables. In the latter case the variables are evaluated once, at the start of the loop. In addition, with time series data you can give the starting and ending values in the form of dates, as in loop i=1950:1..1999:4.

This form of loop control is intended to be quick and easy, and as such it is subject to certain limitations. You cannot do arithmetic within the loop control expression, as in

```
loop i=k..2*k # won't work
```

But one extension is permitted for convenience: you can inflect a loop control variable with a minus sign, as in

```
loop k=-lag..lag # OK
```

Also note that in this sort of loop the index variable is always incremented by one at each iteration. If, for example, you have

```
loop i=m..n
```

where m and n are scalar variables with values m > n at the time of execution, the index will not be decremented; rather, the loop will simply be bypassed.

If you need more complex loop control, see the "for" form below.

The index loop is particularly useful in conjunction with the values() matrix function when some operation must be carried out for each value of some discrete variable (see chapter 8). Consider the following example:

[1] It is common programming practice to use simple, one-character names for such variables. However, you may use any name that is acceptable by gretl: up to 15 characters, starting with a letter, and containing nothing but letters, numerals and the underscore character.

```
open greene22_2
open greene22_2
discrete Z8
v8 = values(Z8)
n = rows(v8)
loop i=1..n
  scalar xi = v8[$i]
  smpl (Z8=xi) --restrict --replace
  printf "mean(Y | Z8 = %g) = %8.5f, sd(Y | Z8 = %g) = %g\n", \
    xi, mean(Y), xi, sd(Y)
end loop
```

In this case, we evaluate the conditional mean and standard deviation of the variable Y for each value of Z8.

### Foreach loop

The fourth form of loop control also uses an index variable, in this case to index a specified list of strings. The loop is executed once for each string in the list. This can be useful for performing repetitive operations on a list of variables. Here is an example of the syntax:

```
loop foreach i peach pear plum
   print "$i"
endloop
```

This loop will execute three times, printing out "peach", "pear" and "plum" on the respective iterations. The numerical value of the index starts at 1 and is incremented by 1 at each iteration.

If you wish to loop across a list of variables that are contiguous in the dataset, you can give the names of the first and last variables in the list, separated by "..", rather than having to type all the names. For example, say we have 50 variables AK, AL, ..., WY, containing income levels for the states of the US. To run a regression of income on time for each of the states we could do:

```
genr time
loop foreach i AL..WY
   ols $i const time
endloop
```

This loop variant can also be used for looping across the elements in a *named list* (see chapter 11). For example:

```
list ylist = y1 y2 y3
loop foreach i ylist
   ols $i const x1 x2
endloop
```

Note that if you use this idiom inside a function (see chapter 10), looping across a list that has been supplied to the function as an argument, it is necessary to use the syntax *listname*.$i to reference the list-member variables. In the context of the example above, this would mean replacing the third line with

```
   ols ylist.$i const x1 x2
```

### For loop

The final form of loop control emulates the for statement in the C programming language. The sytax is loop for, followed by three component expressions, separated by semicolons and surrounded by parentheses. The three components are as follows:

1. Initialization: This is evaluated only once, at the start of the loop. Common example: setting a scalar control variable to some starting value.
2. Continuation condition: this is evaluated at the top of each iteration (including the first). If the expression evaluates as true (non-zero), iteration continues, otherwise it stops. Common example: an inequality expressing a bound on a control variable.
3. Modifier: an expression which modifies the value of some variable. This is evaluated prior to checking the continuation condition, on each iteration after the first. Common example: a control variable is incremented or decremented.

Here's a simple example:

```
loop for (r=0.01; r<.991; r+=.01)
```

In this example the variable `r` will take on the values 0.01, 0.02, `...`, 0.99 across the 99 iterations. Note that due to the finite precision of floating point arithmetic on computers it may be necessary to use a continuation condition such as the above, `r<.991`, rather than the more "natural" `r<=.99`. (Using double-precision numbers on an x86 processor, at the point where you would expect `r` to equal 0.99 it may in fact have value 0.990000000000001.)

Any or all of the three expressions governing a `for` loop may be omitted — the minimal form is `(;;)`. If the continuation test is omitted it is implicitly true, so you have an infinite loop unless you arrange for some other way out, such as a `break` statement.

If the initialization expression in a `for` loop takes the common form of setting a scalar variable to a given value, the string representation of that scalar's value will be available within the loop via the accessor `$`*`varname`*.

## 9.3 Progressive mode

If the `--progressive` option is given for a command loop, special behavior is invoked for certain commands, namely, `print`, `store` and simple estimation commands. By "simple" here we mean commands which (a) estimate a single equation (as opposed to a system of equations) and (b) do so by means of a single command statement (as opposed to a block of statements, as with `nls` and `mle`). The paradigm is `ols`; other possibilities include `tsls`, `wls`, `logit` and so on.

The special behavior is as follows.

Estimators: The results from each individual iteration of the estimator are not printed. Instead, after the loop is completed you get a printout of (a) the mean value of each estimated coefficient across all the repetitions, (b) the standard deviation of those coefficient estimates, (c) the mean value of the estimated standard error for each coefficient, and (d) the standard deviation of the estimated standard errors. This makes sense only if there is some random input at each step.

`print`: When this command is used to print the value of a variable, you do not get a print each time round the loop. Instead, when the loop is terminated you get a printout of the mean and standard deviation of the variable, across the repetitions of the loop. This mode is intended for use with variables that have a scalar value at each iteration, for example the error sum of squares from a regression. Data series cannot be printed in this way.

`store`: This command writes out the values of the specified scalars, from each time round the loop, to a specified file. Thus it keeps a complete record of their values across the iterations. For example, coefficient estimates could be saved in this way so as to permit subsequent examination of their frequency distribution. Only one such `store` can be used in a given loop.

## 9.4 Loop examples

### Monte Carlo example

A simple example of a Monte Carlo loop in “progressive” mode is shown in Example 9.1.

**Example 9.1**: Simple Monte Carlo loop

```
nulldata 50
seed 547
genr x = 100 * uniform()
# open a "progressive" loop, to be repeated 100 times
loop 100 --progressive
   genr u = 10 * normal()
   # construct the dependent variable
   genr y = 10*x + u
   # run OLS regression
   ols y const x
   # grab the coefficient estimates and R-squared
   genr a = $coeff(const)
   genr b = $coeff(x)
   genr r2 = $rsq
   # arrange for printing of stats on these
   print a b r2
   # and save the coefficients to file
   store coeffs.gdt a b
endloop
```

This loop will print out summary statistics for the ‘a’ and ‘b’ estimates and $R^2$ across the 100 repetitions. After running the loop, `coeffs.gdt`, which contains the individual coefficient estimates from all the runs, can be opened in gretl to examine the frequency distribution of the estimates in detail.

The command `nulldata` is useful for Monte Carlo work. Instead of opening a “real” data set, `nulldata 50` (for instance) opens a dummy data set, containing just a constant and an index variable, with a series length of 50. Constructed variables can then be added using the `genr` command. See the `set` command for information on generating repeatable pseudo-random series.

### Iterated least squares

Example 9.2 uses a “while” loop to replicate the estimation of a nonlinear consumption function of the form

$$C = \alpha + \beta Y^{\gamma} + \epsilon$$

as presented in Greene (2000, Example 11.3). This script is included in the gretl distribution under the name `greene11_3.inp`; you can find it in gretl under the menu item “File, Script files, Practice file, Greene...”.

The option `--print-final` for the `ols` command arranges matters so that the regression results will not be printed each time round the loop, but the results from the regression on the last iteration will be printed when the loop terminates.

Example 9.3 shows how a loop can be used to estimate an ARMA model, exploiting the “outer product of the gradient” (OPG) regression discussed by Davidson and MacKinnon in their *Estimation and Inference in Econometrics*.

**Example 9.2**: Nonlinear consumption function

```
open greene11_3.gdt
# run initial OLS
ols C 0 Y
genr essbak = $ess
genr essdiff = 1
genr beta = $coeff(Y)
genr gamma = 1
# iterate OLS till the error sum of squares converges
loop while essdiff > .00001
   # form the linearized variables
   genr C0 = C + gamma * beta * Y^gamma * log(Y)
   genr x1 = Y^gamma
   genr x2 = beta * Y^gamma * log(Y)
   # run OLS
   ols C0 0 x1 x2 --print-final --no-df-corr --vcv
   genr beta = $coeff(x1)
   genr gamma = $coeff(x2)
   genr ess = $ess
   genr essdiff = abs(ess - essbak)/essbak
   genr essbak = ess
endloop
# print parameter estimates using their "proper names"
noecho
printf "alpha = %g\n", $coeff(0)
printf "beta  = %g\n", beta
printf "gamma = %g\n", gamma
```

### Indexed loop examples

Example 9.4 shows an indexed loop in which the `smpl` is keyed to the index variable `i`. Suppose we have a panel dataset with observations on a number of hospitals for the years 1991 to 2000 (where the year of the observation is indicated by a variable named `year`). We restrict the sample to each of these years in turn and print cross-sectional summary statistics for variables 1 through 4.

Example 9.5 illustrates string substitution in an indexed loop.

The first time round this loop the variable `V` will be set to equal `COMP1987` and the dependent variable for the `ols` will be `PBT1987`. The next time round `V` will be redefined as equal to `COMP1988` and the dependent variable in the regression will be `PBT1988`. And so on.

**Example 9.3**: ARMA 1, 1

```
open armaloop.gdt

genr c = 0
genr a = 0.1
genr m = 0.1

series e = 1.0
genr de_c = e
genr de_a = e
genr de_m = e

genr crit = 1
loop while crit > 1.0e-9

   # one-step forecast errors
   genr e = y - c - a*y(-1) - m*e(-1)

   # log-likelihood
   genr loglik = -0.5 * sum(e^2)
   print loglik

   # partials of forecast errors wrt c, a, and m
   genr de_c = -1 - m * de_c(-1)
   genr de_a = -y(-1) -m * de_a(-1)
   genr de_m = -e(-1) -m * de_m(-1)

   # partials of l wrt c, a and m
   genr sc_c = -de_c * e
   genr sc_a = -de_a * e
   genr sc_m = -de_m * e

   # OPG regression
   ols const sc_c sc_a sc_m --print-final --no-df-corr --vcv

   # Update the parameters
   genr dc = $coeff(sc_c)
   genr c = c + dc
   genr da = $coeff(sc_a)
   genr a = a + da
   genr dm = $coeff(sc_m)
   genr m = m + dm

   printf "  constant        = %.8g (gradient = %#.6g)\n", c, dc
   printf "  ar1 coefficient = %.8g (gradient = %#.6g)\n", a, da
   printf "  ma1 coefficient = %.8g (gradient = %#.6g)\n", m, dm

   genr crit = $T - $ess
   print crit
endloop

genr se_c = $stderr(sc_c)
genr se_a = $stderr(sc_a)
genr se_m = $stderr(sc_m)

noecho
print "
printf "constant = %.8g (se = %#.6g, t = %.4f)\n", c, se_c, c/se_c
printf "ar1 term = %.8g (se = %#.6g, t = %.4f)\n", a, se_a, a/se_a
printf "ma1 term = %.8g (se = %#.6g, t = %.4f)\n", m, se_m, m/se_m
```

**Example 9.4**: Panel statistics

```
open hospitals.gdt
loop i=1991..2000
  smpl (year=i) --restrict --replace
  summary 1 2 3 4
endloop
```

**Example 9.5**: String substitution

```
open bea.dat
loop i=1987..2001
  genr V = COMP$i
  genr TC = GOC$i - PBT$i
  genr C = TC - V
  ols PBT$i const TC V
endloop
```

# Chapter 10

# User-defined functions

## 10.1 Defining a function

Since version 1.3.3, gretl has contained a mechanism for defining functions, which may be called via the command line, in the context of a script, or (if packaged appropriately, see section 10.5) via the program's graphical interface.

The syntax for defining a function looks like this:

```
function function-name(parameters)
   function body
end function
```

*function-name* is the unique identifier for the function. Names must start with a letter. They have a maximum length of 31 characters; if you type a longer name it will be truncated. Function names cannot contain spaces. You will get an error if you try to define a function having the same name as an existing gretl command.

The *parameters* for a function are given in the form of a comma-separated list. Parameters can be of any of the types shown below.

| Type | Description |
|---|---|
| `bool` | scalar variable acting as a Boolean switch |
| `int` | scalar variable acting as an integer |
| `scalar` | scalar variable |
| `series` | data series |
| `list` | named list of series |
| `matrix` | named matrix or vector |
| `string` | named string or string literal |

Each element in the listing of parameters must include two terms: a type specifier, and the name by which the parameter shall be known within the function. An example follows:

```
function myfunc(series y, list xvars, bool verbose)
```

Each of the type-specifiers, with the exception of `list` and `string`, may be modified by prepending an asterisk to the associated parameter name, as in

```
function myfunc(series *y, scalar *b)
```

The meaning of this modification is explained below (see section 10.4); it is related to the use of pointer arguments in the C programming language.

### Function parameters: optional refinements

Besides the required elements mentioned above, the specification of a function parameter may include some additional fields.

For a parameter of type `scalar` or `int`, a *minimum*, *maximum* and *default* value may be specified. These values should directly follow the name of the parameter, enclosed in square brackets and with the individual elements separated by colons. For example, suppose we have an integer parameter `order` for which we wish to specify a minimum of 1, a maximum of 12, and a default of 4. We can write

```
int order[1:12:4]
```

If you wish to omit any of the three specifiers, leave the corresponding field empty. For example `[1::4]` would specify a minimum of 1 and a default of 4 while leaving the maximum unlimited.

For a parameter of type `bool`, you can specify a default of 1 (true) or 0 (false), as in

```
bool verbose[0]
```

Finally, for a parameter of any type you can append a short *descriptive string*. This will show up as an aid to the user if the function is packaged (see section 10.5 below) and called via gretl's graphical interface. The string should be enclosed in double quotes, and inserted before the comma that precedes the following parameter (or the closing right parenthesis of the function definition, in the case of the last parameter), as illustrated in the following example.

```
function myfun (series y "dependent variable",
                series x "independent variable")
```

### Void functions

You may define a function that has no parameters (these are called "routines" in some programming languages). In this case, use the keyword `void` in place of the listing of parameters:

```
function myfunc2(void)
```

### The function body

The *function body* is composed of gretl commands, or calls to user-defined functions (that is, function calls may be nested). A function may call itself (that is, functions may be recursive). While the function body may contain function calls, it may not contain function definitions. That is, you cannot define a function inside another function. For further details, see section 10.4.

## 10.2 Calling a function

A user function is called by typing its name followed by zero or more arguments enclosed in parentheses. If there are two or more arguments these should be separated by commas.

There are automatic checks in place to ensure that the number of arguments given in a function call matches the number of parameters, and that the types of the given arguments match the types specified in the definition of the function. An error is flagged if either of these conditions is violated. One qualification: allowance is made for omitting arguments at the end of the list, provided that default values are specified in the function definition. To be precise, the check is that the number of arguments is at least equal to the number of *required* parameters, and is no greater than the total number of parameters.

A scalar, series or matrix argument to a function may be given either as the name of a pre-existing variable or as an expression which evaluates to a variable of the appropriate type. Scalar arguments may also be given as numerical values. List arguments must be specified by name.

The following trivial example illustrates a function call that correctly matches the function definition.

```
# function definition
function ols_ess(series y, list xvars)
  ols y 0 xvars --quiet
  scalar myess = $ess
  printf "ESS = %g\n", myess
  return scalar myess
end function
# main script
open data4-1
list xlist = 2 3 4
# function call (the return value is ignored here)
ols_ess(price, xlist)
```

The function call gives two arguments: the first is a data series specified by name and the second is a named list of regressors. Note that while the function offers the variable `myess` as a return value, it is ignored by the caller in this instance. (As a side note here, if you want a function to calculate some value having to do with a regression, but are not interested in the full results of the regression, you may wish to use the `--quiet` flag with the estimation command as shown above.)

A second example shows how to write a function call that assigns a return value to a variable in the caller:

```
# function definition
function get_uhat(series y, list xvars)
  ols y 0 xvars --quiet
  series uh = $uhat
  return series uh
end function
# main script
open data4-1
list xlist = 2 3 4
# function call
series resid = get_uhat(price, xlist)
```

## 10.3 Deleting a function

If you have defined a function and subsequently wish to clear it out of memory, you can do so using the keywords `delete` or `clear`, as in

```
function myfunc delete
function get_uhat clear
```

Note, however, that if `myfunc` is already a defined function, providing a new definition automatically overwrites the previous one, so it should rarely be necessary to delete functions explicitly.

## 10.4 Function programming details

### Variables versus pointers

Series, scalar, and matrix arguments to functions can be passed in two ways: "as they are", or as pointers. For example, consider the following:

```
function triple1(series x)
  series ret = 3*x
  return series ret
end function
```

```
function triple2(series *x)
  series ret = 3*x
  return series ret
end function
```

These two functions are nearly identical (and yield the same result); the only difference is that you need to feed a series into `triple1`, as in `triple1(myseries)`, while `triple2` must be supplied a *pointer* to a series, as in `triple2(&myseries)`.

Why make the distinction, then? There are two main reasons for doing so: modularity and performance.

By modularity we mean the insulation of a function from the rest of the script which calls it. One of the many benefits of this approach is that your functions are easily reusable in other contexts. To achieve modularity, *variables created within a function are local to that function, and are destroyed when the function exits*, unless they are made available as return values and these values are "picked up" or assigned by the caller.

In addition, functions do not have access to variables in "outer scope" (that is, variables that exist in the script from which the function is called) except insofar as these are explicitly passed to the function as arguments.

By default, when a variable is passed to a function as an argument, what the function actually "gets" is a *copy* of the outer variable, which means that the value of the outer variable is not modified by whatever goes on inside the function. But the use of pointers allows a function and its caller to "cooperate" such that an outer variable can be modified by the function. In effect, this allows a function to "return" more than one value (although only one variable can be returned directly — see below). The parameter in question is marked with a prefix of * in the function definition, and the corresponding argument is marked with the complementary prefix & in the caller. For example,

```
function get_uhat_and_ess(series y, list xvars, scalar *ess)
  ols y 0 xvars --quiet
  ess = $ess
  series uh = $uhat
  return series uh
end function
# main script
open data4-1
list xlist = 2 3 4
# function call
scalar SSR
series resid = get_uhat_and_ess(price, xlist, &SSR)
```

In the above, we may say that the function is given the *address* of the scalar variable `SSR`, and it assigns a value to that variable (under the local name `ess`). (For anyone used to programming in C: note that it is not necessary, or even possible, to "dereference" the variable in question within the function using the * operator. Unembellished use of the name of the variable is sufficient to access the variable in outer scope.)

An "address" parameter of this sort can be used as a means of offering optional information to the caller. (That is, the corresponding argument is not strictly needed, but will be used if present). In that case the parameter should be given a default value of `null` and the the function should test to see if the caller supplied a corresponding argument or not, using the built-in function `isnull()`. For example, here is the simple function shown above, modified to make the filling out of the `ess` value optional.

```
function get_uhat_and_ess(series y, list xvars, scalar *ess[null])
  ols y 0 xvars --quiet
  if !isnull(ess)
```

```
      ess = $ess
    endif
    series uh = $uhat
    return series uh
  end function
```

If the caller does not care to get the ess value, it can use null in place of a real argument:

```
  series resid = get_uhat_and_ess(price, xlist, null)
```

Alternatively, trailing function arguments that have default values may be omitted, so the following would also be a valid call:

```
  series resid = get_uhat_and_ess(price, xlist)
```

Pointer arguments may also be useful for optimizing performance: even if a variable is not modified inside the function, it may be a good idea to pass it as a pointer if it occupies a lot of memory. Otherwise, the time gretl spends transcribing the value of the variable to the local copy may be non-negligible, compared to the time the function spends doing the job it was written for.

Example 10.1 takes this to the extreme. We define two functions which return the number of rows of a matrix (a pretty fast operation). One function gets a matrix as argument, the other one a pointer to a matrix. The two functions are evaluated on a matrix with 2000 rows and 2000 columns; on a typical system, floating-point numbers take 8 bytes of memory, so the space occupied by the matrix is roughly 32 megabytes.

Running the code in example 10.1 will produce output similar to the following (the actual numbers depend on the machine you're running the example on):

```
  Elapsed time:
          without pointers (copy) = 3.66 seconds,
          with pointers (no copy) = 0.01 seconds.
```

If a pointer argument is used for this sort of purpose — and the object to which the pointer points is not modified by the function — it is a good idea to signal this to the user by adding the const qualifier, as shown for function b in Example 10.1. When a pointer argument is qualified in this way, any attempt to modify the object within the function will generate an error.

### List arguments

The use of a named list as an argument to a function gives a means of supplying a function with a set of variables whose number is unknown when the function is written — for example, sets of regressors or instruments. Within the function, the list can be passed on to commands such as ols.

A list argument can also be "unpacked" using a foreach loop construct, but this requires some care. For example, suppose you have a list X and want to calculate the standard deviation of each variable in the list. You can do:

```
  loop foreach i X
     scalar sd_$i = sd(X.$i)
  end loop
```

*Please note*: a special piece of syntax is needed in this context. If we wanted to perform the above task on a list in a regular script (not inside a function), we could do

```
  loop foreach i X
     scalar sd_$i = sd($i)
  end loop
```

**Example 10.1**: Performance comparison: values versus pointer

```
function a(matrix X)
  r = rows(X)
  return scalar r
end function

function b(const matrix *X)
  r = rows(X)
  return scalar r
end function

nulldata 10
set echo off
set messages off
X = zeros(2000,2000)
r = 0

set stopwatch
loop 100
  r = a(X)
end loop
fa = $stopwatch

set stopwatch
loop 100
  r = b(&X)
end loop
fb = $stopwatch

printf "Elapsed time:\n\
\twithout pointers (copy) = %g seconds,\n\
\twith pointers (no copy) = %g seconds.\n", fa, fb
```

where `$i` gets the name of the variable at position *i* in the list, and `sd($i)` gets its standard deviation. But inside a function, working on a list supplied as an argument, if we want to reference an individual variable in the list we must use the syntax *listname.varname*. Hence in the example above we write `sd(X.$i)`.

This is necessary to avoid possible collisions between the name-space of the function and the name-space of the caller script. For example, suppose we have a function that takes a list argument, and that defines a local variable called `y`. Now suppose that this function is passed a list containing a variable named `y`. If the two name-spaces were not separated either we'd get an error, or the external variable `y` would be silently over-written by the local one. It is important, therefore, that list-argument variables should not be "visible" by name within functions. To "get hold of" such variables you need to use the form of identification just mentioned: the name of the list, followed by a dot, followed by the name of the variable.

☞ The treatment of list-argument variables described above is new in gretl 1.7.6. The problem it addresses is quite subtle, and was discovered only recently. Existing functions that use `foreach` loops on list arguments may need to be modified. For a limited time, there is a special switch available that restores the old behavior: that is, it enables support for functions that do not use the *listname.varname* syntax. The command to use is `set protect_lists off`. But we recommend updating old functions as soon as possible.

**Constancy of list arguments** When a named list of variables is passed to a function, the function is actually provided with a copy of the list. The function may modify this copy (for instance, adding or removing members), but the original list at the level of the caller is not modified.

**Optional list arguments** If a list argument to a function is optional, this should be indicated by appending a default value of `null`, as in

```
function myfunc (scalar y, list X[null])
```

In that case, if the caller gives `null` as the list argument (or simply omits the last argument) the named list `X` inside the function will be empty. This possibility can be detected using the `nelem()` function, which returns 0 for an empty list.

### String arguments

String arguments can be used, for example, to provide flexibility in the naming of variables created within a function. In the following example the function `mavg` returns a list containing two moving averages constructed from an input series, with the names of the newly created variables governed by the string argument.

```
function mavg (series y, string vname)
   series @vname_2 = (y+y(-1)) / 2
   series @vname_4 = (y+y(-1)+y(-2)+y(-3)) / 4
   list retlist = @vname_2 @vname_4
   return list retlist
end function

open data9-9
list malist = mavg(nocars, "nocars")
print malist --byobs
```

The last line of the script will print two variables named `nocars_2` and `nocars_4`. For details on the handling of named strings, see chapter 11.

If a string argument is considered optional, it may be given a `null` default value, as in

```
function foo (series y, string vname[null])
```

### Retrieving the names of arguments

The variables given as arguments to a function are known inside the function by the names of the corresponding parameters. For example, within the function whose signature is

```
function somefun (series y)
```

we have the series known as `y`. It may be useful, however, to be able to determine the names of the variables provided as arguments. This can be done using the function `argname`, which takes the name of a function parameter as its single argument and returns a string. Here is a simple illustration:

```
function namefun (series y)
  printf "the series given as 'y' was named %s\n", argname(y)
end function

open data9-7
namefun(QNC)
```

This produces the output

```
the series given as 'y' was named QNC
```

Please note that this will not always work: the arguments given to functions may be anonymous variables, created on the fly, as in `somefun(log(QNC))` or `somefun(CPI/100)`. In that case the `argname` function fails to return a string. Function writers who wish to make use of this facility should check the return from `argname` using the `isstring()` function, which returns 1 when given the name of a string variable, 0 otherwise.

### Return values

Functions can return nothing (just printing a result, perhaps), or they can return a single variable — a scalar, series, list, matrix or string. The return value, if any, is specified via a statement within the function body beginning with the keyword `return`, followed by a type specifier and the name of a variable (as in the listing of parameters). There can be only one such statement. An example of a valid return statement is shown below:

```
return scalar SSR
```

Having a function return a list is one way of permitting the "return" of more than one variable. That is, you can define several variable inside a function and package them as a list; in this case they are not destroyed when the function exits. Here is a simple example, which also illustrates the possibility of setting the descriptive labels for variables generated in a function.

```
function make_cubes (list xlist)
   list cubes = null
   loop foreach i xlist --quiet
      series $i3 = (xlist.$i)^3
      setinfo $i3 -d "cube of $i"
      list cubes += $i3
    end loop
    return list cubes
end function

open data4-1
list xlist = price sqft
list cubelist = make_cubes(xlist)
print xlist cubelist --byobs
labels
```

Note that the `return` statement does *not* cause the function to return (exit) at the point where it appears within the body of the function. Rather, it specifies which variable is available for assignment when the function exits, and a function exits only when (a) the end of the function code is reached, (b) a gretl error occurs, or (c) a `funcerr` statement is reached.

The `funcerr` keyword, which may be followed by a string enclosed in double quotes, causes a function to exit with an error flagged. If a string is provided, this is printed on exit, otherwise a generic error message is printed. This mechanism enables the author of a function to pre-empt an ordinary execution error and/or offer a more specific and helpful error message. For example,

```
if nelem(xlist) = 0
   funcerr "xlist must not be empty"
end if
```

### Error checking

When gretl first reads and "compiles" a function definition there is minimal error-checking: the only checks are that the function name is acceptable, and, so far as the body is concerned, that you are not trying to define a function inside a function (see Section 10.1). Otherwise, if the function body contains invalid commands this will become apparent only when the function is called, and its commands are executed.

### Debugging

The usual mechanism whereby gretl echoes commands and reports on the creation of new variables is by default suppressed when a function is being executed. If you want more verbose output from a particular function you can use either or both of the following commands within the function:

```
set echo on
set messages on
```

Alternatively, you can achieve this effect for all functions via the command `set debug 1`. Usually when you set the value of a state variable using the `set` command, the effect applies only to the current level of function execution. For instance, if you do `set messages on` within function `f1`, which in turn calls function `f2`, then messages will be printed for `f1` but not `f2`. The debug variable, however, acts globally; all functions become verbose regardless of their level.

Further, you can do `set debug 2`: in addition to command echo and the printing of messages, this is equivalent to setting `max_verbose` (which produces verbose output from the BFGS maximizer) at all levels of function execution.

## 10.5 Function packages

As of gretl 1.6.0, there is a mechanism to package functions and make them available to other users of gretl. Here is a walk-through of the process.

### Load a function in memory

There are several ways to load a function:

- If you have a script file containing function definitions, open that file and run it.
- Create a script file from scratch. Include at least one function definition, and run the script.
- Open the GUI console and type a function definition interactively. This method is not particularly recommended; you are probably better composing a function non-interactively.

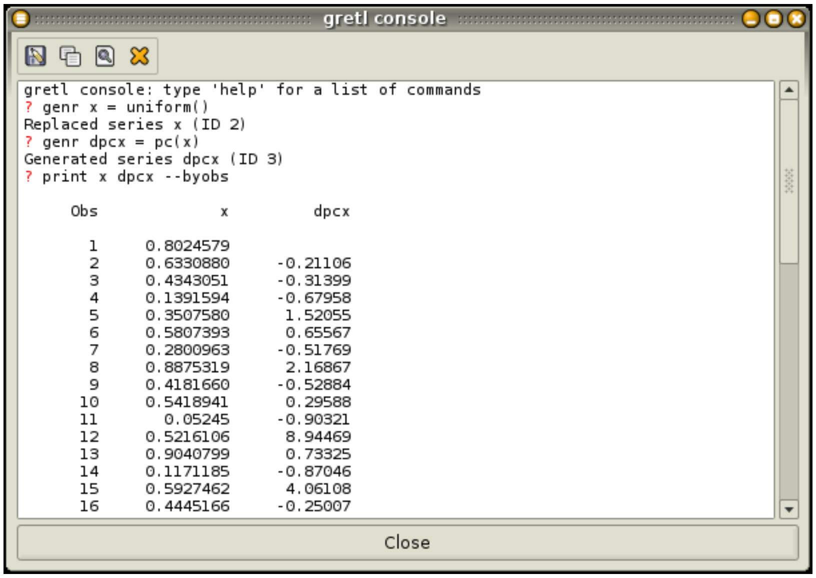
For example, suppose you decide to package a function that returns the percentage change of a time series. Open a script file and type

```
function pc(series y "Series to process")
  series foo = 100 * diff(y)/y(-1)
  return series foo
end function
```

In this case, we have appended a string to the function argument, as explained in section 10.1, so as to make our interface more informative. This is not obligatory: if you omit the descriptive string, gretl will supply a predefined one.

Now run your function. You may want to make sure it works properly by running a few tests. For example, you may open the console and type

```
genr x = uniform()
genr dpcx = pc(x)
print x dpcx --byobs
```



```
gretl console: type 'help' for a list of commands
? genr x = uniform()
Replaced series x (ID 2)
? genr dpcx = pc(x)
Generated series dpcx (ID 3)
? print x dpcx --byobs

     Obs            x         dpcx

       1    0.8024579
       2    0.6330880     -0.21106
       3    0.4343051     -0.31399
       4    0.1391594     -0.67958
       5    0.3507580      1.52055
       6    0.5807393      0.65567
       7    0.2800963     -0.51769
       8    0.8875319      2.16867
       9    0.4181660     -0.52884
      10    0.5418941      0.29588
      11      0.05245     -0.90321
      12    0.5216106      8.94469
      13    0.9040799      0.73325
      14    0.1171185     -0.87046
      15    0.5927462      4.06108
      16    0.4445166     -0.25007
```

**Figure 10.1**: Output of function check

You should see something similar to figure 10.1. The function seems to work ok. Once your function is debugged, you may proceed to the next stage.

### Create a package

Start the GUI program and take a look at the "File, Function files" menu. This menu contains four items: "On local machine", "On server", "Edit package", "New package".

Select "New package". (This will produce an error message unless at least one user-defined function is currently loaded in memory — see the previous point.) In the first dialog you get to select:

- A public function to package.
- Zero or more "private" helper functions.

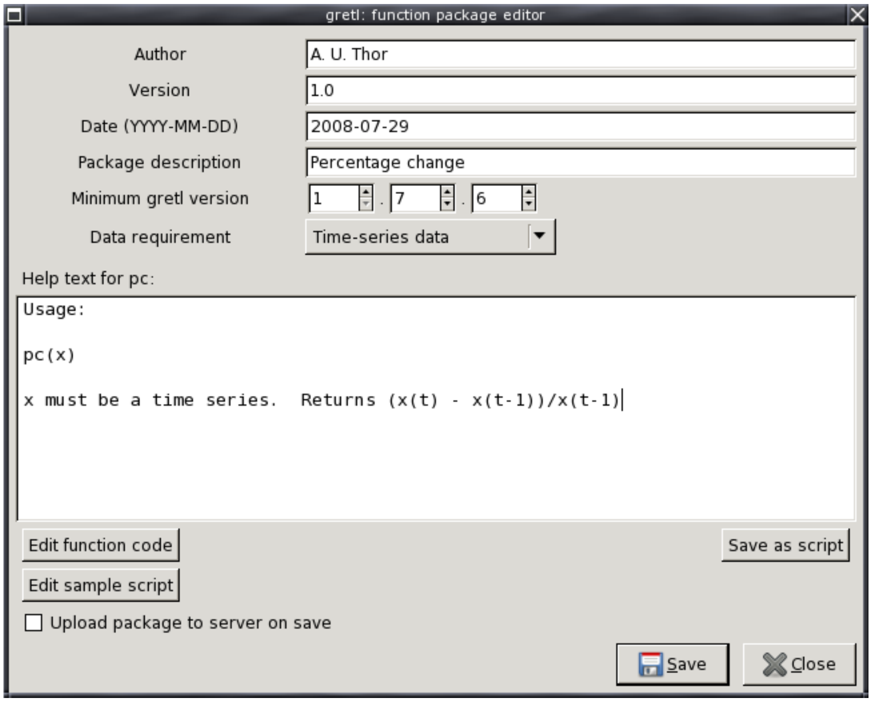
Public functions are directly available to users; private functions are part of the "behind the scenes" mechanism in a function package.

On clicking "OK" a second dialog should appear (see Figure 10.2), where you get to enter the package information (author, version, date, and a short description). You can also enter help text for the public interface. You have a further chance to edit the code of the function(s) to be packaged, by clicking on "Edit function code". (If the package contains more than one function, a drop-down selector will be shown.) And you get to add a sample script that exercises your package. This will be helpful for potential users, and also for testing. A sample script is required if you want to upload the package to the gretl server (for which a check-box is supplied).

You won't need it right now, but the button labeled "Save as script" allows you to "reverse engineer" a function package, writing out a script that contains all the relevant function definitions.

Clicking "Save" in this dialog leads you to a File Save dialog. All being well, this should be pointing towards a directory named `functions`, either under the gretl system directory (if you have write permission on that) or the gretl user directory. This is the recommended place to save function package files, since that is where the program will look in the special routine for opening such files (see below).

Needless to say, the menu command "File, Function files, Edit package" allows you to make changes to a local function package.


gretl: function package editor

Author: A. U. Thor

Version: 1.0

Date (YYYY-MM-DD): 2008-07-29

Package description: Percentage change

Minimum gretl version: 1 . 7 . 6

Data requirement: Time-series data

Help text for pc:

```
Usage:

pc(x)

x must be a time series.  Returns (x(t) - x(t-1))/x(t-1)
```

**Figure 10.2**: The package editor window

A word on the file you just saved. By default, it will have a .gfn extension. This is a "function package" file: unlike an ordinary gretl script file, it is an XML file containing both the function code and the extra information entered in the packager. Hackers might wish to write such a file from scratch rather than using the GUI packager, but most people are likely to find it awkward. Note that XML-special characters in the function code have to be escaped, e.g. & must be represented as &amp;. Also, some elements of the function syntax differ from the standard script representation: the parameters and return values (if any) are represented in XML. Basically, the function is pre-parsed, and ready for fast loading using libxml.

### Load a package

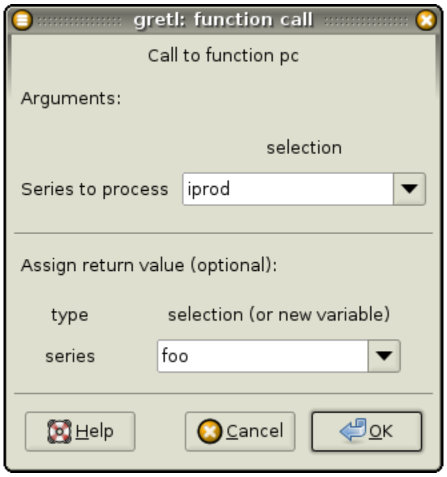
Why package functions in this way? To see what's on offer so far, try the next phase of the walk-through.

Close gretl, then re-open it. Now go to "File, Function files, On local machine". If the previous stage above has gone OK, you should see the file you packaged and saved, with its short description. If you click on "Info" you get a window with all the information gretl has gleaned from the function package. If you click on the "View code" icon in the toolbar of this new window, you get a script view window showing the actual function code. Now, back to the "Function packages" window, if you click on the package's name, the relevant functions are loaded into gretl's workspace, ready to be called by clicking on the "Call" button.

After loading the function(s) from the package, open the GUI console. Try typing help foo, replacing foo with the name of the public interface from the loaded function package: if any help text was provided for the function, it should be presented.

In a similar way, you can browse and load the function packages available on the gretl server, by selecting "File, Function files, On server".

Once your package is installed on your local machine, you can use the function it contains via the graphical interface as described above, or by using the CLI, namely in a script or through the console. In the latter case, you load the function via the include command, specifying the package file as the argument, complete with the .gfn extension.



Call to function pc

Arguments:

| | selection |
|---|---|
| Series to process | iprod |

Assign return value (optional):

| type | selection (or new variable) |
|---|---|
| series | foo |

**Figure 10.3**: Using your package

To continue with our example, load the file np.gdt (supplied with gretl among the sample datasets). Suppose you want to compute the rate of change for the variable iprod via your new function and store the result in a series named foo.

Go to "File, Function files, On local machine". You will be shown a list of the installed packages, including the one you have just created. If you select it and click on "Execute" (or double-click on the name of the function package), a window similar to the one shown in figure 10.3 will appear. Notice that the description string "Series to process", supplied with the function definition, appears to the left of the top series chooser.

Click "Ok" and the series foo will be generated (see figure 10.4). You may have to go to "Data, Refresh data" in order to have your new variable show up in the main window variable list (or just press the "r" key).

Alternatively, the same could have been accomplished by the script

```
include pc.gfn
open np
foo = pc(iprod)
```

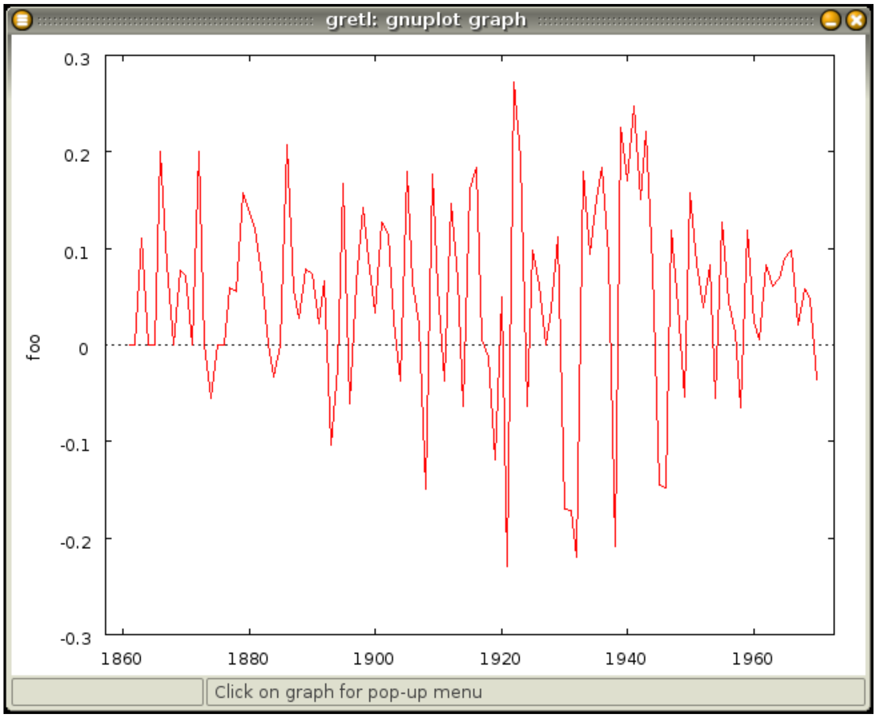


**Figure 10.4**: Percent change in industrial production

Chapter 11

# Named lists and strings

## 11.1 Named lists

Many gretl commands take one or more lists of series as arguments. To make this easier to handle in the context of command scripts, and in particular within user-defined functions, gretl offers the possibility of *named lists*.

### Creating and modifying named lists

A named list is created using the keyword list, followed by the name of the list, an equals sign, and an expression that forms a list. The most basic sort of expression that works in this context is a space-separated list of variables, given either by name or by ID number. For example,

```
list xlist = 1 2 3 4
list reglist = income price
```

Note that the variables in question must be of the series type: you can't include scalars in a named list.

Two special forms are available:

- If you use the keyword null on the right-hand side, you get an empty list.
- If you use the keyword dataset on the right, you get a list containing all the series in the current dataset (except the pre-defined const).

The name of the list must start with a letter, and must be composed entirely of letters, numbers or the underscore character. The maximum length of the name is 15 characters; list names cannot contain spaces.

Once a named list has been created, it will be "remembered" for the duration of the gretl session, and can be used in the context of any gretl command where a list of variables is expected. One simple example is the specification of a list of regressors:

```
list xlist = x1 x2 x3 x4
ols y 0 xlist
```

To get rid of a list, you can use the following syntax:

```
  list xlist delete
```

Be careful: delete xlist will delete the variables contained in the list, so it implies data loss (which may not be what you want). On the other hand, list xlist delete will simply "undefine" the xlist identifier and the variables themselves will not be affected.

Lists can be modified in two ways. To *redefine* an existing list altogether, use the same syntax as for creating a list. For example

```
list xlist = 1 2 3
xlist = 4 5 6
```

After the second assignment, `xlist` contains just variables 4, 5 and 6.

To *append* or *prepend* variables to an existing list, we can make use of the fact that a named list stands in for a “longhand” list. For example, we can do

```
list xlist = xlist 5 6 7
xlist = 9 10 xlist 11 12
```

Another option for appending a term (or a list) to an existing list is to use +=, as in

```
xlist += cpi
```

To drop a variable from a list, use -=:

```
xlist -= cpi
```

In most contexts where lists are used in gretl, it is expected that they do not contain any duplicated elements. If you form a new list by simple concatenation, as in `list L3 = L1 L2` (where `L1` and `L2` are existing lists), it’s possible that the result may contain duplicates. To guard against this you can form a new list as the union of two existing ones:

```
list L3 = L1 || L2
```

The result is a list that contains all the members of `L1`, plus any members of `L2` that are not already in `L1`.

In the same vein, you can construct a new list as the intersection of two existing ones:

```
list L3 = L1 && L2
```

Here `L3` contains all the elements that are present in both `L1` and `L2`.

### Lists and matrices

Another way of forming a list is by assignment from a matrix. The matrix in question must be interpretable as a vector containing ID numbers of (series) variables. It may be either a row or a column vector, and each of its elements must have an integer part that is no greater than the number of variables in the data set. For example:

```
matrix m = {1,2,3,4}
list L = m
```

The above is OK provided the data set contains at least 4 variables.

### Querying a list

You can determine whether an unknown variable actually represents a list using the function `islist()`.

```
series xl1 = log(x1)
series xl2 = log(x2)
list xlogs = xl1 xl2
genr is1 = islist(xlogs)
genr is2 = islist(xl1)
```

The first `genr` command above will assign a value of 1 to `is1` since `xlogs` is in fact a named list. The second genr will assign 0 to `is2` since `xl1` is a data series, not a list.

You can also determine the number of variables or elements in a list using the function `nelem()`.

```
list xlist = 1 2 3
nl = nelem(xlist)
```

The (scalar) variable `nl` will be assigned a value of 3 since `xlist` contains 3 members.

You can display the membership of a named list just by giving its name, as illustrated in this interactive session:

```
? list xlist = x1 x2 x3
Added list 'xlist'
? xlist
 x1 x2 x3
```

Note that `print xlist` will do something different, namely print the values of all the variables in `xlist` (as should be expected).

### Generating lists of transformed variables

Given a named list of variables, you are able to generate lists of transformations of these variables using the functions `log`, `lags`, `diff`, `ldiff`, `sdiff` or `dummify`. For example

```
list xlist = x1 x2 x3
list lxlist = log(xlist)
list difflist = diff(xlist)
```

When generating a list of *lags* in this way, you specify the maximum lag order inside the parentheses, before the list name and separated by a comma. For example

```
list xlist = x1 x2 x3
list laglist = lags(2, xlist)
```

or

```
scalar order = 4
list laglist = lags(order, xlist)
```

These commands will populate `laglist` with the specified number of lags of the variables in `xlist`. You can give the name of a single series in place of a list as the second argument to `lags`: this is equivalent to giving a list with just one member.

The `dummify` function creates a set of dummy variables coding for all but one of the distinct values taken on by the original variable, which should be discrete. (The smallest value is taken as the omitted catgory.) Like lags, this function returns a list even if the input is a single series.

### Generating series from lists

Once a list is defined, gretl offers several functions that apply to the list and return a series. In most cases, these functions also apply to single series and behave as natural extensions when applied to a list, but this is not always the case.

For recognizing and handling missing values, Gretl offers several functions (see the *Gretl Command Reference* for details). In this context, it is worth remarking that the `ok()` function can be used with a list argument. For example,

```
list xlist = x1 x2 x3
series xok = ok(xlist)
```

| | YpcFR | YpcGE | YpcIT | NFR | NGE | NIT |
|---|---|---|---|---|---|---|
| 1997 | 114.9 | 124.6 | 119.3 | 59830.635 | 82034.771 | 56890.372 |
| 1998 | 115.3 | 122.7 | 120.0 | 60046.709 | 82047.195 | 56906.744 |
| 1999 | 115.0 | 122.4 | 117.8 | 60348.255 | 82100.243 | 56916.317 |
| 2000 | 115.6 | 118.8 | 117.2 | 60750.876 | 82211.508 | 56942.108 |
| 2001 | 116.0 | 116.9 | 118.1 | 61181.560 | 82349.925 | 56977.217 |
| 2002 | 116.3 | 115.5 | 112.2 | 61615.562 | 82488.495 | 57157.406 |
| 2003 | 112.1 | 116.9 | 111.0 | 62041.798 | 82534.176 | 57604.658 |
| 2004 | 110.3 | 116.6 | 106.9 | 62444.707 | 82516.260 | 58175.310 |
| 2005 | 112.4 | 115.1 | 105.1 | 62818.185 | 82469.422 | 58607.043 |
| 2006 | 111.9 | 114.2 | 103.3 | 63195.457 | 82376.451 | 58941.499 |

**Table 11.1**: GDP per capita and population in 3 European countries (Source: Eurostat)

After these commands, the series xok will have value 1 for observations where none of x1, x2, or x3 has a missing value, and value 0 for any observations where this condition is not met.

The functions max, min, mean, sd, sum and var behave horizontally rather than vertically when their argument is a list. For instance, the following commands

```
list Xlist = x1 x2 x3
series m = mean(Xlist)
```

produce a series m whose $i$-th element is the average of $x_{1,i}, x_{2,i}$ and $x_{3,i}$; missing values, if any, are implicitly discarded.

In addition, gretl provides three functions for weighted operations: wmean, wsd and wvar. Consider as an illustration Table 11.1: the first three columns are GDP per capita for France, Germany and Italy; columns 4 to 6 contain the population for each country. If we want to compute an aggregate indicator of per capita GDP, all we have to do is

```
list Ypc = YpcFR YpcGE YpcIT
list N = NFR NGE NIT
y = wmean(Ypc, N)
```

so for example

$$y_{1996} = \frac{114.9 \times 59830.635 + 124.6 \times 82034.771 + 119.3 \times 56890.372}{59830.635 + 82034.771 + 56890.372} = 120.163$$

See the *Gretl Command Reference* for more details.

## 11.2 Named strings

For some purposes it may be useful to save a string (that is, a sequence of characters) as a named variable that can be reused. Versions of gretl higher than 1.6.0 offer this facility, but some of the refinements noted below are available only in gretl 1.7.2 and higher.

To *define* a string variable, you can use either of two commands, string or sprintf. The string command is simpler: you can type, for example,

```
string s1 = "some stuff I want to save"
string s2 = getenv("HOME")
string s3 = s1 + 11
```

The first field after `string` is the name under which the string should be saved, then comes an equals sign, then comes a specification of the string to be saved. This can be the keyword `null`, to produce an empty string, or may take any of the following forms:

- a string literal (enclosed in double quotes); or
- the name of an existing string variable; or
- a function that returns a string (see below); or
- any of the above followed by + and an integer offset.

The role of the integer offset is to use a substring of the preceding element, starting at the given character offset. An empty string is returned if the offset is greater than the length of the string in question.

To add to the end of an existing string you can use the operator +=, as in

```
string s1 = "some stuff I want to "
string s1 += "save"
```

or you can use the ~ operator to join two or more strings, as in

```
string s1 = "sweet"
string s2 = "Home, " ~ s1 ~ " home."
```

The `sprintf` command is more flexible. It works exactly as gretl's `printf` command except that the "format" string must be preceded by the name of a string variable. For example,

```
scalar x = 8
sprintf foo "var%d", x
```

To use the *value* of a string variable in a command, give the name of the variable preceded by the "at" sign, `@`. This notation is treated as a "macro". That is, if a sequence of characters in a gretl command following the symbol `@` is recognized as the name of a string variable, the value of that variable is sustituted literally into the command line before the regular parsing of the command is carried out. This is illustrated in the following interactive session:

```
? scalar x = 8
 scalar x = 8
Generated scalar x (ID 2) = 8
? sprintf foo "var%d", x
Saved string as 'foo'
? print "@foo"
var8
```

Note the effect of the quotation marks in the line `print "@foo"`. The line

```
? print @foo
```

would *not* print a literal "`var8`" as above. After pre-processing the line would read

```
print var8
```

It would therefore print the value(s) of the variable `var8`, if such a variable exists, or would generate an error otherwise.

In some contexts, however, one wants to treat string variables as variables in their own right: to do this, give the name of the variable without a leading `@` symbol. This is the way to handle such variables in the following contexts:

- When they appear among the arguments to the commands printf and sprintf.
- On the right-hand side of a string assignment.
- When they appear as an argument to the function taking a string argument.

Here is an illustration of the use of named string arguments with printf:

```
string vstr = "variance"
Generated string vstr
printf "vstr: %12s\n", vstr
vstr:     variance
```

Note that vstr should not be put in quotes in this context. Similarly with

```
? string vstr_copy = vstr
```

### Built-in strings

Apart from any strings that the user may define, some string variables are defined by gretl itself. These may be useful for people writing functions that include shell commands. The built-in strings are as shown in Table 11.2.

| | |
|---|---|
| gretldir | the gretl installation directory |
| workdir | user's current gretl working directory |
| dotdir | the directory gretl uses for temporary files |
| gnuplot | path to, or name of, the gnuplot executable |
| tramo | path to, or name of, the tramo executable |
| x12a | path to, or name of, the x-12-arima executable |
| tramodir | tramo data directory |
| x12adir | x-12-arima data directory |

**Table 11.2**: Built-in string variables

### Reading strings from the environment

In addition, it is possible to read into gretl's named strings, values that are defined in the external environment. To do this you use the function getenv, which takes the name of an environment variable as its argument. For example:

```
? string user = getenv("USER")
Saved string as 'user'
? string home = getenv("HOME")
Saved string as 'home'
? print "@user's home directory is @home"
cottrell's home directory is /home/cottrell
```

To check whether you got a non-empty value from a given call to getenv, you can use the function strlen, which retrieves the length of the string, as in

```
? string temp = getenv("TEMP")
Saved empty string as 'temp'
? scalar x = strlen(temp)
Generated scalar x (ID 2) = 0
```

The function `isstring` returns 1 if its argument is the name of a string variable, 0 otherwise. However, if the return is 1 the string may still be empty.

At present the `getenv` function can only be used on the right-hand side of a `string` assignment, as in the above illustrations.

### Capturing strings via the shell

If shell commands are enabled in gretl, you can capture the output from such commands using the syntax

`string` *stringname* = `$(`*shellcommand*`)`

That is, you enclose a shell command in parentheses, preceded by a dollar sign.

### Reading from a file into a string

You can read the content of a file into a string variable using the syntax

`string` *stringname* = `readfile(`*filename*`)`

The *filename* field may include components that are string variables. For example

`string foo = readfile(x12adir/QNC.rts)`

### The `strstr` function

Invocation of this function takes the form

`string` *stringname* = `strstr(`*s1*`,` *s2*`)`

The effect is to search *s1* for the first occurrence of *s2*. If no such occurrence is found, an empty string is returned; otherwise the portion of *s1* starting with *s2* is returned. For example:

```
? string hw = "hello world"
Saved string as 'hw'
? string w = strstr(hw, "o")
Saved string as 'w'
? print "@w"
o world
```

Chapter 12

# Matrix manipulation

Together with the other two basic types of data (series and scalars), gretl offers a quite comprehensive array of matrix methods. This chapter illustrates the peculiarities of matrix syntax and discusses briefly some of the more complex matrix functions. For a full listing of matrix functions and a comprehensive account of their syntax, please refer to the *Gretl Command Reference*.

## 12.1 Creating matrices

Matrices can be created using any of these methods:

1. By direct specification of the scalar values that compose the matrix — in numerical form, by reference to pre-existing scalar variables, or using computed values.
2. By providing a list of data series.
3. By providing a *named list* of series.
4. Using a formula of the same general type that is used with the genr command, whereby a new matrix is defined in terms of existing matrices and/or scalars, or via some special functions.

To specify a matrix *directly in terms of scalars*, the syntax is, for example:

```
matrix A = { 1, 2, 3 ; 4, 5, 6 }
```

The matrix is defined by rows; the elements on each row are separated by commas and the rows are separated by semi-colons. The whole expression must be wrapped in braces. Spaces within the braces are not significant. The above expression defines a $2 \times 3$ matrix. Each element should be a numerical value, the name of a scalar variable, or an expression that evaluates to a scalar. Directly after the closing brace you can append a single quote (') to obtain the transpose.

To specify a matrix *in terms of data series* the syntax is, for example,

```
matrix A = { x1, x2, x3 }
```

where the names of the variables are separated by commas. Besides names of existing variables, you can use expressions that evaluate to a series. For example, given a series x you could do

```
matrix A = { x, x^2 }
```

Each variable occupies a column (and there can only be one variable per column). You cannot use the semi-colon as a row separator in this case: if you want the series arranged in rows, append the transpose symbol. The range of data values included in the matrix depends on the current setting of the sample range.

☞ While gretl's built-in statistical functions for data series are capable of handling missing values, the matrix arithmetic functions are not. When you build a matrix from series that include missing values, observations for which at least one series has a missing value are skipped.

Instead of giving an explicit list of variables, you may instead provide the *name of a saved list* (see Chapter 11), as in

```
list xlist = x1 x2 x3
matrix A = { xlist }
```

When you provide a named list, the data series are by default placed in columns, as is natural in an econometric context: if you want them in rows, append the transpose symbol.

As a special case of constructing a matrix from a list of variables, you can say

```
matrix A = { dataset }
```

This builds a matrix using all the series in the current dataset, apart from the constant (variable 0). When this dummy list is used, it must be the sole element in the matrix definition `{...}`. You can, however, create a matrix that includes the constant along with all other variables using horizontal concatenation (see below), as in

```
matrix A = {const}~{dataset}
```

The syntax

```
matrix A = {}
```

creates an empty matrix — a matrix with zero rows and zero columns. See section 12.2 for a discussion of this object.

☞ Names of matrices must satisfy the same requirements as names of gretl variables in general: the name can be no longer than 15 characters, must start with a letter, and must be composed of nothing but letters, numbers and the underscore character.

## 12.2 Empty matrices

The main purpose of the concept of an empty matrix is to enable the user to define a starting point for subsequent concatenation operations. For instance, if X is an already defined matrix of any size, the commands

```
  matrix A = {}
  matrix B = A ~ X
```

result in a matrix B identical to X.

From an algebraic point of view, one can make sense of the idea of an empty matrix in terms of vector spaces: if a matrix is an ordered set of vectors, then A={} is the empty set. As a consequence, operations involving addition and multiplications don't have any clear meaning (arguably, they have none at all), but operations involving the cardinality of this set (that is, the dimension of the space spanned by A) are meaningful.

Legal operations on empty matrices are listed in Table 12.1. (All other matrix operations generate an error when an empty matrix is given as an argument.) In line with the above interpretation, some matrix functions return an empty matrix under certain conditions: the functions `diag, vec, vech, unvech` when the arguments is an empty matrix; the functions `I, ones, zeros, mnormal, muniform` when one or more of the arguments is 0; and the function `nullspace` when its argument has full column rank.

## 12.3 Selecting sub-matrices

You can select sub-matrices of a given matrix using the syntax

A[*rows*,*cols*]

where *rows* can take any of these forms:

| *Function* | *Return value* |
|---|---|
| `A', transp(A)` | A |
| `rows(A)` | 0 |
| `cols(A)` | 0 |
| `rank(A)` | 0 |
| `det(A)` | NA |
| `ldet(A)` | NA |
| `tr(A)` | NA |
| `onenorm(A)` | NA |
| `infnorm(A)` | NA |
| `rcond(A)` | NA |

**Table 12.1**: Valid functions on an empty matrix, `A`

|  |  |  |
|---|---|---|
| 1. | empty | selects all rows |
| 2. | a single integer | selects the single specified row |
| 3. | two integers separated by a colon | selects a range of rows |
| 4. | the name of a matrix | selects the specified rows |

With regard to option 2, the integer value can be given numerically, as the name of an existing scalar variable, or as an expression that evaluates to a scalar. With the option 4, the index matrix given in the *rows* field must be either $p \times 1$ or $1 \times p$, and should contain integer values in the range 1 to $n$, where $n$ is the number of rows in the matrix from which the selection is to be made.

The *cols* specification works in the same way, *mutatis mutandis*. Here are some examples.

```
matrix B = A[1,]
matrix B = A[2:3,3:5]
matrix B = A[2,2]
matrix idx = { 1, 2, 6 }
matrix B = A[idx,]
```

The first example selects row 1 from matrix `A`; the second selects a $2\times3$ submatrix; the third selects a scalar; and the fourth selects rows 1, 2, and 6 from matrix `A`.

In addition there is a pre-defined index specification, `diag`, which selects the principal diagonal of a square matrix, as in `B[diag]`, where `B` is square.

You can use selections of this sort on either the right-hand side of a matrix-generating formula or the left. Here is an example of use of a selection on the right, to extract a $2 \times 2$ submatrix $B$ from a $3 \times 3$ matrix $A$:

```
matrix A = { 1, 2, 3; 4, 5, 6; 7, 8, 9 }
matrix B = A[1:2,2:3]
```

And here are examples of selection on the left. The second line below writes a $2 \times 2$ identity matrix into the bottom right corner of the $3 \times 3$ matrix $A$. The fourth line replaces the diagonal of $A$ with 1s.

```
matrix A = { 1, 2, 3; 4, 5, 6; 7, 8, 9 }
matrix A[2:3,2:3] = I(2)
matrix d = { 1, 1, 1 }
matrix A[diag] = d
```

## 12.4 Matrix operators

The following binary operators are available for matrices:

| | |
|---|---|
| + | addition |
| - | subtraction |
| * | ordinary matrix multiplication |
| ’ | pre-multiplication by transpose |
| / | matrix “division” (see below) |
| ~ | column-wise concatenation |
| \| | row-wise concatenation |
| ** | Kronecker product |
| = | test for equality |

In addition, the following operators (“dot” operators) apply on an element-by-element basis:

```
.+   .-   .*   ./   .^   .=   .>   .<
```

Here are explanations of the less obvious cases.

For matrix addition and subtraction, in general the two matrices have to be of the same dimensions but an exception to this rule is granted if one of the operands is a $1 \times 1$ matrix or scalar. The scalar is implicitly promoted to the status of a matrix of the correct dimensions, all of whose elements are equal to the given scalar value. For example, if $A$ is an $m \times n$ matrix and $k$ a scalar, then the commands

```
matrix C = A + k
matrix D = A - k
```

both produce $m \times n$ matrices, with elements $c_{ij} = a_{ij} + k$ and $d_{ij} = a_{ij} - k$ respectively.

By “pre-multiplication by transpose” we mean, for example, that

```
matrix C = X’Y
```

produces the product of $X$-transpose and $Y$. In effect, the expression X’Y is shorthand for X’*Y (which is also valid).

In matrix “division”, the statement

```
matrix C = A/B
```

is interpreted as a request to find the matrix $C$ that solves $BC = A$. If $B$ is a square matrix, this is treated as equivalent to $B^{-1}A$, which fails if $B$ is singular; the numerical method employed here is the LU decomposition. If $B$ is a $T \times k$ matrix with $T > k$, then $C$ is the least-squares solution, $C = (B'B)^{-1}B'A$, which fails if $B'B$ is singular; the numerical method employed here is the QR decomposition. Otherwise, the operation necessarily fails.

In “dot” operations a binary operation is applied element by element; the result of this operation is obvious if the matrices are of the same size. However, there are several other cases where such operators may be applied. For example, if we write

```
matrix C = A .- B
```

then the result $C$ depends on the dimensions of $A$ and $B$. Let $A$ be an $m \times n$ matrix and let $B$ be $p \times q$; the result is as follows:

| *Case* | *Result* |
|---|---|
| Dimensions match ($m = p$ and $n = q$) | $c_{ij} = a_{ij} - b_{ij}$ |
| $A$ is a column vector; rows match ($m = p$; $n = 1$) | $c_{ij} = a_i - b_{ij}$ |
| $B$ is a column vector; rows match ($m = p$; $q = 1$) | $c_{ij} = a_{ij} - b_i$ |
| $A$ is a row vector; columns match ($m = 1$; $n = q$) | $c_{ij} = a_j - b_{ij}$ |
| $B$ is a row vector; columns match ($m = p$; $q = 1$) | $c_{ij} = a_{ij} - b_j$ |
| $A$ is a column vector; $B$ is a row vector ($n = 1$; $p = 1$) | $c_{ij} = a_i - b_j$ |
| $A$ is a row vector; $B$ is a column vector ($m = 1$; $q = 1$) | $c_{ij} = a_j - b_i$ |
| $A$ is a scalar ($m = 1$ and $n = 1$) | $c_{ij} = a - b_{ij}$ |
| $B$ is a scalar ($p = 1$ and $q = 1$) | $c_{ij} = a_{ij} - b$ |

If none of the above conditions are satisfied the result is undefined and an error is flagged.

Note that this convention makes it unnecessary, in most cases, to use diagonal matrices to perform transformations by means of ordinary matrix multiplication: if $Y = XV$, where $V$ is diagonal, it is computationally much more convenient to obtain $Y$ via the instruction

```
matrix Y = X .* v
```

where v is a row vector containing the diagonal of $V$.

In *column-wise concatenation* of an $m \times n$ matrix $A$ and an $m \times p$ matrix $B$, the result is an $m \times (n+p)$ matrix. That is,

```
matrix C = A ~ B
```

produces $C = \left[\begin{array}{cc} A & B \end{array}\right]$.

*Row-wise concatenation* of an $m \times n$ matrix $A$ and an $p \times n$ matrix $B$ produces an $(m + p) \times n$ matrix. That is,

```
matrix C = A | B
```

produces $C = \left[\begin{array}{c} A \\ B \end{array}\right]$.

## 12.5 Matrix-scalar operators

For matrix $A$ and scalar $k$, the operators shown in Table 12.2 are available. (Addition and subtraction were discussed in section 12.4 but we include them in the table for completeness.) In addition, for square $A$ and integer $k \geq 0$, `B = A^k` produces a matrix $B$ which is $A$ raised to the power $k$.

## 12.6 Matrix functions

Most of the gretl functions available for scalars and series also apply to matrices in an element-by-element fashion, and as such their behavior should be pretty obvious. This is the case for functions such as `log`, `exp`, `sin`, etc. These functions have the effects documented in relation to the `genr` command. For example, if a matrix A is already defined, then

```
matrix B = sqrt(A)
```

| *Expression* | *Effect* |
|---|---|
| `matrix B = A * k` | $b_{ij} = ka_{ij}$ |
| `matrix B = A / k` | $b_{ij} = a_{ij}/k$ |
| `matrix B = k / A` | $b_{ij} = k/a_{ij}$ |
| `matrix B = A + k` | $b_{ij} = a_{ij} + k$ |
| `matrix B = A - k` | $b_{ij} = a_{ij} - k$ |
| `matrix B = k - A` | $b_{ij} = k - a_{ij}$ |
| `matrix B = A % k` | $b_{ij} = a_{ij}$ modulo $k$ |

**Table 12.2**: Matrix-scalar operators

generates a matrix such that $b_{ij} = \sqrt{a_{ij}}$. All such functions require a single matrix as argument, or an expression which evaluates to a single matrix.[1]

In this section, we review some aspects of `genr` functions that apply specifically to matrices. A full account of each function is available in the *Gretl Command Reference*.

| | | | | | |
|---|---|---|---|---|---|
| **Creation and I/O** | | | | | |
| `colnames` | `diag` | `I` | `lower` | `makemask` | `mnormal` |
| `mread` | `muniform` | `mwrite` | `ones` | `seq` | `unvech` |
| `upper` | `vec` | `vech` | `zeros` | | |
| **Shape/size/arrangement** | | | | | |
| `cols` | `dsort` | `mshape` | `msortby` | `rows` | `selifc` |
| `selifr` | `sort` | `trimr` | | | |
| **Matrix algebra** | | | | | |
| `cdiv` | `cholesky` | `cmult` | `det` | `eigengen` | `eigensym` |
| `fft` | `ffti` | `ginv` | `infnorm` | `inv` | `invpd` |
| `ldet` | `mexp` | `nullspace` | `onenorm` | `polroots` | `qform` |
| `qrdecomp` | `rank` | `rcond` | `svd` | `toepsolv` | `tr` |
| `transp` | | | | | |
| **Statistics/transformations** | | | | | |
| `cdemean` | `cum` | `imaxc` | `imaxr` | `iminc` | `iminr` |
| `maxc` | `maxr` | `mcorr` | `mcov` | `mcovg` | `meanc` |
| `meanr` | `minc` | `minr` | `mlag` | `mols` | `mpols` |
| `mxtab` | `princomp` | `quantile` | `resample` | `sdc` | `sumc` |
| `sumr` | `values` | | | | |
| **Numerical methods** | | | | | |
| `BFGSmax` | `fdjac` | | | | |
| **Transformations** | | | | | |
| `lincomb` | | | | | |

**Table 12.3**: Matrix functions by category

[1] Note that to find the "matrix square root" you need the `cholesky` function (see below); moreover, the `exp` function computes the exponential element by element, and therefore does *not* return the matrix exponential unless the matrix is diagonal — to get the matrix exponential, use `mexp`.

### Matrix reshaping

In addition to the methods discussed in sections 12.1 and 12.3, a matrix can also be created by re-arranging the elements of a pre-existing matrix. This is accomplished via the mshape function. It takes three arguments: the input matrix, $A$, and the rows and columns of the target matrix, $r$ and $c$ respectively. Elements are read from $A$ and written to the target in column-major order. If $A$ contains fewer elements than $n = r \times c$, they are repeated cyclically; if $A$ has more elements, only the first $n$ are used.

For example:

```
matrix a = mnormal(2,3)
a
matrix b = mshape(a,3,1)
b
matrix b = mshape(a,5,2)
b
```

produces

```
?   a
a

      1.2323      0.99714     -0.39078
     0.54363      0.43928     -0.48467

?   matrix b = mshape(a,3,1)
Generated matrix b
?   b
b

      1.2323
     0.54363
     0.99714

?   matrix b = mshape(a,5,2)
Replaced matrix b
?   b
b

      1.2323     -0.48467
     0.54363       1.2323
     0.99714      0.54363
     0.43928      0.99714
    -0.39078      0.43928
```

### Complex multiplication and division

Gretl has no native provision for complex numbers. However, basic operations can be performed on vectors of complex numbers by using the convention that a vector of $n$ complex numbers is represented as a $n \times 2$ matrix, where the first column contains the real part and the second the imaginary part.

Addition and subtraction are trivial; the functions cmult and cdiv compute the complex product and division, respectively, of two input matrices, $A$ and $B$, representing complex numbers. These matrices must have the same number of rows, $n$, and either one or two columns. The first column contains the real part and the second (if present) the imaginary part. The return value is an $n \times 2$ matrix, or, if the result has no imaginary part, an $n$-vector.

For example, suppose you have $z_1 = [1 + 2i, 3 + 4i]'$ and $z_2 = [1, i]'$:

```
? z1 = {1,2;3,4}
 z1 = {1,2;3,4}
Generated matrix z1
? z2 = I(2)
 z2 = I(2)
Generated matrix z2
? conj_z1 = z1 .* {1,-1}
 conj_z1 = z1 .* {1,-1}
Generated matrix conj_z1
? eval cmult(z1,z2)
 eval cmult(z1,z2)
   1    2
  -4    3

? eval cmult(z1,conj_z1)
 eval cmult(z1,conj_z1)
   5
  25
```

### Multiple returns and the `null` keyword

Some functions take one or more matrices as arguments and compute one or more matrices; these are:

| | |
|---|---|
| `eigensym` | Eigen-analysis of symmetric matrix |
| `eigengen` | Eigen-analysis of general matrix |
| `mols` | Matrix OLS |
| `qrdecomp` | QR decomposition |
| `svd` | Singular value decomposition (SVD) |

The general rule is: the “main” result of the function is always returned as the result proper. Auxiliary returns, if needed, are retrieved using pre-existing matrices, which are passed to the function as pointers (see 10.4). If such values are not needed, the pointer may be substituted with the keyword `null`.

The syntax for `qrdecomp`, `eigensym` and `eigengen` is of the form

```
matrix B = func(A, &C)
```

The first argument, `A`, represents the input data, that is, the matrix whose decomposition or analysis is required. The second argument must be either the name of an existing matrix preceded by `&` (to indicate the “address” of the matrix in question), in which case an auxiliary result is written to that matrix, or the keyword `null`, in which case the auxiliary result is not produced, or is discarded.

In case a non-null second argument is given, the specified matrix will be over-written with the auxiliary result. (It is not required that the existing matrix be of the right dimensions to receive the result.)

The function `eigensym` computes the eigenvalues, and optionally the right eigenvectors, of a symmetric $n \times n$ matrix. The eigenvalues are returned directly in a column vector of length $n$; if the eigenvectors are required, they are returned in an $n \times n$ matrix. For example:

```
matrix V
matrix E = eigensym(M, &V)
matrix E = eigensym(M, null)
```

In the first case `E` holds the eigenvalues of `M` and `V` holds the eigenvectors. In the second, `E` holds the eigenvalues but the eigenvectors are not computed.

The function eigengen computes the eigenvalues, and optionally the eigenvectors, of a general $n \times n$ matrix. The eigenvalues are returned directly in an $n \times 2$ matrix, the first column holding the real components and the second column the imaginary components.

If the eigenvectors are required (that is, if the second argument to eigengen is not null), they are returned in an $n \times n$ matrix. The column arrangement of this matrix is somewhat non-trivial: the eigenvectors are stored in the same order as the eigenvalues, but the real eigenvectors occupy one column, whereas complex eigenvectors take two (the real part comes first); the total number of columns is still $n$, because the conjugate eigenvector is skipped. Example 12.1 provides a (hopefully) clarifying example (see also subsection 12.6).

**Example 12.1**: Complex eigenvalues and eigenvectors

```
set seed 34756

matrix v
A = mnormal(3,3)

/* do the eigen-analysis */
l = eigengen(A,&v)
/* eigenvalue 1 is real, 2 and 3 are complex conjugates */
print l
print v

/*
  column 1 contains the first eigenvector (real)
*/

B = A*v[,1]
c = l[1,1] * v[,1]
/* B should equal c */
print B
print c


/*
  columns 2:3 contain the real and imaginary parts
  of eigenvector 2
*/

B = A*v[,2:3]
c = cmult(ones(3,1)*(l[2,]),v[,2:3])
/* B should equal c */
print B
print c
```

The qrdecomp function computes the QR decomposition of an $m \times n$ matrix $A$: $A = QR$, where $Q$ is an $m \times n$ orthogonal matrix and $R$ is an $n \times n$ upper triangular matrix. The matrix $Q$ is returned directly, while $R$ can be retrieved via the second argument. Here are two examples:

```
matrix R
matrix Q = qrdecomp(M, &R)
matrix Q = qrdecomp(M, null)
```

In the first example, the triangular $R$ is saved as R; in the second, $R$ is discarded. The first line above shows an example of a "simple declaration" of a matrix: R is declared to be a matrix variable but is not given any explicit value. In this case the variable is initialized as a $1 \times 1$ matrix whose single element equals zero.

The syntax for svd is

```
matrix B = func(A, &C, &D)
```

The function svd computes all or part of the singular value decomposition of the real $m \times n$ matrix $A$. Let $k = \min(m, n)$. The decomposition is

$$A = U\Sigma V'$$

where $U$ is an $m \times k$ orthogonal matrix, $\Sigma$ is an $k \times k$ diagonal matrix, and $V$ is an $k \times n$ orthogonal matrix.[2] The diagonal elements of $\Sigma$ are the singular values of $A$; they are real and non-negative, and are returned in descending order. The first $k$ columns of $U$ and $V$ are the left and right singular vectors of $A$.

The svd function returns the singular values, in a vector of length $k$. The left and/or right singular vectors may be obtained by supplying non-null values for the second and/or third arguments respectively. For example:

```
matrix s = svd(A, &U, &V)
matrix s = svd(A, null, null)
matrix s = svd(A, null, &V)
```

In the first case both sets of singular vectors are obtained, in the second case only the singular values are obtained; and in the third, the right singular vectors are obtained but $U$ is not computed. *Please note*: when the third argument is non-null, it is actually $V'$ that is provided. To reconstitute the original matrix from its SVD, one can do:

```
matrix s = svd(A, &U, &V)
matrix B = (U.*s)*V
```

Finally, the syntax for mols is

```
matrix B = mols(Y, X, &U)
```

This function returns the OLS estimates obtained by regressing the $T \times n$ matrix $Y$ on the $T \times k$ matrix $X$, that is, a $k \times n$ matrix holding $(X'X)^{-1}X'Y$. The Cholesky decomposition is used. The matrix $U$, if not null, is used to store the residuals.

### Reading and writing matrices from/to text files

The two functions mread and mwrite can be used for basic matrix input/output. This can be useful to enable gretl to exchange data with other programs.

The mread function accepts one string parameter: the name of the (plain text) file from which the matrix is to be read. The file in question must conform to the following rules:

1. The columns must be separated by spaces or tab characters.

2. The decimal separator must be the dot "." character.

3. The first line in the file must contain two integers, separated by a space or a tab, indicating the number of rows and columns, respectively.

[2] This is not the only definition of the SVD: some writers define $U$ as $m \times m$, $\Sigma$ as $m \times n$ (with $k$ non-zero diagonal elements) and $V$ as $n \times n$.

Should an error occur (such as the file being badly formatted or inaccessible), an empty matrix (see section 12.2) is returned.

The complementary function `mwrite` produces text files formatted as described above. The column separator is the tab character, so import into spreadsheets should be straightforward. Usage is illustrated in example 12.2. Matrices stored via the `mwrite` command can be easily read by other programs; the following table summarizes the appropriate commands for reading a matrix A from a file called `a.mat` in some widely-used programs.[3]

| Program | Sample code |
|---:|---|
| GAUSS | `tmp[] = load a.mat;` |
| | `A = reshape(tmp[3:rows(tmp)],tmp[1],tmp[2]);` |
| Octave | `fd = fopen("a.mat");` |
| | `[r,c] = fscanf(fd, "%d %d", "C");` |
| | `A = reshape(fscanf(fd, "%g", r*c),c,r)’;` |
| | `fclose(fd);` |
| Ox | `decl A = loadmat("a.mat");` |
| R | `A <- as.matrix(read.table("a.mat", skip=1))` |

**Example 12.2**: Matrix input/output via text files

```
nulldata 64
scalar n = 3
string f1 = "a.csv"
string f2 = "b.csv"

matrix a = mnormal(n,n)
matrix b = inv(a)

err = mwrite(a, f1)

if err != 0
  fprintf "Failed to write %s\n", f1
else
  err = mwrite(b, f2)
endif

if err != 0
  fprintf "Failed to write %s\n", f2
else
  c = mread(f1)
  d = mread(f2)
  a = c*d
  printf "The following matrix should be an identity matrix\n"
  print a
endif
```

[3] Matlab users may find the Octave example helpful, since the two programs are mostly compatible with one another.

## 12.7 Matrix accessors

In addition to the matrix functions discussed above, various "accessor" strings allow you to create copies of internal matrices associated with models previously estimated. These are set out in Table 12.4.

| | |
|---|---|
| `$coeff` | vector of estimated coefficients |
| `$compan` | companion matrix (after VAR or VECM estimation) |
| `$jalpha` | matrix $\alpha$ (loadings) from Johansen's procedure |
| `$jbeta` | matrix $\beta$ (cointegration vectors) from Johansen's procedure |
| `$jvbeta` | covariance matrix for the unrestricted elements of $\beta$ from Johansen's procedure |
| `$rho` | autoregressive coefficients for error process |
| `$sigma` | residual covariance matrix |
| `$stderr` | vector of estimated standard errors |
| `$uhat` | matrix of residuals |
| `$vcv` | covariance matrix of parameter estimates |
| `$yhat` | matrix of fitted values |

**Table 12.4**: Matrix accessors for model data

Many of the accessors in Table 12.4 behave somewhat differently depending on the sort of model that is referenced, as follows:

- Single-equation models: `$sigma` gets a scalar (the standard error of the residuals); `$uhat` and `$yhat` get series.
- All system estimators: `$sigma` gets the cross-equation residual covariance matrix, `$uhat` gets a matrix of residuals, one column per equation.
- VARs and VECMs: `$stderr` and `$yhat` are not available; `$coeff` gets a matrix of coefficients, one column per equation.

If the accessors are given without any prefix, they retrieve results from the last model estimated, if any. Alternatively, they may be prefixed with the name of a saved model plus a period (`.`), in which case they retrieve results from the specified model. Here are some examples:

```
matrix u = $uhat
matrix b = m1.$coeff
matrix v2 = m1.$vcv[1:2,1:2]
```

The first command grabs the residuals from the last model; the second grabs the coefficient vector from model `m1`; and the third (which uses the mechanism of sub-matrix selection described above) grabs a portion of the covariance matrix from model `m1`.

If the model in question a VAR or VECM (only) `$compan` returns the companion matrix.

After a vector error correction model is estimated via Johansen's procedure, the matrices `$jalpha` and `$jbeta` are also available. These have a number of columns equal to the chosen cointegration rank; therefore, the product

```
matrix Pi = $jalpha * $jbeta'
```

returns the reduced-rank estimate of $A(1)$. Since $\beta$ is automatically identified via the Phillips normalization (see section 21.5), its unrestricted elements do have a proper covariance matrix, which can be retrieved through the `$jvbeta` accessor.

## 12.8 Namespace issues

Matrices share a common namespace with data series and scalar variables. In other words, no two objects of any of these types can have the same name. It is an error to attempt to change the type of an existing variable, for example:

```
scalar x = 3
matrix x = ones(2,2) # wrong!
```

It is possible, however, to delete or rename an existing variable then reuse the name for a variable of a different type:

```
scalar x = 3
delete x
matrix x = ones(2,2) # OK
```

## 12.9 Creating a data series from a matrix

Section 12.1 above describes how to create a matrix from a data series or set of series. You may sometimes wish to go in the opposite direction, that is, to copy values from a matrix into a regular data series. The syntax for this operation is

`series` *`sname`* `=` *`mspec`*

where *`sname`* is the name of the series to create and *`mspec`* is the name of the matrix to copy from, possibly followed by a matrix selection expression. Here are two examples.

```
series s = x
series u1 = U[,1]
```

It is assumed that `x` and `U` are pre-existing matrices. In the second example the series `u1` is formed from the first column of the matrix `U`.

For this operation to work, the matrix (or matrix selection) must be a vector with length equal to either the full length of the current dataset, $n$, or the length of the current sample range, $n'$. If $n' < n$ then only $n'$ elements are drawn from the matrix; if the matrix or selection comprises $n$ elements, the $n'$ values starting at element $t_1$ are used, where $t_1$ represents the starting observation of the sample range. Any values in the series that are not assigned from the matrix are set to the missing code.

## 12.10 Matrices and lists

To facilitate the manipulation of named lists of variables (see Chapter 11), it is possible to convert between matrices and lists. In section 12.1 above we mentioned the facility for creating a matrix from a list of variables, as in

```
matrix M = { listname }
```

That formulation, with the name of the list enclosed in braces, builds a matrix whose columns hold the variables referenced in the list. What we are now describing is a different matter: if we say

```
matrix M = listname
```

(without the braces), we get a row vector whose elements are the ID numbers of the variables in the list. This special case of matrix generation cannot be embedded in a compound expression. The syntax must be as shown above, namely simple assignment of a list to a matrix.

To go in the other direction, you can include a matrix on the right-hand side of an expression that defines a list, as in

```
list Xl = M
```

where M is a matrix. The matrix must be suitable for conversion; that is, it must be a row or column vector containing non-negative whole-number values, none of which exceeds the highest ID number of a variable (series or scalar) in the current dataset.

Example 12.3 illustrates the use of this sort of conversion to “normalize” a list, moving the constant (variable 0) to first position.

**Example 12.3**: Manipulating a list

```
function normalize_list (matrix *x)
  # If the matrix (representing a list) contains var 0,
  # but not in first position, move it to first position

  if (x[1] != 0)
     scalar k = cols(x)
     loop for (i=2; i<=k; i++) --quiet
        if (x[i] = 0)
            x[i] = x[1]
            x[1] = 0
            break
         endif
     end loop
  end if
end function

open data9-7
list Xl = 2 3 0 4
matrix x = Xl
normalize_list(&x)
list Xl = x
```

## 12.11 Deleting a matrix

To delete a matrix, just write

```
delete M
```

where M is the name of the matrix to be deleted.

## 12.12 Printing a matrix

To print a matrix, the easiest way is to give the name of the matrix in question on a line by itself, which is equivalent to using the print command:

```
matrix M = mnormal(100,2)
M
print M
```

You can get finer control on the formatting of output by using the printf command: for example, the following code

```
matrix Id = I(2)
printf "%10.3f", Id
```

produces

```
? print Id
 print Id
Id (2 x 2)

  1   0
  0   1

? printf "%10.3f", Id
     1.000     0.000
     0.000     1.000
```

For presentation purposes you may wish to give titles to the columns of a matrix. For this you can use the `colnames` function: the first argument is a matrix and the second is either a named list of variables, whose names will be used as headings, or a string that contains as many space-separated substrings as the matrix has columns. For example,

```
? matrix M = mnormal(3,3)
? colnames(M, "foo bar baz")
? print M
M (3 x 3)

          foo          bar          baz
       1.7102     -0.76072     0.089406
     -0.99780      -1.9003     -0.25123
     -0.91762     -0.39237      -1.6114
```

## 12.13 Example: OLS using matrices

Example 12.4 shows how matrix methods can be used to replicate gretl’s built-in OLS functionality.

**Example 12.4**: OLS via matrix methods

```
open data4-1
matrix X = { const, sqft }
matrix y = { price }
matrix b = invpd(X’X) * X’y
print "estimated coefficient vector"
b
matrix u = y - X*b
scalar SSR = u’u
scalar s2 = SSR / (rows(X) - rows(b))
matrix V = s2 * inv(X’X)
V
matrix se = sqrt(diag(V))
print "estimated standard errors"
se
# compare with built-in function
ols price const sqft --vcv
```

# Chapter 13

# Cheat sheet

This chapter explains how to perform some common — and some not so common — tasks in gretl's scripting language. Some but not all of the techniques listed here are also available through the graphical interface. Although the graphical interface may be more intuitive and less intimidating at first, we encourage users to take advantage of the power of gretl's scripting language as soon as they feel comfortable with the program.

## 13.1 Dataset handling

### "Weird" periodicities

*Problem:* You have data sampled each 3 minutes from 9am onwards; you'll probably want to specify the hour as 20 periods.

*Solution:*

```
setobs 20 9:1 --special
```

*Comment:* Now functions like `sdiff()` ("seasonal" difference) or estimation methods like seasonal ARIMA will work as expected.

### Help, my data are backwards!

*Problem:* Gretl expects time series data to be in chronological order (most recent observation last), but you have imported third-party data that are in reverse order (most recent first).

*Solution:*

```
setobs 1 1 --cross-section
genr sortkey = -obs
dataset sortby sortkey
setobs 1 1950 --time-series
```

*Comment:* The first line is required only if the data currently have a time series interpretation: it removes that interpretation, because (for fairly obvious reasons) the `dataset sortby` operation is not allowed for time series data. The following two lines reverse the data, using the negative of the built-in index variable `obs`. The last line is just illustrative: it establishes the data as annual time series, starting in 1950.

If you have a dataset that is mostly the right way round, but a particular variable is wrong, you can reverse that variable as follows:

```
genr x = sortby(-obs, x)
```

### Dropping missing observations selectively

*Problem:* You have a dataset with many variables and want to restrict the sample to those observations for which there are no missing observations for the variables `x1`, `x2` and `x3`.

*Solution:*

```
list X = x1 x2 x3
genr sel = ok(X)
smpl sel --restrict
```

*Comment:* You can now save the file via a `store` command to preserve a subsampled version of the dataset.

### "By" operations

*Problem:* You have a discrete variable d and you want to run some commands (for example, estimate a model) by splitting the sample according to the values of d.

*Solution:*

```
matrix vd = values(d)
m = rows(vd)
loop for i=1..m
  scalar sel = vd[i]
  smpl (d=sel) --restrict --replace
  ols y const x
end loop
smpl full
```

*Comment:* The main ingredient here is a loop. You can have gretl perform as many instructions as you want for each value of d, as long as they are allowed inside a loop.

## 13.2 Creating/modifying variables

### Generating a dummy variable for a specific observation

*Problem:* Generate $d_t = 0$ for all observation but one, for which $d_t = 1$.

*Solution:*

```
  genr d = (t="1984:2")
```

*Comment:* The internal variable `t` is used to refer to observations in string form, so if you have a cross-section sample you may just use `d = (t="123")`; of course, if the dataset has data labels, use the corresponding label. For example, if you open the dataset `mrw.gdt`, supplied with gretl among the examples, a dummy variable for Italy could be generated via

```
  genr DIta = (t="Italy")
```

Note that this method does not require scripting at all. In fact, you might as well use the GUI Menu "Add/Define new variable" for the same purpose, with the same syntax.

### Generating an ARMA(1,1)

*Problem:* Generate $y_t = 0.9y_{t-1} + \varepsilon_t - 0.5\varepsilon_{t-1}$, with $\varepsilon_t \sim \mathit{NIID}(0,1)$.

*Solution:*

```
alpha = 0.9
theta = -0.5
series e = normal()
series y = 0
series y = alpha * y(-1) + e + theta * e(-1)
```

*Comment:* The statement `series y = 0` is necessary because the next statement evaluates `y` recursively, so `y[1]` must be set. Note that you must use the keyword `series` here instead of writing `genr y = 0` or simply `y = 0`, to ensure that `y` is a series and not a scalar.

### Conditional assignment

*Problem:* Generate $y_t$ via the following rule:

$$y_t = \begin{cases} x_t & \text{for} \quad d_t > a \\ z_t & \text{for} \quad d_t \leq a \end{cases}$$

*Solution:*

```
series y = (d > a) ? x : z
```

*Comment:* There are several alternatives to the one presented above. One is a brute force solution using loops. Another one, more efficient but still suboptimal, would be

```
series y = (d>a)*x + (d<=a)*z
```

However, the ternary conditional assignment operator is not only the most numerically efficient way to accomplish what we want, it is also remarkably transparent to read when one gets used to it. Some readers may find it helpful to note that the conditional assignment operator works exactly the same way as the `=IF()` function in spreadsheets.

### Generating a time index for panel datasets

*Problem:* Gretl has a `$unit` accessor, but not the equivalent for time. What should I use?

*Solution:*

```
series x = time
```

*Comment:* The special construct `genr time` and its variants are aware of whether a dataset is a panel.

## 13.3 Neat tricks

### Interaction dummies

*Problem:* You want to estimate the model $y_i = \mathbf{x}_i\beta_1 + \mathbf{z}_i\beta_2 + d_i\beta_3 + (d_i \cdot \mathbf{z}_i)\beta_4 + \varepsilon_t$, where $d_i$ is a dummy variable while $\mathbf{x}_i$ and $\mathbf{z}_i$ are vectors of explanatory variables.

*Solution:*

```
list X = x1 x2 x3
list Z = z1 z2
list dZ = null
loop foreach i Z
  series d$i = d * $i
  list dZ = dZ d$i
end loop

ols y X Z d dZ
```

*Comment:* It's amazing what string substitution can do for you, isn't it?

### Realized volatility

*Problem:* Given data by the minute, you want to compute the "realized volatility" for the hour as $RV_t = \frac{1}{60}\sum_{\tau=1}^{60} y_{t:\tau}^2$. Imagine your sample starts at time 1:1.

*Solution:*

```
smpl full
genr time
genr minute = int(time/60) + 1
genr second = time % 60
setobs minute second --panel
genr rv = psd(y)^2
setobs 1 1
smpl second=1 --restrict
store foo rv
```

*Comment:* Here we trick gretl into thinking that our dataset is a panel dataset, where the minutes are the "units" and the seconds are the "time"; this way, we can take advantage of the special function `psd()`, panel standard deviation. Then we simply drop all observations but one per minute and save the resulting data (`store foo rv` translates as "store in the gretl datafile `foo.gdt` the series `rv`").

### Looping over two paired lists

*Problem:* Suppose you have two lists with the same number of elements, and you want to apply some command to corresponding elements over a loop.

*Solution:*

```
list L1 = a b c
list L2 = x y z

k1 = 1
loop foreach i L1 --quiet
    k2 = 1
    loop foreach j L2 --quiet
        if k1=k2
            ols $i 0 $j
        endif
        k2++
    end loop
    k1++
end loop
```

*Comment:* The simplest way to achieve the result is to loop over all possible combinations and filter out the unneeded ones via an `if` condition, as above. That said, in some cases variable names can help. For example, if

```
list Lx = x1 x2 x3
list Ly = y1 y2 y3
```

looping over the integers is quite intuitive and certainly more elegant:

```
loop for i=1..3
  ols y$i const x$i
end loop
```

# Part II

# Econometric methods

## Chapter 14

# Robust covariance matrix estimation

## 14.1 Introduction

Consider (once again) the linear regression model

$$y = X\beta + u \tag{14.1}$$

where $y$ and $u$ are $T$-vectors, $X$ is a $T \times k$ matrix of regressors, and $\beta$ is a $k$-vector of parameters. As is well known, the estimator of $\beta$ given by Ordinary Least Squares (OLS) is

$$\hat{\beta} = (X'X)^{-1}X'y \tag{14.2}$$

If the condition $E(u|X) = 0$ is satisfied, this is an unbiased estimator; under somewhat weaker conditions the estimator is biased but consistent. It is straightforward to show that when the OLS estimator is unbiased (that is, when $E(\hat{\beta} - \beta) = 0$), its variance is

$$\text{Var}(\hat{\beta}) = E\left((\hat{\beta} - \beta)(\hat{\beta} - \beta)'\right) = (X'X)^{-1}X'\Omega X(X'X)^{-1} \tag{14.3}$$

where $\Omega = E(uu')$ is the covariance matrix of the error terms.

Under the assumption that the error terms are independently and identically distributed (iid) we can write $\Omega = \sigma^2 I$, where $\sigma^2$ is the (common) variance of the errors (and the covariances are zero). In that case (14.3) simplifies to the "classical" formula,

$$\text{Var}(\hat{\beta}) = \sigma^2(X'X)^{-1} \tag{14.4}$$

If the iid assumption is not satisfied, two things follow. First, it is possible in principle to construct a more efficient estimator than OLS — for instance some sort of Feasible Generalized Least Squares (FGLS). Second, the simple "classical" formula for the variance of the least squares estimator is no longer correct, and hence the conventional OLS standard errors — which are just the square roots of the diagonal elements of the matrix defined by (14.4) — do not provide valid means of statistical inference.

In the recent history of econometrics there are broadly two approaches to the problem of non-iid errors. The "traditional" approach is to use an FGLS estimator. For example, if the departure from the iid condition takes the form of time-series dependence, and if one believes that this could be modeled as a case of first-order autocorrelation, one might employ an AR(1) estimation method such as Cochrane–Orcutt, Hildreth–Lu, or Prais–Winsten. If the problem is that the error variance is non-constant across observations, one might estimate the variance as a function of the independent variables and then perform weighted least squares, using as weights the reciprocals of the estimated variances.

While these methods are still in use, an alternative approach has found increasing favor: that is, use OLS but compute standard errors (or more generally, covariance matrices) that are robust with respect to deviations from the iid assumption. This is typically combined with an emphasis on using large datasets — large enough that the researcher can place some reliance on the (asymptotic) consistency property of OLS. This approach has been enabled by the availability of cheap computing power. The computation of robust standard errors and the handling of very large datasets were daunting tasks at one time, but now they are unproblematic. The other point favoring the newer methodology is that while FGLS offers an efficiency advantage in principle, it often involves making additional statistical assumptions which may or may not be justified, which may not be easy to test rigorously, and which may threaten the consistency of the estimator — for example, the "common factor restriction" that is implied by traditional FGLS "corrections" for autocorrelated errors.

James Stock and Mark Watson's *Introduction to Econometrics* illustrates this approach at the level of undergraduate instruction: many of the datasets they use comprise thousands or tens of thousands of observations; FGLS is downplayed; and robust standard errors are reported as a matter of course. In fact, the discussion of the classical standard errors (labeled "homoskedasticity-only") is confined to an Appendix.

Against this background it may be useful to set out and discuss all the various options offered by gretl in respect of robust covariance matrix estimation. The first point to notice is that gretl produces "classical" standard errors by default (in all cases apart from GMM estimation). In script mode you can get robust standard errors by appending the `--robust` flag to estimation commands. In the GUI program the model specification dialog usually contains a "Robust standard errors" check box, along with a "configure" button that is activated when the box is checked. The configure button takes you to a configuration dialog (which can also be reached from the main menu bar: Tools → Preferences → General → HCCME). There you can select from a set of possible robust estimation variants, and can also choose to make robust estimation the default.

The specifics of the available options depend on the nature of the data under consideration — cross-sectional, time series or panel — and also to some extent the choice of estimator. (Although we introduced robust standard errors in the context of OLS above, they may be used in conjunction with other estimators too.) The following three sections of this chapter deal with matters that are specific to the three sorts of data just mentioned. Note that additional details regarding covariance matrix estimation in the context of GMM are given in chapter 18.

We close this introduction with a brief statement of what "robust standard errors" can and cannot achieve. They can provide for asymptotically valid statistical inference in models that are basically correctly specified, but in which the errors are not iid. The "asymptotic" part means that they may be of little use in small samples. The "correct specification" part means that they are not a magic bullet: if the error term is correlated with the regressors, so that the parameter estimates themselves are biased and inconsistent, robust standard errors will not save the day.

## 14.2 Cross-sectional data and the HCCME

With cross-sectional data, the most likely departure from iid errors is heteroskedasticity (non-constant variance).[1] In some cases one may be able to arrive at a judgment regarding the likely form of the heteroskedasticity, and hence to apply a specific correction. The more common case, however, is where the heteroskedasticity is of unknown form. We seek an estimator of the covariance matrix of the parameter estimates that retains its validity, at least asymptotically, in face of unspecified heteroskedasticity. It is not obvious, a priori, that this should be possible, but White (1980) showed that

$$\widehat{\mathrm{Var}}_{\mathrm{h}}(\hat{\beta}) = (X'X)^{-1}X'\hat{\Omega}X(X'X)^{-1} \tag{14.5}$$

does the trick. (As usual in statistics, we need to say "under certain conditions", but the conditions are not very restrictive.) $\hat{\Omega}$ is in this context a diagonal matrix, whose non-zero elements may be estimated using squared OLS residuals. White referred to (14.5) as a heteroskedasticity-consistent covariance matrix estimator (HCCME).

Davidson and MacKinnon (2004, chapter 5) offer a useful discussion of several variants on White's HCCME theme. They refer to the original variant of (14.5) — in which the diagonal elements of $\hat{\Omega}$ are estimated directly by the squared OLS residuals, $\hat{u}_t^2$ — as $\mathrm{HC}_0$. (The associated standard errors are often called "White's standard errors".) The various refinements of White's proposal share a

[1] In some specialized contexts spatial autocorrelation may be an issue. Gretl does not have any built-in methods to handle this and we will not discuss it here.

common point of departure, namely the idea that the squared OLS residuals are likely to be "too small" on average. This point is quite intuitive. The OLS parameter estimates, $\hat{\beta}$, satisfy by design the criterion that the sum of squared residuals,

$$\sum \hat{u}_t^2 = \sum \left(y_t - X_t\hat{\beta}\right)^2$$

is minimized for given $X$ and $y$. Suppose that $\hat{\beta} \neq \beta$. This is almost certain to be the case: even is OLS is not biased, it would be a miracle if the $\hat{\beta}$ calculated from any finite sample were exactly equal to $\beta$. But in that case the sum of squares of the true, unobserved *errors*, $\sum u_t^2 = \sum(y_t - X_t\beta)^2$ is bound to be greater than $\sum \hat{u}_t^2$. The elaborated variants on $\text{HC}_0$ take this point on board as follows:

- $\text{HC}_1$: Applies a degrees-of-freedom correction, multiplying the $\text{HC}_0$ matrix by $T/(T-k)$.
- $\text{HC}_2$: Instead of using $\hat{u}_t^2$ for the diagonal elements of $\hat{\Omega}$, uses $\hat{u}_t^2/(1-h_t)$, where $h_t = X_t(X'X)^{-1}X_t'$, the $t^{\text{th}}$ diagonal element of the projection matrix, $P$, which has the property that $P \cdot y = \hat{y}$. The relevance of $h_t$ is that if the variance of all the $u_t$ is $\sigma^2$, the expectation of $\hat{u}_t^2$ is $\sigma^2(1-h_t)$, or in other words, the ratio $\hat{u}_t^2/(1-h_t)$ has expectation $\sigma^2$. As Davidson and MacKinnon show, $0 \leq h_t < 1$ for all $t$, so this adjustment cannot reduce the the diagonal elements of $\hat{\Omega}$ and in general revises them upward.
- $\text{HC}_3$: Uses $\hat{u}_t^2/(1-h_t)^2$. The additional factor of $(1-h_t)$ in the denominator, relative to $\text{HC}_2$, may be justified on the grounds that observations with large variances tend to exert a lot of influence on the OLS estimates, so that the corresponding residuals tend to be underestimated. See Davidson and MacKinnon for a fuller explanation.

The relative merits of these variants have been explored by means of both simulations and theoretical analysis. Unfortunately there is not a clear consensus on which is "best". Davidson and MacKinnon argue that the original $\text{HC}_0$ is likely to perform worse than the others; nonetheless, "White's standard errors" are reported more often than the more sophisticated variants and therefore, for reasons of comparability, $\text{HC}_0$ is the default HCCME in gretl.

If you wish to use $\text{HC}_1$, $\text{HC}_2$ or $\text{HC}_3$ you can arrange for this in either of two ways. In script mode, you can do, for example,

```
set hc_version 2
```

In the GUI program you can go to the HCCME configuration dialog, as noted above, and choose any of these variants to be the default.

## 14.3 Time series data and HAC covariance matrices

Heteroskedasticity may be an issue with time series data too, but it is unlikely to be the only, or even the primary, concern.

One form of heteroskedasticity is common in macroeconomic time series, but is fairly easily dealt with. That is, in the case of strongly trending series such as Gross Domestic Product, aggregate consumption, aggregate investment, and so on, higher levels of the variable in question are likely to be associated with higher variability in absolute terms. The obvious "fix", employed in many macroeconometric studies, is to use the logs of such series rather than the raw levels. Provided the *proportional* variability of such series remains roughly constant over time, the log transformation is effective.

Other forms of heteroskedasticity may resist the log transformation, but may demand a special treatment distinct from the calculation of robust standard errors. We have in mind here *autoregressive conditional* heteroskedasticity, for example in the behavior of asset prices, where large disturbances to the market may usher in periods of increased volatility. Such phenomena call for specific estimation strategies, such as GARCH (see chapter 20).

Despite the points made above, some residual degree of heteroskedasticity may be present in time series data: the key point is that in most cases it is likely to be combined with serial correlation (autocorrelation), hence demanding a special treatment. In White's approach, $\hat{\Omega}$, the estimated covariance matrix of the $u_t$, remains conveniently diagonal: the variances, $E(u_t^2)$, may differ by $t$ but the covariances, $E(u_t u_s)$, are all zero. Autocorrelation in time series data means that at least some of the the off-diagonal elements of $\hat{\Omega}$ should be non-zero. This introduces a substantial complication and requires another piece of terminology; estimates of the covariance matrix that are asymptotically valid in face of both heteroskedasticity and autocorrelation of the error process are termed HAC (heteroskedasticity and autocorrelation consistent).

The issue of HAC estimation is treated in more technical terms in chapter 18. Here we try to convey some of the intuition at a more basic level. We begin with a general comment: residual autocorrelation is not so much a property of the data, as a symptom of an inadequate model. Data may be persistent though time, and if we fit a model that does not take this aspect into account properly, we end up with a model with autocorrelated disturbances. Conversely, it is often possible to mitigate or even eliminate the problem of autocorrelation by including relevant lagged variables in a time series model, or in other words, by specifying the dynamics of the model more fully. HAC estimation should *not* be seen as the first resort in dealing with an autocorrelated error process.

That said, the "obvious" extension of White's HCCME to the case of autocorrelated errors would seem to be this: estimate the off-diagonal elements of $\hat{\Omega}$ (that is, the autocovariances, $E(u_t u_s)$) using, once again, the appropriate OLS residuals: $\hat{\omega}_{ts} = \hat{u}_t \hat{u}_s$. This is basically right, but demands an important amendment. We seek a *consistent* estimator, one that converges towards the true $\Omega$ as the sample size tends towards infinity. This can't work if we allow unbounded serial dependence. Bigger samples will enable us to estimate more of the true $\omega_{ts}$ elements (that is, for $t$ and $s$ more widely separated in time) but will *not* contribute ever-increasing information regarding the maximally separated $\omega_{ts}$ pairs, since the maximal separation itself grows with the sample size. To ensure consistency, we have to confine our attention to processes exhibiting temporally limited dependence, or in other words cut off the computation of the $\hat{\omega}_{ts}$ values at some maximum value of $p = t - s$ (where $p$ is treated as an increasing function of the sample size, $T$, although it cannot increase in proportion to $T$).

The simplest variant of this idea is to truncate the computation at some finite lag order $p$, where $p$ grows as, say, $T^{1/4}$. The trouble with this is that the resulting $\hat{\Omega}$ may not be a positive definite matrix. In practical terms, we may end up with negative estimated variances. One solution to this problem is offered by The Newey–West estimator (Newey and West, 1987), which assigns declining weights to the sample autocovariances as the temporal separation increases.

To understand this point it is helpful to look more closely at the covariance matrix given in (14.5), namely,

$$(X'X)^{-1}(X'\hat{\Omega}X)(X'X)^{-1}$$

This is known as a "sandwich" estimator. The bread, which appears on both sides, is $(X'X)^{-1}$. This is a $k \times k$ matrix, and is also the key ingredient in the computation of the classical covariance matrix. The filling in the sandwich is

$$\underset{(k\times k)}{\hat{\Sigma}} = \underset{(k\times T)}{X'} \quad \underset{(T\times T)}{\hat{\Omega}} \quad \underset{(T\times k)}{X}$$

Since $\Omega = E(uu')$, the matrix being estimated here can also be written as

$$\Sigma = E(X'u\,u'X)$$

which expresses $\Sigma$ as the long-run covariance of the random $k$-vector $X'u$.

From a computational point of view, it is not necessary or desirable to store the (potentially very large) $T \times T$ matrix $\hat{\Omega}$ as such. Rather, one computes the sandwich filling by summation as

$$\hat{\Sigma} = \hat{\Gamma}(0) + \sum_{j=1}^{p} w_j \left(\hat{\Gamma}(j) + \hat{\Gamma}'(j)\right)$$

where the $k \times k$ sample autocovariance matrix $\hat{\Gamma}(j)$, for $j \geq 0$, is given by

$$\hat{\Gamma}(j) = \frac{1}{T} \sum_{t=j+1}^{T} \hat{u}_t \hat{u}_{t-j} X_t' X_{t-j}$$

and $w_j$ is the weight given to the autocovariance at lag $j > 0$.

This leaves two questions. How exactly do we determine the maximum lag length or "bandwidth", $p$, of the HAC estimator? And how exactly are the weights $w_j$ to be determined? We will return to the (difficult) question of the bandwidth shortly. As regards the weights, Gretl offers three variants. The default is the Bartlett kernel, as used by Newey and West. This sets

$$w_j = \begin{cases} 1 - \frac{j}{p+1} & j \leq p \\ 0 & j > p \end{cases}$$

so the weights decline linearly as $j$ increases. The other two options are the Parzen kernel and the Quadratic Spectral (QS) kernel. For the Parzen kernel,

$$w_j = \begin{cases} 1 - 6a_j^2 + 6a_j^3 & 0 \leq a_j \leq 0.5 \\ 2(1 - a_j)^3 & 0.5 < a_j \leq 1 \\ 0 & a_j > 1 \end{cases}$$

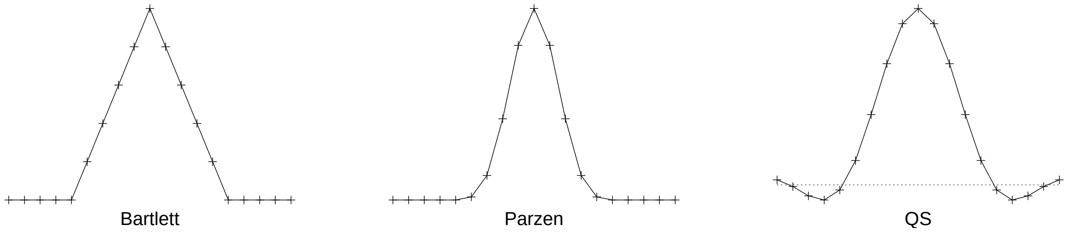
where $a_j = j/(p+1)$, and for the QS kernel,

$$w_j = \frac{25}{12\pi^2 d_j^2} \left( \frac{\sin m_j}{m_j} - \cos m_j \right)$$

where $d_j = j/p$ and $m_j = 6\pi d_i/5$.

Figure 14.1 shows the weights generated by these kernels, for $p = 4$ and $j = 1$ to 9.

**Figure 14.1**: Three HAC kernels



In gretl you select the kernel using the `set` command with the `hac_kernel` parameter:

```
set hac_kernel parzen
set hac_kernel qs
set hac_kernel bartlett
```

### Selecting the HAC bandwidth

The asymptotic theory developed by Newey, West and others tells us in general terms how the HAC bandwidth, $p$, should grow with the sample size, $T$ — that is, $p$ should grow in proportion to some fractional power of $T$. Unfortunately this is of little help to the applied econometrician, working with a given dataset of fixed size. Various rules of thumb have been suggested, and gretl implements two such. The default is $p = 0.75T^{1/3}$, as recommended by Stock and Watson (2003). An alternative is $p = 4(T/100)^{2/9}$, as in Wooldridge (2002b). In each case one takes the integer part of the result. These variants are labeled `nw1` and `nw2` respectively, in the context of the `set` command with the `hac_lag` parameter. That is, you can switch to the version given by Wooldridge with

```
set hac_lag nw2
```

As shown in Table 14.1 the choice between nw1 and nw2 does not make a great deal of difference.

| $T$ | $p$ (nw1) | $p$ (nw2) |
|---|---|---|
| 50 | 2 | 3 |
| 100 | 3 | 4 |
| 150 | 3 | 4 |
| 200 | 4 | 4 |
| 300 | 5 | 5 |
| 400 | 5 | 5 |

**Table 14.1**: HAC bandwidth: two rules of thumb

You also have the option of specifying a fixed numerical value for $p$, as in

```
set hac_lag 6
```

In addition you can set a distinct bandwidth for use with the Quadratic Spectral kernel (since this need not be an integer). For example,

```
set qs_bandwidth 3.5
```

### Prewhitening and data-based bandwidth selection

An alternative approach is to deal with residual autocorrelation by attacking the problem from two sides. The intuition behind the technique known as *VAR prewhitening* (Andrews and Monahan, 1992) can be illustrated by a simple example. Let $x_t$ be a sequence of first-order autocorrelated random variables

$$x_t = \rho x_{t-1} + u_t$$

The long-run variance of $x_t$ can be shown to be

$$V_{LR}(x_t) = \frac{V_{LR}(u_t)}{(1-\rho)^2}$$

In most cases, $u_t$ is likely to be less autocorrelated than $x_t$, so a smaller bandwidth should suffice. Estimation of $V_{LR}(x_t)$ can therefore proceed in three steps: (1) estimate $\rho$; (2) obtain a HAC estimate of $\hat{u}_t = x_t - \hat{\rho} x_{t-1}$; and (3) divide the result by $(1-\rho)^2$.

The application of the above concept to our problem implies estimating a finite-order Vector Autoregression (VAR) on the vector variables $\xi_t = X_t \hat{u}_t$. In general, the VAR can be of any order, but in most cases 1 is sufficient; the aim is not to build a watertight model for $\xi_t$, but just to "mop up" a substantial part of the autocorrelation. Hence, the following VAR is estimated

$$\xi_t = A\xi_{t-1} + \varepsilon_t$$

Then an estimate of the matrix $X'\Omega X$ can be recovered via

$$(I - \hat{A})^{-1}\hat{\Sigma}_{\varepsilon}(I - \hat{A}')^{-1}$$

where $\hat{\Sigma}_{\varepsilon}$ is any HAC estimator, applied to the VAR residuals.

You can ask for prewhitening in gretl using

```
set hac_prewhiten on
```

There is at present no mechanism for specifying an order other than 1 for the initial VAR.

A further refinement is available in this context, namely data-based bandwidth selection. It makes intuitive sense that the HAC bandwidth should not simply be based on the size of the sample, but should somehow take into account the time-series properties of the data (and also the kernel chosen). A nonparametric method for doing this was proposed by Newey and West (1994); a good concise account of the method is given in Hall (2005). This option can be invoked in gretl via

```
set hac_lag nw3
```

This option is the default when prewhitening is selected, but you can override it by giving a specific numerical value for hac_lag.

Even the Newey–West data-based method does not fully pin down the bandwidth for any particular sample. The first step involves calculating a series of residual covariances. The length of this series is given as a function of the sample size, but only up to a scalar multiple — for example, it is given as $O(T^{2/9})$ for the Bartlett kernel. Gretl uses an implied multiple of 1.

## 14.4 Special issues with panel data

Since panel data have both a time-series and a cross-sectional dimension one might expect that, in general, robust estimation of the covariance matrix would require handling both heteroskedasticity and autocorrelation (the HAC approach). In addition, some special features of panel data require attention.

- The variance of the error term may differ across the cross-sectional units.
- The covariance of the errors across the units may be non-zero in each time period.
- If the "between" variation is not removed, the errors may exhibit autocorrelation, not in the usual time-series sense but in the sense that the mean error for unit $i$ may differ from that of unit $j$. (This is particularly relevant when estimation is by pooled OLS.)

Gretl currently offers two robust covariance matrix estimators specifically for panel data. These are available for models estimated via fixed effects, pooled OLS, and pooled two-stage least squares. The default robust estimator is that suggested by Arellano (2003), which is HAC provided the panel is of the "large $n$, small $T$" variety (that is, many units are observed in relatively few periods). The Arellano estimator is

$$\hat{\Sigma}_{\mathrm{A}} = (X'X)^{-1}\left(\sum_{i=1}^{n} X_i'\hat{u}_i\hat{u}_i'X_i\right)(X'X)^{-1}$$

where $X$ is the matrix of regressors (with the group means subtracted, in the case of fixed effects) $\hat{u}_i$ denotes the vector of residuals for unit $i$, and $n$ is the number of cross-sectional units. Cameron and Trivedi (2005) make a strong case for using this estimator; they note that the ordinary White HCCME can produce misleadingly small standard errors in the panel context because it fails to take autocorrelation into account.

In cases where autocorrelation is not an issue, however, the estimator proposed by Beck and Katz (1995) and discussed by Greene (2003, chapter 13) may be appropriate. This estimator, which takes into account contemporaneous correlation across the units and heteroskedasticity by unit, is

$$\hat{\Sigma}_{\mathrm{BK}} = (X'X)^{-1}\left(\sum_{i=1}^{n}\sum_{j=1}^{n} \hat{\sigma}_{ij}X_i'X_j\right)(X'X)^{-1}$$

The covariances $\hat{\sigma}_{ij}$ are estimated via

$$\hat{\sigma}_{ij} = \frac{\hat{u}_i'\hat{u}_j}{T}$$

where $T$ is the length of the time series for each unit. Beck and Katz call the associated standard errors “Panel-Corrected Standard Errors” (PCSE). This estimator can be invoked in gretl via the command

```
set pcse on
```

The Arellano default can be re-established via

```
set pcse off
```

(Note that regardless of the `pcse` setting, the robust estimator is not used unless the `--robust` flag is given, or the “Robust” box is checked in the GUI program.)

# Chapter 15

# Panel data

## 15.1 Estimation of panel models

### Pooled Ordinary Least Squares

The simplest estimator for panel data is pooled OLS. In most cases this is unlikely to be adequate, but it provides a baseline for comparison with more complex estimators.

If you estimate a model on panel data using OLS an additional test item becomes available. In the GUI model window this is the item "panel diagnostics" under the `Tests` menu; the script counterpart is the `hausman` command.

To take advantage of this test, you should specify a model without any dummy variables representing cross-sectional units. The test compares pooled OLS against the principal alternatives, the fixed effects and random effects models. These alternatives are explained in the following section.

### The fixed and random effects models

In gretl version 1.6.0 and higher, the fixed and random effects models for panel data can be estimated in their own right. In the graphical interface these options are found under the menu item "Model/Panel/Fixed and random effects". In the command-line interface one uses the `panel` command, with or without the `--random-effects` option.

This section explains the nature of these models and comments on their estimation via gretl.

The pooled OLS specification may be written as

$$y_{it} = X_{it}\beta + u_{it} \tag{15.1}$$

where $y_{it}$ is the observation on the dependent variable for cross-sectional unit $i$ in period $t$, $X_{it}$ is a $1 \times k$ vector of independent variables observed for unit $i$ in period $t$, $\beta$ is a $k \times 1$ vector of parameters, and $u_{it}$ is an error or disturbance term specific to unit $i$ in period $t$.

The fixed and random effects models have in common that they decompose the unitary pooled error term, $u_{it}$. For the *fixed effects* model we write $u_{it} = \alpha_i + \varepsilon_{it}$, yielding

$$y_{it} = X_{it}\beta + \alpha_i + \varepsilon_{it} \tag{15.2}$$

That is, we decompose $u_{it}$ into a unit-specific and time-invariant component, $\alpha_i$, and an observation-specific error, $\varepsilon_{it}$.[1] The $\alpha_i$s are then treated as fixed parameters (in effect, unit-specific $y$-intercepts), which are to be estimated. This can be done by including a dummy variable for each cross-sectional unit (and suppressing the global constant). This is sometimes called the Least Squares Dummy Variables (LSDV) method. Alternatively, one can subtract the group mean from each of variables and estimate a model without a constant. In the latter case the dependent variable may be written as

$$\tilde{y}_{it} = y_{it} - \bar{y}_i$$

The "group mean", $\bar{y}_i$, is defined as

$$\bar{y}_i = \frac{1}{T_i}\sum_{t=1}^{T_i} y_{it}$$

[1] It is possible to break a third component out of $u_{it}$, namely $w_t$, a shock that is time-specific but common to all the units in a given period. In the interest of simplicity we do not pursue that option here.

where $T_i$ is the number of observations for unit $i$. An exactly analogous formulation applies to the independent variables. Given parameter estimates, $\hat{\beta}$, obtained using such de-meaned data we can recover estimates of the $\alpha_i$s using

$$\hat{\alpha}_i = \frac{1}{T_i} \sum_{t=1}^{T_i} \left( y_{it} - X_{it}\hat{\beta} \right)$$

These two methods (LSDV, and using de-meaned data) are numerically equivalent. Gretl takes the approach of de-meaning the data. If you have a small number of cross-sectional units, a large number of time-series observations per unit, and a large number of regressors, it is more economical in terms of computer memory to use LSDV. If need be you can easily implement this manually. For example,

```
genr unitdum
ols y x du_*
```

(See Chapter 5 for details on `unitdum`).

The $\hat{\alpha}_i$ estimates are not printed as part of the standard model output in gretl (there may be a large number of these, and typically they are not of much inherent interest). However you can retrieve them after estimation of the fixed effects model if you wish. In the graphical interface, go to the "Save" menu in the model window and select "per-unit constants". In command-line mode, you can do `genr` *newname* = `$ahat`, where *newname* is the name you want to give the series.

For the *random effects* model we write $u_{it} = v_i + \varepsilon_{it}$, so the model becomes

$$y_{it} = X_{it}\beta + v_i + \varepsilon_{it} \tag{15.3}$$

In contrast to the fixed effects model, the $v_i$s are not treated as fixed parameters, but as random drawings from a given probability distribution.

The celebrated Gauss–Markov theorem, according to which OLS is the best linear unbiased estimator (BLUE), depends on the assumption that the error term is independently and identically distributed (IID). In the panel context, the IID assumption means that $E(u_{it}^2)$, in relation to equation 15.1, equals a constant, $\sigma_u^2$, for all $i$ and $t$, while the covariance $E(u_{is}u_{it})$ equals zero for all $s \neq t$ and the covariance $E(u_{jt}u_{it})$ equals zero for all $j \neq i$.

If these assumptions are not met — and they are unlikely to be met in the context of panel data — OLS is not the most efficient estimator. Greater efficiency may be gained using generalized least squares (GLS), taking into account the covariance structure of the error term.

Consider observations on a given unit $i$ at two different times $s$ and $t$. From the hypotheses above it can be worked out that $\mathrm{Var}(u_{is}) = \mathrm{Var}(u_{it}) = \sigma_v^2 + \sigma_\varepsilon^2$, while the covariance between $u_{is}$ and $u_{it}$ is given by $E(u_{is}u_{it}) = \sigma_v^2$.

In matrix notation, we may group all the $T_i$ observations for unit $i$ into the vector $\mathbf{y}_i$ and write it as

$$\mathbf{y}_i = \mathbf{X}_i\beta + \mathbf{u}_i \tag{15.4}$$

The vector $\mathbf{u}_i$, which includes all the disturbances for individual $i$, has a variance–covariance matrix given by

$$\mathrm{Var}(\mathbf{u}_i) = \Sigma_i = \sigma_\varepsilon^2 I + \sigma_v^2 J \tag{15.5}$$

where $J$ is a square matrix with all elements equal to 1. It can be shown that the matrix

$$K_i = I - \frac{\theta}{T_i} J,$$

where $\theta = 1 - \sqrt{\frac{\sigma_\varepsilon^2}{\sigma_\varepsilon^2 + T_i\sigma_v^2}}$, has the property

$$K_i \Sigma K_i' = \sigma_\varepsilon^2 I$$

It follows that the transformed system

$$K_i \mathbf{y}_i = K_i \mathbf{X}_i \beta + K_i \mathbf{u}_i \tag{15.6}$$

satisfies the Gauss–Markov conditions, and OLS estimation of (15.6) provides efficient inference. But since

$$K_i \mathbf{y}_i = \mathbf{y}_i - \theta \bar{\mathbf{y}}_i$$

GLS estimation is equivalent to OLS using "quasi-demeaned" variables; that is, variables from which we subtract a fraction $\theta$ of their average. Notice that for $\sigma_\varepsilon^2 \to 0$, $\theta \to 1$, while for $\sigma_v^2 \to 0$, $\theta \to 0$. This means that if all the variance is attributable to the individual effects, then the fixed effects estimator is optimal; if, on the other hand, individual effects are negligible, then pooled OLS turns out, unsurprisingly, to be the optimal estimator.

To implement the GLS approach we need to calculate $\theta$, which in turn requires estimates of the variances $\sigma_\varepsilon^2$ and $\sigma_v^2$. (These are often referred to as the "within" and "between" variances respectively, since the former refers to variation within each cross-sectional unit and the latter to variation between the units). Several means of estimating these magnitudes have been suggested in the literature (see Baltagi, 1995); gretl uses the method of Swamy and Arora (1972): $\sigma_\varepsilon^2$ is estimated by the residual variance from the fixed effects model, and the sum $\sigma_\varepsilon^2 + T_i \sigma_v^2$ is estimated as $T_i$ times the residual variance from the "between" estimator,

$$\bar{y}_i = \bar{X}_i \beta + e_i$$

The latter regression is implemented by constructing a data set consisting of the group means of all the relevant variables.

### Choice of estimator

Which panel method should one use, fixed effects or random effects?

One way of answering this question is in relation to the nature of the data set. If the panel comprises observations on a fixed and relatively small set of units of interest (say, the member states of the European Union), there is a presumption in favor of fixed effects. If it comprises observations on a large number of randomly selected individuals (as in many epidemiological and other longitudinal studies), there is a presumption in favor of random effects.

Besides this general heuristic, however, various statistical issues must be taken into account.

1. Some panel data sets contain variables whose values are specific to the cross-sectional unit but which do not vary over time. If you want to include such variables in the model, the fixed effects option is simply not available. When the fixed effects approach is implemented using dummy variables, the problem is that the time-invariant variables are perfectly collinear with the per-unit dummies. When using the approach of subtracting the group means, the issue is that after de-meaning these variables are nothing but zeros.

2. A somewhat analogous prohibition applies to the random effects estimator. This estimator is in effect a matrix-weighted average of pooled OLS and the "between" estimator. Suppose we have observations on $n$ units or individuals and there are $k$ independent variables of interest. If $k > n$, the "between" estimator is undefined — since we have only $n$ effective observations — and hence so is the random effects estimator.

If one does not fall foul of one or other of the prohibitions mentioned above, the choice between fixed effects and random effects may be expressed in terms of the two econometric *desiderata*, efficiency and consistency.

From a purely statistical viewpoint, we could say that there is a tradeoff between robustness and efficiency. In the fixed effects approach, we do not make any hypotheses on the "group effects" (that is, the time-invariant differences in mean between the groups) beyond the fact that they exist

— and that can be tested; see below. As a consequence, once these effects are swept out by taking deviations from the group means, the remaining parameters can be estimated.

On the other hand, the random effects approach attempts to model the group effects as drawings from a probability distribution instead of removing them. This requires that individual effects are representable as a legitimate part of the disturbance term, that is, zero-mean random variables, uncorrelated with the regressors.

As a consequence, the fixed-effects estimator "always works", but at the cost of not being able to estimate the effect of time-invariant regressors. The richer hypothesis set of the random-effects estimator ensures that parameters for time-invariant regressors can be estimated, and that estimation of the parameters for time-varying regressors is carried out more efficiently. These advantages, though, are tied to the validity of the additional hypotheses. If, for example, there is reason to think that individual effects may be correlated with some of the explanatory variables, then the random-effects estimator would be inconsistent, while fixed-effects estimates would still be valid. It is precisely on this principle that the Hausman test is built (see below): if the fixed- and random-effects estimates agree, to within the usual statistical margin of error, there is no reason to think the additional hypotheses invalid, and as a consequence, no reason *not* to use the more efficient RE estimator.

### Testing panel models

If you estimate a fixed effects or random effects model in the graphical interface, you may notice that the number of items available under the "Tests" menu in the model window is relatively limited. Panel models carry certain complications that make it difficult to implement all of the tests one expects to see for models estimated on straight time-series or cross-sectional data.

Nonetheless, various panel-specific tests are printed along with the parameter estimates as a matter of course, as follows.

When you estimate a model using *fixed effects*, you automatically get an $F$-test for the null hypothesis that the cross-sectional units all have a common intercept. That is to say that all the $\alpha_i$s are equal, in which case the pooled model (15.1), with a column of 1s included in the $X$ matrix, is adequate.

When you estimate using *random effects*, the Breusch–Pagan and Hausman tests are presented automatically.

The Breusch–Pagan test is the counterpart to the $F$-test mentioned above. The null hypothesis is that the variance of $v_i$ in equation (15.3) equals zero; if this hypothesis is not rejected, then again we conclude that the simple pooled model is adequate.

The Hausman test probes the consistency of the GLS estimates. The null hypothesis is that these estimates are consistent — that is, that the requirement of orthogonality of the $v_i$ and the $X_i$ is satisfied. The test is based on a measure, $H$, of the "distance" between the fixed-effects and random-effects estimates, constructed such that under the null it follows the $\chi^2$ distribution with degrees of freedom equal to the number of time-varying regressors in the matrix $X$. If the value of $H$ is "large" this suggests that the random effects estimator is not consistent and the fixed-effects model is preferable.

There are two ways of calculating $H$, the matrix-difference method and the regression method. The procedure for the matrix-difference method is this:

- Collect the fixed-effects estimates in a vector $\tilde{\beta}$ and the corresponding random-effects estimates in $\hat{\beta}$, then form the difference vector $(\tilde{\beta} - \hat{\beta})$.
- Form the covariance matrix of the difference vector as $\mathrm{Var}(\tilde{\beta} - \hat{\beta}) = \mathrm{Var}(\tilde{\beta}) - \mathrm{Var}(\hat{\beta}) = \Psi$, where $\mathrm{Var}(\tilde{\beta})$ and $\mathrm{Var}(\hat{\beta})$ are estimated by the sample variance matrices of the fixed- and random-effects models respectively.[2]

[2] Hausman (1978) showed that the covariance of the difference takes this simple form when $\hat{\beta}$ is an efficient estimator

- Compute $H = \left(\tilde{\beta} - \hat{\beta}\right)' \Psi^{-1} \left(\tilde{\beta} - \hat{\beta}\right)$.

Given the relative efficiencies of $\tilde{\beta}$ and $\hat{\beta}$, the matrix $\Psi$ "should be" positive definite, in which case $H$ is positive, but in finite samples this is not guaranteed and of course a negative $\chi^2$ value is not admissible. The regression method avoids this potential problem. The procedure is:

- Treat the random-effects model as the restricted model, and record its sum of squared residuals as $\text{SSR}_r$.
- Estimate via OLS an unrestricted model in which the dependent variable is quasi-demeaned $y$ and the regressors include both quasi-demeaned $X$ (as in the RE model) and the de-meaned variants of all the time-varying variables (i.e. the fixed-effects regressors); record the sum of squared residuals from this model as $\text{SSR}_u$.
- Compute $H = n\left(\text{SSR}_r - \text{SSR}_u\right)/\text{SSR}_u$, where $n$ is the total number of observations used. On this variant $H$ cannot be negative, since adding additional regressors to the RE model cannot raise the SSR.

By default gretl computes the Hausman test via the matrix-difference method (largely for comparability with other software), but it uses the regression method if you pass the option `--hausman-reg` to the `panel` command.

### Robust standard errors

For most estimators, gretl offers the option of computing an estimate of the covariance matrix that is robust with respect to heteroskedasticity and/or autocorrelation (and hence also robust standard errors). In the case of panel data, robust covariance matrix estimators are available for the pooled and fixed effects model but not currently for random effects. Please see section 14.4 for details.

## 15.2 Dynamic panel models

Special problems arise when a lag of the dependent variable is included among the regressors in a panel model. Consider a dynamic variant of the pooled model (15.1):

$$y_{it} = X_{it}\beta + \rho y_{it-1} + u_{it} \tag{15.7}$$

First, if the error $u_{it}$ includes a group effect, $v_i$, then $y_{it-1}$ is bound to be correlated with the error, since the value of $v_i$ affects $y_i$ at all $t$. That means that OLS applied to (15.7) will be inconsistent as well as inefficient. The fixed-effects model sweeps out the group effects and so overcomes this particular problem, but a subtler issue remains, which applies to both fixed and random effects estimation. Consider the de-meaned representation of fixed effects, as applied to the dynamic model,

$$\tilde{y}_{it} = \tilde{X}_{it}\beta + \rho\tilde{y}_{i,t-1} + \varepsilon_{it}$$

where $\tilde{y}_{it} = y_{it} - \bar{y}_i$ and $\varepsilon_{it} = u_{it} - \bar{u}_i$ (or $u_{it} - \alpha_i$, using the notation of equation 15.2). The trouble is that $\tilde{y}_{i,t-1}$ will be correlated with $\varepsilon_{it}$ via the group mean, $\bar{y}_i$. The disturbance $\varepsilon_{it}$ influences $y_{it}$ directly, which influences $\bar{y}_i$, which, by construction, affects the value of $\tilde{y}_{it}$ for all $t$. The same issue arises in relation to the quasi-demeaning used for random effects. Estimators which ignore this correlation will be consistent only as $T \to \infty$ (in which case the marginal effect of $\varepsilon_{it}$ on the group mean of $y$ tends to vanish).

One strategy for handling this problem, and producing consistent estimates of $\beta$ and $\rho$, was proposed by Anderson and Hsiao (1981). Instead of de-meaning the data, they suggest taking the first difference of (15.7), an alternative tactic for sweeping out the group effects:

$$\Delta y_{it} = \Delta X_{it}\beta + \rho\Delta y_{i,t-1} + \eta_{it} \tag{15.8}$$

and $\tilde{\beta}$ is inefficient.

where $\eta_{it} = \Delta u_{it} = \Delta(v_i + \varepsilon_{it}) = \varepsilon_{it} - \varepsilon_{i,t-1}$. We're not in the clear yet, given the structure of the error $\eta_{it}$: the disturbance $\varepsilon_{i,t-1}$ is an influence on both $\eta_{it}$ and $\Delta y_{i,t-1} = y_{it} - y_{i,t-1}$. The next step is then to find an instrument for the "contaminated" $\Delta y_{i,t-1}$. Anderson and Hsiao suggest using either $y_{i,t-2}$ or $\Delta y_{i,t-2}$, both of which will be uncorrelated with $\eta_{it}$ provided that the underlying errors, $\varepsilon_{it}$, are not themselves serially correlated.

The Anderson–Hsiao estimator is not provided as a built-in function in gretl, since gretl's sensible handling of lags and differences for panel data makes it a simple application of regression with instrumental variables — see Example 15.1, which is based on a study of country growth rates by Nerlove (1999).[3]

**Example 15.1**: The Anderson–Hsiao estimator for a dynamic panel model

```
# Penn World Table data as used by Nerlove
open penngrow.gdt
# Fixed effects (for comparison)
panel Y 0 Y(-1) X
# Random effects (for comparison)
panel Y 0 Y(-1) X --random-effects
# take differences of all variables
diff Y X
# Anderson-Hsiao, using Y(-2) as instrument
tsls d_Y d_Y(-1) d_X ; 0 d_X Y(-2)
# Anderson-Hsiao, using d_Y(-2) as instrument
tsls d_Y d_Y(-1) d_X ; 0 d_X d_Y(-2)
```

Although the Anderson–Hsiao estimator is consistent, it is not most efficient: it does not make the fullest use of the available instruments for $\Delta y_{i,t-1}$, nor does it take into account the differenced structure of the error $\eta_{it}$. It is improved upon by the methods of Arellano and Bond (1991) and Blundell and Bond (1998).

Gretl implements natively the Arellano–Bond estimator. The rationale behind it is, strictly speaking, that of a GMM estimator, but it can be illustrated briefly as follows (see Arellano (2003) for a comprehensive exposition). Consider again equation (15.8): if for each individual we have observations dated from 1 to $T$, we may write the following system:

$$\Delta y_{i,3} = \Delta X_{i,3}\beta + \rho\Delta y_{i,2} + \eta_{i,3} \tag{15.9}$$

$$\Delta y_{i,4} = \Delta X_{i,4}\beta + \rho\Delta y_{i,4} + \eta_{i,4} \tag{15.10}$$

$$\vdots$$

$$\Delta y_{i,T} = \Delta X_{i,T}\beta + \rho\Delta y_{i,T} + \eta_{i,T} \tag{15.11}$$

Following the same logic as for the Anderson–Hsiao estimator, we see that the only possible instrument for $\Delta y_{i,2}$ in equation (15.9) is $y_{i,1}$, but for equation (15.10) we can use *both* $y_{i,1}$ and $y_{i,2}$ as instruments for $\Delta y_{i,3}$, thereby gaining efficiency. Likewise, for the final period $T$ we can use as instruments all values of $y_{i,t}$ up to $t = T - 2$. The Arellano–Bond technique estimates the above system, with an increasing number of instruments for each equation.

Estimation is typically carried out in two steps: in step 1 the parameters are estimated on the

[3] Also see Clint Cummins' benchmarks page, http://www.stanford.edu/~clint/bench/.

assumption that the covariance matrix of the $\eta_{i,t}$ terms is proportional to

$$\begin{bmatrix} 2 & -1 & 0 & \cdots & 0 \\ -1 & 2 & -1 & \cdots & 0 \\ 0 & -1 & 2 & \cdots & 0 \\ & \vdots & & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & 2 \end{bmatrix}$$

as should be the case if the disturbances in the original model $u_{i,t}$ were homoskedastic and uncorrelated. This yields a consistent, but not necessarily efficient, estimator.

Step 2 uses the parameters estimated in step 1 to compute an estimate of the covariance of the $\eta_{i,t}$, and re-estimates the parameters based on that. This procedure has the double effect of handling heteroskedasticity and/or serial correlation, plus producing estimators that are asymptotically efficient.

One-step estimators have sometimes been preferred on the grounds that they are more robust. Moreover, computing the covariance matrix of the 2-step estimator via the standard GMM formulae has been shown to produce grossly biased results in finite samples. Gretl, however, implements the finite-sample correction devised by Windmeijer (2005), so standard errors for the 2-step estimator can be considered relatively accurate.

By default, gretl's `arbond` command estimates the parameters in

$$A(L)y_{i,t} = X_{i,t}\beta + v_i + u_{i,t}$$

via the 1-step procedure. The dependent variable is automatically differenced (but note that the right-hand side variables are not automatically differenced), and all available instruments are used. However, these choices (plus some others) can be overridden: please see the documentation for the `arbond` command in the *Gretl Command Reference* and the `arbond91` example file supplied with gretl.

## 15.3 Panel illustration: the Penn World Table

The Penn World Table (homepage at pwt.econ.upenn.edu) is a rich macroeconomic panel dataset, spanning 152 countries over the years 1950–1992. The data are available in gretl format; please see the gretl data site (this is a free download, although it is not included in the main gretl package).

Example 15.2 opens `pwt56_60_89.gdt`, a subset of the PWT containing data on 120 countries, 1960–89, for 20 variables, with no missing observations (the full data set, which is also supplied in the pwt package for gretl, has many missing observations). Total growth of real GDP, 1960–89, is calculated for each country and regressed against the 1960 level of real GDP, to see if there is evidence for "convergence" (i.e. faster growth on the part of countries starting from a low base).

**Example 15.2**: Use of the Penn World Table

```
open pwt56_60_89.gdt
# for 1989 (the last obs), lag 29 gives 1960, the first obs
genr gdp60 = RGDPL(-29)
# find total growth of real GDP over 30 years
genr gdpgro = (RGDPL - gdp60)/gdp60
# restrict the sample to a 1989 cross-section
smpl --restrict YEAR=1989
# convergence: did countries with a lower base grow faster?
ols gdpgro const gdp60
# result: No! Try an inverse relationship?
genr gdp60inv = 1/gdp60
ols gdpgro const gdp60inv
# no again.  Try treating Africa as special?
genr afdum = (CCODE = 1)
genr afslope = afdum * gdp60
ols gdpgro const afdum gdp60 afslope
```

# Chapter 16

# Nonlinear least squares

## 16.1 Introduction and examples

Gretl supports nonlinear least squares (NLS) using a variant of the Levenberg–Marquardt algorithm. The user must supply a specification of the regression function; prior to giving this specification the parameters to be estimated must be "declared" and given initial values. Optionally, the user may supply analytical derivatives of the regression function with respect to each of the parameters. The tolerance (criterion for terminating the iterative estimation procedure) can be adjusted using the `set` command.

The syntax for specifying the function to be estimated is the same as for the `genr` command. Here are two examples, with accompanying derivatives.

**Example 16.1**: Consumption function from Greene

```
nls C = alpha + beta * Y^gamma
deriv alpha = 1
deriv beta = Y^gamma
deriv gamma = beta * Y^gamma * log(Y)
end nls
```

**Example 16.2**: Nonlinear function from Russell Davidson

```
nls y = alpha + beta * x1 + (1/beta) * x2
deriv alpha = 1
deriv beta = x1 - x2/(beta*beta)
end nls
```

Note the command words `nls` (which introduces the regression function), `deriv` (which introduces the specification of a derivative), and `end nls`, which terminates the specification and calls for estimation. If the `--vcv` flag is appended to the last line the covariance matrix of the parameter estimates is printed.

## 16.2 Initializing the parameters

The parameters of the regression function must be given initial values prior to the `nls` command. This can be done using the `genr` command (or, in the GUI program, via the menu item "Variable, Define new variable").

In some cases, where the nonlinear function is a generalization of (or a restricted form of) a linear model, it may be convenient to run an `ols` and initialize the parameters from the OLS coefficient estimates. In relation to the first example above, one might do:

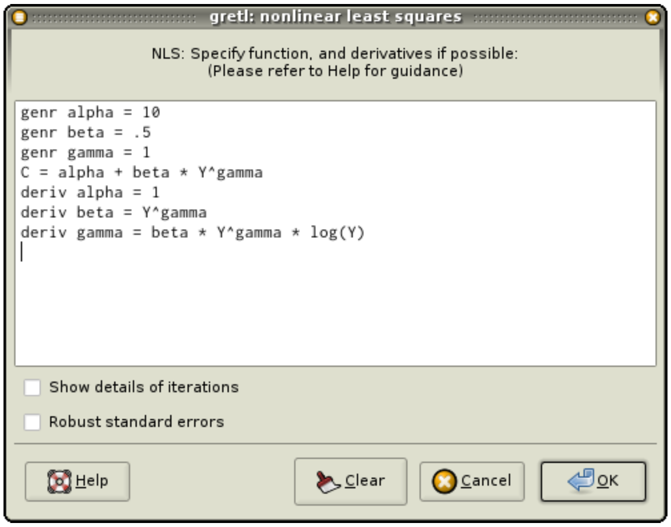
```
ols C 0 Y
genr alpha = $coeff(0)
genr beta = $coeff(Y)
genr gamma = 1
```

And in relation to the second example one might do:

```
ols y 0 x1 x2
genr alpha = $coeff(0)
genr beta = $coeff(x1)
```

## 16.3 NLS dialog window

It is probably most convenient to compose the commands for NLS estimation in the form of a gretl script but you can also do so interactively, by selecting the item "Nonlinear Least Squares" under the "Model, Nonlinear models" menu. This opens a dialog box where you can type the function specification (possibly prefaced by `genr` lines to set the initial parameter values) and the derivatives, if available. An example of this is shown in Figure 16.1. Note that in this context you do not have to supply the `nls` and `end nls` tags.



NLS: Specify function, and derivatives if possible:
(Please refer to Help for guidance)

```
genr alpha = 10
genr beta = .5
genr gamma = 1
C = alpha + beta * Y^gamma
deriv alpha = 1
deriv beta = Y^gamma
deriv gamma = beta * Y^gamma * log(Y)
```

□ Show details of iterations

□ Robust standard errors

**Figure 16.1**: NLS dialog box

## 16.4 Analytical and numerical derivatives

If you are able to figure out the derivatives of the regression function with respect to the parameters, it is advisable to supply those derivatives as shown in the examples above. If that is not possible, gretl will compute approximate numerical derivatives. The properties of the NLS algorithm may not be so good in this case (see Section 16.7).

If analytical derivatives are supplied, they are checked for consistency with the given nonlinear function. If the derivatives are clearly incorrect estimation is aborted with an error message. If the derivatives are "suspicious" a warning message is issued but estimation proceeds. This warning may sometimes be triggered by incorrect derivatives, but it may also be triggered by a high degree of collinearity among the derivatives.

Note that you cannot mix analytical and numerical derivatives: you should supply expressions for all of the derivatives or none.

## 16.5 Controlling termination

The NLS estimation procedure is an iterative process. Iteration is terminated when the criterion for convergence is met or when the maximum number of iterations is reached, whichever comes first.

Let $k$ denote the number of parameters being estimated. The maximum number of iterations is $100 \times (k + 1)$ when analytical derivatives are given, and $200 \times (k + 1)$ when numerical derivatives are used.

Let $\epsilon$ denote a small number. The iteration is deemed to have converged if at least one of the following conditions is satisfied:

- Both the actual and predicted relative reductions in the error sum of squares are at most $\epsilon$.
- The relative error between two consecutive iterates is at most $\epsilon$.

This default value of $\epsilon$ is the machine precision to the power 3/4,[1] but it can be adjusted using the `set` command with the parameter `nls_toler`. For example

```
set nls_toler .0001
```

will relax the value of $\epsilon$ to 0.0001.

## 16.6 Details on the code

The underlying engine for NLS estimation is based on the minpack suite of functions, available from netlib.org. Specifically, the following minpack functions are called:

| | |
|---|---|
| `lmder` | Levenberg–Marquardt algorithm with analytical derivatives |
| `chkder` | Check the supplied analytical derivatives |
| `lmdif` | Levenberg–Marquardt algorithm with numerical derivatives |
| `fdjac2` | Compute final approximate Jacobian when using numerical derivatives |
| `dpmpar` | Determine the machine precision |

On successful completion of the Levenberg–Marquardt iteration, a Gauss–Newton regression is used to calculate the covariance matrix for the parameter estimates. If the `--robust` flag is given a robust variant is computed. The documentation for the `set` command explains the specific options available in this regard.

Since NLS results are asymptotic, there is room for debate over whether or not a correction for degrees of freedom should be applied when calculating the standard error of the regression (and the standard errors of the parameter estimates). For comparability with OLS, and in light of the reasoning given in Davidson and MacKinnon (1993), the estimates shown in gretl *do* use a degrees of freedom correction.

## 16.7 Numerical accuracy

Table 16.1 shows the results of running the gretl NLS procedure on the 27 Statistical Reference Datasets made available by the U.S. National Institute of Standards and Technology (NIST) for testing nonlinear regression software.[2] For each dataset, two sets of starting values for the parameters

[1] On a 32-bit Intel Pentium machine a likely value for this parameter is $1.82 \times 10^{-12}$.

[2] For a discussion of gretl's accuracy in the estimation of linear models, see Appendix D.

are given in the test files, so the full test comprises 54 runs. Two full tests were performed, one using all analytical derivatives and one using all numerical approximations. In each case the default tolerance was used.[3]

Out of the 54 runs, gretl failed to produce a solution in 4 cases when using analytical derivatives, and in 5 cases when using numeric approximation. Of the four failures in analytical derivatives mode, two were due to non-convergence of the Levenberg–Marquardt algorithm after the maximum number of iterations (on MGH09 and Bennett5, both described by NIST as of "Higher difficulty") and two were due to generation of range errors (out-of-bounds floating point values) when computing the Jacobian (on BoxBOD and MGH17, described as of "Higher difficulty" and "Average difficulty" respectively). The additional failure in numerical approximation mode was on MGH10 ("Higher difficulty", maximum number of iterations reached).

The table gives information on several aspects of the tests: the number of outright failures, the average number of iterations taken to produce a solution and two sorts of measure of the accuracy of the estimates for both the parameters and the standard errors of the parameters.

For each of the 54 runs in each mode, if the run produced a solution the parameter estimates obtained by gretl were compared with the NIST certified values. We define the "minimum correct figures" for a given run as the number of significant figures to which the *least accurate* gretl estimate agreed with the certified value, for that run. The table shows both the average and the worst case value of this variable across all the runs that produced a solution. The same information is shown for the estimated standard errors.[4]

The second measure of accuracy shown is the percentage of cases, taking into account all parameters from all successful runs, in which the gretl estimate agreed with the certified value to at least the 6 significant figures which are printed by default in the gretl regression output.

**Table 16.1**: Nonlinear regression: the NIST tests

| | *Analytical derivatives* | *Numerical derivatives* |
|---|---|---|
| Failures in 54 tests | 4 | 5 |
| Average iterations | 32 | 127 |
| Mean of min. correct figures, parameters | 8.120 | 6.980 |
| Worst of min. correct figures, parameters | 4 | 3 |
| Mean of min. correct figures, standard errors | 8.000 | 5.673 |
| Worst of min. correct figures, standard errors | 5 | 2 |
| Percent correct to at least 6 figures, parameters | 96.5 | 91.9 |
| Percent correct to at least 6 figures, standard errors | 97.7 | 77.3 |

Using analytical derivatives, the worst case values for both parameters and standard errors were

[3] The data shown in the table were gathered from a pre-release build of gretl version 1.0.9, compiled with gcc 3.3, linked against glibc 2.3.2, and run under Linux on an i686 PC (IBM ThinkPad A21m).

[4] For the standard errors, I excluded one outlier from the statistics shown in the table, namely Lanczos1. This is an odd case, using generated data with an almost-exact fit: the standard errors are 9 or 10 orders of magnitude smaller than the coefficients. In this instance gretl could reproduce the certified standard errors to only 3 figures (analytical derivatives) and 2 figures (numerical derivatives).

improved to 6 correct figures on the test machine when the tolerance was tightened to 1.0e−14. Using numerical derivatives, the same tightening of the tolerance raised the worst values to 5 correct figures for the parameters and 3 figures for standard errors, at a cost of one additional failure of convergence.

Note the overall superiority of analytical derivatives: on average solutions to the test problems were obtained with substantially fewer iterations and the results were more accurate (most notably for the estimated standard errors). Note also that the six-digit results printed by gretl are not 100 percent reliable for difficult nonlinear problems (in particular when using numerical derivatives). Having registered this caveat, the percentage of cases where the results were good to six digits or better seems high enough to justify their printing in this form.

# Chapter 17

# Maximum likelihood estimation

## 17.1 Generic ML estimation with gretl

Maximum likelihood estimation is a cornerstone of modern inferential procedures. Gretl provides a way to implement this method for a wide range of estimation problems, by use of the `mle` command. We give here a few examples.

To give a foundation for the examples that follow, we start from a brief reminder on the basics of ML estimation. Given a sample of size $T$, it is possible to define the density function[1] for the whole sample, namely the joint distribution of all the observations $f(\mathbf{Y};\theta)$, where $\mathbf{Y} = \{y_1, \ldots, y_T\}$. Its shape is determined by a $k$-vector of unknown parameters $\theta$, which we assume is contained in a set $\Theta$, and which can be used to evaluate the probability of observing a sample with any given characteristics.

After observing the data, the values $\mathbf{Y}$ are given, and this function can be evaluated for any legitimate value of $\theta$. In this case, we prefer to call it the *likelihood* function; the need for another name stems from the fact that this function works as a density when we use the $y_t$s as arguments and $\theta$ as parameters, whereas in this context $\theta$ is taken as the function's argument, and the data $\mathbf{Y}$ only have the role of determining its shape.

In standard cases, this function has a unique maximum. The location of the maximum is unaffected if we consider the logarithm of the likelihood (or log-likelihood for short): this function will be denoted as

$$\ell(\theta) = \log f(\mathbf{Y};\theta)$$

The log-likelihood functions that gretl can handle are those where $\ell(\theta)$ can be written as

$$\ell(\theta) = \sum_{t=1}^{T} \ell_t(\theta)$$

which is true in most cases of interest. The functions $\ell_t(\theta)$ are called the log-likelihood contributions.

Moreover, the location of the maximum is obviously determined by the data $\mathbf{Y}$. This means that the value

$$\hat{\theta}(\mathbf{Y}) = \underset{\theta\in\Theta}{\text{Argmax}}\, \ell(\theta) \tag{17.1}$$

is some function of the observed data (a statistic), which has the property, under mild conditions, of being a consistent, asymptotically normal and asymptotically efficient estimator of $\theta$.

Sometimes it is possible to write down explicitly the function $\hat{\theta}(\mathbf{Y})$; in general, it need not be so. In these circumstances, the maximum can be found by means of numerical techniques. These often rely on the fact that the log-likelihood is a smooth function of $\theta$, and therefore on the maximum its partial derivatives should all be 0. The *gradient vector*, or *score vector*, is a function that enjoys many interesting statistical properties in its own right; it will be denoted here as $\mathbf{g}(\theta)$. It is a

[1] We are supposing here that our data are a realization of continuous random variables. For discrete random variables, everything continues to apply by referring to the probability function instead of the density. In both cases, the distribution may be conditional on some exogenous variables.

$k$-vector with typical element

$$g_i(\theta) = \frac{\partial \ell(\theta)}{\partial \theta_i} = \sum_{t=1}^{T} \frac{\partial \ell_t(\theta)}{\partial \theta_i}$$

Gradient-based methods can be shortly illustrated as follows:

1. pick a point $\theta_0 \in \Theta$;
2. evaluate $\mathbf{g}(\theta_0)$;
3. if $\mathbf{g}(\theta_0)$ is "small", stop. Otherwise, compute a direction vector $d(\mathbf{g}(\theta_0))$;
4. evaluate $\theta_1 = \theta_0 + d(\mathbf{g}(\theta_0))$;
5. substitute $\theta_0$ with $\theta_1$;
6. restart from 2.

Many algorithms of this kind exist; they basically differ from one another in the way they compute the direction vector $d(\mathbf{g}(\theta_0))$, to ensure that $\ell(\theta_1) > \ell(\theta_0)$ (so that we eventually end up on the maximum).

The method gretl uses to maximize the log-likelihood is a gradient-based algorithm known as the **BFGS** (Broyden, Fletcher, Goldfarb and Shanno) method. This technique is used in most econometric and statistical packages, as it is well-established and remarkably powerful. Clearly, in order to make this technique operational, it must be possible to compute the vector $\mathbf{g}(\theta)$ for any value of $\theta$. In some cases this vector can be written explicitly as a function of $\mathbf{Y}$. If this is not possible or too difficult the gradient may be evaluated numerically.

The choice of the starting value, $\theta_0$, is crucial in some contexts and inconsequential in others. In general, however, it is advisable to start the algorithm from "sensible" values whenever possible. If a consistent estimator is available, this is usually a safe and efficient choice: this ensures that in large samples the starting point will be likely close to $\hat{\theta}$ and convergence can be achieved in few iterations.

The maxmimum number of iterations allowed for the BFGS procedure, and the relative tolerance for assessing convergence, can be adjusted using the `set` command: the relevant variables are `bfgs_maxiter` (default value 500) and `bfgs_toler` (default value, the machine precision to the power 3/4).

### Covariance matrix and standard errors

By default the covariance matrix of the parameter estimates is based on the Outer Product of the Gradient. That is,

$$\widehat{\mathrm{Var}}_{\mathrm{OPG}}(\hat{\theta}) = \left(G'(\hat{\theta})G(\hat{\theta})\right)^{-1}$$

where $G(\hat{\theta})$ is the $T \times k$ matrix of contributions to the gradient. Two other options are available. If the `--hessian` flag is given, the covariance matrix is computed from a numerical approximation to the Hessian at convergence. If the `--robust` option is selected, the quasi-ML "sandwich" estimator is used:

$$\widehat{\mathrm{Var}}_{\mathrm{QML}}(\hat{\theta}) = H(\hat{\theta})^{-1}G'(\hat{\theta})G(\hat{\theta})H(\hat{\theta})^{-1}$$

where $H$ denotes the numerical approximation to the Hessian.

## 17.2 Gamma estimation

Suppose we have a sample of $T$ independent and identically distributed observations from a Gamma distribution. The density function for each observation $x_t$ is

$$f(x_t) = \frac{\alpha^p}{\Gamma(p)} x_t^{p-1} \exp\left(-\alpha x_t\right) \tag{17.2}$$

The log-likelihood for the entire sample can be written as the logarithm of the joint density of all the observations. Since these are independent and identical, the joint density is the product of the individual densities, and hence its log is

$$\ell(\alpha, p) = \sum_{t=1}^{T} \log\left[\frac{\alpha^p}{\Gamma(p)} x_t^{p-1} \exp\left(-\alpha x_t\right)\right] = \sum_{t=1}^{T} \ell_t \tag{17.3}$$

where

$$\ell_t = p \cdot \log(\alpha x_t) - \gamma(p) - \log x_t - \alpha x_t$$

and $\gamma(\cdot)$ is the log of the gamma function. In order to estimate the parameters $\alpha$ and $p$ via ML, we need to maximize (17.3) with respect to them. The corresponding gretl code snippet is

```
scalar alpha = 1
scalar p = 1

mle logl =  p*ln(alpha * x) - lngamma(p) - ln(x) - alpha * x
end mle
```

The two statements

```
alpha = 1
p = 1
```

are necessary to ensure that the variables `p` and `alpha` exist before the computation of `logl` is attempted. The values of these variables will be changed by the execution of the `mle` command; upon successful completion, they will be replaced by the ML estimates. The starting value is 1 for both; this is arbitrary and does not matter much in this example (more on this later).

The above code can be made more readable, and marginally more efficient, by defining a variable to hold $\alpha \cdot x_t$. This command can be embedded into the `mle` block as follows:

```
scalar alpha = 1
scalar p = 1

mle logl =  p*ln(ax) - lngamma(p) - ln(x) - ax
  series ax = alpha*x
  params alpha p
end mle
```

In this case, it is necessary to include the line `params alpha p` to set the symbols `p` and `alpha` apart from `ax`, which is a temporarily generated variable and not a parameter to be estimated.

In a simple example like this, the choice of the starting values is almost inconsequential; the algorithm is likely to converge no matter what the starting values are. However, consistent method-of-moments estimators of $p$ and $\alpha$ can be simply recovered from the sample mean $m$ and variance $V$: since it can be shown that

$$E(x_t) = p/\alpha \qquad V(x_t) = p/\alpha^2$$

it follows that the following estimators

$$\begin{aligned} \bar{\alpha} &= m/V \\ \bar{p} &= m \cdot \bar{\alpha} \end{aligned}$$

are consistent, and therefore suitable to be used as starting point for the algorithm. The gretl script code then becomes

```
scalar m = mean(x)
scalar alpha = m/var(x)
scalar p = m*alpha

mle logl =  p*ln(ax) - lngamma(p) - ln(x) - ax
  series ax = alpha*x
  params alpha p
end mle
```

Another thing to note is that sometimes parameters are constrained within certain boundaries: in this case, for example, both $\alpha$ and $p$ must be positive numbers. Gretl does not check for this: it is the user's responsibility to ensure that the function is always evaluated at an admissible point in the parameter space during the iterative search for the maximum. An effective technique is to define a variable for checking that the parameters are admissible and setting the log-likelihood as undefined if the check fails. An example, which uses the conditional assignment operator, follows:

```
scalar m = mean(x)
scalar alpha = m/var(x)
scalar p = m*alpha

mle logl = check ? p*ln(ax) - lngamma(p) - ln(x) - ax : NA
  series ax = alpha*x
  scalar check = (alpha>0) & (p>0)
params alpha p
end mle
```

## 17.3 Stochastic frontier cost function

When modeling a cost function, it is sometimes worthwhile to incorporate explicitly into the statistical model the notion that firms may be inefficient, so that the observed cost deviates from the theoretical figure not only because of unobserved heterogeneity between firms, but also because two firms could be operating at a different efficiency level, despite being identical under all other respects. In this case we may write

$$C_i = C_i^* + u_i + v_i$$

where $C_i$ is some variable cost indicator, $C_i^*$ is its "theoretical" value, $u_i$ is a zero-mean disturbance term and $v_i$ is the inefficiency term, which is supposed to be nonnegative by its very nature.

A linear specification for $C_i^*$ is often chosen. For example, the Cobb–Douglas cost function arises when $C_i^*$ is a linear function of the logarithms of the input prices and the output quantities.

The *stochastic frontier* model is a linear model of the form $y_i = x_i\beta + \varepsilon_i$ in which the error term $\varepsilon_i$ is the sum of $u_i$ and $v_i$. A common postulate is that $u_i \sim N(0, \sigma_u^2)$ and $v_i \sim \left|N(0, \sigma_v^2)\right|$. If independence between $u_i$ and $v_i$ is also assumed, then it is possible to show that the density function of $\varepsilon_i$ has the form:

$$f(\varepsilon_i) = \sqrt{\frac{2}{\pi}} \Phi\left(\frac{\lambda\varepsilon_i}{\sigma}\right) \frac{1}{\sigma} \phi\left(\frac{\varepsilon_i}{\sigma}\right) \tag{17.4}$$

where $\Phi(\cdot)$ and $\phi(\cdot)$ are, respectively, the distribution and density function of the standard normal, $\sigma = \sqrt{\sigma_u^2 + \sigma_v^2}$ and $\lambda = \frac{\sigma_u}{\sigma_v}$.

As a consequence, the log-likelihood for one observation takes the form (apart form an irrelevant constant)

$$\ell_t = \log\Phi\left(\frac{\lambda\varepsilon_i}{\sigma}\right) - \left[\log(\sigma) + \frac{\varepsilon_i^2}{2\sigma^2}\right]$$

Therefore, a Cobb–Douglas cost function with stochastic frontier is the model described by the following equations:

$$\begin{aligned}
\log C_i &= \log C_i^* + \varepsilon_i \\
\log C_i^* &= c + \sum_{j=1}^{m}\beta_j \log y_{ij} + \sum_{j=1}^{n}\alpha_j \log p_{ij} \\
\varepsilon_i &= u_i + v_i \\
u_i &\sim N(0, \sigma_u^2) \\
v_i &\sim \left|N(0, \sigma_v^2)\right|
\end{aligned}$$

In most cases, one wants to ensure that the homogeneity of the cost function with respect to the prices holds by construction. Since this requirement is equivalent to $\sum_{j=1}^{n}\alpha_j = 1$, the above equation for $C_i^*$ can be rewritten as

$$\log C_i - \log p_{in} = c + \sum_{j=1}^{m}\beta_j \log y_{ij} + \sum_{j=2}^{n}\alpha_j(\log p_{ij} - \log p_{in}) + \varepsilon_i \tag{17.5}$$

The above equation could be estimated by OLS, but it would suffer from two drawbacks: first, the OLS estimator for the intercept $c$ is inconsistent because the disturbance term has a non-zero expected value; second, the OLS estimators for the other parameters are consistent, but inefficient in view of the non-normality of $\varepsilon_i$. Both issues can be addressed by estimating (17.5) by maximum likelihood. Nevertheless, OLS estimation is a quick and convenient way to provide starting values for the MLE algorithm.

Example 17.1 shows how to implement the model described so far. The `banks91` file contains part of the data used in Lucchetti, Papi and Zazzaro (2001).

## 17.4 GARCH models

GARCH models are handled by gretl via a native function. However, it is instructive to see how they can be estimated through the `mle` command.

The following equations provide the simplest example of a GARCH(1,1) model:

$$\begin{aligned}
y_t &= \mu + \varepsilon_t \\
\varepsilon_t &= u_t \cdot \sigma_t \\
u_t &\sim N(0, 1) \\
h_t &= \omega + \alpha\varepsilon_{t-1}^2 + \beta h_{t-1}.
\end{aligned}$$

Since the variance of $y_t$ depends on past values, writing down the log-likelihood function is not simply a matter of summing the log densities for individual observations. As is common in time series models, $y_t$ cannot be considered independent of the other observations in our sample, and consequently the density function for the whole sample (the joint density for all observations) is not just the product of the marginal densities.

Maximum likelihood estimation, in these cases, is achieved by considering *conditional* densities, so what we maximize is a conditional likelihood function. If we define the information set at time $t$ as

$$F_t = \{y_t, y_{t-1}, \ldots\},$$

**Example 17.1**: Estimation of stochastic frontier cost function

```
open banks91

# Cobb-Douglas cost function

ols cost const y p1 p2 p3

# Cobb-Douglas cost function with homogeneity restrictions

genr rcost = cost - p3
genr rp1 = p1 - p3
genr rp2 = p2 - p3

ols rcost const y rp1 rp2

# Cobb-Douglas cost function with homogeneity restrictions
# and inefficiency

scalar b0 = $coeff(const)
scalar b1 = $coeff(y)
scalar b2 = $coeff(rp1)
scalar b3 = $coeff(rp2)

scalar su = 0.1
scalar sv = 0.1

mle logl = ln(cnorm(e*lambda/ss)) - (ln(ss) + 0.5*(e/ss)^2)
  scalar ss = sqrt(su^2 + sv^2)
  scalar lambda = su/sv
  series e = rcost - b0*const - b1*y - b2*rp1 - b3*rp2
  params b0 b1 b2 b3 su sv
end mle
```

then the density of $y_t$ conditional on $F_{t-1}$ is normal:

$$y_t|F_{t-1} \sim N\left[\mu, h_t\right].$$

By means of the properties of conditional distributions, the joint density can be factorized as follows

$$f(y_t, y_{t-1}, \ldots) = \left[\prod_{t=1}^{T} f(y_t|F_{t-1})\right] \cdot f(y_0)$$

If we treat $y_0$ as fixed, then the term $f(y_0)$ does not depend on the unknown parameters, and therefore the conditional log-likelihood can then be written as the sum of the individual contributions as

$$\ell(\mu, \omega, \alpha, \beta) = \sum_{t=1}^{T} \ell_t \qquad (17.6)$$

where

$$\ell_t = \log\left[\frac{1}{\sqrt{h_t}}\phi\left(\frac{y_t - \mu}{\sqrt{h_t}}\right)\right] = -\frac{1}{2}\left[\log(h_t) + \frac{(y_t - \mu)^2}{h_t}\right]$$

The following script shows a simple application of this technique, which uses the data file `djclose`;

it is one of the example dataset supplied with gretl and contains daily data from the Dow Jones stock index.

```
open djclose

series y = 100*ldiff(djclose)

scalar mu = 0.0
scalar omega = 1
scalar alpha = 0.4
scalar beta = 0.0

mle ll = -0.5*(log(h) + (e^2)/h)
  series e = y - mu
  series h = var(y)
  series h = omega + alpha*(e(-1))^2 + beta*h(-1)
  params mu omega alpha beta
end mle
```

## 17.5 Analytical derivatives

Computation of the score vector is essential for the working of the BFGS method. In all the previous examples, no explicit formula for the computation of the score was given, so the algorithm was fed numerically evaluated gradients. Numerical computation of the score for the $i$-th parameter is performed via a finite approximation of the derivative, namely

$$\frac{\partial \ell(\theta_1, \ldots, \theta_n)}{\partial \theta_i} \simeq \frac{\ell(\theta_1, \ldots, \theta_i + h, \ldots, \theta_n) - \ell(\theta_1, \ldots, \theta_i - h, \ldots, \theta_n)}{2h}$$

where $h$ is a small number.

In many situations, this is rather efficient and accurate. However, one might want to avoid the approximation and specify an exact function for the derivatives. As an example, consider the following script:

```
nulldata 1000

genr x1 = normal()
genr x2 = normal()
genr x3 = normal()

genr ystar = x1 + x2 + x3 + normal()
genr y = (ystar > 0)

scalar b0 = 0
scalar b1 = 0
scalar b2 = 0
scalar b3 = 0

mle logl = y*ln(P) + (1-y)*ln(1-P)
  series ndx = b0 + b1*x1 + b2*x2 + b3*x3
  series P = cnorm(ndx)
  params b0 b1 b2 b3
end mle --verbose
```

Here, 1000 data points are artificially generated for an ordinary probit model:[2] $y_t$ is a binary variable, which takes the value 1 if $y_t^* = \beta_1 x_{1t} + \beta_2 x_{2t} + \beta_3 x_{3t} + \varepsilon_t > 0$ and 0 otherwise. Therefore,

[2] Again, gretl does provide a native `probit` command (see section 22.1), but a probit model makes for a nice example here.

$y_t = 1$ with probability $\Phi(\beta_1 x_{1t} + \beta_2 x_{2t} + \beta_3 x_{3t}) = \pi_t$. The probability function for one observation can be written as

$$P(y_t) = \pi_t^{y_t}(1 - \pi_t)^{1-y_t}$$

Since the observations are independent and identically distributed, the log-likelihood is simply the sum of the individual contributions. Hence

$$\ell = \sum_{t=1}^{T} y_t \log(\pi_t) + (1 - y_t) \log(1 - \pi_t)$$

The `--verbose` switch at the end of the `end mle` statement produces a detailed account of the iterations done by the BFGS algorithm.

In this case, numerical differentiation works rather well; nevertheless, computation of the analytical score is straightforward, since the derivative $\frac{\partial \ell}{\partial \beta_i}$ can be written as

$$\frac{\partial \ell}{\partial \beta_i} = \frac{\partial \ell}{\partial \pi_t} \cdot \frac{\partial \pi_t}{\partial \beta_i}$$

via the chain rule, and it is easy to see that

$$\begin{aligned} \frac{\partial \ell}{\partial \pi_t} &= \frac{y_t}{\pi_t} - \frac{1 - y_t}{1 - \pi_t} \\ \frac{\partial \pi_t}{\partial \beta_i} &= \phi(\beta_1 x_{1t} + \beta_2 x_{2t} + \beta_3 x_{3t}) \cdot x_{it} \end{aligned}$$

The `mle` block in the above script can therefore be modified as follows:

```
mle logl = y*ln(P) + (1-y)*ln(1-P)
  series ndx = b0 + b1*x1 + b2*x2 + b3*x3
  series P = cnorm(ndx)
  series tmp = dnorm(ndx)*(y/P - (1-y)/(1-P))
  deriv b0 = tmp
  deriv b1 = tmp*x1
  deriv b2 = tmp*x2
  deriv b3 = tmp*x3
end mle --verbose
```

Note that the `params` statement has been replaced by a series of `deriv` statements; these have the double function of identifying the parameters over which to optimize and providing an analytical expression for their respective score elements.

## 17.6 Debugging ML scripts

We have discussed above the main sorts of statements that are permitted within an `mle` block, namely

- auxiliary commands to generate helper variables;
- `deriv` statements to specify the gradient with respect to each of the parameters; and
- a `params` statement to identify the parameters in case analytical derivatives are not given.

For the purpose of debugging ML estimators one additional sort of statement is allowed: you can print the value of a relevant variable at each step of the iteration. This facility is more restricted then the regular `print` command. The command word `print` should be followed by the name of just one variable (a scalar, series or matrix).

In the last example above a key variable named tmp was generated, forming the basis for the analytical derivatives. To track the progress of this variable one could add a print statement within the ML block, as in

```
series tmp = dnorm(ndx)*(y/P - (1-y)/(1-P))
print tmp
```

## 17.7 Using functions

The mle command allows you to estimate models that gretl does not provide natively: in some cases, it may be a good idea to wrap up the mle block in a user-defined function (see Chapter 10), so as to extend gretl's capabilities in a modular and flexible way.

As an example, we will take a simple case of a model that gretl does not yet provide natively: the zero-inflated Poisson model, or ZIP for short.[3] In this model, we assume that we observe a mixed population: for some individuals, the variable $y_t$ is (conditionally on a vector of exogenous covariates $x_t$) distributed as a Poisson random variate; for some others, $y_t$ is identically 0. The trouble is, we don't know which category a given individual belongs to.

For instance, suppose we have a sample of women, and the variable $y_t$ represents the number of children that woman $t$ has. There may be a certain proportion, $\alpha$, of women for whom $y_t = 0$ with certainty (maybe out of a personal choice, or due to physical impossibility). But there may be other women for whom $y_t = 0$ just as a matter of chance — they haven't happened to have any children at the time of observation.

In formulae:

$$\begin{aligned}
P(y_t = k|x_t) &= \alpha d_t + (1-\alpha)\left[e^{-\mu_t}\frac{\mu_t^{y_t}}{y_t!}\right] \\
\mu_t &= \exp(x_t\beta) \\
d_t &= \begin{cases} 1 & \text{for} \quad y_t = 0 \\ 0 & \text{for} \quad y_t > 0 \end{cases}
\end{aligned}$$

Writing a mle block for this model is not difficult:

```
mle ll = logprob
  series xb = exp(b0 + b1 * x)
  series d = (y=0)
  series poiprob = exp(-xb) * xb^y / gamma(y+1)
  series logprob = (alpha>0) && (alpha<1) ? \
    log(alpha*d + (1-alpha)*poiprob) : NA
  params alpha b0 b1
end mle -v
```

However, the code above has to be modified each time we change our specification by, say, adding an explanatory variable. Using functions, we can simplify this task considerably and eventually be able to write something easy like

```
list X = const x
zip(y, X)
```

Let's see how this can be done. First we need to define a function called zip() that will take two arguments: a dependent variable y and a list of explanatory variables X. An example of such function can be seen in script 17.2. By inspecting the function code, you can see that the actual estimation does not happen here: rather, the zip() function merely formats and prints out the results coming from another user-written function, namely zip_estimate().

[3] The actual ZIP model is in fact a bit more general than the one presented here. The specialized version discussed in this section was chosen for the sake of simplicity. For futher details, see Greene (2003).

**Example 17.2**: Zero-inflated Poisson Model — user-level function

```
/*
  user-level function: estimate the model and print out
  the results
*/
function zip(series y, list X)
    matrix ret = zip_estimate(y, X)
    matrix coef = ret[,1]
    matrix vcv = ret[,2:cols(ret)]

    printf "\nZero-inflated Poisson model:\n\n"
    scalar c = coef[1]
    scalar se = sqrt(vcv[1,1])
    scalar zs = c/se
    scalar pv = 2*pvalue(n, zs)
    printf "     alpha%9.4f%9.4f%8.3f%8.3f\n", c, se, zs, pv

    k = 2
    loop foreach i X -q
        sprintf s "$i"
        scalar c = coef[k]
        scalar se = sqrt(vcv[k,k])
        scalar zs = c/se
        scalar pv = 2*pvalue(n, zs)
        printf "%10s%9.4f%9.4f%8.3f%8.3f\n", s, c, se, zs, pv
        k++
    end loop
end function
```

The function `zip_estimate()` is not meant to be executed directly; it just contains the number-crunching part of the job, whose results are then picked up by the end function `zip()`. In turn, `zip_estimate()` calls other user-written functions to perform other tasks. The whole set of "internal" functions is shown in the panel 17.3.

All the functions shown in 17.2 and 17.3 can be stored in a separate `inp` file and executed once, at the beginning of our job, by means of the `include` command. Assuming the name of this script file is `zip_est.inp`, the following is an example script which

- includes the script file;
- generates a simulated dataset;
- performs the estimation of a ZIP model on the artificial data.

```
set echo off
set messages off

# include the user-written functions
include zip_est.inp

# generate the artificial data
nulldata 1000
set seed 732237
scalar truep = 0.2
scalar b0 = 0.2
scalar b1 = 0.5
series x = normal()
series y = (uniform()<truep) ? 0 : genpois(exp(b0 + b1*x))
list X = const x

# estimate the zero-inflated Poisson model
zip(y, X)
```

The results are as follows:

```
Zero-inflated Poisson model:

     alpha   0.2031   0.0238   8.531   0.000
     const   0.2570   0.0417   6.162   0.000
         x   0.4667   0.0321  14.527   0.000
```

A further step may then be creating a function package for accessing your new `zip()` function via gretl's graphical interface. For details on how to do this, see section 10.5.

**Example 17.3**: Zero-inflated Poisson Model — internal functions

```
/*
  compute the log probabilities for the plain Poisson model
*/
function ln_poi_prob(series y, list X, matrix beta)
    series xb = lincomb(X, beta)
    series ret = -exp(xb) + y*xb - lngamma(y+1)
    return series ret
end function

/*
  compute the log probabilities for the zero-inflated Poisson model
*/
function ln_zip_prob(series y, list X, matrix beta, scalar p0)
    # check if the probability is in [0,1]; otherwise, return NA
    if (p0>1) || (p0<0)
        series ret = NA
    else
        series ret = ln_poi_prob(y, X, beta) + ln(1-p0)
        series ret = (y=0) ? ln(p0 + exp(ret)) : ret
    endif
    return series ret
end function

/*
  do the actual estimation (silently)
*/
function zip_estimate(series y, list X)
    # initialize alpha to a "sensible" value: half the frequency
    # of zeros in the sample
    scalar alpha = mean(y=0)/2
    # initialize the coeffs (we assume the first explanatory
    # variable is the constant here)
    matrix coef = zeros(nelem(X), 1)
    coef[1] = mean(y) / (1-alpha)
    # do the actual ML estimation
    mle ll = ln_zip_prob(y, X, coef, alpha)
        params alpha coef
    end mle --hessian --quiet
    matrix ret = $coeff ~ $vcv
    return matrix ret
end function
```

# Chapter 18

# GMM estimation

## 18.1 Introduction and terminology

The Generalized Method of Moments (GMM) is a very powerful and general estimation method, which encompasses practically all the parametric estimation techniques used in econometrics. It was introduced in Hansen (1982) and Hansen and Singleton (1982); an excellent and thorough treatment is given in Davidson and MacKinnon (1993), chapter 17.

The basic principle on which GMM is built is rather straightforward. Suppose we wish to estimate a scalar parameter $\theta$ based on a sample $x_1, x_2, \ldots, x_T$. Let $\theta_0$ indicate the "true" value of $\theta$. Theoretical considerations (either of statistical or economic nature) may suggest that a relationship like the following holds:

$$E\left[x_t - g(\theta)\right] = 0 \Leftrightarrow \theta = \theta_0, \tag{18.1}$$

with $g(\cdot)$ a continuous and invertible function. That is to say, there exists a function of the data and the parameter, with the property that it has expectation zero if and only if it is evaluated at the true parameter value. For example, economic models with rational expectations lead to expressions like (18.1) quite naturally.

If the sampling model for the $x_t$s is such that some version of the Law of Large Numbers holds, then

$$\bar{X} = \frac{1}{T}\sum_{t=1}^{T} x_t \xrightarrow{\text{p}} g(\theta_0);$$

hence, since $g(\cdot)$ is invertible, the statistic

$$\hat{\theta} = g^{-1}(\bar{X}) \xrightarrow{\text{p}} \theta_0,$$

so $\hat{\theta}$ is a consistent estimator of $\theta$. A different way to obtain the same outcome is to choose, as an estimator of $\theta$, the value that minimizes the objective function

$$F(\theta) = \left[\frac{1}{T}\sum_{t=1}^{T}(x_t - g(\theta))\right]^2 = \left[\bar{X} - g(\theta)\right]^2; \tag{18.2}$$

the minimum is trivially reached at $\hat{\theta} = g^{-1}(\bar{X})$, since the expression in square brackets equals 0.

The above reasoning can be generalized as follows: suppose $\theta$ is an $n$-vector and we have $m$ relations like

$$E\left[f_i(x_t, \theta)\right] = 0 \quad \text{for } i = 1 \ldots m, \tag{18.3}$$

where $E[\cdot]$ is a conditional expectation on a set of $p$ variables $z_t$, called the *instruments*. In the above simple example, $m = 1$ and $f(x_t, \theta) = x_t - g(\theta)$, and the only instrument used is $z_t = 1$. Then, it must also be true that

$$E\left[f_i(x_t, \theta) \cdot z_{j,t}\right] = E\left[f_{i,j,t}(\theta)\right] = 0 \quad \text{for } i = 1 \ldots m \quad \text{and} \quad j = 1 \ldots p; \tag{18.4}$$

equation (18.4) is known as an *orthogonality condition*, or *moment condition*. The GMM estimator is defined as the minimum of the quadratic form

$$F(\theta, W) = \bar{\mathbf{f}}' W \bar{\mathbf{f}}, \tag{18.5}$$

where $\bar{\mathbf{f}}$ is a $(1 \times m \cdot p)$ vector holding the average of the orthogonality conditions and $W$ is some symmetric, positive definite matrix, known as the *weights* matrix. A necessary condition for the minimum to exist is the order condition $n \leq m \cdot p$.

The statistic

$$\hat{\theta} = \underset{\theta}{\text{Argmin}}\, F(\theta, W) \tag{18.6}$$

is a consistent estimator of $\theta$ whatever the choice of $W$. However, to achieve maximum asymptotic efficiency $W$ must be proportional to the inverse of the long-run covariance matrix of the orthogonality conditions; if $W$ is not known, a consistent estimator will suffice.

These considerations lead to the following empirical strategy:

1. Choose a positive definite $W$ and compute the *one-step* GMM estimator $\hat{\theta}_1$. Customary choices for $W$ are $I_{m \cdot p}$ or $I_m \otimes (Z'Z)^{-1}$.

2. Use $\hat{\theta}_1$ to estimate $V(f_{i,j,t}(\theta))$ and use its inverse as the weights matrix. The resulting estimator $\hat{\theta}_2$ is called the *two-step* estimator.

3. Re-estimate $V(f_{i,j,t}(\theta))$ by means of $\hat{\theta}_2$ and obtain $\hat{\theta}_3$; iterate until convergence. Asymptotically, these extra steps are unnecessary, since the two-step estimator is consistent and efficient; however, the iterated estimator often has better small-sample properties and should be independent of the choice of $W$ made at step 1.

In the special case when the number of parameters $n$ is equal to the total number of orthogonality conditions $m \cdot p$, the GMM estimator $\hat{\theta}$ is the same for any choice of the weights matrix $W$, so the first step is sufficient; in this case, the objective function is 0 at the minimum.

If, on the contrary, $n < m \cdot p$, the second step (or successive iterations) is needed to achieve efficiency, and the estimator so obtained can be very different, in finite samples, from the one-step estimator. Moreover, the value of the objective function at the minimum, suitably scaled by the number of observations, yields *Hansen's J statistic*; this statistic can be interpreted as a test statistic that has a $\chi^2$ distribution with $m \cdot p - n$ degrees of freedom under the null hypothesis of correct specification. See Davidson and MacKinnon (1993), section 17.6 for details.

In the following sections we will show how these ideas are implemented in gretl through some examples.

## 18.2 OLS as GMM

It is instructive to start with a somewhat contrived example: consider the linear model $y_t = x_t\beta + u_t$. Although most of us are used to read it as the sum of a hazily defined "systematic part" plus an equally hazy "disturbance", a more rigorous interpretation of this familiar expression comes from the *hypothesis* that the conditional mean $E(y_t|x_t)$ is linear and the *definition* of $u_t$ as $y_t - E(y_t|x_t)$.

From the definition of $u_t$, it follows that $E(u_t|x_t) = 0$. The following orthogonality condition is therefore available:

$$E\left[f(\beta)\right] = 0, \tag{18.7}$$

where $f(\beta) = (y_t - x_t\beta)x_t$. The definitions given in the previous section therefore specialize here to:

- $\theta$ is $\beta$;

- the instrument is $x_t$;

- $f_{i,j,t}(\theta)$ is $(y_t - x_t\beta)x_t = u_t x_t$; the orthogonality condition is interpretable as the requirement that the regressors should be uncorrelated with the disturbances;

- $W$ can be any symmetric positive definite matrix, since the number of parameters equals the number of orthogonality conditions. Let's say we choose $I$.
- The function $F(\theta, W)$ is in this case

$$F(\theta, W) = \left[ \frac{1}{T} \sum_{t=1}^{T} (\hat{u}_t x_t) \right]^2$$

  and it is easy to see why OLS and GMM coincide here: the GMM objective function has the same minimizer as the objective function of OLS, the residual sum of squares. Note, however, that the two functions are not equal to one another: at the minimum, $F(\theta, W) = 0$ while the minimized sum of squared residuals is zero only in the special case of a perfect linear fit.

The code snippet contained in Example 18.1 uses gretl's gmm command to make the above operational.

**Example 18.1**: OLS via GMM

```
/* initialize stuff */
series e = 0
scalar beta = 0
matrix V = I(1)

/* proceed with estimation */
gmm
  series e = y - x*beta
  orthog e ; x
  weights V
  params beta
end gmm
```

We feed gretl the necessary ingredients for GMM estimation in a command block, starting with `gmm` and ending with `end gmm`. After the `end gmm` statement two mutually exclusive options can be specified: `--two-step` or `--iterate`, whose meaning should be obvious.

Three elements are compulsory within a `gmm` block:

1. one or more `orthog` statements
2. one `weights` statement
3. one `params` statement

The three elements should be given in the stated order.

The `orthog` statements are used to specify the orthogonality conditions. They must follow the syntax

```
  orthog x ; Z
```

where `x` may be a series, matrix or list of series and `Z` may also be a series, matrix or list. In example 18.1, the series `e` holds the "residuals" and the series `x` holds the regressor. If `x` had been a list (a matrix), the `orthog` statement would have generated one orthogonality condition for each element (column) of `x`. Note the structure of the orthogonality condition: it is assumed that the term to the left of the semicolon represents a quantity that depends on the estimated parameters (and so must be updated in the process of iterative estimation), while the term on the right is a constant function of the data.

The `weights` statement is used to specify the initial weighting matrix and its syntax is straightforward. Note, however, that when more than one step is required that matrix will contain the *final* weight matrix, which most likely will be different from its initial value.

The `params` statement specifies the parameters with respect to which the GMM criterion should be minimized; it follows the same logic and rules as in the `mle` and `nls` commands.

The minimum is found through numerical minimization via BFGS (see section 5.9 and chapter 17). The progress of the optimization procedure can be observed by appending the `--verbose` switch to the `end gmm` line. (In this example GMM estimation is clearly a rather silly thing to do, since a closed form solution is easily given by OLS.)

## 18.3 TSLS as GMM

Moving closer to the proper domain of GMM, we now consider two-stage least squares (TSLS) as a case of GMM.

TSLS is employed in the case where one wishes to estimate a linear model of the form $y_t = X_t\beta + u_t$, but where one or more of the variables in the matrix $X$ are potentially endogenous — correlated with the error term, $u$. We proceed by identifying a set of instruments, $Z_t$, which are explanatory for the endogenous variables in $X$ but which are plausibly uncorrelated with $u$. The classic two-stage procedure is (1) regress the endogenous elements of $X$ on $Z$; then (2) estimate the equation of interest, with the endogenous elements of $X$ replaced by their fitted values from (1).

An alternative perspective is given by GMM. We define the residual $\hat{u}_t$ as $y_t - X_t\hat{\beta}$, as usual. But instead of relying on $E(u|X) = 0$ as in OLS, we base estimation on the condition $E(u|Z) = 0$. In this case it is natural to base the initial weighting matrix on the covariance matrix of the instruments. Example 18.2 presents a model from Stock and Watson's *Introduction to Econometrics*. The demand for cigarettes is modeled as a linear function of the logs of price and income; income is treated as exogenous while price is taken to be endogenous and two measures of tax are used as instruments. Since we have two instruments and one endogenous variable the model is over-identified and therefore the weights matrix will influence the solution. Partial output from this script is shown in 18.3. The estimated standard errors from GMM are robust by default; if we supply the `--robust` option to the `tsls` command we get identical results.[1]

## 18.4 Covariance matrix options

The covariance matrix of the estimated parameters depends on the choice of $W$ through

$$\hat{\Sigma} = (J'WJ)^{-1}J'W\Omega WJ(J'WJ)^{-1} \tag{18.8}$$

where $J$ is a Jacobian term

$$J_{ij} = \frac{\partial \bar{f}_i}{\partial \theta_j}$$

and $\Omega$ is the long-run covariance matrix of the orthogonality conditions.

Gretl computes $J$ by numeric differentiation (there is no provision for specifying a user-supplied analytical expression for $J$ at the moment). As for $\Omega$, a consistent estimate is needed. The simplest choice is the sample covariance matrix of the $f_t$s:

$$\hat{\Omega}_0(\theta) = \frac{1}{T}\sum_{t=1}^{T} f_t(\theta)f_t(\theta)' \tag{18.9}$$

This estimator is robust with respect to heteroskedasticity, but not with respect to autocorrelation. A heteroskedasticity- and autocorrelation-consistent (HAC) variant can be obtained using the

[1] The data file used in this example is available in the Stock and Watson package for gretl. See http://gretl.sourceforge.net/gretl_data.html.

**Example 18.2**: TSLS via GMM

```
open cig_ch10.gdt
# real avg price including sales tax
genr ravgprs = avgprs / cpi
# real avg cig-specific tax
genr rtax = tax / cpi
# real average total tax
genr rtaxs = taxs / cpi
# real average sales tax
genr rtaxso = rtaxs - rtax
# logs of consumption, price, income
genr lpackpc = log(packpc)
genr lravgprs = log(ravgprs)
genr perinc = income / (pop*cpi)
genr lperinc = log(perinc)
# restrict sample to 1995 observations
smpl --restrict year=1995
# Equation (10.16) by tsls
list xlist = const lravgprs lperinc
list zlist = const rtaxso rtax lperinc
tsls lpackpc xlist ; zlist --robust

# setup for gmm
matrix Z = { zlist }
matrix W = inv(Z'Z)
series e = 0
scalar b0 = 1
scalar b1 = 1
scalar b2 = 1

gmm e = lpackpc - b0 - b1*lravgprs - b2*lperinc
  orthog e ; Z
  weights W
  params b0 b1 b2
end gmm
```

Bartlett kernel or similar. A univariate version of this is used in the context of the `lrvar()` function — see equation (5.1). The multivariate version is set out in equation (18.10).

$$\hat{\Omega}_k(\theta) = \frac{1}{T}\sum_{t=k}^{T-k}\left[\sum_{i=-k}^{k} w_i f_t(\theta) f_{t-i}(\theta)'\right], \tag{18.10}$$

Gretl computes the HAC covariance matrix by default when a GMM model is estimated on time series data. You can control the kernel and the bandwidth (that is, the value of $k$ in 18.10) using the `set` command. See chapter 14 for further discussion of HAC estimation. You can also ask gretl *not* to use the HAC version by saying

```
set force_hc on
```

**Example 18.3**: TSLS via GMM: partial output

```
Model 1: TSLS estimates using the 48 observations 1-48
Dependent variable: lpackpc
Instruments: rtaxso rtax
Heteroskedasticity-robust standard errors, variant HC0

      VARIABLE       COEFFICIENT        STDERROR      T STAT    P-VALUE

  const               9.89496          0.928758     10.654   <0.00001 ***
  lravgprs           -1.27742          0.241684     -5.286   <0.00001 ***
  lperinc             0.280405         0.245828      1.141    0.25401

Model 2: 1-step GMM estimates using the 48 observations 1-48
e = lpackpc - b0 - b1*lravgprs - b2*lperinc

      PARAMETER       ESTIMATE          STDERROR      T STAT    P-VALUE

  b0                  9.89496          0.928758     10.654   <0.00001 ***
  b1                 -1.27742          0.241684     -5.286   <0.00001 ***
  b2                  0.280405         0.245828      1.141    0.25401

  GMM criterion = 0.0110046
```

## 18.5 A real example: the Consumption Based Asset Pricing Model

To illustrate gretl's implementation of GMM, we will replicate the example given in chapter 3 of Hall (2005). The model to estimate is a classic application of GMM, and provides an example of a case when orthogonality conditions do not stem from statistical considerations, but rather from economic theory.

A rational individual who must allocate his income between consumption and investment in a financial asset must in fact choose the consumption path of his whole lifetime, since investment translates into future consumption. It can be shown that an optimal consumption path should satisfy the following condition:

$$pU'(c_t) = \delta^k E\left[r_{t+k}U'(c_{t+k})|\mathcal{F}_t\right], \qquad (18.11)$$

where $p$ is the asset price, $U(\cdot)$ is the individual's utility function, $\delta$ is the individual's subjective discount rate and $r_{t+k}$ is the asset's rate of return between time $t$ and time $t+k$. $\mathcal{F}_t$ is the *information set* at time $t$; equation (18.11) says that the utility "lost" at time $t$ by purchasing the asset instead of consumption goods must be matched by a corresponding increase in the (discounted) future utility of the consumption financed by the asset's return. Since the future is uncertain, the individual considers his expectation, conditional on what is known at the time when the choice is made.

We have said nothing about the nature of the asset, so equation (18.11) should hold whatever asset we consider; hence, it is possible to build a system of equations like (18.11) for each asset whose price we observe.

If we are willing to believe that

- the economy as a whole can be represented as a single gigantic and immortal representative individual, and
- the function $U(x) = \frac{x^\alpha - 1}{\alpha}$ is a faithful representation of the individual's preferences,

then, setting $k = 1$, equation (18.11) implies the following for any asset $j$:

$$E\left[\delta \frac{r_{j,t+1}}{p_{j,t}} \left(\frac{C_{t+1}}{C_t}\right)^{\alpha-1} \middle| \mathcal{F}_t\right] = 1, \tag{18.12}$$

where $C_t$ is aggregate consumption and $\alpha$ and $\delta$ are the risk aversion and discount rate of the representative individual. In this case, it is easy to see that the "deep" parameters $\alpha$ and $\delta$ can be estimated via GMM by using

$$e_t = \delta \frac{r_{j,t+1}}{p_{j,t}} \left(\frac{C_{t+1}}{C_t}\right)^{\alpha-1} - 1$$

as the moment condition, while any variable known at time $t$ may serve as an instrument.

**Example 18.4**: Estimation of the Consumption Based Asset Pricing Model

```
open hall.gdt
set force_hc on

scalar alpha = 0.5
scalar delta = 0.5
series e = 0

list inst = const consrat(-1) consrat(-2) ewr(-1) ewr(-2)

matrix V0 = 100000*I(nelem(inst))
matrix Z = { inst }
matrix V1 = $nobs*inv(Z'Z)

gmm e = delta*ewr*consrat^(alpha-1) - 1
  orthog e ; inst
  weights V0
  params alpha delta
end gmm

gmm e = delta*ewr*consrat^(alpha-1) - 1
  orthog e ; inst
  weights V1
  params alpha delta
end gmm

gmm e = delta*ewr*consrat^(alpha-1) - 1
  orthog e ; inst
  weights V0
  params alpha delta
end gmm --iterate

gmm e = delta*ewr*consrat^(alpha-1) - 1
  orthog e ; inst
  weights V1
  params alpha delta
end gmm --iterate
```

In the example code given in 18.4, we replicate selected portions of table 3.7 in Hall (2005). The variable `consrat` is defined as the ratio of monthly consecutive real per capita consumption (services and nondurables) for the US, and `ewr` is the return–price ratio of a fictitious asset constructed by averaging all the stocks in the NYSE. The instrument set contains the constant and two lags of each variable.

The command `set force_hc on` on the second line of the script has the sole purpose of replicating the given example: as mentioned above, it forces gretl to compute the long-run variance of the orthogonality conditions according to equation (18.9) rather than (18.10).

We run `gmm` four times: one-step estimation for each of two initial weights matrices, then iterative estimation starting from each set of initial weights. Since the number of orthogonality conditions (5) is greater than the number of estimated parameters (2), the choice of intial weights should make a difference, and indeed we see fairly substantial differences between the one-step estimates (Models 1 and 2). On the other hand, iteration reduces these differences almost to the vanishing point (Models 3 and 4).

Part of the output is given in 18.5. It should be noted that the $J$ test leads to a rejection of the hypothesis of correct specification. This is perhaps not surprising given the heroic assumptions required to move from the microeconomic principle in equation (18.11) to the aggregate system that is actually estimated.

## 18.6 Caveats

A few words of warning are in order: despite its ingenuity, GMM is possibly the most fragile estimation method in econometrics. The number of non-obvious choices one has to make when using GMM is high, and in finite samples each of these can have dramatic consequences on the eventual output. Some of the factors that may affect the results are:

1. Orthogonality conditions can be written in more than one way: for example, if $E(x_t - \mu) = 0$, then $E(x_t/\mu - 1) = 0$ holds too. It is possible that a different specification of the moment conditions leads to different results.

2. As with all other numerical optimization algorithms, weird things may happen when the objective function is nearly flat in some directions or has multiple minima. BFGS is usually quite good, but there is no guarantee that it always delivers a sensible solution, if one at all.

3. The 1-step and, to a lesser extent, the 2-step estimators may be sensitive to apparently trivial details, like the re-scaling of the instruments. Different choices for the initial weights matrix can also have noticeable consequences.

4. With time-series data, there is no hard rule on the appropriate number of lags to use when computing the long-run covariance matrix (see section 18.4). Our advice is to go by trial and error, since results may be greatly influenced by a poor choice. Future versions of gretl will include more options on covariance matrix estimation.

One of the consequences of this state of things is that replicating various well-known published studies may be extremely difficult. Any non-trivial result is virtually impossible to reproduce unless all details of the estimation procedure are carefully recorded.

**Example 18.5**: Estimation of the Consumption Based Asset Pricing Model — output

```
Model 1: 1-step GMM estimates using the 465 observations 1959:04-1997:12
e = d*ewr*consrat^(alpha-1) - 1

      PARAMETER       ESTIMATE          STDERROR      T STAT   P-VALUE

  alpha                -3.14475          6.84439      -0.459   0.64590
  d                     0.999215         0.0121044    82.549  <0.00001 ***

  GMM criterion = 2778.08

Model 2: 1-step GMM estimates using the 465 observations 1959:04-1997:12
e = d*ewr*consrat^(alpha-1) - 1

      PARAMETER       ESTIMATE          STDERROR      T STAT   P-VALUE

  alpha                 0.398194         2.26359       0.176   0.86036
  d                     0.993180         0.00439367  226.048  <0.00001 ***

  GMM criterion = 14.247

Model 3: Iterated GMM estimates using the 465 observations 1959:04-1997:12
e = d*ewr*consrat^(alpha-1) - 1

      PARAMETER       ESTIMATE          STDERROR      T STAT   P-VALUE

  alpha                -0.344325         2.21458      -0.155   0.87644
  d                     0.991566         0.00423620  234.070  <0.00001 ***

  GMM criterion = 5491.78
  J test: Chi-square(3) = 11.8103 (p-value 0.0081)

Model 4: Iterated GMM estimates using the 465 observations 1959:04-1997:12
e = d*ewr*consrat^(alpha-1) - 1

      PARAMETER       ESTIMATE          STDERROR      T STAT   P-VALUE

  alpha                -0.344315         2.21359      -0.156   0.87639
  d                     0.991566         0.00423469  234.153  <0.00001 ***

  GMM criterion = 5491.78
  J test: Chi-square(3) = 11.8103 (p-value 0.0081)
```

# Chapter 19

# Model selection criteria

## 19.1 Introduction

In some contexts the econometrician chooses between alternative models based on a formal hypothesis test. For example, one might choose a more general model over a more restricted one if the restriction in question can be formulated as a testable null hypothesis, and the null is rejected on an appropriate test.

In other contexts one sometimes seeks a criterion for model selection that somehow measures the balance between goodness of fit or likelihood, on the one hand, and parsimony on the other. The balancing is necessary because the addition of extra variables to a model cannot reduce the degree of fit or likelihood, and is very likely to increase it somewhat even if the additional variables are not truly relevant to the data-generating process.

The best known such criterion, for linear models estimated via least squares, is the adjusted $R^2$,

$$\bar{R}^2 = 1 - \frac{\text{SSR}/(n-k)}{\text{TSS}/(n-1)}$$

where $n$ is the number of observations in the sample, $k$ denotes the number of parameters estimated, and SSR and TSS denote the sum of squared residuals and the total sum of squares for the dependent variable, respectively. Compared to the ordinary coefficient of determination or unadjusted $R^2$,

$$R^2 = 1 - \frac{\text{SSR}}{\text{TSS}}$$

the “adjusted” calculation penalizes the inclusion of additional parameters, other things equal.

## 19.2 Information criteria

A more general criterion in a similar spirit is Akaike’s (1974) “Information Criterion” (AIC). The original formulation of this measure is

$$\text{AIC} = -2\ell(\hat{\theta}) + 2k \tag{19.1}$$

where $\ell(\hat{\theta})$ represents the maximum loglikelihood as a function of the vector of parameter estimates, $\hat{\theta}$, and $k$ (as above) denotes the number of “independently adjusted parameters within the model.” In this formulation, with AIC negatively related to the likelihood and positively related to the number of parameters, the researcher seeks the minimum AIC.

The AIC can be confusing, in that several variants of the calculation are “in circulation.” For example, Davidson and MacKinnon (2004) present a simplified version,

$$\text{AIC} = \ell(\hat{\theta}) - k$$

which is just $-2$ times the original: in this case, obviously, one wants to maximize AIC.

In the case of models estimated by least squares, the loglikelihood can be written as

$$\ell(\hat{\theta}) = -\frac{n}{2}(1 + \log 2\pi - \log n) - \frac{n}{2}\log \text{SSR} \tag{19.2}$$

Substituting (19.2) into (19.1) we get

$$\mathrm{AIC} = n(1 + \log 2\pi - \log n) + n \log \mathrm{SSR} + 2k$$

which can also be written as

$$\mathrm{AIC} = n \log \left( \frac{\mathrm{SSR}}{n} \right) + 2k + n(1 + \log 2\pi) \tag{19.3}$$

Some authors simplify the formula for the case of models estimated via least squares. For instance, William Greene writes

$$\mathrm{AIC} = \log \left( \frac{\mathrm{SSR}}{n} \right) + \frac{2k}{n} \tag{19.4}$$

This variant can be derived from (19.3) by dividing through by $n$ and subtracting the constant $1 + \log 2\pi$. That is, writing $\mathrm{AIC}_G$ for the version given by Greene, we have

$$\mathrm{AIC}_G = \frac{1}{n}\mathrm{AIC} - (1 + \log 2\pi)$$

Finally, Ramanathan gives a further variant:

$$\mathrm{AIC}_R = \left( \frac{\mathrm{SSR}}{n} \right) e^{2k/n}$$

which is the exponential of the one given by Greene.

Gretl began by using the Ramanathan variant, but since version 1.3.1 the program has used the original Akaike formula (19.1), and more specifically (19.3) for models estimated via least squares.

Although the Akaike criterion is designed to favor parsimony, arguably it does not go far enough in that direction. For instance, if we have two nested models with $k - 1$ and $k$ parameters respectively, and if the null hypothesis that parameter $k$ equals 0 is true, in large samples the AIC will nonetheless tend to select the less parsimonious model about 16 percent of the time (see Davidson and MacKinnon, 2004, chapter 15).

An alternative to the AIC which avoids this problem is the Schwarz (1978) "Bayesian information criterion" (BIC). The BIC can be written (in line with Akaike's formulation of the AIC) as

$$\mathrm{BIC} = -2\ell(\hat{\theta}) + k \log n$$

The multiplication of $k$ by $\log n$ in the BIC means that the penalty for adding extra parameters grows with the sample size. This ensures that, asymptotically, one will not select a larger model over a correctly specified parsimonious model.

A further alternative to AIC, which again tends to select more parsimonious models than AIC, is the Hannan–Quinn criterion or HQC (Hannan and Quinn, 1979). Written consistently with the formulations above, this is

$$\mathrm{HQC} = -2\ell(\hat{\theta}) + 2k \log \log n$$

The Hannan–Quinn calculation is based on the law of the iterated logarithm (note that the last term is the log of the log of the sample size). The authors argue that their procedure provides a "strongly consistent estimation procedure for the order of an autoregression", and that "compared to other strongly consistent procedures this procedure will underestimate the order to a lesser degree."

Gretl reports the AIC, BIC and HQC (calculated as explained above) for most sorts of models. The key point in interpreting these values is to know whether they are calculated such that smaller values are better, or such that larger values are better. In gretl, smaller values are better: one wants to minimize the chosen criterion.

# Chapter 20

# Time series models

## 20.1 Introduction

Time series models are discussed in this chapter and the next. In this chapter we concentrate on ARIMA models, unit root tests, and GARCH. The following chapter deals with cointegration and error correction.

## 20.2 ARIMA models

### Representation and syntax

The `arma` command performs estimation of AutoRegressive, Integrated, Moving Average (ARIMA) models. These are models that can be written in the form

$$\phi(L)y_t = \theta(L)\epsilon_t \tag{20.1}$$

where $\phi(L)$, and $\theta(L)$ are polynomials in the lag operator, $L$, defined such that $L^n x_t = x_{t-n}$, and $\epsilon_t$ is a white noise process. The exact content of $y_t$, of the AR polynomial $\phi()$, and of the MA polynomial $\theta()$, will be explained in the following.

### Mean terms

The process $y_t$ as written in equation (20.1) has, without further qualifications, mean zero. If the model is to be applied to real data, it is necessary to include some term to handle the possibility that $y_t$ has non-zero mean. There are two possible ways to represent processes with nonzero mean: one is to define $\mu_t$ as the *unconditional* mean of $y_t$, namely the central value of its marginal distribution. Therefore, the series $\tilde{y}_t = y_t - \mu_t$ has mean 0, and the model (20.1) applies to $\tilde{y}_t$. In practice, assuming that $\mu_t$ is a linear function of some observable variables $x_t$, the model becomes

$$\phi(L)(y_t - x_t\beta) = \theta(L)\epsilon_t \tag{20.2}$$

This is sometimes known as a "regression model with ARMA errors"; its structure may be more apparent if we represent it using two equations:

$$\begin{aligned} y_t &= x_t\beta + u_t \\ \phi(L)u_t &= \theta(L)\epsilon_t \end{aligned}$$

The model just presented is also sometimes known as "ARMAX" (ARMA + eXogenous variables). It seems to us, however, that this label is more appropriately applied to a different model: another way to include a mean term in (20.1) is to base the representation on the *conditional* mean of $y_t$, that is the central value of the distribution of $y_t$ *given its own past*. Assuming, again, that this can be represented as a linear combination of some observable variables $z_t$, the model would expand to

$$\phi(L)y_t = z_t\gamma + \theta(L)\epsilon_t \tag{20.3}$$

The formulation (20.3) has the advantage that $\gamma$ can be immediately interpreted as the vector of marginal effects of the $z_t$ variables on the conditional mean of $y_t$. And by adding lags of $z_t$ to this specification one can estimate *Transfer Function models* (which generalize ARMA by adding the effects of exogenous variable distributed across time).

Gretl provides a way to estimate both forms. Models written as in (20.2) are estimated by maximum likelihood; models written as in (20.3) are estimated by conditional maximum likelihood. (For more on these options see the section on "Estimation" below.)

In the special case when $x_t = z_t = 1$ (that is, the models include a constant but no exogenous variables) the two specifications discussed above reduce to

$$\phi(L)(y_t - \mu) = \theta(L)\epsilon_t \tag{20.4}$$

and

$$\phi(L)y_t = \alpha + \theta(L)\epsilon_t \tag{20.5}$$

respectively. These formulations are essentially equivalent, but if they represent one and the same process $\mu$ and $\alpha$ are, fairly obviously, not numerically identical; rather

$$\alpha = \left(1 - \phi_1 - \ldots - \phi_p\right)\mu$$

The gretl syntax for estimating (20.4) is simply

```
arma p q ; y
```

The AR and MA lag orders, p and q, can be given either as numbers or as pre-defined scalars. The parameter $\mu$ can be dropped if necessary by appending the option --nc ("no constant") to the command. If estimation of (20.5) is needed, the switch --conditional must be appended to the command, as in

```
arma p q ; y --conditional
```

Generalizing this principle to the estimation of (20.2) or (20.3), you get that

```
arma p q ; y const x1 x2
```

would estimate the following model:

$$y_t - x_t\beta = \phi_1\left(y_{t-1} - x_{t-1}\beta\right) + \ldots + \phi_p\left(y_{t-p} - x_{t-p}\beta\right) + \epsilon_t + \theta_1\epsilon_{t-1} + \ldots + \theta_q\epsilon_{t-q}$$

where in this instance $x_t\beta = \beta_0 + x_{t,1}\beta_1 + x_{t,2}\beta_2$. Appending the --conditional switch, as in

```
arma p q ; y const x1 x2 --conditional
```

would estimate the following model:

$$y_t = x_t\gamma + \phi_1 y_{t-1} + \ldots + \phi_p y_{t-p} + \epsilon_t + \theta_1\epsilon_{t-1} + \ldots + \theta_q\epsilon_{t-q}$$

Ideally, the issue broached above could be made moot by writing a more general specification that nests the alternatives; that is

$$\phi(L)\left(y_t - x_t\beta\right) = z_t\gamma + \theta(L)\epsilon_t; \tag{20.6}$$

we would like to generalize the arma command so that the user could specify, for any estimation method, whether certain exogenous variables should be treated as $x_t$s or $z_t$s, but we're not yet at that point (and neither are most other software packages).

### Seasonal models

A more flexible lag structure is desirable when analyzing time series that display strong seasonal patterns. Model (20.1) can be expanded to

$$\phi(L)\Phi(L^s)y_t = \theta(L)\Theta(L^s)\epsilon_t. \tag{20.7}$$

For such cases, a fuller form of the syntax is available, namely,

```
arma p q ; P Q ; y
```

where p and q represent the non-seasonal AR and MA orders, and P and Q the seasonal orders. For example,

```
arma 1 1 ; 1 1 ; y
```

would be used to estimate the following model:

$$(1 - \phi L)(1 - \Phi L^s)(y_t - \mu) = (1 + \theta L)(1 + \Theta L^s)\epsilon_t$$

If $y_t$ is a quarterly series (and therefore $s = 4$), the above equation can be written more explicitly as

$$y_t - \mu = \phi(y_{t-1} - \mu) + \Phi(y_{t-4} - \mu) - (\phi \cdot \Phi)(y_{t-5} - \mu) + \epsilon_t + \theta\epsilon_{t-1} + \Theta\epsilon_{t-4} + (\theta \cdot \Theta)\epsilon_{t-5}$$

Such a model is known as a “multiplicative seasonal ARMA model”.

### Gaps in the lag structure

The standard way to specify an ARMA model in gretl is via the AR and MA orders, $p$ and $q$ respectively. In this case all lags from 1 to the given order are included. In some cases one may wish to include only certain specific AR and/or MA lags. This can be done in either of two ways.

- One can construct a matrix containing the desired lags (positive integer values) and supply the name of this matrix in place of $p$ or $q$.
- One can give a space-separated list of lags, enclosed in braces, in place of $p$ or $q$.

The following code illustrates these options:

```
matrix pvec = {1, 4}
arma pvec 1 ; y
arma {1 4} 1 ; y
```

Both forms above specify an ARMA model in which AR lags 1 and 4 are used (but not 2 and 3).

This facility is available only for the non-seasonal component of the ARMA specification.

### Differencing and ARIMA

The above discussion presupposes that the time series $y_t$ has already been subjected to all the transformations deemed necessary for ensuring stationarity (see also section 20.3). Differencing is the most common of these transformations, and gretl provides a mechanism to include this step into the arma command: the syntax

```
arma p d q ; y
```

would estimate an ARMA$(p, q)$ model on $\Delta^d y_t$. It is functionally equivalent to

```
series tmp = y
loop for i=1..d
  tmp = diff(tmp)
end loop
arma p q ; tmp
```

except with regard to forecasting after estimation (see below).

When the series $y_t$ is differenced before performing the analysis the model is known as ARIMA ("I" for Integrated); for this reason, gretl provides the `arima` command as an alias for `arma`.

Seasonal differencing is handled similarly, with the syntax

```
arma p d q ; P D Q ; y
```

where `D` is the order for seasonal differencing. Thus, the command

```
arma 1 0 0 ; 1 1 1 ; y
```

would produce the same parameter estimates as

```
genr dsy = sdiff(y)
arma 1 0 ; 1 1 ; dsy
```

where we use the `sdiff` function to create a seasonal difference (e.g. for quarterly data, $y_t - y_{t-4}$).

### Estimation

The default estimation method for ARMA models is exact maximum likelihood estimation (under the assumption that the error term is normally distributed), using the Kalman filter in conjunction with the BFGS maximization algorithm. The gradient of the log-likelihood with respect to the parameter estimates is approximated numerically. This method produces results that are directly comparable with many other software packages. The constant, and any exogenous variables, are treated as in equation (20.2). The covariance matrix for the parameters is computed using a numerical approximation to the Hessian at convergence.

The alternative method, invoked with the `--conditional` switch, is conditional maximum likelihood (CML), also known as "conditional sum of squares" — see Hamilton (1994, p. 132). This method was exemplified in the script 9.3, and only a brief description will be given here. Given a sample of size $T$, the CML method minimizes the sum of squared one-step-ahead prediction errors generated by the model for the observations $t_0, \ldots, T$. The starting point $t_0$ depends on the orders of the AR polynomials in the model. The numerical maximization method used is BHHH, and the covariance matrix is computed using a Gauss–Newton regression.

The CML method is nearly equivalent to maximum likelihood under the hypothesis of normality; the difference is that the first $(t_0 - 1)$ observations are considered fixed and only enter the likelihood function as conditioning variables. As a consequence, the two methods are asymptotically equivalent under standard conditions — except for the fact, discussed above, that our CML implementation treats the constant and exogenous variables as per equation (20.3).

The two methods can be compared as in the following example

```
open data10-1
arma 1 1 ; r
arma 1 1 ; r --conditional
```

which produces the estimates shown in Table 20.1. As you can see, the estimates of $\phi$ and $\theta$ are quite similar. The reported constants differ widely, as expected — see the discussion following equations (20.4) and (20.5). However, dividing the CML constant by $1 - \phi$ we get 7.38, which is not far from the ML estimate of 6.93.

**Table 20.1**: ML and CML estimates

| Parameter | ML | | CML | |
|---|---|---|---|---|
| $\mu$ | 6.93042 | (0.923882) | 1.07322 | (0.488661) |
| $\phi$ | 0.855360 | (0.0511842) | 0.852772 | (0.0450252) |
| $\theta$ | 0.588056 | (0.0986096) | 0.591838 | (0.0456662) |

### Convergence and initialization

The numerical methods used to maximize the likelihood for ARMA models are not guaranteed to converge. Whether or not convergence is achieved, and whether or not the true maximum of the likelihood function is attained, may depend on the starting values for the parameters. Gretl employs one of the following two initialization mechanisms, depending on the specification of the model and the estimation method chosen.

1. Estimate a pure AR model by Least Squares (nonlinear least squares if the model requires it, otherwise OLS). Set the AR parameter values based on this regression and set the MA parameters to a small positive value (0.0001).
2. The Hannan–Rissanen method: First estimate an autoregressive model by OLS and save the residuals. Then in a second OLS pass add appropriate lags of the first-round residuals to the model, to obtain estimates of the MA parameters.

To see the details of the ARMA estimation procedure, add the `--verbose` option to the command. This prints a notice of the initialization method used, as well as the parameter values and log-likelihood at each iteration.

Besides the build-in initialization mechanisms, the user has the option of specifying a set of starting values manually. This is done via the `set` command: the first argument should be the keyword `initvals` and the second should be the name of a pre-specified matrix containing starting values. For example

```
matrix start = { 0, 0.85, 0.34 }
set initvals start
arma 1 1 ; y
```

The specified matrix should have just as many parameters as the model: in the example above there are three parameters, since the model implicitly includes a constant. The constant, if present, is always given first; otherwise the order in which the parameters are expected is the same as the order of specification in the `arma` or `arima` command. In the example the constant is set to zero, $\phi_1$ to 0.85, and $\theta_1$ to 0.34.

You can get gretl to revert to automatic initialization via the command `set initvals auto`.

### Estimation via X-12-ARIMA

As an alternative to estimating ARMA models using "native" code, gretl offers the option of using the external program X-12-ARIMA. This is the seasonal adjustment software produced and maintained by the U.S. Census Bureau; it is used for all official seasonal adjustments at the Bureau.

Gretl includes a module which interfaces with X-12-ARIMA: it translates `arma` commands using the syntax outlined above into a form recognized by X-12-ARIMA, executes the program, and retrieves the results for viewing and further analysis within gretl. To use this facility you have to install X-12-ARIMA separately. Packages for both MS Windows and GNU/Linux are available from the gretl website, http://gretl.sourceforge.net/.

To invoke X-12-ARIMA as the estimation engine, append the flag `--x-12-arima`, as in

```
arma p q ; y --x-12-arima
```

As with native estimation, the default is to use exact ML but there is the option of using conditional ML with the `--conditional` flag. However, please note that when X-12-ARIMA is used in conditional ML mode, the comments above regarding the variant treatments of the mean of the process $y_t$ *do not apply*. That is, when you use X-12-ARIMA the model that is estimated is (20.2), regardless of whether estimation is by exact ML or conditional ML.

### Forecasting

ARMA models are often used for forecasting purposes. The autoregressive component, in particular, offers the possibility of forecasting a process "out of sample" over a substantial time horizon.

Gretl supports forecasting on the basis of ARMA models using the method set out by Box and Jenkins (1976).[1] The Box and Jenkins algorithm produces a set of integrated AR coefficients which take into account any differencing of the dependent variable (seasonal and/or non-seasonal) in the ARIMA context, thus making it possible to generate a forecast for the level of the original variable. By contrast, if you first difference a series manually and then apply ARMA to the differenced series, forecasts will be for the differenced series, not the level. This point is illustrated in Example 20.1. The parameter estimates are identical for the two models. The forecasts differ but are mutually consistent: the variable `fcdiff` emulates the ARMA forecast (static, one step ahead within the sample range, and dynamic out of sample).

## 20.3 Unit root tests

### The ADF test

The Augmented Dickey–Fuller (ADF) test is, as implemented in gretl, the $t$-statistic on $\varphi$ in the following regression:

$$\Delta y_t = \mu_t + \varphi y_{t-1} + \sum_{i=1}^{p} \gamma_i \Delta y_{t-i} + \epsilon_t . \tag{20.8}$$

This test statistic is probably the best-known and most widely used unit root test. It is a one-sided test whose null hypothesis is $\varphi = 0$ versus the alternative $\varphi < 0$. Under the null, $y_t$ must be differenced at least once to achieve stationarity; under the alternative, $y_t$ is already stationary and no differencing is required. Hence, large negative values of the test statistic lead to the rejection of the null.

One peculiar aspect of this test is that its limit distribution is non-standard under the null hypothesis: moreover, the shape of the distribution, and consequently the critical values for the test, depends on the form of the $\mu_t$ term. A full analysis of the various cases is inappropriate here: Hamilton (1994) contains an excellent discussion, but any recent time series textbook covers this topic. Suffice it to say that gretl allows the user to choose the specification for $\mu_t$ among four different alternatives:

| $\mu_t$ | command option |
|---|---|
| 0 | `--nc` |
| $\mu_0$ | `--c` |
| $\mu_0 + \mu_1 t$ | `--ct` |
| $\mu_0 + \mu_1 t + \mu_1 t^2$ | `--ctt` |

[1] See in particular their "Program 4" on p. 505ff.

These options are not mutually exclusive; when they are used together the statistic will be reported separately for each case. By default, gretl uses by default the combination `--c --ct --ctt`. For each case, approximate p-values are calculated by means of the algorithm developed in MacKinnon (1996).

The gretl command used to perform the test is `adf`; for example

```
adf 4 x1 --c --ct
```

would compute the test statistic as the t-statistic for $\varphi$ in equation 20.8 with $p = 4$ in the two cases $\mu_t = \mu_0$ and $\mu_t = \mu_0 + \mu_1 t$.

The number of lags ($p$ in equation 20.8) should be chosen as to ensure that (20.8) is a parametrization flexible enough to represent adequately the short-run persistence of $\Delta y_t$. Setting $p$ too low results in size distortions in the test, whereas setting $p$ too high would lead to low power. As a convenience to the user, the parameter $p$ can be automatically determined. Setting $p$ to a negative number triggers a sequential procedure that starts with $p$ lags and decrements $p$ until the $t$-statistic for the parameter $\gamma_p$ exceeds 1.645 in absolute value.

### The KPSS test

The KPSS test (Kwiatkowski, Phillips, Schmidt and Shin, 1992) is a unit root test in which the null hypothesis is opposite to that in the ADF test: under the null, the series in question is stationary; the alternative is that the series is $I(1)$.

The basic intuition behind this test statistic is very simple: if $y_t$ can be written as $y_t = \mu + u_t$, where $u_t$ is some zero-mean stationary process, then not only does the sample average of the $y_t$'s provide a consistent estimator of $\mu$, but the long-run variance of $u_t$ is a well-defined, finite number. Neither of these properties hold under the alternative.

The test itself is based on the following statistic:

$$\eta = \frac{\sum_{i=1}^{T} S_t^2}{T^2 \bar{\sigma}^2} \tag{20.9}$$

where $S_t = \sum_{s=1}^{t} e_s$ and $\bar{\sigma}^2$ is an estimate of the long-run variance of $e_t = (y_t - \bar{y})$. Under the null, this statistic has a well-defined (nonstandard) asymptotic distribution, which is free of nuisance parameters and has been tabulated by simulation. Under the alternative, the statistic diverges.

As a consequence, it is possible to construct a one-sided test based on $\eta$, where $H_0$ is rejected if $\eta$ is bigger than the appropriate critical value; gretl provides the 90%, 95%, 97.5% and 99% quantiles.

Usage example:

```
kpss m y
```

where `m` is an integer representing the bandwidth or window size used in the formula for estimating the long run variance:

$$\bar{\sigma}^2 = \sum_{i=-m}^{m} \left(1 - \frac{|i|}{m+1}\right) \hat{\gamma}_i$$

The $\hat{\gamma}_i$ terms denote the empirical autocovariances of $e_t$ from order $-m$ through $m$. For this estimator to be consistent, $m$ must be large enough to accommodate the short-run persistence of $e_t$, but not too large compared to the sample size $T$. In the GUI interface of gretl, this value defaults to the integer part of $4\left(\frac{T}{100}\right)^{1/4}$.

The above concept can be generalized to the case where $y_t$ is thought to be stationary around a deterministic trend. In this case, formula (20.9) remains unchanged, but the series $e_t$ is defined as the residuals from an OLS regression of $y_t$ on a constant and a linear trend. This second form of the test is obtained by appending the `--trend` option to the `kpss` command:

```
kpss n y --trend
```

Note that in this case the asymptotic distribution of the test is different and the critical values reported by gretl differ accordingly.

### Cointegration tests

FIXME discuss Engle—Granger here, and refer forward to the next chapter for the Johansen tests.

## 20.4 ARCH and GARCH

Heteroskedasticity means a non-constant variance of the error term in a regression model. Autoregressive Conditional Heteroskedasticity (ARCH) is a phenomenon specific to time series models, whereby the variance of the error displays autoregressive behavior; for instance, the time series exhibits successive periods where the error variance is relatively large, and successive periods where it is relatively small. This sort of behavior is reckoned to be quite common in asset markets: an unsettling piece of news can lead to a period of increased volatility in the market.

An ARCH error process of order $q$ can be represented as

$$u_t = \sigma_t \varepsilon_t; \qquad \sigma_t^2 \equiv \mathrm{E}(u_t^2|\Omega_{t-1}) = \alpha_0 + \sum_{i=1}^{q} \alpha_i u_{t-i}^2$$

where the $\varepsilon_t$s are independently and identically distributed (iid) with mean zero and variance 1, and where $\sigma_t$ is taken to be the positive square root of $\sigma_t^2$. $\Omega_{t-1}$ denotes the information set as of time $t-1$ and $\sigma_t^2$ is the conditional variance: that is, the variance conditional on information dated $t-1$ and earlier.

It is important to notice the difference between ARCH and an ordinary autoregressive error process. The simplest (first-order) case of the latter can be written as

$$u_t = \rho u_{t-1} + \varepsilon_t; \qquad -1 < \rho < 1$$

where the $\varepsilon_t$s are independently and identically distributed with mean zero and variance $\sigma^2$. With an AR(1) error, if $\rho$ is positive then a positive value of $u_t$ will tend to be followed, with probability greater than 0.5, by a positive $u_{t+1}$. With an ARCH error process, a disturbance $u_t$ of large absolute value will tend to be followed by further large absolute values, but with no presumption that the successive values will be of the same sign. ARCH in asset prices is a "stylized fact" and is consistent with market efficiency; on the other hand autoregressive behavior of asset prices would violate market efficiency.

One can test for ARCH of order $q$ in the following way:

1. Estimate the model of interest via OLS and save the squared residuals, $\hat{u}_t^2$.
2. Perform an auxiliary regression in which the current squared residual is regressed on a constant and $q$ lags of itself.
3. Find the $TR^2$ value (sample size times unadjusted $R^2$) for the auxiliary regression.
4. Refer the $TR^2$ value to the $\chi^2$ distribution with $q$ degrees of freedom, and if the p-value is "small enough" reject the null hypothesis of homoskedasticity in favor of the alternative of ARCH($q$).

This test is implemented in gretl via the arch command. This command may be issued following the estimation of a time-series model by OLS, or by selection from the "Tests" menu in the model window (again, following OLS estimation). The result of the test is reported and if the $TR^2$ from the auxiliary regression has a p-value less than 0.10, ARCH estimates are also reported. These estimates take the form of Generalized Least Squares (GLS), specifically weighted least squares, using weights that are inversely proportional to the predicted variances of the disturbances, $\hat{\sigma}_t$, derived from the auxiliary regression.

In addition, the ARCH test is available after estimating a vector autoregression (VAR). In this case, however, there is no provision to re-estimate the model via GLS.

### GARCH

The simple ARCH($q$) process is useful for introducing the general concept of conditional heteroskedasticity in time series, but it has been found to be insufficient in empirical work. The dynamics of the error variance permitted by ARCH($q$) are not rich enough to represent the patterns found in financial data. The generalized ARCH or GARCH model is now more widely used.

The representation of the variance of a process in the GARCH model is somewhat (but not exactly) analogous to the ARMA representation of the level of a time series. The variance at time $t$ is allowed to depend on both past values of the variance and past values of the realized squared disturbance, as shown in the following system of equations:

$$y_t = X_t\beta + u_t \tag{20.10}$$

$$u_t = \sigma_t\varepsilon_t \tag{20.11}$$

$$\sigma_t^2 = \alpha_0 + \sum_{i=1}^{q}\alpha_i u_{t-i}^2 + \sum_{j=1}^{p}\delta_i\sigma_{t-j}^2 \tag{20.12}$$

As above, $\varepsilon_t$ is an iid sequence with unit variance. $X_t$ is a matrix of regressors (or in the simplest case, just a vector of 1s allowing for a non-zero mean of $y_t$). Note that if $p = 0$, GARCH collapses to ARCH($q$): the generalization is embodied in the $\delta_i$ terms that multiply previous values of the error variance.

In principle the underlying innovation, $\varepsilon_t$, could follow any suitable probability distribution, and besides the obvious candidate of the normal or Gaussian distribution the $t$ distribution has been used in this context. Currently gretl only handles the case where $\varepsilon_t$ is assumed to be Gaussian. However, when the `--robust` option to the `garch` command is given, the estimator gretl uses for the covariance matrix can be considered Quasi-Maximum Likelihood even with non-normal disturbances. See below for more on the options regarding the GARCH covariance matrix.

Example:

```
garch p q ; y const x
```

where `p` $\geq 0$ and `q` $> 0$ denote the respective lag orders as shown in equation (20.12). These values can be supplied in numerical form or as the names of pre-defined scalar variables.

### GARCH estimation

Estimation of the parameters of a GARCH model is by no means a straightforward task. (Consider equation 20.12: the conditional variance at any point in time, $\sigma_t^2$, depends on the conditional variance in earlier periods, but $\sigma_t^2$ is not observed, and must be inferred by some sort of Maximum Likelihood procedure.) Gretl uses the method proposed by Fiorentini, Calzolari and Panattoni (1996),[2] which was adopted as a benchmark in the study of GARCH results by McCullough and Renfro (1998). It employs analytical first and second derivatives of the log-likelihood, and uses a mixed-gradient algorithm, exploiting the information matrix in the early iterations and then switching to the Hessian in the neighborhood of the maximum likelihood. (This progress can be observed if you append the `--verbose` option to gretl's `garch` command.)

[2] The algorithm is based on Fortran code deposited in the archive of the *Journal of Applied Econometrics* by the authors, and is used by kind permission of Professor Fiorentini.

Several options are available for computing the covariance matrix of the parameter estimates in connection with the `garch` command. At a first level, one can choose between a “standard” and a “robust” estimator. By default, the Hessian is used unless the `--robust` option is given, in which case the QML estimator is used. A finer choice is available via the `set` command, as shown in Table 20.2.

**Table 20.2**: Options for the GARCH covariance matrix

| *command* | *effect* |
|---|---|
| `set garch_vcv hessian` | Use the Hessian |
| `set garch_vcv im` | Use the Information Matrix |
| `set garch_vcv op` | Use the Outer Product of the Gradient |
| `set garch_vcv qml` | QML estimator |
| `set garch_vcv bw` | Bollerslev–Wooldridge “sandwich” estimator |

It is not uncommon, when one estimates a GARCH model for an arbitrary time series, to find that the iterative calculation of the estimates fails to converge. For the GARCH model to make sense, there are strong restrictions on the admissible parameter values, and it is not always the case that there exists a set of values inside the admissible parameter space for which the likelihood is maximized.

The restrictions in question can be explained by reference to the simplest (and much the most common) instance of the GARCH model, where $p = q = 1$. In the GARCH(1, 1) model the conditional variance is

$$\sigma_t^2 = \alpha_0 + \alpha_1 u_{t-1}^2 + \delta_1 \sigma_{t-1}^2 \tag{20.13}$$

Taking the unconditional expectation of (20.13) we get

$$\sigma^2 = \alpha_0 + \alpha_1 \sigma^2 + \delta_1 \sigma^2$$

so that

$$\sigma^2 = \frac{\alpha_0}{1 - \alpha_1 - \delta_1}$$

For this unconditional variance to exist, we require that $\alpha_1 + \delta_1 < 1$, and for it to be positive we require that $\alpha_0 > 0$.

A common reason for non-convergence of GARCH estimates (that is, a common reason for the non-existence of $\alpha_i$ and $\delta_i$ values that satisfy the above requirements and at the same time maximize the likelihood of the data) is misspecification of the model. It is important to realize that GARCH, in itself, allows *only* for time-varying volatility in the data. If the *mean* of the series in question is not constant, or if the error process is not only heteroskedastic but also autoregressive, it is necessary to take this into account when formulating an appropriate model. For example, it may be necessary to take the first difference of the variable in question and/or to add suitable regressors, $X_t$, as in (20.10).

**Example 20.1**: ARIMA forecasting

```
open greene18_2.gdt
# log of quarterly U.S. nominal GNP, 1950:1 to 1983:4
genr y = log(Y)
# and its first difference
genr dy = diff(y)
# reserve 2 years for out-of-sample forecast
smpl ; 1981:4
# Estimate using ARIMA
arima 1 1 1 ; y
# forecast over full period
smpl --full
fcast fc1
# Return to sub-sample and run ARMA on the first difference of y
smpl ; 1981:4
arma 1 1 ; dy
smpl --full
fcast fc2
genr fcdiff = (t<=1982:1)*(fc1 - y(-1)) + (t>1982:1)*(fc1 - fc1(-1))
# compare the forecasts over the later period
smpl 1981:1 1983:4
print y fc1 fc2 fcdiff --byobs
```

The output from the last command is:

```
                    y           fc1          fc2        fcdiff
  1981:1       7.964086     7.940930      0.02668      0.02668
  1981:2       7.978654     7.997576      0.03349      0.03349
  1981:3       8.009463     7.997503      0.01885      0.01885
  1981:4       8.015625     8.033695      0.02423      0.02423
  1982:1       8.014997     8.029698      0.01407      0.01407
  1982:2       8.026562     8.046037      0.01634      0.01634
  1982:3       8.032717     8.063636      0.01760      0.01760
  1982:4       8.042249     8.081935      0.01830      0.01830
  1983:1       8.062685     8.100623      0.01869      0.01869
  1983:2       8.091627     8.119528      0.01891      0.01891
  1983:3       8.115700     8.138554      0.01903      0.01903
  1983:4       8.140811     8.157646      0.01909      0.01909
```

Chapter 21

# Cointegration and Vector Error Correction Models

## 21.1 Introduction

The twin concepts of cointegration and error correction have drawn a good deal of attention in macroeconometrics over recent years. The attraction of the Vector Error Correction Model (VECM) is that it allows the researcher to embed a representation of economic equilibrium relationships within a relatively rich time-series specification. This approach overcomes the old dichotomy between (a) structural models that faithfully represented macroeconomic theory but failed to fit the data, and (b) time-series models that were accurately tailored to the data but difficult if not impossible to interpret in economic terms.

The basic idea of cointegration relates closely to the concept of unit roots (see section 20.3). Suppose we have a set of macroeconomic variables of interest, and we find we cannot reject the hypothesis that some of these variables, considered individually, are non-stationary. Specifically, suppose we judge that a subset of the variables are individually integrated of order 1, or I(1). That is, while they are non-stationary in their levels, their first differences are stationary. Given the statistical problems associated with the analysis of non-stationary data (for example, the threat of spurious regression), the traditional approach in this case was to take first differences of all the variables before proceeding with the analysis.

But this can result in the loss of important information. It may be that while the variables in question are I(1) when taken individually, there exists a linear combination of the variables that is stationary without differencing, or I(0). (There could be more than one such linear combination.) That is, while the ensemble of variables may be "free to wander" over time, nonetheless the variables are "tied together" in certain ways. And it may be possible to interpret these ties, or *cointegrating vectors*, as representing equilibrium conditions.

For example, suppose we find some or all of the following variables are I(1): money stock, $M$, the price level, $P$, the nominal interest rate, $R$, and output, $Y$. According to standard theories of the demand for money, we would nonetheless expect there to be an equilibrium relationship between real balances, interest rate and output; for example

$$m - p = \gamma_0 + \gamma_1 y + \gamma_2 r \qquad \gamma_1 > 0, \gamma_2 < 0$$

where lower-case variable names denote logs. In equilibrium, then,

$$m - p - \gamma_1 y - \gamma_2 r = \gamma_0$$

Realistically, we should not expect this condition to be satisfied each period. We need to allow for the possibility of short-run disequilibrium. But if the system moves back towards equilibrium following a disturbance, it follows that the vector $x = (m, p, y, r)'$ is bound by a cointegrating vector $\beta' = (\beta_1, \beta_2, \beta_3, \beta_4)$, such that $\beta' x$ is stationary (with a mean of $\gamma_0$). Furthermore, if equilibrium is correctly characterized by the simple model above, we have $\beta_2 = -\beta_1$, $\beta_3 < 0$ and $\beta_4 > 0$. These things are testable within the context of cointegration analysis.

There are typically three steps in this sort of analysis:

1. Test to determine the number of cointegrating vectors, the *cointegrating rank* of the system.
2. Estimate a VECM with the appropriate rank, but subject to no further restrictions.

3. Probe the interpretation of the cointegrating vectors as equilibrium conditions by means of restrictions on the elements of these vectors.

The following sections expand on each of these points, giving further econometric details and explaining how to implement the analysis using gretl.

## 21.2 Vector Error Correction Models as representation of a cointegrated system

Consider a VAR of order $p$ with a deterministic part given by $\mu_t$ (typically, a polynomial in time). One can write the $n$-variate process $y_t$ as

$$y_t = \mu_t + A_1 y_{t-1} + A_2 y_{t-2} + \cdots + A_p y_{t-p} + \epsilon_t \tag{21.1}$$

But since $y_{t-1} \equiv y_t - \Delta y_t$ and $y_{t-i} \equiv y_{t-1} - (\Delta y_{t-1} + \Delta y_{t-2} + \cdots + \Delta y_{t-i+1})$, we can re-write the above as

$$\Delta y_t = \mu_t + \Pi y_{t-1} + \sum_{i=1}^{p-1} \Gamma_i \Delta y_{t-i} + \epsilon_t, \tag{21.2}$$

where $\Pi = \sum_{i=1}^{p} A_i$ and $\Gamma_k = -\sum_{i=k}^{p} A_i$. This is the VECM representation of (21.1).

The interpretation of (21.2) depends crucially on $r$, the rank of the matrix $\Pi$.

- If $r = 0$, the processes are all I(1) and not cointegrated.
- If $r = n$, then $\Pi$ is invertible and the processes are all I(0).
- Cointegration occurs in between, when $0 < r < n$ and $\Pi$ can be written as $\alpha\beta'$. In this case, $y_t$ is I(1), but the combination $z_t = \beta' y_t$ is I(0). If, for example, $r = 1$ and the first element of $\beta$ was $-1$, then one could write $z_t = -y_{1,t} + \beta_2 y_{2,t} + \cdots + \beta_n y_{n,t}$, which is equivalent to saying that

  $$y_{1_t} = \beta_2 y_{2,t} + \cdots + \beta_n y_{n,t} - z_t$$

  is a long-run equilibrium relationship: the deviations $z_t$ may not be 0 but they are stationary. In this case, (21.2) can be written as

  $$\Delta y_t = \mu_t + \alpha\beta' y_{t-1} + \sum_{i=1}^{p-1} \Gamma_i \Delta y_{t-i} + \epsilon_t. \tag{21.3}$$

  If $\beta$ were known, then $z_t$ would be observable and all the remaining parameters could be estimated via OLS. In practice, the procedure estimates $\beta$ first and then the rest.

The rank of $\Pi$ is investigated by computing the eigenvalues of a closely related matrix whose rank is the same as $\Pi$: however, this matrix is by construction symmetric and positive semidefinite. As a consequence, all its eigenvalues are real and non-negative, and tests on the rank of $\Pi$ can therefore be carried out by testing how many eigenvalues are 0.

If all the eigenvalues are significantly different from 0, then all the processes are stationary. If, on the contrary, there is at least one zero eigenvalue, then the $y_t$ process is integrated, although some linear combination $\beta' y_t$ might be stationary. At the other extreme, if no eigenvalues are significantly different from 0, then not only is the process $y_t$ non-stationary, but the same holds for any linear combination $\beta' y_t$; in other words, no cointegration occurs.

Estimation typically proceeds in two stages: first, a sequence of tests is run to determine $r$, the cointegration rank. Then, for a given rank the parameters in equation (21.3) are estimated. The two commands that gretl offers for estimating these systems are `coint2` and `vecm`, respectively.

The syntax for `coint2` is

```
coint2 p ylist [ ; xlist [ ; zlist ] ]
```

where p is the number of lags in (21.1); ylist is a list containing the $y_t$ variables; xlist is an optional list of exogenous variables; and zlist is another optional list of exogenous variables whose effects are assumed to be confined to the cointegrating relationships.

The syntax for vecm is

```
    vecm p r ylist [ ; xlist [ ; zlist ] ]
```

where p is the number of lags in (21.1); r is the cointegration rank; and the lists ylist, xlist and zlist have the same interpretation as in coint2.

Both commands can be given specific options to handle the treatment of the deterministic component $\mu_t$. These are discussed in the following section.

## 21.3 Interpretation of the deterministic components

Statistical inference in the context of a cointegrated system depends on the hypotheses one is willing to make on the deterministic terms, which leads to the famous "five cases."

In equation (21.2), the term $\mu_t$ is usually understood to take the form

$$\mu_t = \mu_0 + \mu_1 \cdot t.$$

In order to have the model mimic as closely as possible the features of the observed data, there is a preliminary question to settle. Do the data appear to follow a deterministic trend? If so, is it linear or quadratic?

Once this is established, one should impose restrictions on $\mu_0$ and $\mu_1$ that are consistent with this judgement. For example, suppose that the data do not exhibit a discernible trend. This means that $\Delta y_t$ is on average zero, so it is reasonable to assume that its expected value is also zero. Write equation (21.2) as

$$\Gamma(L)\Delta y_t = \mu_0 + \mu_1 \cdot t + \alpha z_{t-1} + \epsilon_t, \tag{21.4}$$

where $z_t = \beta' y_t$ is assumed to be stationary and therefore to possess finite moments. Taking unconditional expectations, we get

$$0 = \mu_0 + \mu_1 \cdot t + \alpha m_z.$$

Since the left-hand side does not depend on $t$, the restriction $\mu_1 = 0$ is a safe bet. As for $\mu_0$, there are just two ways to make the above expression true: either $\mu_0 = 0$ with $m_z = 0$, or $\mu_0$ equals $-\alpha m_z$. The latter possibility is less restrictive in that the vector $\mu_0$ may be non-zero, but is constrained to be a linear combination of the columns of $\alpha$. In that case, $\mu_0$ can be written as $\alpha \cdot c$, and one may write (21.4) as

$$\Gamma(L)\Delta y_t = \alpha \begin{bmatrix} \beta' & c \end{bmatrix} \begin{bmatrix} y_{t-1} \\ 1 \end{bmatrix} + \epsilon_t.$$

The long-run relationship therefore contains an intercept. This type of restriction is usually written

$$\alpha'_\perp \mu_0 = 0,$$

where $\alpha_\perp$ is the left null space of the matrix $\alpha$.

An intuitive understanding of the issue can be gained by means of a simple example. Consider a series $x_t$ which behaves as follows

$$x_t = m + x_{t-1} + \varepsilon_t$$

where $m$ is a real number and $\varepsilon_t$ is a white noise process: $x_t$ is then a random walk with drift $m$. In the special case $m = 0$, the drift disappears and $x_t$ is a pure random walk.

Consider now another process $y_t$, defined by

$$y_t = k + x_t + u_t$$

where, again, $k$ is a real number and $u_t$ is a white noise process. Since $u_t$ is stationary by definition, $x_t$ and $y_t$ cointegrate: that is, their difference

$$z_t = y_t - x_t = k + u_t$$

is a stationary process. For $k = 0$, $z_t$ is simple zero-mean white noise, whereas for $k \neq 0$ the process $z_t$ is white noise with a non-zero mean.

After some simple substitutions, the two equations above can be represented jointly as a VAR(1) system

$$\begin{bmatrix} y_t \\ x_t \end{bmatrix} = \begin{bmatrix} k+m \\ m \end{bmatrix} + \begin{bmatrix} 0 & 1 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} y_{t-1} \\ x_{t-1} \end{bmatrix} + \begin{bmatrix} u_t + \varepsilon_t \\ \varepsilon_t \end{bmatrix}$$

or in VECM form

$$\begin{aligned} \begin{bmatrix} \Delta y_t \\ \Delta x_t \end{bmatrix} &= \begin{bmatrix} k+m \\ m \end{bmatrix} + \begin{bmatrix} -1 & 1 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} y_{t-1} \\ x_{t-1} \end{bmatrix} + \begin{bmatrix} u_t + \varepsilon_t \\ \varepsilon_t \end{bmatrix} = \\ &= \begin{bmatrix} k+m \\ m \end{bmatrix} + \begin{bmatrix} -1 \\ 0 \end{bmatrix} \begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} y_{t-1} \\ x_{t-1} \end{bmatrix} + \begin{bmatrix} u_t + \varepsilon_t \\ \varepsilon_t \end{bmatrix} = \\ &= \mu_0 + \alpha\beta' \begin{bmatrix} y_{t-1} \\ x_{t-1} \end{bmatrix} + \eta_t = \mu_0 + \alpha z_{t-1} + \eta_t, \end{aligned}$$

where $\beta$ is the cointegration vector and $\alpha$ is the "loadings" or "adjustments" vector.

We are now ready to consider three possible cases:

1. $m \neq 0$: In this case $x_t$ is trended, as we just saw; it follows that $y_t$ also follows a linear trend because on average it keeps at a fixed distance $k$ from $x_t$. The vector $\mu_0$ is unrestricted.

2. $m = 0$ and $k \neq 0$: In this case, $x_t$ is not trended and as a consequence neither is $y_t$. However, the mean distance between $y_t$ and $x_t$ is non-zero. The vector $\mu_0$ is given by

   $$\mu_0 = \begin{bmatrix} k \\ 0 \end{bmatrix}$$

   which is not null and therefore the VECM shown above does have a constant term. The constant, however, is subject to the restriction that its second element must be 0. More generally, $\mu_0$ is a multiple of the vector $\alpha$. Note that the VECM could also be written as

   $$\begin{bmatrix} \Delta y_t \\ \Delta x_t \end{bmatrix} = \begin{bmatrix} -1 \\ 0 \end{bmatrix} \begin{bmatrix} 1 & -1 & -k \end{bmatrix} \begin{bmatrix} y_{t-1} \\ x_{t-1} \\ 1 \end{bmatrix} + \begin{bmatrix} u_t + \varepsilon_t \\ \varepsilon_t \end{bmatrix}$$

   which incorporates the intercept into the cointegration vector. This is known as the "restricted constant" case.

3. $m = 0$ and $k = 0$: This case is the most restrictive: clearly, neither $x_t$ nor $y_t$ are trended, and the mean distance between them is zero. The vector $\mu_0$ is also 0, which explains why this case is referred to as "no constant."

In most cases, the choice between these three possibilities is based on a mix of empirical observation and economic reasoning. If the variables under consideration seem to follow a linear trend then we should not place any restriction on the intercept. Otherwise, the question arises of whether it makes sense to specify a cointegration relationship which includes a non-zero intercept. One example where this is appropriate is the relationship between two interest rates: generally these are not trended, but the VAR might still have an intercept because the difference between the two (the "interest rate spread") might be stationary around a non-zero mean (for example, because of a risk or liquidity premium).

The previous example can be generalized in three directions:

1. If a VAR of order greater than 1 is considered, the algebra gets more convoluted but the conclusions are identical.
2. If the VAR includes more than two endogenous variables the cointegration rank $r$ can be greater than 1. In this case, $\alpha$ is a matrix with $r$ columns, and the case with restricted constant entails the restriction that $\mu_0$ should be some linear combination of the columns of $\alpha$.
3. If a linear trend is included in the model, the deterministic part of the VAR becomes $\mu_0 + \mu_1 t$. The reasoning is practically the same as above except that the focus now centers on $\mu_1$ rather than $\mu_0$. The counterpart to the "restricted constant" case discussed above is a "restricted trend" case, such that the cointegration relationships include a trend but the first differences of the variables in question do not. In the case of an unrestricted trend, the trend appears in both the cointegration relationships and the first differences, which corresponds to the presence of a quadratic trend in the variables themselves (in levels).

In order to accommodate the five cases, gretl provides the following options to the `coint2` and `vecm` commands:

| $\mu_t$ | *option flag* | *description* |
|---|---|---|
| $0$ | `--nc` | no constant |
| $\mu_0, \alpha'_\perp \mu_0 = 0$ | `--rc` | restricted constant |
| $\mu_0$ | default | unrestricted constant |
| $\mu_0 + \mu_1 t, \alpha'_\perp \mu_1 = 0$ | `--crt` | constant + restricted trend |
| $\mu_0 + \mu_1 t$ | `--ct` | constant + unrestricted trend |

Note that for this command the above options are mutually exclusive. In addition, you have the option of using the `--seasonal` options, for augmenting $\mu_t$ with centered seasonal dummies. In each case, p-values are computed via the approximations by Doornik (1998).

## 21.4 The Johansen cointegration tests

The two Johansen tests for cointegration are used to establish the rank of $\beta$; in other words, how many cointegration vectors the system has. These are the "$\lambda$-max" test, for hypotheses on individual eigenvalues, and the "trace" test, for joint hypotheses. Suppose that the eigenvalues $\lambda_i$ are sorted from largest to smallest. The null hypothesis for the "$\lambda$-max" test on the $i$-th eigenvalue is that $\lambda_i = 0$. The corresponding trace test, instead, considers the hypothesis $\lambda_j = 0$ for all $j \geq i$.

The gretl command `coint2` performs these two tests. The corresponding menu entry in the GUI is "Model, Time Series, Cointegration Test, Johansen".

As in the ADF test, the asymptotic distribution of the tests varies with the deterministic component $\mu_t$ one includes in the VAR (see section 21.3 above). The following code uses the `denmark` data file, supplied with gretl, to replicate Johansen's example found in his 1995 book.

```
open denmark
coint2 2 LRM LRY IBO IDE --rc --seasonal
```

In this case, the vector $y_t$ in equation (21.2) comprises the four variables `LRM`, `LRY`, `IBO`, `IDE`. The number of lags equals $p$ in (21.2) (that is, the number of lags of the model written in VAR form). Part of the output is reported below:

```
Johansen test:
Number of equations = 4
Lag order = 2
Estimation period: 1974:3 - 1987:3 (T = 53)

Case 2: Restricted constant
Rank Eigenvalue Trace test p-value   Lmax test  p-value
   0    0.43317     49.144 [0.1284]     30.087 [0.0286]
   1    0.17758     19.057 [0.7833]     10.362 [0.8017]
   2    0.11279     8.6950 [0.7645]     6.3427 [0.7483]
   3   0.043411     2.3522 [0.7088]     2.3522 [0.7076]
```

Both the trace and λ-max tests accept the null hypothesis that the smallest eigenvalue is 0 (see the last row of the table), so we may conclude that the series are in fact non-stationary. However, some linear combination may be I(0), since the λ-max test rejects the hypothesis that the rank of $\Pi$ is 0 (though the trace test gives less clear-cut evidence for this, with a p-value of 0.1284).

## 21.5 Identification of the cointegration vectors

The core problem in the estimation of equation (21.2) is to find an estimate of $\Pi$ that has by construction rank $r$, so it can be written as $\Pi = \alpha\beta'$, where $\beta$ is the matrix containing the cointegration vectors and $\alpha$ contains the "adjustment" or "loading" coefficients whereby the endogenous variables respond to deviation from equilibrium in the previous period.

Without further specification, the problem has multiple solutions (in fact, infinitely many). The parameters $\alpha$ and $\beta$ are under-identified: if all columns of $\beta$ are cointegration vectors, then any arbitrary linear combinations of those columns is a cointegration vector too. To put it differently, if $\Pi = \alpha_0\beta_0'$ for specific matrices $\alpha_0$ and $\beta_0$, then $\Pi$ also equals $(\alpha_0 Q)(Q^{-1}\beta_0')$ for any conformable non-singular matrix $Q$. In order to find a unique solution, it is therefore necessary to impose some restrictions on $\alpha$ and/or $\beta$. It can be shown that the minimum number of restrictions that is necessary to guarantee identification is $r^2$. Normalizing one coefficient per column to 1 (or $-1$, according to taste) is a trivial first step, which also helps in that the remaining coefficients can be interpreted as the parameters in the equilibrium relations, but this only suffices when $r = 1$.

The method that gretl uses by default is known as the "Phillips normalization", or "triangular representation".[1] The starting point is writing $\beta$ in partitioned form as in

$$\beta = \left[ \begin{array}{c} \beta_1 \\ \beta_2 \end{array} \right],$$

where $\beta_1$ is an $r \times r$ matrix and $\beta_2$ is $(n - r) \times r$. Assuming that $\beta_1$ has full rank, $\beta$ can be post-multiplied by $\beta_1^{-1}$, giving

$$\hat{\beta} = \left[ \begin{array}{c} I \\ \beta_2\beta_1^{-1} \end{array} \right] = \left[ \begin{array}{c} I \\ -B \end{array} \right],$$

The coefficients that gretl produces are $\hat{\beta}$, with $B$ known as the matrix of unrestricted coefficients. In terms of the underlying equilibrium relationship, the Phillips normalization expresses the system

[1] For comparison with other studies, you may wish to normalize $\beta$ differently. Using the `set` command you can do `set vecm_norm diag` to select a normalization that simply scales the columns of the original $\beta$ such that $\beta_{ij} = 1$ for $i = j$ and $i \leq r$, as used in the empirical section of Boswijk and Doornik (2004). Another alternative is `set vecm_norm first`, which scales $\beta$ such that the elements on the first row equal 1. To suppress normalization altogether, use `set vecm_norm none`. (To return to the default: `set vecm_norm phillips`.)

of $r$ equilibrium relations as

$$\begin{aligned}
y_{1,t} &= b_{1,r+1}y_{r+1,t} + \ldots + b_{1,n}y_{n,t} \\
y_{2,t} &= b_{2,r+1}y_{r+1,t} + \ldots + b_{2,n}y_{n,t} \\
&\vdots \\
y_{r,t} &= b_{r,r+1}y_{r+1,t} + \ldots + b_{r,n}y_{r,t}
\end{aligned}$$

where the first $r$ variables are expressed as functions of the remaining $n - r$.

Although the triangular representation ensures that the statistical problem of estimating $\beta$ is solved, the resulting equilibrium relationships may be difficult to interpret. In this case, the user may want to achieve identification by specifying manually the system of $r^2$ constraints that gretl will use to produce an estimate of $\beta$.

As an example, consider the money demand system presented in section 9.6 of Verbeek (2004). The variables used are m (the log of real money stock M1), infl (inflation), cpr (the commercial paper rate), y (log of real GDP) and tbr (the Treasury bill rate).[2]

Estimation of $\beta$ can be performed via the commands

```
open money.gdt
smpl 1954:1 1994:4
vecm 6 2 m infl cpr y tbr --rc
```

and the relevant portion of the output reads

```
Maximum likelihood estimates, observations 1954:1-1994:4 (T = 164)
Cointegration rank = 2
Case 2: Restricted constant

beta (cointegrating vectors, standard errors in parentheses)

m            1.0000       0.0000
            (0.0000)     (0.0000)
infl         0.0000       1.0000
            (0.0000)     (0.0000)
cpr         0.56108      -24.367
           (0.10638)     (4.2113)
y          -0.40446     -0.91166
           (0.10277)     (4.0683)
tbr        -0.54293       24.786
           (0.10962)     (4.3394)
const       -3.7483       16.751
           (0.78082)     (30.909)
```

Interpretation of the coefficients of the cointegration matrix $\beta$ would be easier if a meaning could be attached to each of its columns. This is possible by hypothesizing the existence of two long-run relationships: a money demand equation

$$\texttt{m} = c_1 + \beta_1\texttt{infl} + \beta_2\texttt{y} + \beta_3\texttt{tbr}$$

and a risk premium equation

$$\texttt{cpr} = c_2 + \beta_4\texttt{infl} + \beta_5\texttt{y} + \beta_6\texttt{tbr}$$

[2] This data set is available in the verbeek data package; see http://gretl.sourceforge.net/gretl_data.html.

which imply that the cointegration matrix can be normalized as

$$\beta = \begin{bmatrix} -1 & 0 \\ \beta_1 & \beta_4 \\ 0 & -1 \\ \beta_2 & \beta_5 \\ \beta_3 & \beta_6 \\ c_1 & c_2 \end{bmatrix}$$

This renormalization can be accomplished by means of the `restrict` command, to be given after the `vecm` command or, in the graphical interface, by selecting the "Test, Linear Restrictions" menu entry. The syntax for entering the restrictions should be fairly obvious:[3]

```
restrict
  b[1,1] = -1
  b[1,3] = 0
  b[2,1] = 0
  b[2,3] = -1
end restrict
```

which produces

```
Cointegrating vectors (standard errors in parentheses)

m           -1.0000       0.0000
            (0.0000)     (0.0000)
infl     -0.023026      0.041039
        (0.0054666)   (0.027790)
cpr         0.0000      -1.0000
           (0.0000)     (0.0000)
y          0.42545     -0.037414
         (0.033718)    (0.17140)
tbr      -0.027790        1.0172
        (0.0045445)   (0.023102)
const       3.3625       0.68744
          (0.25318)     (1.2870)
```

## 21.6 Over-identifying restrictions

One purpose of imposing restrictions on a VECM system is simply to achieve identification. If these restrictions are simply normalizations, they are not testable and should have no effect on the maximized likelihood. In addition, however, one may wish to formulate constraints on $\beta$ and/or $\alpha$ that derive from the economic theory underlying the equilibrium relationships; substantive restrictions of this sort are then testable via a likelihood-ratio statistic.

Gretl is capable of testing general linear restrictions of the form

$$R_b \text{vec}(\beta) = q \tag{21.5}$$

and/or

$$R_a \text{vec}(\alpha) = 0 \tag{21.6}$$

Note that the $\beta$ restriction may be non-homogeneous ($q \neq 0$) but the $\alpha$ restriction must be homogeneous. Nonlinear restrictions are not supported, and neither are restrictions that cross between

[3] Note that in this context we are bending the usual matrix indexation convention, using the leading index to refer to the *column* of $\beta$ (the particular cointegrating vector). This is standard practice in the literature, and defensible insofar as it is the columns of $\beta$ (the cointegrating relations or equilibrium errors) that are of primary interest.

$\beta$ and $\alpha$. In the case where $r > 1$ such restrictions may be in common across all the columns of $\beta$ (or $\alpha$) or may be specific to certain columns of these matrices. This is the case discussed in Boswijk (1995) and Boswijk and Doornik (2004, section 4.4).

The restrictions (21.5) and (21.6) may be written in explicit form as

$$\mathrm{vec}(\beta) = H\phi + h_0 \tag{21.7}$$

and

$$\mathrm{vec}(\alpha') = G\psi \tag{21.8}$$

respectively, where $\phi$ and $\psi$ are the free parameter vectors associated with $\beta$ and $\alpha$ respectively. We may refer to the free parameters collectively as $\theta$ (the column vector formed by concatenating $\phi$ and $\psi$). Gretl uses this representation internally when testing the restrictions.

If the list of restrictions that is passed to the `restrict` command contains more constraints than necessary to achieve identification, then an LR test is performed; moreover, the `restrict` command can be given the `--full` switch, in which case full estimates for the restricted system are printed (including the $\Gamma_i$ terms), and the system thus restricted becomes the "current model" for the purposes of further tests. Thus you are able to carry out cumulative tests, as in Chapter 7 of Johansen (1995).

### Syntax

The full syntax for specifying the restriction is an extension of the one exemplified in the previous section. Inside a `restrict...end restrict` block, valid statements are of the form

*parameter linear combination* = *scalar*

where a parameter linear combination involves a weighted sum of individual elements of $\beta$ or $\alpha$ (but not both in the same combination); the scalar on the right-hand side must be 0 for combinations involving $\alpha$, but can be any real number for combinations involving $\beta$. Below, we give a few examples of valid restrictions:

```
    b[1,1] = 1.618
    b[1,4] + 2*b[2,5] = 0
    a[1,3] = 0
    a[1,1] - a[1,2] = 0
```

A special syntax is reserved for the case when a certain constraint should be applied to all columns of $\beta$: in this case, one index is given for each `b` term, and the square brackets are dropped. Hence, the following syntax

```
  restrict
    b1 + b2 = 0
  end restrict
```

corresponds to

$$\beta = \begin{bmatrix} \beta_{11} & \beta_{21} \\ -\beta_{11} & -\beta_{21} \\ \beta_{13} & \beta_{23} \\ \beta_{14} & \beta_{24} \end{bmatrix}$$

The same convention is used for $\alpha$: when only one index is given for each `a` term, the restriction is presumed to apply to all $r$ rows of $\alpha$, or in other words the given variables are weakly exogenous. For instance, the formulation

```
restrict
  a3 = 0
  a4 = 0
end restrict
```

specifies that variables 3 and 4 do not respond to the deviation from equilibrium in the previous period.

Finally, a short-cut is available for setting up complex restrictions (but currently only in relation to $\beta$): you can specify $R_b$ and $q$, as in $R_b\text{vec}(\beta) = q$, by giving the names of previously defined matrices. For example,

```
matrix I4 = I(4)
matrix vR = I4**(I4~zeros(4,1))
matrix vq = mshape(I4,16,1)
restrict
  R = vR
  q = vq
end restrict
```

which manually imposes Phillips normalization on the $\beta$ estimates for a system with cointegrating rank 4.

### An example

Brand and Cassola (2004) propose a money demand system for the Euro area, in which they postulate three long-run equilibrium relationships:

| | |
|---|---|
| money demand | $m = \beta_l l + \beta_y y$ |
| Fisher equation | $\pi = \phi l$ |
| Expectation theory of interest rates | $l = s$ |

where $m$ is real money demand, $l$ and $s$ are long- and short-term interest rates, $y$ is output and $\pi$ is inflation.[4] (The names for these variables in the gretl data file are `m_p`, `rl`, `rs`, `y` and `infl`, respectively.)

The cointegration rank assumed by the authors is 3 and there are 5 variables, giving 15 elements in the $\beta$ matrix. $3 \times 3 = 9$ restrictions are required for identification, and a just-identified system would have $15 - 9 = 6$ free parameters. However, the postulated long-run relationships feature only three free parameters, so the over-identification rank is 3.

Example 21.1 replicates Table 4 on page 824 of the Brand and Cassola article.[5] Note that we use the `$lnl` accessor after the `vecm` command to store the unrestricted log-likelihood and the `$rlnl` accessor after `restrict` for its restricted counterpart.

The example continues in script 21.2, where we perform further testing to check whether (a) the income elasticity in the money demand equation is 1 ($\beta_y = 1$) and (b) the Fisher relation is homogeneous ($\phi = 1$). Since the `--full` switch was given to the initial `restrict` command, additional restrictions can be applied without having to repeat the previous ones. (The second script contains a few `printf` commands, which are not strictly necessary, to format the output nicely.) It turns out that both of the additional hypotheses are rejected by the data, with p-values of 0.002 and 0.004.

[4] A traditional formulation of the Fisher equation would reverse the roles of the variables in the second equation, but this detail is immaterial in the present context; moreover, the expectation theory of interest rates implies that the third equilibrium relationship should include a constant for the liquidity premium. However, since in this example the system is estimated with the constant term unrestricted, the liquidity premium gets merged in the system intercept and disappears from $z_t$.

[5] Modulo what appear to be a few typos in the article.

**Example 21.1**: Estimation of a money demand system with constraints on $\beta$

Input:

```
open brand_cassola.gdt

# perform a few transformations
m_p = m_p*100
y = y*100
infl = infl/4
rs = rs/4
rl = rl/4

# replicate table 4, page 824
vecm 2 3 m_p infl rl rs y -q
genr ll0 = $lnl

restrict --full
  b[1,1] = 1
  b[1,2] = 0
  b[1,4] = 0
  b[2,1] = 0
  b[2,2] = 1
  b[2,4] = 0
  b[2,5] = 0
  b[3,1] = 0
  b[3,2] = 0
  b[3,3] = 1
  b[3,4] = -1
  b[3,5] = 0
end restrict
genr ll1 = $rlnl
```

Partial output:

```
Unrestricted loglikelihood (lu) = 116.60268
Restricted loglikelihood (lr) = 115.86451
2 * (lu - lr) = 1.47635
P(Chi-Square(3) > 1.47635) = 0.68774

beta (cointegrating vectors, standard errors in parentheses)

m_p        1.0000       0.0000       0.0000
          (0.0000)     (0.0000)     (0.0000)
infl       0.0000       1.0000       0.0000
          (0.0000)     (0.0000)     (0.0000)
rl         1.6108     -0.67100       1.0000
         (0.62752)   (0.049482)     (0.0000)
rs         0.0000       0.0000      -1.0000
          (0.0000)     (0.0000)     (0.0000)
y         -1.3304       0.0000       0.0000
        (0.030533)     (0.0000)     (0.0000)
```

**Example 21.2**: Further testing of money demand system

Input:

```
restrict
  b[1,5] = -1
end restrict
genr ll_uie = $rlnl

restrict
  b[2,3] = -1
end restrict
genr ll_hfh = $rlnl

# replicate table 5, page 824
printf "Testing zero restrictions in cointegration space:\n"
printf "  LR-test, rank = 3: chi^2(3) = %6.4f [%6.4f]\n", 2*(ll0-ll1), \
        pvalue(X, 3, 2*(ll0-ll1))

printf "Unit income elasticity: LR-test, rank = 3:\n"
printf "  chi^2(4) = %g [%6.4f]\n", 2*(ll0-ll_uie), \
        pvalue(X, 4, 2*(ll0-ll_uie))

printf "Homogeneity in the Fisher hypothesis:\n"
printf "  LR-test, rank = 3: chi^2(4) = %6.3f [%6.4f]\n", 2*(ll0-ll_hfh), \
        pvalue(X, 4, 2*(ll0-ll_hfh))
```

Output:

```
Testing zero restrictions in cointegration space:
  LR-test, rank = 3: chi^2(3) = 1.4763 [0.6877]
Unit income elasticity: LR-test, rank = 3:
  chi^2(4) = 17.2071 [0.0018]
Homogeneity in the Fisher hypothesis:
  LR-test, rank = 3: chi^2(4) = 15.547 [0.0037]
```

Another type of test that is commonly performed is the "weak exogeneity" test. In this context, a variable is said to be weakly exogenous if all coefficients on the corresponding row in the $\alpha$ matrix are zero. If this is the case, that variable does not adjust to deviations from any of the long-run equilibria and can be considered an autonomous driving force of the whole system.

The code in Example 21.3 performs this test for each variable in turn, thus replicating the first column of Table 6 on page 825 of Brand and Cassola (2004). The results show that weak exogeneity might perhaps be accepted for the long-term interest rate and real GDP (p-values 0.07 and 0.08 respectively).

### Identification and testability

One point regarding VECM restrictions that can be confusing at first is that identification (does the restriction identify the system?) and testability (is the restriction testable?) are quite separate matters. Restrictions can be identifying but not testable; less obviously, they can be testable but not identifying.

This can be seen quite easily in relation to a rank-1 system. The restriction $\beta_1 = 1$ is identifying (it pins down the scale of $\beta$) but, being a pure scaling, it is not testable. On the other hand, the restriction $\beta_1 + \beta_2 = 0$ is testable — the system with this requirement imposed will almost certainly have a lower maximized likelihood — but it is not identifying; it still leaves open the scale of $\beta$.

We said above that the number of restrictions must equal at least $r^2$, where $r$ is the cointegrating

**Example 21.3**: Testing for weak exogeneity

Input:

```
restrict
  a1 = 0
end restrict
ts_m = 2*(ll0 - $rlnl)

restrict
  a2 = 0
end restrict
ts_p = 2*(ll0 - $rlnl)

restrict
  a3 = 0
end restrict
ts_l = 2*(ll0 - $rlnl)

restrict
  a4 = 0
end restrict
ts_s = 2*(ll0 - $rlnl)

restrict
  a5 = 0
end restrict
ts_y = 2*(ll0 - $rlnl)

loop foreach i m p l s y --quiet
  printf "\Delta $i\t%6.3f [%6.4f]\n", ts_$i, pvalue(X, 6, ts_$i)
end loop
```

Output (variable, LR test, p-value):

```
\Delta m        18.111 [0.0060]
\Delta p        21.067 [0.0018]
\Delta l        11.819 [0.0661]
\Delta s        16.000 [0.0138]
\Delta y        11.335 [0.0786]
```

rank, for identification. This is a necessary and not a sufficient condition. In fact, when $r > 1$ it can be quite tricky to assess whether a given set of restrictions is identifying. Gretl uses the method suggested by Doornik (1995), where identification is assessed via the rank of the information matrix.

It can be shown that for restrictions of the sort (21.7) and (21.8) the information matrix has the same rank as the Jacobian matrix

$$\mathcal{J}(\theta) = \left[(I_p \otimes \beta)G : (\alpha \otimes I_{p_1})H\right]$$

A sufficient condition for identification is that the rank of $\mathcal{J}(\theta)$ equals the number of free parameters. The rank of this matrix is evaluated by examination of its singular values at a randomly selected point in the parameter space. For practical purposes we treat this condition as if it were both necessary and sufficient; that is, we disregard the special cases where identification could be achieved without this condition being met.[6]

[6] See Boswijk and Doornik (2004, pp. 447–8) for discussion of this point.

## 21.7 Numerical solution methods

In general, the ML estimator for the restricted VECM problem has no closed form solution, hence the maximum must be found via numerical methods.[7] In some cases convergence may be difficult, and gretl provides several choices to solve the problem.

### Switching and LBFGS

Two maximization methods are available in gretl. The default is the switching algorithm set out in Boswijk and Doornik (2004). The alternative is a limited-memory variant of the BFGS algorithm (LBFGS), using analytical derivatives. This is invoked using the `--lbfgs` flag with the `restrict` command.

The switching algorithm works by explicitly maximizing the likelihood at each iteration, with respect to $\hat{\phi}$, $\hat{\psi}$ and $\hat{\Omega}$ (the covariance matrix of the residuals) in turn. This method shares a feature with the basic Johansen eigenvalues procedure, namely, it can handle a set of restrictions that does not fully identify the parameters.

LBFGS, on the other hand, requires that the model be fully identified. When using LBFGS, therefore, you may have to supplement the restrictions of interest with normalizations that serve to identify the parameters. For example, one might use all or part of the Phillips normalization (see section 21.5).

Neither the switching algorithm nor LBFGS is guaranteed to find the global ML solution.[8] The optimizer may end up at a local maximum (or, in the case of the switching algorithm, at a saddle point).

The solution (or lack thereof) may be sensitive to the initial value selected for $\theta$. By default, gretl selects a starting point using a deterministic method based on Boswijk (1995), but two further options are available: the initialization may be adjusted using simulated annealing, or the user may supply an explicit initial value for $\theta$.

The default initialization method is:

1. Calculate the unrestricted ML $\hat{\beta}$ using the Johansen procedure.
2. If the restriction on $\beta$ is non-homogeneous, use the method proposed by Boswijk (1995):

$$\phi_0 = -[(I_r \otimes \hat{\beta}_\perp)'H]^+(I_r \otimes \hat{\beta}_\perp)'h_0 \tag{21.9}$$

   where $\hat{\beta}'_\perp\hat{\beta} = 0$ and $A^+$ denotes the Moore–Penrose inverse of $A$. Otherwise

$$\phi_0 = (H'H)^{-1}H'\text{vec}(\hat{\beta}) \tag{21.10}$$

3. $\text{vec}(\beta_0) = H\phi_0 + h_0$.
4. Calculate the unrestricted ML $\hat{\alpha}$ conditional on $\beta_0$, as per Johansen:

$$\hat{\alpha} = S_{01}\beta_0(\beta_0'S_{11}\beta_0)^{-1} \tag{21.11}$$

5. If $\alpha$ is restricted by $\text{vec}(\alpha') = G\psi$, then $\psi_0 = (G'G)^{-1}G'\,\text{vec}(\hat{\alpha}')$ and $\text{vec}(\alpha_0') = G\psi_0$.

[7] The exception is restrictions that are homogeneous, common to all $\beta$ or all $\alpha$ (in case $r > 1$), and involve either $\beta$ only or $\alpha$ only. Such restrictions are handled via the modified eigenvalues method set out by Johansen (1995). We solve directly for the ML estimator, without any need for iterative methods.

[8] In developing gretl's VECM-testing facilities we have considered a fair number of "tricky cases" from various sources. We'd like to thank Luca Fanelli of the University of Bologna and Sven Schreiber of Goethe University Frankfurt for their help in devising torture-tests for gretl's VECM code.

### Alternative initialization methods

As mentioned above, gretl offers the option of adjusting the initialization using **simulated annealing.** This is invoked by adding the `--jitter` option to the `restrict` command.

The basic idea is this: we start at a certain point in the parameter space, and for each of $n$ iterations (currently $n = 4096$) we randomly select a new point within a certain radius of the previous one, and determine the likelihood at the new point. If the likelihood is higher, we jump to the new point; otherwise, we jump with probability $P$ (and remain at the previous point with probability $1 - P$). As the iterations proceed, the system gradually "cools" — that is, the radius of the random perturbation is reduced, as is the probability of making a jump when the likelihood fails to increase.

In the course of this procedure many points in the parameter space are evaluated, starting with the point arrived at by the deterministic method, which we'll call $\theta_0$. One of these points will be "best" in the sense of yielding the highest likelihood: call it $\theta^*$. This point may or may not have a greater likelihood than $\theta_0$. And the procedure has an end point, $\theta_n$, which may or may not be "best".

The rule followed by gretl in selecting an initial value for $\theta$ based on simulated annealing is this: use $\theta^*$ if $\theta^* > \theta_0$, otherwise use $\theta_n$. That is, if we get an improvement in the likelihood via annealing, we make full use of this; on the other hand, if we fail to get an improvement we nonetheless allow the annealing to randomize the starting point. Experiments indicated that the latter effect can be helpful.

Besides annealing, a further alternative is **manual initialization.** This is done by passing a predefined vector to the `set` command with parameter `initvals`, as in

```
set initvals myvec
```

The details depend on whether the switching algorithm or LBFGS is used. For the switching algorithm, there are two options for specifying the initial values. The more user-friendly one (for most people, we suppose) is to specify a matrix that contains $\text{vec}(\beta)$ followed by $\text{vec}(\alpha)$. For example:

```
open denmark.gdt
vecm 2 1 LRM LRY IBO IDE --rc --seasonals

matrix BA = {1, -1, 6, -6, -6, -0.2, 0.1, 0.02, 0.03}
set initvals BA
restrict
  b[1] = 1
  b[1] + b[2] = 0
  b[3] + b[4] = 0
end restrict
```

In this example — from Johansen (1995) — the cointegration rank is 1 and there are 4 variables. However, the model includes a restricted constant (the `--rc` flag) so that $\beta$ has 5 elements. The $\alpha$ matrix has 4 elements, one per equation. So the matrix BA may be read as

$$(\beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \alpha_1, \alpha_2, \alpha_3, \alpha_4)$$

The other option, which is compulsory when using LBFGS, is to specify the initial values in terms of the free parameters, $\phi$ and $\psi$. Getting this right is somewhat less obvious. As mentioned above, the implicit-form restriction $R\text{vec}(\beta) = q$ has explicit form $\text{vec}(\beta) = H\phi + h_0$, where $H = R_{\perp}$, the right nullspace of $R$. The vector $\phi$ is shorter, by the number of restrictions, than $\text{vec}(\beta)$. The savvy user will then see what needs to be done. The other point to take into account is that if $\alpha$ is unrestricted, the *effective* length of $\psi$ is 0, since it is then optimal to compute $\alpha$ using Johansen's formula, conditional on $\beta$ (equation 21.11 above). The example above could be rewritten as:

```
open denmark.gdt
vecm 2 1 LRM LRY IBO IDE --rc --seasonals
```

```
matrix phi = {-8, -6}
set initvals phi
restrict --lbfgs
  b[1] = 1
  b[1] + b[2] = 0
  b[3] + b[4] = 0
end restrict
```

In this more economical formulation the initializer specifies only the two free parameters in $\phi$ (5 elements in $\beta$ minus 3 restrictions). There is no call to give values for $\psi$ since $\alpha$ is unrestricted.

### Scale removal

Consider a simpler version of the restriction discussed in the previous section, namely,

```
restrict
  b[1] = 1
  b[1] + b[2] = 0
end restrict
```

This restriction comprises a substantive, testable requirement — that $\beta_1$ and $\beta_2$ sum to zero — and a normalization or scaling, $\beta_1 = 1$. The question arises, might it be easier and more reliable to maximize the likelihood without imposing $\beta_1 = 1$?[9] If so, we could record this normalization, remove it for the purpose of maximizing the likelihood, then reimpose it by scaling the result.

Unfortunately it is not possible to say in advance whether "scale removal" of this sort will give better results, for any particular estimation problem. However, this does seem to be the case more often than not. Gretl therefore performs scale removal where feasible, unless you

- explicitly forbid this, by giving the `--no-scaling` option flag to the restrict command; or
- provide a specific vector of initial values; or
- select the LBFGS algorithm for maximization.

Scale removal is deemed infeasible if there are any cross-column restrictions on $\beta$, or any non-homogeneous restrictions involving more than one element of $\beta$.

In addition, experimentation has suggested to us that scale removal is inadvisable if the system is just identified with the normalization(s) included, so we do not do it in that case. By "just identified" we mean that the system would not be identified if any of the restrictions were removed. On that criterion the above example is not just identified, since the removal of the second restriction would not affect identification; and gretl would in fact perform scale removal in this case unless the user specified otherwise.

[9] As a numerical matter, that is. In principle this should make no difference.

## Chapter 22

# Discrete and censored dependent variables

### 22.1 Logit and probit models

It often happens that one wants to specify and estimate a model in which the dependent variable is not continuous, but discrete. A typical example is a model in which the dependent variable is the occupational status of an individual (1 = employed, 0 = unemployed). A convenient way of formalizing this situation is to consider the variable $y_i$ as a Bernoulli random variable and analyze its distribution conditional on the explanatory variables $x_i$. That is,

$$y_i = \begin{cases} 1 & P_i \\ 0 & 1 - P_i \end{cases} \tag{22.1}$$

where $P_i = P(y_i = 1|x_i)$ is a given function of the explanatory variables $x_i$.

In most cases, the function $P_i$ is a cumulative distribution function $F$, applied to a linear combination of the $x_i$s. In the probit model, the normal cdf is used, while the logit model employs the logistic function $\Lambda()$. Therefore, we have

$$\text{probit} \qquad P_i = F(z_i) = \Phi(z_i) \tag{22.2}$$

$$\text{logit} \qquad P_i = F(z_i) = \Lambda(z_i) = \frac{1}{1 + e^{-z_i}} \tag{22.3}$$

$$z_i = \sum_{j=1}^{k} x_{ij}\beta_j \tag{22.4}$$

where $z_i$ is commonly known as the *index* function. Note that in this case the coefficients $\beta_j$ cannot be interpreted as the partial derivatives of $E(y_i|x_i)$ with respect to $x_{ij}$. However, for a given value of $x_i$ it is possible to compute the vector of "slopes", that is

$$\text{slope}_j(\bar{x}) = \left. \frac{\partial F(z)}{\partial x_j} \right|_{z=\bar{z}}$$

Gretl automatically computes the slopes, setting each explanatory variable at its sample mean.

Another, equivalent way of thinking about this model is in terms of an unobserved variable $y_i^*$ which can be described thus:

$$y_i^* = \sum_{j=1}^{k} x_{ij}\beta_j + \varepsilon_i = z_i + \varepsilon_i \tag{22.5}$$

We observe $y_i = 1$ whenever $y_i^* > 0$ and $y_i = 0$ otherwise. If $\varepsilon_i$ is assumed to be normal, then we have the probit model. The logit model arises if we assume that the density function of $\varepsilon_i$ is

$$\lambda(\varepsilon_i) = \frac{\partial \Lambda(\varepsilon_i)}{\partial \varepsilon_i} = \frac{e^{-\varepsilon_i}}{(1 + e^{-\varepsilon_i})^2}$$

Both the probit and logit model are estimated in gretl via maximum likelihood, where the log-likelihood can be written as

$$L(\beta) = \sum_{y_i=0} \ln[1 - F(z_i)] + \sum_{y_i=1} \ln F(z_i), \tag{22.6}$$

which is always negative, since $0 < F(\cdot) < 1$. Since the score equations do not have a closed form solution, numerical optimization is used. However, in most cases this is totally transparent to the user, since usually only a few iterations are needed to ensure convergence. The `--verbose` switch can be used to track the maximization algorithm.

**Example 22.1**: Estimation of simple logit and probit models

```
open greene19_1

logit GRADE const GPA TUCE PSI
probit GRADE const GPA TUCE PSI
```

As an example, we reproduce the results given in Greene (2000), chapter 21, where the effectiveness of a program for teaching economics is evaluated by the improvements of students' grades. Running the code in example 22.1 gives the following output:

```
  Model 1: Logit estimates using the 32 observations 1-32
  Dependent variable: GRADE

        VARIABLE       COEFFICIENT        STDERROR      T STAT       SLOPE
                                                                    (at mean)
    const               -13.0213           4.93132      -2.641
    GPA                   2.82611          1.26294       2.238      0.533859
    TUCE                  0.0951577        0.141554      0.672      0.0179755
    PSI                   2.37869          1.06456       2.234      0.449339

    Mean of GRADE = 0.344
    Number of cases 'correctly predicted' = 26 (81.2%)
    f(beta'x) at mean of independent vars = 0.189
    McFadden's pseudo-R-squared = 0.374038
    Log-likelihood = -12.8896
    Likelihood ratio test: Chi-square(3) = 15.4042 (p-value 0.001502)
    Akaike information criterion (AIC) = 33.7793
    Schwarz Bayesian criterion (BIC) = 39.6422
    Hannan-Quinn criterion (HQC) = 35.7227

             Predicted
               0    1
    Actual 0  18    3
           1   3    8

  Model 2: Probit estimates using the 32 observations 1-32
  Dependent variable: GRADE

        VARIABLE       COEFFICIENT        STDERROR      T STAT       SLOPE
                                                                    (at mean)
    const                -7.45232          2.54247      -2.931
    GPA                   1.62581          0.693883      2.343      0.533347
    TUCE                  0.0517288        0.0838903     0.617      0.0169697
    PSI                   1.42633          0.595038      2.397      0.467908

    Mean of GRADE = 0.344
    Number of cases 'correctly predicted' = 26 (81.2%)
    f(beta'x) at mean of independent vars = 0.328
```

```
McFadden's pseudo-R-squared = 0.377478
Log-likelihood = -12.8188
Likelihood ratio test: Chi-square(3) = 15.5459 (p-value 0.001405)
Akaike information criterion (AIC) = 33.6376
Schwarz Bayesian criterion (BIC) = 39.5006
Hannan-Quinn criterion (HQC) = 35.581

         Predicted
           0    1
Actual 0  18    3
       1   3    8
```

In this context, the `$uhat` accessor function takes a special meaning: it returns generalized residuals as defined in Gourieroux *et al* (1987), which can be interpreted as unbiased estimators of the latent disturbances $\varepsilon_t$. These are defined as

$$u_i = \begin{cases} y_i - \hat{P}_i & \text{for the logit model} \\ y_i \cdot \frac{\phi(\hat{z}_i)}{\Phi(\hat{z}_i)} - (1 - y_i) \cdot \frac{\phi(\hat{z}_i)}{1-\Phi(\hat{z}_i)} & \text{for the probit model} \end{cases} \tag{22.7}$$

Among other uses, generalized residuals are often used for diagnostic purposes. For example, it is very easy to set up an omitted variables test equivalent to the familiar LM test in the context of a linear regression; example 22.2 shows how to perform a variable addition test.

**Example 22.2**: Variable addition test in a probit model

```
open greene19_1

probit GRADE const GPA PSI
series u = $uhat
%$
ols u const GPA PSI TUCE -q
printf "Variable addition test for TUCE:\n"
printf "Rsq * T = %g (p. val. = %g)\n", $trsq, pvalue(X,1,$trsq)
```

### The perfect prediction problem

One curious characteristic of logit and probit models is that (quite paradoxically) estimation is not feasible if a model fits the data perfectly; this is called the *perfect prediction problem*. The reason why this problem arises is easy to see by considering equation (22.6): if for some vector $\beta$ and scalar $k$ it's the case that $z_i < k$ whenever $y_i = 0$ and $z_i > k$ whenever $y_i = 1$, the same thing is true for any multiple of $\beta$. Hence, $L(\beta)$ can be made arbitrarily close to 0 simply by choosing enormous values for $\beta$. As a consequence, the log-likelihood has no maximum, despite being bounded.

Gretl has a mechanism for preventing the algorithm from iterating endlessly in search of a non-existent maximum. One sub-case of interest is when the perfect prediction problem arises because of a single binary explanatory variable. In this case, the offending variable is dropped from the model and estimation proceeds with the reduced specification. Nevertheless, it may happen that no single "perfect classifier" exists among the regressors, in which case estimation is simply impossible and the algorithm stops with an error. This behavior is triggered during the iteration process if

$$\max_{i:y_i=0} z_i < \min_{i:y_i=1} z_i$$

If this happens, unless your model is trivially mis-specified (like predicting if a country is an oil exporter on the basis of oil revenues), it is normally a small-sample problem: you probably just don't have enough data to estimate your model. You may want to drop some of your explanatory variables.

## 22.2 Ordered response models

These models constitute a simple variation on ordinary logit/probit models, and are usually applied when the dependent variable is a discrete and ordered measurement — not simply binary, but on an ordinal rather than an interval scale. For example, this sort of model may be applied when the dependent variable is a qualitative assessment such as "Good", "Average" and "Bad".

In the general case, consider an ordered response variable, $y$, that can take on any of the $J+1$ values $0, 1, 2, \ldots, J$. We suppose, as before, that underlying the observed response is a latent variable,

$$y^* = X\beta + \varepsilon = z + \varepsilon$$

Now define "cut points", $\alpha_1 < \alpha_2 < \cdots < \alpha_J$, such that

$$\begin{array}{ll} y = 0 & \text{if } y^* \le \alpha_1 \\ y = 1 & \text{if } \alpha_1 < y^* \le \alpha_2 \\ \vdots & \\ y = J & \text{if } y^* > \alpha_J \end{array}$$

For example, if the response takes on three values there will be two such cut points, $\alpha_1$ and $\alpha_2$.

The probability that individual $i$ exhibits response $j$, conditional on the characteristics $x_i$, is then given by

$$P(y_i = j \,|\, x_i) = \begin{cases} P(y^* \le \alpha_1 \,|\, x_i) = F(\alpha_1 - z_i) & \text{for } j = 0 \\ P(\alpha_j < y^* \le \alpha_{j+1} \,|\, x_i) = F(\alpha_{j+1} - z_i) - F(\alpha_j - z_i) & \text{for } 0 < j < J \\ P(y^* > \alpha_J \,|\, x_i) = 1 - F(\alpha_J - z_i) & \text{for } j = J \end{cases} \tag{22.8}$$

The unknown parameters $\alpha_j$ are estimated jointly with the $\beta$s via maximum likelihood. The $\hat{\alpha}_j$ estimates are reported by gretl as `cut1`, `cut2` and so on.

In order to apply these models in gretl, the dependent variable must either take on only non-negative integer values, or be explicitly marked as discrete. (In case the variable has non-integer values, it will be recoded internally.) Note that gretl does not provide a separate command for ordered models: the `logit` and `probit` commands automatically estimate the ordered version if the dependent variable is acceptable, but not binary.

Example 22.3 reproduces the results presented in section 15.10 of Wooldridge (2002a). The question of interest in this analysis is what difference it makes, to the allocation of assets in pension funds, whether individual plan participants have a choice in the matter. The response variable is an ordinal measure of the weight of stocks in the pension portfolio. Having reported the results of estimation of the ordered model, Wooldridge illustrates the effect of the `choice` variable by reference to an "average" participant. The example script shows how one can compute this effect in gretl.

After estimating ordered models, the `$uhat` accessor yields generalized residuals as in binary models; additionally, the `$yhat` accessor function returns $\hat{z}_i$, so it is possible to compute an unbiased estimator of the latent variable $y_i^*$ simply by adding the two together.

## 22.3 Multinomial logit

When the dependent variable is not binary and does not have a natural ordering, *multinomial* models are used. Gretl does not provide a native implementation of these yet, but simple models

**Example 22.3**: Ordered probit model

```
/*
  Replicate the results in Wooldridge, Econometric Analysis of Cross
  Section and Panel Data, section 15.10, using pension-plan data from
  Papke (AER, 1998).

  The dependent variable, pctstck (percent stocks), codes the asset
  allocation responses of "mostly bonds", "mixed" and "mostly stocks"
  as {0, 50, 100}.

  The independent variable of interest is "choice", a dummy indicating
  whether individuals are able to choose their own asset allocations.
*/

open pension.gdt

# demographic characteristics of participant
list DEMOG = age educ female black married
# dummies coding for income level
list INCOME = finc25 finc35 finc50 finc75 finc100 finc101

# Papke’s OLS approach
ols pctstck const choice DEMOG INCOME wealth89 prftshr
# save the OLS choice coefficient
choice_ols = $coeff(choice)

# estimate ordered probit
probit pctstck choice DEMOG INCOME wealth89 prftshr

k = $ncoeff
matrix b = $coeff[1:k-2]
a1 = $coeff[k-1]
a2 = $coeff[k]

/*
   Wooldridge illustrates the ’choice’ effect in the ordered probit
   by reference to a single, non-black male aged 60, with 13.5 years
   of education, income in the range $50K - $75K and wealth of $200K,
   participating in a plan with profit sharing.
*/
matrix X = {60, 13.5, 0, 0, 0, 0, 0, 0, 1, 0, 0, 200, 1}

# with ’choice’ = 0
scalar Xb = (0 ~ X) * b
P0 = cdf(N, a1 - Xb)
P50 = cdf(N, a2 - Xb) - P0
P100 = 1 - cdf(N, a2 - Xb)
E0 = 50 * P50 + 100 * P100

# with ’choice’ = 1
Xb = (1 ~ X) * b
P0 = cdf(N, a1 - Xb)
P50 = cdf(N, a2 - Xb) - P0
P100 = 1 - cdf(N, a2 - Xb)
E1 = 50 * P50 + 100 * P100

printf "\nWith choice, E(y) = %.2f, without E(y) = %.2f\n", E1, E0
printf "Estimated choice effect via ML = %.2f (OLS = %.2f)\n", E1 - E0,
  choice_ols
```

can be handled via the `mle` command (see chapter 17). We give here an example of a multinomial logit model. Let the dependent variable, $y_i$, take on integer values $0, 1, \ldots p$. The probability that $y_i = k$ is given by

$$P(y_i = k|x_i) = \frac{\exp(x_i\beta_k)}{\sum_{j=0}^{p}\exp(x_i\beta_j)}$$

For the purpose of identification one of the outcomes must be taken as the “baseline”; it is usually assumed that $\beta_0 = 0$, in which case

$$P(y_i = k|x_i) = \frac{\exp(x_i\beta_k)}{1 + \sum_{j=1}^{p}\exp(x_i\beta_j)}$$

and

$$P(y_i = 0|x_i) = \frac{1}{1 + \sum_{j=1}^{p}\exp(x_i\beta_j)}.$$

Example 22.4 reproduces Table 15.2 in Wooldridge (2002a), based on data on career choice from Keane and Wolpin (1997). The dependent variable is the occupational status of an individual (0 = in school; 1 = not in school and not working; 2 = working), and the explanatory variables are education and work experience (linear and square) plus a “black” binary variable. The full data set is a panel; here the analysis is confined to a cross-section for 1987. For explanations of the matrix methods employed in the script, see chapter 12.

**Example 22.4**: Multinomial logit

```
function mlogitlogprobs(series y, matrix X, matrix theta)

  scalar n = max(y)
  scalar k = cols(X)
  matrix b = mshape(theta,k,n)

  matrix tmp = X*b
  series ret = -ln(1 + sumr(exp(tmp)))

  loop for i=1..n --quiet
    series x = tmp[,i]
    ret += (y=$i) ? x : 0
  end loop

  return series ret

end function

open Keane.gdt
status = status-1 # dep. var. must be 0-based
smpl (year=87 & ok(status)) --restrict

matrix X = { educ exper expersq black const }
scalar k = cols(X)
matrix theta = zeros(2*k, 1)

mle loglik = mlogitlogprobs(status,X,theta)
  params theta
end mle --verbose --hessian
```

## 22.4 The Tobit model

The Tobit model is used when the dependent variable of a model is *censored*.[1] Assume a latent variable $y_i^*$ can be described as

$$y_i^* = \sum_{j=1}^{k} x_{ij}\beta_j + \varepsilon_i,$$

where $\varepsilon_i \sim N(0, \sigma^2)$. If $y_i^*$ were observable, the model's parameters could be estimated via ordinary least squares. On the contrary, suppose that we observe $y_i$, defined as

$$y_i = \begin{cases} y_i^* & \text{for} \quad y_i^* > 0 \\ 0 & \text{for} \quad y_i^* \leq 0 \end{cases} \tag{22.9}$$

In this case, regressing $y_i$ on the $x_i$s does not yield consistent estimates of the parameters $\beta$, because the conditional mean $E(y_i|x_i)$ is not equal to $\sum_{j=1}^{k} x_{ij}\beta_j$. It can be shown that restricting the sample to non-zero observations would not yield consistent estimates either. The solution is to estimate the parameters via maximum likelihood. The syntax is simply

```
tobit depvar indvars
```

As usual, progress of the maximization algorithm can be tracked via the `--verbose` switch, while `$uhat` returns the generalized residuals. Note that in this case the generalized residual is defined as $\hat{u}_i = E(\varepsilon_i|y_i = 0)$ for censored observations, so the familiar equality $\hat{u}_i = y_i - \hat{y}_i$ only holds for uncensored observations, that is, when $y_i > 0$.

An important difference between the Tobit estimator and OLS is that the consequences of non-normality of the disturbance term are much more severe: non-normality implies inconsistency for the Tobit estimator. For this reason, the output for the tobit model includes the Chesher–Irish (1987) normality test by default.

## 22.5 Interval regression

The interval regression model arises when the dependent variable is unobserved for some (possibly all) observations; what we observe instead is an interval in which the dependent variable lies. In other words, the data generating process is assumed to be

$$y_i^* = x_i\beta + \epsilon_i$$

but we only know that $m_i \leq y_i^* \leq M_i$, where the interval may be left- or right-unbounded (but not both). If $m_i = M_i$, we effectively observe $y_i^*$ and no information loss occurs. In practice, each observation belongs to one of four categories:

1. left-unbounded, when $m_i = -\infty$,
2. right-unbounded, when $M_i = \infty$,
3. bounded, when $-\infty < m_i < M_i < \infty$ and
4. point observations when $m_i = M_i$.

It is interesting to note that this model bears similarities to other models in several special cases:

- When all observations are point observations the model trivially reduces to the ordinary linear regression model.

[1] We assume here that censoring occurs from below at 0. Censoring from above, or at a point different from zero, can be rather easily handled by re-defining the dependent variable appropriately. For the more general case of two-sided censoring the `intreg` command may be used (see below).

- When $m_i = M_i$ when $y_i^* > 0$, while $m_i = -\infty$ and $M_i = 0$ otherwise, we have the Tobit model (see 22.4).
- The interval model could be thought of an ordered probit model (see 22.2) in which the cut points (the $\alpha_j$ coefficients in eq. 22.8) are observed and don't need to be estimated.

The gretl command `intreg` estimates interval models by maximum likelihood, assuming normality of the disturbance term $\epsilon_i$. Its syntax is

```
intreg minvar maxvar X
```

where `minvar` contains the $m_i$ series, with NAs for left-unbounded observations, and `maxvar` contains $M_i$, with NAs for right-unbounded observations. By default, standard errors are computed using the negative inverse of the Hessian. If the `--robust` flag is given, then QML or Huber–White standard errors are calculated instead. In this case the estimated covariance matrix is a "sandwich" of the inverse of the estimated Hessian and the outer product of the gradient.

If the model specification contains regressors other than just a constant, the output includes a chi-square statistic for testing the joint null hypothesis that none of these regressors has any effect on the outcome. This is a Wald statistic based on the estimated covariance matrix. If you wish to construct a likelihood ratio test, this is easily done by estimating both the full model and the null model (containing only the constant), saving the log-likelihood in both cases via the `$lnl` accessor, and then referring twice the difference between the two log-likelihoods to the chi-square distribution with $k$ degrees of freedom, where $k$ is the number of additional regressors (see the `pvalue` command in the *Gretl Command Reference*). An example is contained in the sample script `wtp.inp`, provided with the gretl distribution.

As with the probit and Tobit models, after a model has been estimated the `$uhat` accessor returns the generalized residual, which is an estimate of $\epsilon_i$: more precisely, it equals $y_i - x_i\hat{\beta}$ for point observations and $E(\epsilon_i|m_i, M_i, x_i)$ otherwise. Note that it is possible to compute an unbiased predictor of $y_i^*$ by summing this estimate to $x_i\hat{\beta}$. Script 22.5 shows an example. As a further similarity with Tobit, the interval regression model may deliver inconsistent estimates if the disturbances are non-normal; hence, the Chesher–Irish (1987) test for normality is included by default here too.

## 22.6 Sample selection model

In the sample selection model (also known as "Tobit II" model), there are two latent variables:

$$y_i^* = \sum_{j=1}^{k} x_{ij}\beta_j + \varepsilon_i \qquad (22.10)$$

$$s_i^* = \sum_{j=1}^{p} z_{ij}\gamma_j + \eta_i \qquad (22.11)$$

and the observation rule is given by

$$y_i = \begin{cases} y_i^* & \text{for} \quad s_i^* > 0 \\ \blacklozenge & \text{for} \quad s_i^* \leq 0 \end{cases} \qquad (22.12)$$

In this context, the ◆ symbol indicates that for some observations we simply do not have data on $y$: $y_i$ may be 0, or missing, or anything else. A dummy variable $d_i$ is normally used to set censored observations apart.

One of the most popular applications of this model in econometrics is a wage equation coupled with a labor force participation equation: we only observe the wage for the employed. If $y_i^*$ and $s_i^*$ were (conditionally) independent, there would be no reason not to use OLS for estimating equation (22.10); otherwise, OLS does not yield consistent estimates of the parameters $\beta_j$.

Since conditional independence between $y_i^*$ and $s_i^*$ is equivalent to conditional independence between $\varepsilon_i$ and $\eta_i$, one may model the co-dependence between $\varepsilon_i$ and $\eta_i$ as

$$\varepsilon_i = \lambda\eta_i + v_i;$$

substituting the above expression in (22.10), you obtain the model that is actually estimated:

$$y_i = \sum_{j=1}^{k} x_{ij}\beta_j + \lambda\hat{\eta}_i + v_i,$$

so the hypothesis that censoring does not matter is equivalent to the hypothesis $H_0 : \lambda = 0$, which can be easily tested.

The parameters can be estimated via maximum likelihood under the assumption of joint normality of $\varepsilon_i$ and $\eta_i$; however, a widely used alternative method yields the so-called *Heckit* estimator, named after Heckman (1979). The procedure can be briefly outlined as follows: first, a probit model is fit on equation (22.11); next, the generalized residuals are inserted in equation (22.10) to correct for the effect of sample selection.

Gretl provides the `heckit` command to carry out estimation; its syntax is

```
heckit y X ; d Z
```

where `y` is the dependent variable, `X` is a list of regressors, `d` is a dummy variable holding 1 for uncensored observations and `Z` is a list of explanatory variables for the censoring equation.

Since in most cases maximum likelihood is the method of choice, by default gretl computes ML estimates. The 2-step Heckit estimates can be obtained by using the `--two-step` option. After estimation, the `$uhat` accessor contains the generalized residuals. As in the ordinary Tobit model, the residuals equal the difference between actual and fitted $y_i$ only for uncensored observations (those for which $d_i = 1$).

Example 22.6 shows two estimates from the dataset used in Mroz (1987): the first one replicates Table 22.7 in Greene (2003),[2] while the second one replicates table 17.1 in Wooldridge (2002a).

[2] Note that the estimates given by gretl do not coincide with those found in the printed volume. They do, however, match those found on the errata web page for Greene's book: http://pages.stern.nyu.edu/~wgreene/Text/Errata/ERRATA5.htm.

**Example 22.5**: Interval model on artificial data

Input:

```
nulldata 100
# generate artificial data
set seed 201449
x = normal()
epsilon = 0.2*normal()
ystar = 1 + x + epsilon
lo_bound = floor(ystar)
hi_bound = ceil(ystar)

# run the interval model
intreg lo_bound hi_bound const x

# estimate ystar
gen_resid = $uhat
yhat = $yhat + gen_resid
corr ystar yhat
```

Output (selected portions):

```
Model 1: Interval estimates using the 100 observations 1-100
Lower limit: lo_bound, Upper limit: hi_bound

             coefficient   std. error   t-ratio    p-value
  ---------------------------------------------------------
  const       0.993762     0.0338325     29.37    1.22e-189 ***
  x           0.986662     0.0319959     30.84    8.34e-209 ***

Chi-square(1)        950.9270   p-value              8.3e-209
Log-likelihood      -44.21258   Akaike criterion     94.42517
Schwarz criterion    102.2407   Hannan-Quinn         97.58824

sigma = 0.223273
Left-unbounded observations: 0
Right-unbounded observations: 0
Bounded observations: 100
Point observations: 0

...

corr(ystar, yhat) = 0.98960092
Under the null hypothesis of no correlation:
 t(98) = 68.1071, with two-tailed p-value 0.0000
```

**Example 22.6**: Heckit model

```
open mroz87.gdt

genr EXP2 = AX^2
genr WA2 = WA^2
genr KIDS = (KL6+K618)>0

# Greene's specification

list X = const AX EXP2 WE CIT
list Z = const WA WA2 FAMINC KIDS WE

heckit WW X ; LFP Z --two-step
heckit WW X ; LFP Z

# Wooldridge's specification

series NWINC = FAMINC - WW*WHRS
series lww = log(WW)
list X = const WE AX EXP2
list Z = X NWINC WA KL6 K618

heckit lww X ; LFP Z --two-step
```

Chapter 23

# Quantile regression

## 23.1 Introduction

In Ordinary Least Squares (OLS) regression, the fitted values, $\hat{y}_i = X_i \hat{\beta}$, represent the *conditional mean* of the dependent variable — conditional, that is, on the regression function and the values of the independent variables. In median regression, by contrast and as the name implies, fitted values represent the *conditional median* of the dependent variable. It turns out that the principle of estimation for median regression is easily stated (though not so easily computed), namely, choose $\hat{\beta}$ so as to minimize the sum of absolute residuals. Hence the method is known as Least Absolute Deviations or LAD. While the OLS problem has a straightforward analytical solution, LAD is a linear programming problem.

Quantile regression is a generalization of median regression: the regression function predicts the conditional $\tau$-quantile of the dependent variable — for example the first quartile ($\tau = .25$) or the ninth decile ($\tau = .90$).

If the classical conditions for the validity of OLS are satisfied — that is, if the error term is independently and identically distributed, conditional on $X$ — then quantile regression is redundant: all the conditional quantiles of the dependent variable will march in lockstep with the conditional mean. Conversely, if quantile regression reveals that the conditional quantiles behave in a manner quite distinct from the conditional mean, this suggests that OLS estimation is problematic.

As of version 1.7.5, gretl offers quantile regression functionality (in addition to basic LAD regression, which has been available since early in gretl's history via the `lad` command).[1]

## 23.2 Basic syntax

The basic invocation of quantile regression is

`quantreg` *tau reglist*

where

- *reglist* is a standard gretl regression list (dependent variable followed by regressors, including the constant if an intercept is wanted); and
- *tau* is the desired conditional quantile, in the range 0.01 to 0.99, given either as a numerical value or the name of a pre-defined scalar variable (but see below for a further option).

Estimation is via the Frisch–Newton interior point solver (Portnoy and Koenker, 1997), which is substantially faster than the "traditional" Barrodale–Roberts (1974) simplex approach for large problems.

[1] We gratefully acknowledge our borrowing from the `quantreg` package for GNU R (version 4.17). The core of the `quantreg` package is composed of Fortran code written by Roger Koenker; this is accompanied by various driver and auxiliary functions written in the R language by Koenker and Martin Mächler. The latter functions have been re-worked in C for gretl. We have added some guards against potential numerical problems in small samples.

By default, standard errors are computed according to the asymptotic formula given by Koenker and Bassett (1978). Alternatively, if the `--robust` option is given, we use the sandwich estimator developed in Koenker and Zhao (1994).[2]

## 23.3 Confidence intervals

An option `--intervals` is available. When this is given we print confidence intervals for the parameter estimates instead of standard errors. These intervals are computed using the rank inversion method and in general they are asymmetrical about the point estimates — that is, they are not simply "plus or minus so many standard errors". The specifics of the calculation are inflected by the `--robust` option: without this, the intervals are computed on the assumption of IID errors (Koenker, 1994); with it, they use the heteroskedasticity-robust estimator developed by Koenker and Machado (1999).

By default, 90 percent intervals are produced. You can change this by appending a confidence value (expressed as a decimal fraction) to the intervals option, as in

```
quantreg tau reglist --intervals=.95
```

When the confidence intervals option is selected, the parameter estimates are calculated using the Barrodale–Roberts method. This is simply because the Frisch–Newton code does not currently support the calculation of confidence intervals.

Two further details. First, the mechanisms for generating confidence intervals for quantile estimates require that the model has at least two regressors (including the constant). If the `--intervals` option is given for a model containing only one regressor, an error is flagged. Second, when a model is estimated in this mode, you can retrieve the confidence intervals using the accessor `$coeff_ci`. This produces a $k \times 2$ matrix, where $k$ is the number of regressors. The lower bounds are in the first column, the upper bounds in the second. See also section 23.5 below.

## 23.4 Multiple quantiles

As a further option, you can give *tau* as a matrix — either the name of a predefined matrix or in numerical form, as in `{.05, .25, .5, .75, .95}`. The given model is estimated for all the $\tau$ values and the results are printed in a special form, as shown below (in this case the `--intervals` option was also given).

```
Model 1: Quantile estimates using the 235 observations 1-235
Dependent variable: foodexp
With 90 percent confidence intervals

      VARIABLE       TAU    COEFFICIENT      LOWER        UPPER

  const             0.05      124.880      98.3021      130.517
                    0.25      95.4835      73.7861      120.098
                    0.50      81.4822      53.2592      114.012
                    0.75      62.3966      32.7449      107.314
                    0.95      64.1040      46.2649      83.5790

  income            0.05     0.343361     0.343327     0.389750
                    0.25     0.474103     0.420330     0.494329
                    0.50     0.560181     0.487022     0.601989
                    0.75     0.644014     0.580155     0.690413
                    0.95     0.709069     0.673900     0.734441
```

[2] These correspond to the `iid` and `nid` options in R's `quantreg` package, respectively.

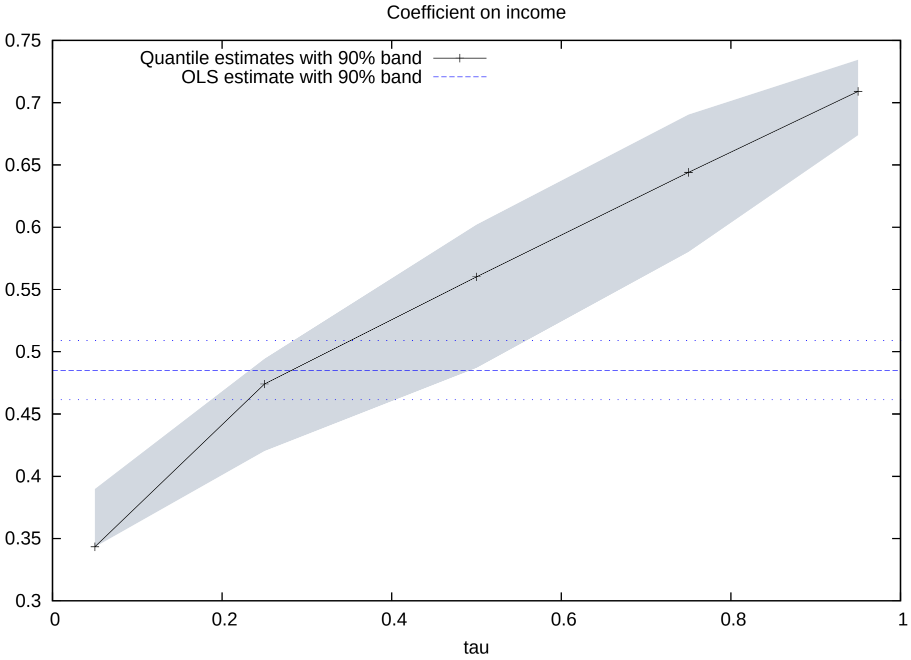


**Figure 23.1**: Regression of food expenditure on income; Engel's data

The gretl GUI has an entry for Quantile Regression (under /Model/Robust estimation), and you can select multiple quantiles there too. In that context, just give space-separated numerical values (as per the predefined options, shown in a drop-down list).

When you estimate a model in this way most of the standard menu items in the model window are disabled, but one extra item is available — graphs showing the $\tau$ sequence for a given coefficient in comparison with the OLS coefficient. An example is shown in Figure 23.1. This sort of graph provides a simple means of judging whether quantile regression is redundant (OLS is fine) or informative.

In the example shown — based on data on household income and food expenditure gathered by Ernst Engel (1821–1896) — it seems clear that simple OLS regression is potentially misleading. The "crossing" of the OLS estimate by the quantile estimates is very marked.

However, it is not always clear what implications should be drawn from this sort of conflict. With the Engel data there are two issues to consider. First, Engel's famous "law" claims an income-elasticity of food consumption that is less than one, and talk of elasticities suggests a logarithmic formulation of the model. Second, there are two apparently anomalous observations in the data set: household 105 has the third-highest income but unexpectedly low expenditure on food (as judged from a simple scatter plot), while household 138 (which also has unexpectedly low food consumption) has much the highest income, almost twice that of the next highest.

With $n = 235$ it seems reasonable to consider dropping these observations. If we do so, and adopt a log–log formulation, we get the plot shown in Figure 23.2. The quantile estimates still cross the OLS estimate, but the "evidence against OLS" is much less compelling: the 90 percent confidence bands of the respective estimates overlap at all the quantiles considered.

## 23.5 Large datasets

As noted above, when you give the `--intervals` option with the `quantreg` command, which calls for estimation of confidence intervals via rank inversion, gretl switches from the default Frisch–Newton algorithm to the Barrodale–Roberts simplex method.

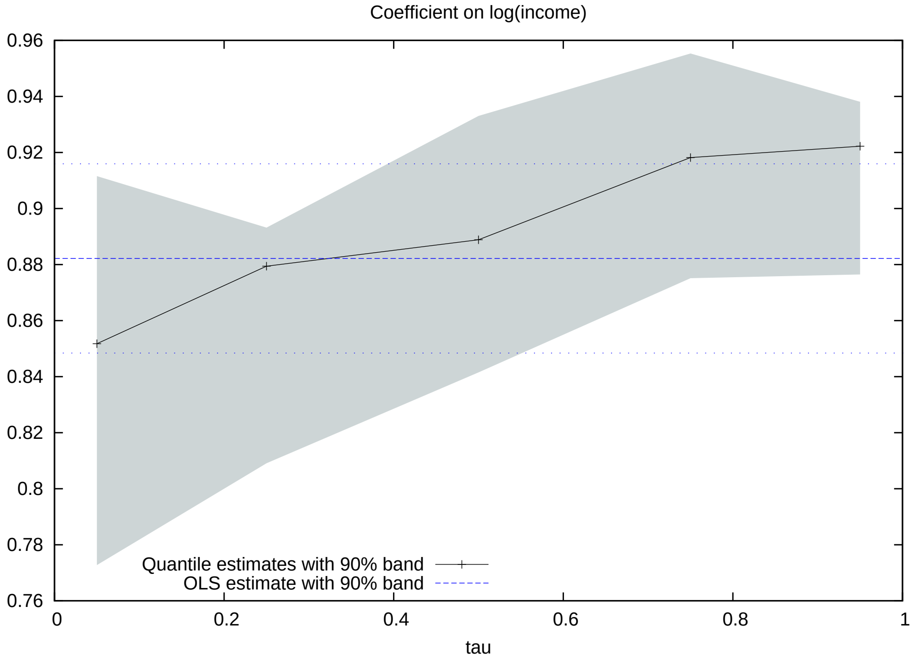


**Figure 23.2**: Log–log regression; 2 observations dropped from full Engel data set.

This is OK for moderately large datasets (up to, say, a few thousand observations) but on very large problems the simplex algorithm may become seriously bogged down. For example, Koenker and Hallock (2001) present an analysis of the determinants of birth weights, using 198377 observations and with 15 regressors. Generating confidence intervals via Barrodale–Roberts for a single value of $\tau$ took about half an hour on a Lenovo Thinkpad T60p with 1.83GHz Intel Core 2 processor.

If you want confidence intervals in such cases, you are advised not to use the `--intervals` option, but to compute them using the method of "plus or minus so many standard errors". (One Frisch–Newton run took about 8 seconds on the same machine, showing the superiority of the interior point method.) The script below illustrates:

```
quantreg .10 y 0 xlist
scalar crit = qnorm(.95)
matrix ci = $coeff - crit * $stderr
ci = ci~($coeff + crit * $stderr)
print ci
```

The matrix `ci` will contain the lower and upper bounds of the (symmetrical) 90 percent confidence intervals.

To avoid a situation where gretl becomes unresponsive for a very long time we have set the maximum number of iterations for the Borrodale–Roberts algorithm to the (somewhat arbitrary) value of 1000. We will experiment further with this, but for the meantime if you really want to use this method on a large dataset, and don't mind waiting for the results, you can increase the limit using the `set` command with parameter `rq_maxiter`, as in

```
set rq_maxiter 5000
```

# Part III

# Technical details

Chapter 24

# Gretl and TEX

## 24.1 Introduction

TEX — initially developed by Donald Knuth of Stanford University and since enhanced by hundreds of contributors around the world — is the gold standard of scientific typesetting. Gretl provides various hooks that enable you to preview and print econometric results using the TEX engine, and to save output in a form suitable for further processing with TEX.

This chapter explains the finer points of gretl's TEX-related functionality. The next section describes the relevant menu items; section 24.3 discusses ways of fine-tuning TEX output; section 24.4 explains how to handle the encoding of characters not found in English; and section 24.5 gives some pointers on installing (and learning) TEX if you do not already have it on your computer. (Just to be clear: TEX is not included with the gretl distribution; it is a separate package, including several programs and a large number of supporting files.)

Before proceeding, however, it may be useful to set out briefly the stages of production of a final document using TEX. For the most part you don't have to worry about these details, since, in regard to previewing at any rate, gretl handles them for you. But having some grasp of what is going on behind the scences will enable you to understand your options better.

The first step is the creation of a plain text "source" file, containing the text or mathematics to be typeset, interspersed with mark-up that defines how it should be formatted. The second step is to run the source through a processing engine that does the actual formatting. Typically this is either:

- a program called latex that generates so-called DVI (device-independent) output, or
- a program called pdflatex that generates PDF output.[1]

For previewing, one uses either a DVI viewer (typically xdvi on GNU/Linux systems) or a PDF viewer (for example, Adobe's Acrobat Reader or xpdf), depending on how the source was processed. If the DVI route is taken, there's then a third step to produce printable output, typically using the program dvips to generate a PostScript file. If the PDF route is taken, the output is ready for printing without any further processing.

On the MS Windows and Mac OS X platforms, gretl calls pdflatex to process the source file, and expects the operating system to be able to find the default viewer for PDF output; DVI is not supported. On GNU/Linux the default is to take the DVI route, but if you prefer to use PDF you can do the following: select the menu item "Tools, Preferences, General" then the "Programs" tab. Find the item titled "Command to compile TeX files", and set this to `pdflatex`. Make sure the "Command to view PDF files" is set to something appropriate.

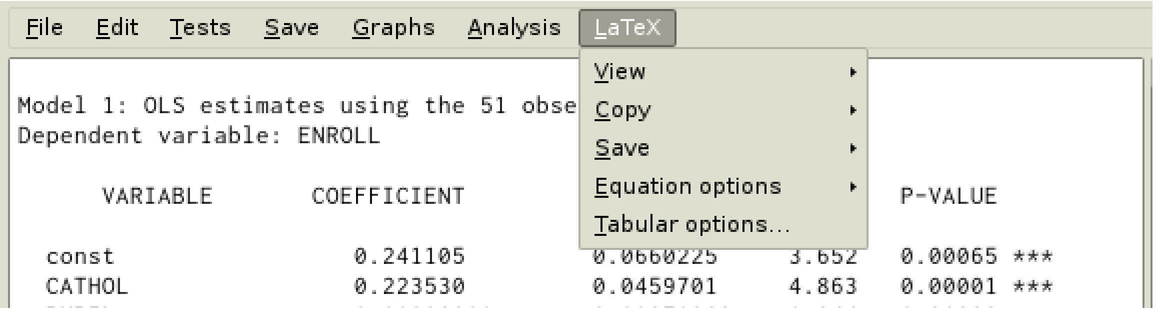
## 24.2 TEX-related menu items

### The model window

The fullest TEX support in gretl is found in the GUI model window. This has a menu item titled "LaTeX" with sub-items "View", "Copy", "Save" and "Equation options" (see Figure 24.1).

[1] Experts will be aware of something called "plain TEX", which is processed using the program tex. The great majority of TEX users, however, use the LATEX macros, initially developed by Leslie Lamport. Gretl does not support plain TEX.

Figure 24.1: LATEX menu in model window



```
Model 1: OLS estimates using the 51 obse
Dependent variable: ENROLL

     VARIABLE       COEFFICIENT                                    P-VALUE

  const                0.241105      0.0660225      3.652      0.00065 ***
  CATHOL               0.223530      0.0459701      4.863      0.00001 ***
```

The first three sub-items have branches titled “Tabular” and “Equation”. By “Tabular” we mean that the model is represented in the form of a table; this is the fullest and most explicit presentation of the results. See Table 24.1 for an example; this was pasted into the manual after using the “Copy, Tabular” item in gretl (a few lines were edited out for brevity).

Table 24.1: Example of LATEX tabular output

Model 1: OLS estimates using the 51 observations 1–51
Dependent variable: ENROLL

| Variable | Coefficient | Std. Error | $t$-statistic | p-value |
|---|---|---|---|---|
| const | 0.241105 | 0.0660225 | 3.6519 | 0.0007 |
| CATHOL | 0.223530 | 0.0459701 | 4.8625 | 0.0000 |
| PUPIL | −0.00338200 | 0.00271962 | −1.2436 | 0.2198 |
| WHITE | −0.152643 | 0.0407064 | −3.7499 | 0.0005 |

| | |
|---|---|
| Mean of dependent variable | 0.0955686 |
| S.D. of dependent variable | 0.0522150 |
| Sum of squared residuals | 0.0709594 |
| Standard error of residuals ($\hat{\sigma}$) | 0.0388558 |
| Unadjusted $R^2$ | 0.479466 |
| Adjusted $\bar{R}^2$ | 0.446241 |
| $F(3,47)$ | 14.4306 |

The “Equation” option is fairly self-explanatory — the results are written across the page in equation format, as below:

$$\widehat{\rm ENROLL} = \underset{(0.066022)}{0.241105} + \underset{(0.04597)}{0.223530}\,{\rm CATHOL} - \underset{(0.0027196)}{0.00338200}\,{\rm PUPIL} - \underset{(0.040706)}{0.152643}\,{\rm WHITE}$$

$$T = 51 \quad \bar{R}^2 = 0.4462 \quad F(3,47) = 14.431 \quad \hat{\sigma} = 0.038856$$

(standard errors in parentheses)

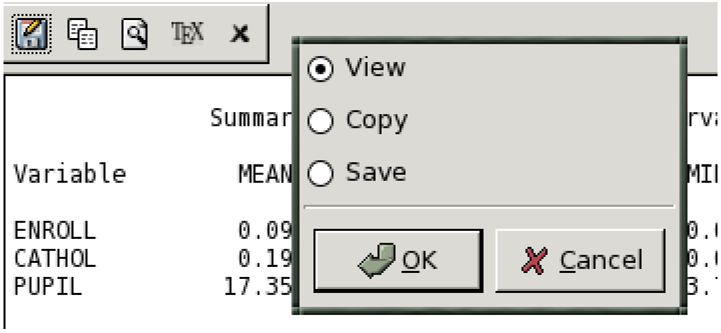
The distinction between the “Copy” and “Save” options (for both tabular and equation) is twofold. First, “Copy” puts the TEX source on the clipboard while with “Save” you are prompted for the name of a file into which the source should be saved. Second, with “Copy” the material is copied as a "fragment" while with "Save" it is written as a complete file. The point is that a well-formed TeX source file must have a header that defines the `documentclass` (article, report, book or whatever) and tags that say `\begin{document}` and `\end{document}`. This material is included when you do "Save" but not when you do "Copy", since in the latter case the expectation is that you will paste the data into an existing TeX source file that already has the relevant apparatus in place.

The items under "Equation options" should be self-explanatory: when printing the model in equation form, do you want standard errors or $t$-ratios displayed in parentheses under the parameter estimates? The default is to show standard errors; if you want $t$-ratios, select that item.

### Other windows

Several other sorts of output windows also have TeX preview, copy and save enabled. In the case of windows having a graphical toolbar, look for the TeX button. Figure 24.2 shows this icon (second from the right on the toolbar) along with the dialog that appears when you press the button.

**Figure 24.2**: TeX icon and dialog



● View
○ Copy
○ Save

```
                     Summar                  rv
Variable              MEAN                   MI

ENROLL                0.09                   0.
CATHOL                0.19                   0.
PUPIL                17.35                   3.
```

One aspect of gretl's TeX support that is likely to be particularly useful for publication purposes is the ability to produce a typeset version of the "model table" (see section 3.4). An example of this is shown in Table 24.2.

## 24.3 Fine-tuning typeset output

There are three aspects to this: adjusting the appearance of the output produced by gretl in LaTeX preview mode; adjusting the formatting of gretl's tabular output for models when using the `tabprint` command; and incorporating gretl's output into your own TeX files.

### Previewing in the GUI

As regards *preview mode*, you can control the appearance of gretl's output using a file named `gretlpre.tex`, which should be placed in your gretl user directory (see the *Gretl Command Reference*). If such a file is found, its contents will be used as the "preamble" to the TeX source. The default value of the preamble is as follows:

```
\documentclass[11pt]{article}
\usepackage[latin1]{inputenc} %% but see below
\usepackage{amsmath}
\usepackage{dcolumn,longtable}
\begin{document}
\thispagestyle{empty}
```

**Table 24.2**: Example of model table output

OLS estimates
Dependent variable: ENROLL

| | Model 1 | Model 2 | Model 3 |
|---|---|---|---|
| const | 0.2907** | 0.2411** | 0.08557 |
| | (0.07853) | (0.06602) | (0.05794) |
| CATHOL | 0.2216** | 0.2235** | 0.2065** |
| | (0.04584) | (0.04597) | (0.05160) |
| PUPIL | −0.003035 | −0.003382 | −0.001697 |
| | (0.002727) | (0.002720) | (0.003025) |
| WHITE | −0.1482** | −0.1526** | |
| | (0.04074) | (0.04071) | |
| ADMEXP | −0.1551 | | |
| | (0.1342) | | |
| $n$ | 51 | 51 | 51 |
| $\bar{R}^2$ | 0.4502 | 0.4462 | 0.2956 |
| $\ell$ | 96.09 | 95.36 | 88.69 |

Standard errors in parentheses
* indicates significance at the 10 percent level
** indicates significance at the 5 percent level

Note that the amsmath and dcolumn packages are required. (For some sorts of output the longtable package is also needed.) Beyond that you can, for instance, change the type size or the font by altering the documentclass declaration or including an alternative font package.

The line \usepackage[latin1]{inputenc} is automatically changed if gretl finds itself running on a system where UTF-8 is the default character encoding — see section 24.4 below.

In addition, if you should wish to typeset gretl output in more than one language, you can set up per-language preamble files. A "localized" preamble file is identified by a name of the form gretlpre_xx.tex, where xx is replaced by the first two letters of the current setting of the LANG environment variable. For example, if you are running the program in Polish, using LANG=pl_PL, then gretl will do the following when writing the preamble for a TEX source file.

1. Look for a file named gretlpre_pl.tex in the gretl user directory. If this is not found, then
2. look for a file named gretlpre.tex in the gretl user directory. If this is not found, then
3. use the default preamble.

Conversely, suppose you usually run gretl in a language other than English, and have a suitable gretlpre.tex file in place for your native language. If on some occasions you want to produce TEX output in English, then you could create an additional file gretlpre_en.tex: this file will be used for the preamble when gretl is run with a language setting of, say, en_US.

### Command-line options

After estimating a model via a script — or interactively via the gretl console or using the command-line program gretlcli — you can use the commands `tabprint` or `eqnprint` to print the model to file in tabular format or equation format respectively. These options are explained in the *Gretl Command Reference*.

If you wish alter the appearance of gretl's tabular output for models in the context of the `tabprint` command, you can specify a custom row format using the `--format` flag. The format string must be enclosed in double quotes and must be tied to the flag with an equals sign. The pattern for the format string is as follows. There are four fields, representing the coefficient, standard error, *t*-ratio and p-value respectively. These fields should be separated by vertical bars; they may contain a `printf`-type specification for the formatting of the numeric value in question, or may be left blank to suppress the printing of that column (subject to the constraint that you can't leave all the columns blank). Here are a few examples:

```
--format="%.4f|%.4f|%.4f|%.4f"
--format="%.4f|%.4f|%.3f|"
--format="%.5f|%.4f||%.4f"
--format="%.8g|%.8g||%.4f"
```

The first of these specifications prints the values in all columns using 4 decimal places. The second suppresses the p-value and prints the *t*-ratio to 3 places. The third omits the *t*-ratio. The last one again omits the *t*, and prints both coefficient and standard error to 8 significant figures.

Once you set a custom format in this way, it is remembered and used for the duration of the gretl session. To revert to the default formatting you can use the special variant `--format=default`.

### Further editing

Once you have pasted gretl's TEX output into your own document, or saved it to file and opened it in an editor, you can of course modify the material in any wish you wish. In some cases, machine-generated TEX is hard to understand, but gretl's output is intended to be human-readable and -editable. In addition, it does not use any non-standard style packages. Besides the standard LATEX document classes, the only files needed are, as noted above, the `amsmath`, `dcolumn` and `longtable` packages. These should be included in any reasonably full TEX implementation.

## 24.4 Character encodings

People using gretl in English-speaking locales are unlikely to have a problem with this, but if you're generating TEX output in a locale where accented characters (not in the ASCII character set) are employed, you may want to pay attention here.

Gretl generates TEX output using whatever character encoding is standard on the local system. If the system encoding is in the ISO-8859 family, this will probably be OK wihout any special effort on the part of the user. Newer GNU/Linux systems, however, typically use Unicode (UTF-8). This is also OK so long as your TEX system can handle UTF-8 input, which requires use of the latex-ucs package. So: if you are using gretl to generate TEX in a non-English locale, where the system encoding is UTF-8, you will need to ensure that the latex-ucs package is installed. This package may or may not be installed by default when you install TEX.

For reference, if gretl detects a UTF-8 environment, the following lines are used in the TEX preamble:

```
\usepackage{ucs}
\usepackage[utf8x]{inputenc}
```

## 24.5 Installing and learning TEX

This is not the place for a detailed exposition of these matters, but here are a few pointers.

So far as we know, every GNU/Linux distribution has a package or set of packages for TEX, and in fact these are likely to be installed by default. Check the documentation for your distribution. For MS Windows, several packaged versions of TEX are available: one of the most popular is MiKTEX at http://www.miktex.org/. For Mac OS X a nice implementation is iTEXMac, at http://itexmac.sourceforge.net/. An essential starting point for online TEX resources is the Comprehensive TEX Archive Network (CTAN) at http://www.ctan.org/.

As for learning TEX, many useful resources are available both online and in print. Among online guides, Tony Roberts' "LATEX: from quick and dirty to style and finesse" is very helpful, at

http://www.sci.usq.edu.au/staff/robertsa/LaTeX/latexintro.html

An excellent source for advanced material is *The LATEX Companion* (Goossens *et al.*, 2004).

Chapter 25

# Gretl and R

## 25.1 Introduction

R is, by far, the largest free statistical project.[1] Like gretl, it is a GNU project and the two have a lot in common; however, gretl's approach focuses on ease of use much more than R, which instead aims to encompass the widest possible range of statistical procedures.

As is natural in the free software ecosystem, we don't view ourselves as competitors to R,[2] but rather as projects sharing a common goal who should support each other whenever possible. For this reason, gretl provides a way to interact with R and thus enable users to pool the capabilities of the two packages.

In this chapter, we will explain how to exploit R's power from within gretl. We assume that the reader has a working installation of R available and a basic grasp of R's syntax.[3]

Despite several valiant attempts, no graphical shell has gained wide acceptance in the R community: by and large, the standard method of working with R is by writing scripts, or by typing commands at the R prompt, much in the same way as one would write gretl scripts or work with the gretl console. In this chapter, the focus will be on the methods available to execute R commands without leaving gretl.

## 25.2 Starting an interactive R session

The easiest way to use R from gretl is in interactive mode. Once you have your data loaded in gretl, you can select the menu item "Tools, Start GNU R" and an interactive R session will be started, with your dataset automatically pre-loaded.

### A simple example: OLS on cross-section data

For this example we use Ramanathan's dataset data4-1, one of the sample files supplied with gretl. We first run, in gretl, an OLS regression of price on sqft, bedrms and baths. The basic results are shown in Table 25.1.

**Table 25.1**: OLS house price regression via gretl

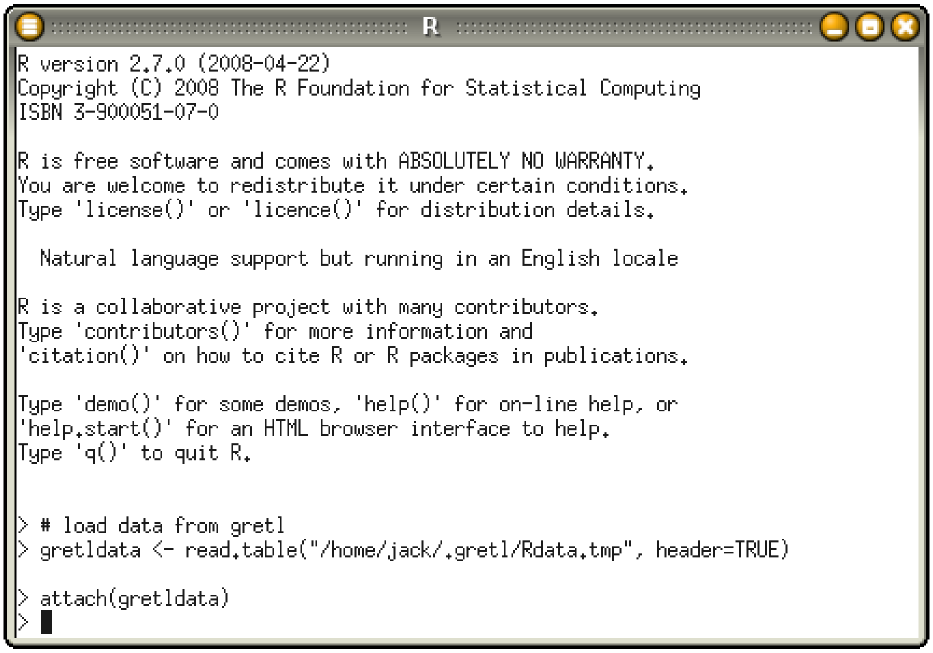
| Variable | Coefficient | Std. Error | $t$-statistic | p-value |
|---|---|---|---|---|
| const | 129.062 | 88.3033 | 1.4616 | 0.1746 |
| sqft | 0.154800 | 0.0319404 | 4.8465 | 0.0007 |
| bedrms | −21.587 | 27.0293 | −0.7987 | 0.4430 |
| baths | −12.192 | 43.2500 | −0.2819 | 0.7838 |

[1] R's homepage is at http://www.r-project.org/.

[2] OK, who are we kidding? But it's *friendly* competition!

[3] The main reference for R documentation is http://cran.r-project.org/manuals.html. In addition, R tutorials abound on the Net; as always, Google is your friend.

We will now replicate the above results using R. Select the menu item “Tools, Start GNU R”. A window similar to the one shown in figure 25.1 should appear.



```
R version 2.7.0 (2008-04-22)
Copyright (C) 2008 The R Foundation for Statistical Computing
ISBN 3-900051-07-0

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.


> # load data from gretl
> gretldata <- read.table("/home/jack/.gretl/Rdata.tmp", header=TRUE)

> attach(gretldata)
> 
```

**Figure 25.1**: R window

The actual look of the R window may be somewhat different from what you see in Figure 25.1 (especially for Windows users), but this is immaterial. The important point is that you have a window where you can type commands to R. If the above procedure doesn’t work and no R window opens, it means that gretl was unable to launch R. You should ensure that R is installed and working on your system and that gretl knows where it is. The relevant settings can be found by selecting the “Tools, Preferences, General” menu entry, under the “Programs” tab.

Assuming R was launched successfully, you will notice that two commands have been executed automatically:

```
gretldata <- read.table("/home/jack/.gretl/Rdata.tmp", header=TRUE)
attach(gretldata)
```

These commands have the effect of loading our dataset into the R workspace in the form of a *data frame* (one of several forms in which R can store data). Use of a data frame enables the subsequent `attach()` command, which sets things up so that the variable names defined in the gretl workspace are available as valid identifiers within R.

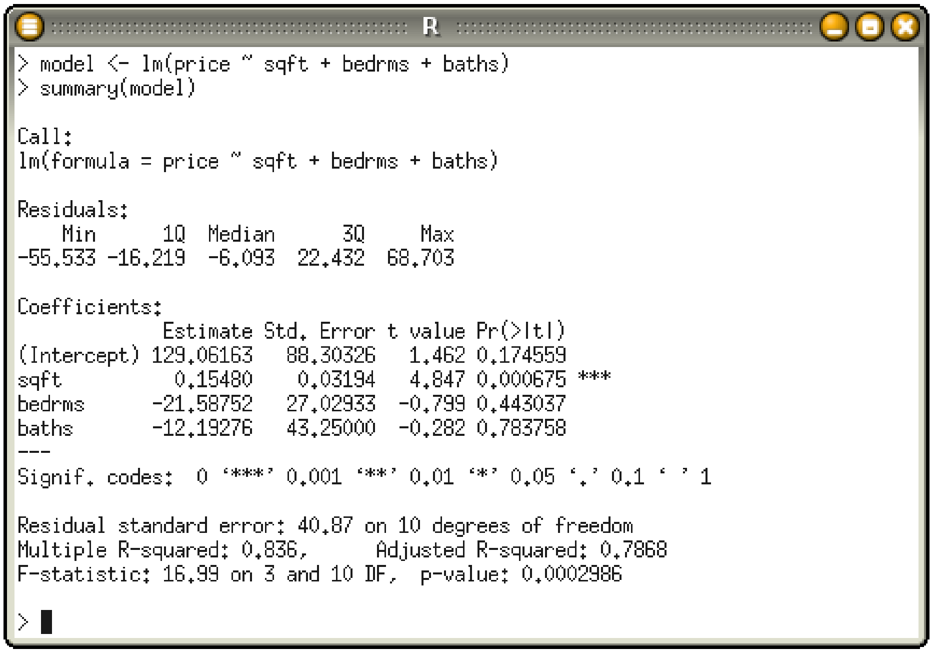
In order to replicate gretl’s OLS estimation, go into the R window and type at the prompt

```
model <- lm(price ~ sqft + bedrms + baths)
summary(model)
```

You should see something similar to Figure 25.2. Surprise — the estimates coincide! To get out, just close the R window or type `q()` at the R prompt.

### Time series data

We now turn to an example which uses time series data: we will compare gretl’s and R’s estimates of Box and Jenkins’ immortal “airline” model. The data are contained in the `bjg` sample dataset. The following gretl code



```
> model <- lm(price ~ sqft + bedrms + baths)
> summary(model)

Call:
lm(formula = price ~ sqft + bedrms + baths)

Residuals:
    Min      1Q  Median      3Q     Max
-55.533 -16.219  -6.093  22.432  68.703

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 129.06163   88.30326   1.462 0.174559
sqft          0.15480    0.03194   4.847 0.000675 ***
bedrms      -21.58752   27.02933  -0.799 0.443037
baths       -12.19276   43.25000  -0.282 0.783758
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 40.87 on 10 degrees of freedom
Multiple R-squared: 0.836,     Adjusted R-squared: 0.7868
F-statistic: 16.99 on 3 and 10 DF,  p-value: 0.0002986

> 
```

**Figure 25.2**: OLS regression on house prices via R

```
open bjg
arima 0 1 1 ; 0 1 1 ; lg --nc
```

produces the estimates shown in Table 25.2.

**Table 25.2**: Airline model from Box and Jenkins (1976) — selected portion of gretl's estimates

| Variable | Coefficient | Std. Error | $t$-statistic | p-value |
|---|---|---|---|---|
| $\theta_1$ | −0.401824 | 0.0896421 | −4.4825 | 0.0000 |
| $\Theta_1$ | −0.556936 | 0.0731044 | −7.6184 | 0.0000 |
| | Variance of innovations | | 0.00134810 | |
| | Log-likelihood | | 244.696 | |
| | Akaike information criterion | | −483.39 | |

If we now open an R session as described in the previous subsection, the data-passing mechanism is slightly different. The R commands that read the data from gretl are in this case

```
# load data from gretl
gretldata <- read.table("/home/jack/.gretl/Rdata.tmp", header=TRUE)
gretldata <- ts(gretldata, start=c(1949, 1), frequency = 12)
```

Since our data were defined in gretl as time series, we use an R *time-series* object (*ts* for short) for the transfer. In this way we can retain in R useful information such as the periodicity of the data and the sample limits. The downside is that the names of individual series, as defined in gretl, are not valid identifiers. In order to extract the variable `lg`, one needs to use the syntax `lg <- gretldata[, "lg"]`.

ARIMA estimation can be carried out by issuing the following two R commands:

```
lg <- gretldata[, "lg"]
arima(lg, c(0,1,1), seasonal=c(0,1,1))
```

which yield

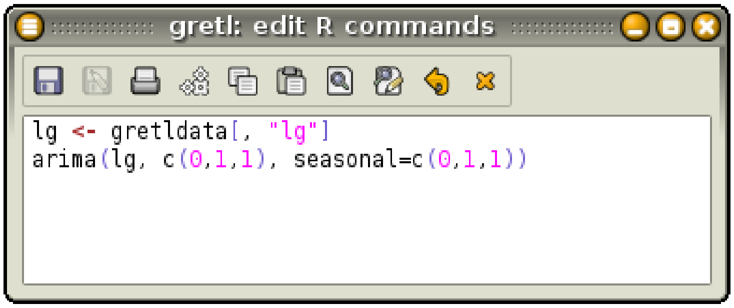
```
Coefficients:
          ma1     sma1
      -0.4018  -0.5569
s.e.   0.0896   0.0731

sigma^2 estimated as 0.001348:  log likelihood = 244.7,  aic = -483.4
```

Happily, the estimates again coincide.

## 25.3 Running an R script

Opening an R window and keying in commands is a convenient method when the job is small. In some cases, however, it would be preferable to have R execute a script prepared in advance. One way to do this is via the `source()` command in R. Alternatively, gretl offers the facility to edit an R script and run it, having the current dataset pre-loaded automatically. This feature can be accessed via the "File, Script Files" menu entry. By selecting "User file", one can load a pre-existing R script; if you want to create a new script instead, select the "New script, R script" menu entry.



```
lg <- gretldata[, "lg"]
arima(lg, c(0,1,1), seasonal=c(0,1,1))
```

**Figure 25.3**: Editing window for R scripts

In either case, you are presented with a window very similar to the editor window used for ordinary gretl scripts, as in Figure 25.3.

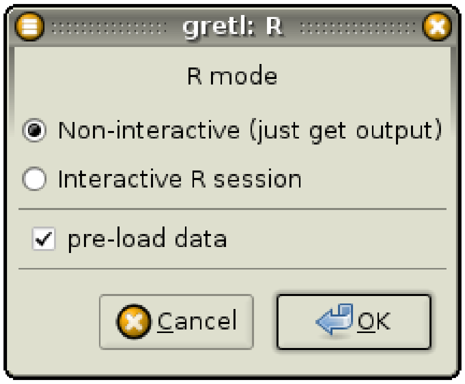
There are two main differences. First, you get syntax highlighting for R's syntax instead of gretl's. Second, clicking on the Execute button (the gears icon), launches an instance of R in which your commands are executed. Before R is actually run, you are asked if you want to run R interactively or not (see Figure 25.4).

An interactive run opens an R instance similar to the one seen in the previous section: your data will be pre-loaded (if the "pre-load data" box is checked) and your commands will be executed. Once this is done, you will find yourself at the R prompt, where you can enter more commands.

A non-interactive run, on the other hand, will execute your script, collect the output from R and present it to you in an output window; R will be run in the background. If, for example, the script in Figure 25.3 is run non-interactively, a window similar to Figure 25.5 will appear.

## 25.4 Taking stuff back and forth

As regards the passing of data between the two programs, so far we have only considered passing series from gretl to R. In order to achieve a satisfactory degree of interoperability, more is needed. In the following sub-sections we see how matrices can be exchanged, and how data can be passed from R back to gretl.



gretl: R

R mode

● Non-interactive (just get output)

○ Interactive R session

☑ pre-load data

**Figure 25.4**: Editing window for R scripts

### Passing matrices from gretl to R

For passing matrices from gretl to R, you can use the mwrite matrix function described in section 12.6. For example, the following gretl code fragment generates the matrix

$$A = \begin{bmatrix} 3 & 7 & 11 \\ 4 & 8 & 12 \\ 5 & 9 & 13 \\ 6 & 10 & 14 \end{bmatrix}$$

and stores it into the file mymatfile.mat.

```
matrix A = mshape(seq(3,14),4,3)
err = mwrite(A, "mymatfile.mat")
```

In order to retrieve this matrix from R, all you have to do is

```
A <- as.matrix(read.table("mymatfile.mat", skip=1))
```

Although in principle you can give your matrix file any valid filename, a couple of conventions may prove useful. First, you may want to use an informative file suffix such as ".mat", but this is a matter of taste. More importantly, the exact location of the file created by mwrite could be an issue. By default, if no path is specified in the file name, gretl stores matrix files in the current work directory. However, it may be wise for the purpose at hand to use the directory in which gretl stores all its temporary files, whose name is stored in the built-in string dotdir (see section 11.2). The value of this string is automatically passed to R as the string variable gretl.dotdir, so the above example may be rewritten more cleanly as

Gretl side:

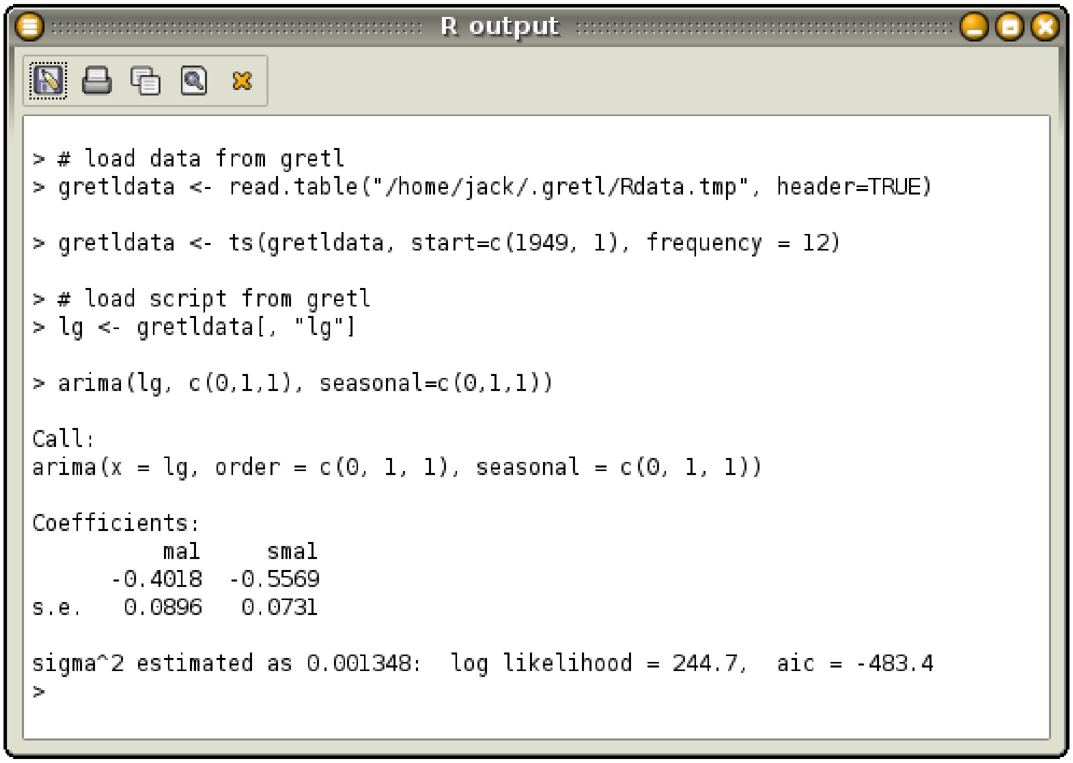
```
matrix A = mshape(seq(3,14),4,3)
err = mwrite(A, "@dotdir/mymatfile.mat")
```

R side:

```
fname <- paste(gretl.dotdir, "mymatfile.mat", sep="")
A <- as.matrix(read.table(fname, skip=1))
```

### Passing data from R to gretl

For passing data in the opposite direction, gretl defines a special function that can be used in the R environment. An R object will be written as a temporary file in gretl's dotdir directory, from where it can be easily retrieved from within gretl.



```
> # load data from gretl
> gretldata <- read.table("/home/jack/.gretl/Rdata.tmp", header=TRUE)

> gretldata <- ts(gretldata, start=c(1949, 1), frequency = 12)

> # load script from gretl
> lg <- gretldata[, "lg"]

> arima(lg, c(0,1,1), seasonal=c(0,1,1))

Call:
arima(x = lg, order = c(0, 1, 1), seasonal = c(0, 1, 1))

Coefficients:
          ma1     sma1
      -0.4018  -0.5569
s.e.   0.0896   0.0731

sigma^2 estimated as 0.001348:  log likelihood = 244.7,  aic = -483.4
>
```

**Figure 25.5**: Output from a non-interactive R run

The name of this function is `gretl.export()`, and it accepts one argument, the object to be exported. At present, the objects that can be exported with this method are matrices, data frames and time-series objects. The function creates a text file, with the same name as the exported object, in gretl's temporary directory. Data frames and time-series objects are stored as CSV files, and can be retrieved by using gretl's append command. Matrices are stored in a special text format that is understood by gretl (see section 12.6); the file suffix is in this case `.mat`, and to read the matrix in gretl you must use the `mread()` function.

As an example, we take the airline data and use them to estimate a structural time series model à la Harvey (1989). The model we will use is the *Basic Structural Model* (BSM), in which a time series is decomposed into three terms:

$$y_t = \mu_t + \gamma_t + \varepsilon_t$$

where $\mu_t$ is a trend component, $\gamma_t$ is a seasonal component and $\varepsilon_t$ is a noise term. In turn, the following is assumed to hold:

$$\begin{aligned} \Delta\mu_t &= \beta_{t-1} + \eta_t \\ \Delta\beta_t &= \zeta_t \\ \Delta_s\gamma_t &= \Delta\omega_t \end{aligned}$$

where $\Delta_s$ is the seasonal differencing operator, $(1 - L^s)$, and $\eta_t$, $\zeta_t$ and $\omega_t$ are mutually uncorrelated white noise processes. The object of the analysis is to estimate the variances of the noise components (which may be zero) and to recover estimates of the latent processes $\mu_t$ (the "level"), $\beta_t$ (the "slope") and $\gamma_t$.

Gretl does not provide (yet) a command for estimating this class of models, so we will use R's `StructTS` command and import the results back into gretl. Once the `bjg` dataset is loaded in gretl, we pass the data to R and execute the following script:

```
# extract the log series
```

```
y <- gretldata[, "lg"]
# estimate the model
strmod <- StructTS(y)
# save the fitted components (smoothed)
compon <- as.ts(tsSmooth(strmod))
# save the estimated variances
vars <- as.matrix(strmod$coef)

# export into gretl's temp dir
gretl.export(compon)
gretl.export(vars)
```

In this case, running the above in R produces nothing more that the echoing of commands:

```
> # load data from gretl
> gretldata <- read.table("/home/jack/.gretl/Rdata.tmp", header=TRUE)

> gretldata <- ts(gretldata, start=c(1949, 1), frequency = 12)

> # load script from gretl
> # extract the log series
> y <- gretldata[, "lg"]

> # estimate the model
> strmod <- StructTS(y)

> # save the fitted components (smoothed)
> compon <- as.ts(tsSmooth(strmod))

> # save the estimated variances
> vars <- as.matrix(strmod$coef)

> # export into gretl's temp dir
> gretl.export(compon)

> gretl.export(vars)
```

However, we see from the output that the two `gretl.export()` commands ran without errors. Hence, we are ready to pull the results back into gretl by executing the following commands, either from the console or by creating a small script:[4]

```
append @dotdir/compon.csv
vars = mread("@dotdir/vars.mat")
```

The first command reads the estimated time-series components from a CSV file, which is the format that the passing mechanism employs for series. The matrix `vars` is read from the file `vars.mat`.

After the above commands have been executed, three new series will have appeared in the gretl workspace, namely the estimates of the three components; by plotting them together with the original data, you should get a graph similar to Figure 25.6. The estimates of the variances can be seen by printing the `vars` matrix, as in

```
? print vars
vars (4 x 1)

  0.00077185
```

[4] This example will work on Linux and presumably on OSX without modifications. On the Windows platform, you may have to substitute the "/" character with "\".

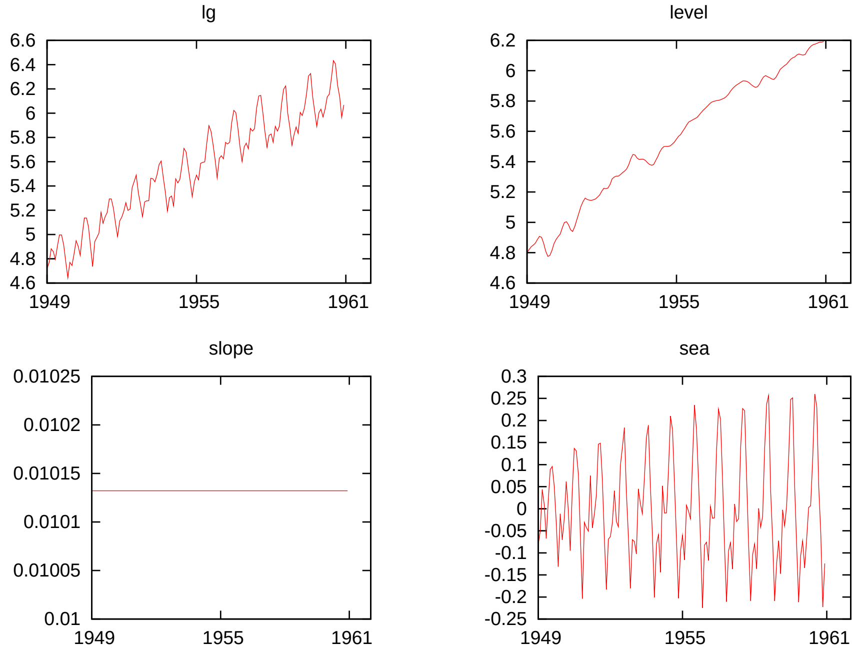


**Figure 25.6**: Estimated components from BSM

```
     0.0000
  0.0013969
     0.0000
```

That is,

$$\hat{\sigma}^2_\eta = 0.00077185, \quad \hat{\sigma}^2_\zeta = 0, \quad \hat{\sigma}^2_\omega = 0.0013969, \quad \hat{\sigma}^2_\varepsilon = 0$$

Notice that, since $\hat{\sigma}^2_\zeta = 0$, the estimate for $\beta_t$ is constant and the level component is simply a random walk with a drift.

## 25.5 Interacting with R from the command line

Up to this point we have spoken only of interaction with R via the GUI program. In order to do the same from the command line interface, gretl provides the foreign command. This enables you to embed non-native commands within a gretl script.[5]

A “foreign” block takes the form

```
foreign language=R [--send-data] [--quiet]
    ... R commands ...
end foreign
```

and achieves the same effect as submitting the enclosed R commands via the GUI in the non-interactive mode (see section 25.3 above). The --send-data option arranges for auto-loading of the data present in the gretl session. The --quiet option prevents the output from R from being echoed in the gretl output.

Using this method, replicating the example in the previous subsection is rather easy: basically, all it takes is encapsulating the content of the R script in a foreign...end foreign block; see example 25.1.

[5] In future this facility may be extended to handle interaction with other programs, but for the present only R commands are accepted.

**Example 25.1**: Estimation of the Basic Structural Model — simple

```
open bjg.gdt

foreign language=R --send-data
    y <- gretldata[, "lg"]
    strmod <- StructTS(y)
    compon <- as.ts(tsSmooth(strmod))
    vars <- as.matrix(strmod$coef)

    gretl.export(compon)
    gretl.export(vars)
end foreign

append @dotdir/compon.csv
rename level lg_level
rename slope lg_slope
rename sea lg_seas

vars = mread("@dotdir/vars.mat")
```

**Example 25.2**: Estimation of the Basic Structural Model — via a function

```
function RStructTS(series myseries)

    smpl ok(myseries) --restrict
    sx = argname(myseries)

    foreign language=R --send-data --quiet
        @sx <- gretldata[, "myseries"]
        strmod <- StructTS(@sx)
        compon <- as.ts(tsSmooth(strmod))
        gretl.export(compon)
    end foreign

    append @dotdir/compon.csv
    rename level @sx_level
    rename slope @sx_slope
    rename sea @sx_seas

    list ret = @sx_level @sx_slope @sx_seas
    return list ret
end function

# ------------ main -------------------------

open bjg.gdt
list X = RStructTS(lg)
```

The above syntax, despite being already quite useful by itself, shows its full power when it is used in conjunction with user-written functions. Example 25.2 shows how to define a gretl function that calls R internally.

A note on performance: at present, when R is called from within gretl using a foreign block, the R program is started up on each invocation, which can be quite time consuming. For maximum performance, you should organize your script so as to group together as many R operations as possible, hence minimizing the number of distinct foreign blocks.[6]

[6] In future we may be able to improve on this, using calls to the R shared library in place of invocations of the program.

Chapter 26

# Troubleshooting gretl

## 26.1 Bug reports

Bug reports are welcome. Hopefully, you are unlikely to find bugs in the actual calculations done by gretl (although this statement does not constitute any sort of warranty). You may, however, come across bugs or oddities in the behavior of the graphical interface. Please remember that the usefulness of bug reports is greatly enhanced if you can be as specific as possible: what *exactly* went wrong, under what conditions, and on what operating system? If you saw an error message, what precisely did it say?

## 26.2 Auxiliary programs

As mentioned above, gretl calls some other programs to accomplish certain tasks (gnuplot for graphing, LaTeX for high-quality typesetting of regression output, GNU R). If something goes wrong with such external links, it is not always easy for gretl to produce an informative error message. If such a link fails when accessed from the gretl graphical interface, you may be able to get more information by starting gretl from the command prompt rather than via a desktop menu entry or icon. On the X window system, start gretl from the shell prompt in an `xterm`; on MS Windows, start the program `gretlw32.exe` from a console window or "DOS box" using the `-g` or `--debug` option flag. Additional error messages may be displayed on the terminal window.

Also please note that for most external calls, gretl assumes that the programs in question are available in your "path" — that is, that they can be invoked simply via the name of the program, without supplying the program's full location.[1] Thus if a given program fails, try the experiment of typing the program name at the command prompt, as shown below.

| | *Graphing* | *Typesetting* | *GNU R* |
|---|---|---|---|
| X window system | gnuplot | latex, xdvi | R |
| MS Windows | wgnuplot.exe | pdflatex | RGui.exe |

If the program fails to start from the prompt, it's not a gretl issue but rather that the program's home directory is not in your path, or the program is not installed (properly). For details on modifying your path please see the documentation or online help for your operating system or shell.

[1] The exception to this rule is the invocation of gnuplot under MS Windows, where a full path to the program is given.

# Chapter 27

# The command line interface

The gretl package includes the command-line program gretlcli. On Linux it can be run from a terminal window (xterm, rxvt, or similar), or at the text console. Under MS Windows it can be run in a console window (sometimes inaccurately called a "DOS box"). gretlcli has its own help file, which may be accessed by typing "help" at the prompt. It can be run in batch mode, sending output directly to a file (see also the *Gretl Command Reference*).

If gretlcli is linked to the readline library (this is automatically the case in the MS Windows version; also see Appendix C), the command line is recallable and editable, and offers command completion. You can use the Up and Down arrow keys to cycle through previously typed commands. On a given command line, you can use the arrow keys to move around, in conjunction with Emacs editing keystokes.[1] The most common of these are:

| *Keystroke* | *Effect* |
|---|---|
| `Ctrl-a` | go to start of line |
| `Ctrl-e` | go to end of line |
| `Ctrl-d` | delete character to right |

where "`Ctrl-a`" means press the "`a`" key while the "`Ctrl`" key is also depressed. Thus if you want to change something at the beginning of a command, you *don't* have to backspace over the whole line, erasing as you go. Just hop to the start and add or delete characters. If you type the first letters of a command name then press the Tab key, readline will attempt to complete the command name for you. If there's a unique completion it will be put in place automatically. If there's more than one completion, pressing Tab a second time brings up a list.

Probably the most useful mode for heavy-duty work with gretlcli is batch (non-interactive) mode, in which the program reads and processes a script, and sends the output to file. For example

```
gretlcli -b scriptfile > outputfile
```

Note that *scriptfile* is treated as a program argument; only the output file requires redirection (>). Don't forget the `-b` (batch) switch, otherwise the program will wait for user input after executing the script (and if output is redirected, the program will appear to "hang").

[1] Actually, the key bindings shown below are only the defaults; they can be customized. See the readline manual.

# Part IV

# Appendices

# Appendix A

# Data file details

## A.1 Basic native format

In gretl's native data format, a data set is stored in XML (extensible mark-up language). Data files correspond to the simple DTD (document type definition) given in `gretldata.dtd`, which is supplied with the gretl distribution and is installed in the system data directory (e.g. `/usr/share/gretl/data` on Linux.) Data files may be plain text or gzipped. They contain the actual data values plus additional information such as the names and descriptions of variables, the frequency of the data, and so on.

Most users will probably not have need to read or write such files other than via gretl itself, but if you want to manipulate them using other software tools you should examine the DTD and also take a look at a few of the supplied practice data files: `data4-1.gdt` gives a simple example; `data4-10.gdt` is an example where observation labels are included.

## A.2 Traditional ESL format

For backward compatibility, gretl can also handle data files in the "traditional" format inherited from Ramanathan's ESL program. In this format (which was the default in gretl prior to version 0.98) a data set is represented by two files. One contains the actual data and the other information on how the data should be read. To be more specific:

1. *Actual data*: A rectangular matrix of white-space separated numbers. Each column represents a variable, each row an observation on each of the variables (spreadsheet style). Data columns can be separated by spaces or tabs. The filename should have the suffix `.gdt`. By default the data file is ASCII (plain text). Optionally it can be gzip-compressed to save disk space. You can insert comments into a data file: if a line begins with the hash mark (#) the entire line is ignored. This is consistent with gnuplot and octave data files.

2. *Header*: The data file must be accompanied by a header file which has the same basename as the data file plus the suffix `.hdr`. This file contains, in order:

   - (Optional) *comments* on the data, set off by the opening string `(*` and the closing string `*)`, each of these strings to occur on lines by themselves.
   - (Required) list of white-space separated *names of the variables* in the data file. Names are limited to 8 characters, must start with a letter, and are limited to alphanumeric characters plus the underscore. The list may continue over more than one line; it is terminated with a semicolon, `;`.
   - (Required) *observations* line of the form `1 1 85`. The first element gives the data frequency (1 for undated or annual data, 4 for quarterly, 12 for monthly). The second and third elements give the starting and ending observations. Generally these will be 1 and the number of observations respectively, for undated data. For time-series data one can use dates of the form `1959.1` (quarterly, one digit after the point) or `1967.03` (monthly, two digits after the point). See Chapter 15 for special use of this line in the case of panel data.
   - The keyword `BYOBS`.

Here is an example of a well-formed data header file.

```
(*
  DATA9-6:
  Data on log(money), log(income) and interest rate from US.
  Source: Stock and Watson (1993) Econometrica
  (unsmoothed data) Period is 1900-1989 (annual data).
  Data compiled by Graham Elliott.
*)
lmoney lincome intrate ;
1 1900 1989 BYOBS
```

The corresponding data file contains three columns of data, each having 90 entries. Three further features of the "traditional" data format may be noted.

1. If the BYOBS keyword is replaced by BYVAR, and followed by the keyword BINARY, this indicates that the corresponding data file is in binary format. Such data files can be written from gretlcli using the `store` command with the `-s` flag (single precision) or the `-o` flag (double precision).

2. If BYOBS is followed by the keyword MARKERS, gretl expects a data file in which the *first column* contains strings (8 characters maximum) used to identify the observations. This may be handy in the case of cross-sectional data where the units of observation are identifiable: countries, states, cities or whatever. It can also be useful for irregular time series data, such as daily stock price data where some days are not trading days — in this case the observations can be marked with a date string such as 10/01/98. (Remember the 8-character maximum.) Note that BINARY and MARKERS are mutually exclusive flags. Also note that the "markers" are not considered to be a variable: this column does not have a corresponding entry in the list of variable names in the header file.

3. If a file with the same base name as the data file and header files, but with the suffix `.lbl`, is found, it is read to fill out the descriptive labels for the data series. The format of the label file is simple: each line contains the name of one variable (as found in the header file), followed by one or more spaces, followed by the descriptive label. Here is an example: `price New car price index, 1982 base year`

If you want to save data in traditional format, use the `-t` flag with the `store` command, either in the command-line program or in the console window of the GUI program.

## A.3 Binary database details

A gretl database consists of two parts: an ASCII index file (with filename suffix `.idx`) containing information on the series, and a binary file (suffix `.bin`) containing the actual data. Two examples of the format for an entry in the `idx` file are shown below:

```
G0M910  Composite index of 11 leading indicators (1987=100)
M 1948.01 - 1995.11  n = 575
currbal Balance of Payments: Balance on Current Account; SA
Q 1960.1 - 1999.4 n = 160
```

The first field is the series name. The second is a description of the series (maximum 128 characters). On the second line the first field is a frequency code: M for monthly, Q for quarterly, A for annual, B for business-daily (daily with five days per week) and D for daily (seven days per week). No other frequencies are accepted at present. Then comes the starting date (N.B. with two digits following the point for monthly data, one for quarterly data, none for annual), a space, a hyphen, another space, the ending date, the string “n = ” and the integer number of observations. In the case of daily data the starting and ending dates should be given in the form YYYY/MM/DD. This format must be respected exactly.

Optionally, the first line of the index file may contain a short comment (up to 64 characters) on the source and nature of the data, following a hash mark. For example:

```
# Federal Reserve Board (interest rates)
```

The corresponding binary database file holds the data values, represented as “floats”, that is, single-precision floating-point numbers, typically taking four bytes apiece. The numbers are packed “by variable”, so that the first *n* numbers are the observations of variable 1, the next *m* the observations on variable 2, and so on.

## Appendix B

# Data import via ODBC

Since version 1.7.5, gretl provides a method for retrieving data from databases which support the ODBC standard. Most users won't be interested in this, but there may be some for whom this feature matters a lot: typically, those who work in an environment where huge data collections are accessible via a Data Base Management System (DBMS).

ODBC is the *de facto* standard for interacting with such systems. In the next section we provide some background information on how ODBC works. What you actually need to do to have gretl retrieve data from a database is explained in section B.2.

## B.1 ODBC base concepts

ODBC is short for *Open DataBase Connectivity*, a group of software methods that enable a *client* to interact with a database *server*. The most common operation is when the client fetches some data from the server. ODBC acts as an intermediate layer between client and server, so the client "talks" to ODBC rather than accessing the server directly (see Figure B.1).

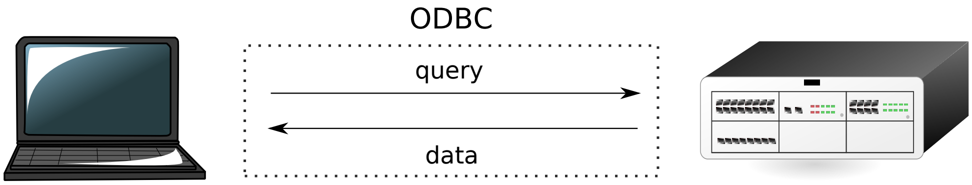


**Figure B.1**: Retrieving data via ODBC

For the above mechanism to work, it is necessary that the relevant ODBC software is installed and working on the client machine (contact your DB administrator for details). At this point, the database (or databases) that the server provides will be accessible to the client as a *data source* with a specific identifier (a Data Source Name or DSN); in most cases, a username and a password are required to connect to the data source.

Once the connection is established, the user sends a *query* to ODBC, which contacts the database manager, collects the results and sends them back to the user. The query is almost invariably formulated in a special language used for the purpose, namely SQL.[1] We will not provide here an SQL tutorial: there are many such tutorials on the Net; besides, each database manager tends to support its own SQL dialect so the precise form of an SQL query may vary slightly if the DBMS on the other end is Oracle, MySQL, PostgreSQL or something else.

Suffice it to say that the main statement for retrieving data is the SELECT statement. Within a DBMS, data are organized in *tables*, which are roughly equivalent to spreadsheets. The SELECT statement returns a subset of a table, which is itself a table. For example, imagine that the database holds a table called "NatAccounts", containing the data shown in Table B.1.

The SQL statement

```
SELECT qtr, tradebal, gdp FROM NatAccounts WHERE year=1970;
```

[1] See http://en.wikipedia.org/wiki/SQL.

| year | qtr | gdp | consump | tradebal |
|---|---|---|---|---|
| 1970 | 1 | 584763 | 344746.9 | −5891.01 |
| 1970 | 2 | 597746 | 350176.9 | −7068.71 |
| 1970 | 3 | 604270 | 355249.7 | −8379.27 |
| 1970 | 4 | 609706 | 361794.7 | −7917.61 |
| 1971 | 1 | 609597 | 362490 | −6274.3 |
| 1971 | 2 | 617002 | 368313.6 | −6658.76 |
| 1971 | 3 | 625536 | 372605 | −4795.89 |
| 1971 | 4 | 630047 | 377033.9 | −6498.13 |

**Table B.1**: The “NatAccounts” table

produces the subset of the original data shown in Table B.2.

| qtr | tradebal | gdp |
|---|---|---|
| 1 | −5891.01 | 584763 |
| 2 | −7068.71 | 597746 |
| 3 | −8379.27 | 604270 |
| 4 | −7917.61 | 609706 |

**Table B.2**: Result of a SELECT statement

Gretl provides a mechanism for forwarding your query to the DBMS via ODBC and including the results in your currently open dataset.

## B.2 Syntax

At present, ODBC import is only possible via the command line interface.[2] The two commands that gretl uses at present for fetching data via an ODBC connection are `open` and `data`.

The `open` command is used for connecting to a DBMS: its syntax is

```
open dsn=database [user=username] [password=password] --odbc
```

The `user` and `password` items are optional; the effect of this command is to initiate an ODBC connection. It is assumed that the machine gretl runs on has a working ODBC client installed.

In order to actually retrieve the data, the `data` command is used. Its syntax is:

```
data series [obs-format=format-string] query-string --odbc
```

where:

***series*** is the name of the gretl series to contain the incoming data, which needs not exist prior to the query. Note that the `data` command imports one series at a time.

***format-string*** is an optional parameter, used to handle cases when a “rectangular” organisation of the database cannot be assumed (more on this later);

***query-string*** is a string containing the SQL statement used to extract the data.

[2] Since designing a graphical interface for this is conceptually simple but rather time-consuming, what we’re aiming at is a robust and reasonably powerful implementation of the data transfer. Once all the issues are sorted out, we’ll start implementing a GUI interface.

The *query-string* can, in principle, contain any valid SQL statement which results in a table: a "`;`" character at the end will be added automatically. This string may be specified directly within the command, as in

```
data x "SELECT foo FROM bar" --odbc
```

which will store into the gretl variable `x` the content of the column `foo` from the table `bar`. However, since in a real-life situation the string containing the SQL statement will be rather long, it may be best to create it just before the call to `data`. For example:

```
string SqlQry = "SELECT foo FROM bar"
data x SqlQry --odbc
```

If the optional parameter `obs-format` is absent, as in the above example, the SQL query should return *exactly one* column of data, which is used to fill the variable `x` sequentially. It may be necessary to include a `smpl` command before the `data` command to set up the right "window" for the incoming data. In addition, if one cannot assume that the data will be delivered in the correct order (typically, chronological order), the SQL query should contain an appropriate `ORDER BY` clause.

The optional format string is used for those cases when there is no certainty that the data from the query will arrive in the same order as the gretl dataset. This may happen when missing values are interspersed within a column, or with data that do not have a natural ordering, e.g. cross-sectional data. In this case, the SQL statement should return a table with $n$ columns, where the first $n - 1$ columns are used to identify which observation the value in the $n$-th column belongs to. The format string is used to translate the first $n - 1$ fields into a string which matches the string gretl uses to identify observations in the currently open dataset. At present, $n$ should be between 2 and 4, which should cover most, if not all, cases.

For example, consider the following fictitious case: we have a 5-days-per-week dataset, to which we want to add the stock index for the Verdurian market;[3] it so happens that in Verduria Saturdays are working days but Wednesdays are not. We want a column which does *not* contain data on Saturdays, because we wouldn't know where to put them, but at the same time we want to place missing values on all the Wednesdays.

In this case, the following syntax could be used

```
string QRY="SELECT year,month,day,VerdSE FROM AlmeaIndexes"
data y obs-format="%d/%d/%d" @QRY --odbc
```

The column `VerdSE` holds the data to be fetched, which will go into the gretl series `y`. The first three columns are used to construct a string which identifies the day. Since a string like `"2008/04/26"` does not correspond to any observation in our dataset (it's a Saturday), that row is simply discarded. On the other hand, since no string `"2008/04/23"` was found in the data coming from the DBMS (it's a Wednesday), that entry is left blank in our variable `y`.

## B.3 Examples

In the following examples, we will assume that access is available to a database known to ODBC with the data source name "AWM", with username "Otto" and password "Bingo". The database "AWM" contains quarterly data in two tables (see B.3 and B.4):

The table `Consump` is the classic "rectangular" dataset; that is, its internal organization is the same as in a spreadsheet or in an econometrics package like gretl itself: each row is a data point and each column is a variable. On the other hand, the structure of the `DATA` table is different: each record is one figure, stored in the column `xval`, and the other fields keep track of which variable it belongs to, for which date.

[3] See `http://www.almeopedia.com/index.php/Verduria`.

Table Consump

| Field | Type |
|---|---|
| time | decimal(7,2) |
| income | decimal(16,6) |
| consump | decimal(16,6) |

Table DATA

| Field | Type |
|---|---|
| year | decimal(4,0) |
| qtr | decimal(1,0) |
| varname | varchar(16) |
| xval | decimal(20,10) |

**Table B.3**: Example AWM database – structure

Table Consump

| | | |
|---|---|---|
| 1970.00 | 424278.975500 | 344746.944000 |
| 1970.25 | 433218.709400 | 350176.890400 |
| 1970.50 | 440954.219100 | 355249.672300 |
| 1970.75 | 446278.664700 | 361794.719900 |
| 1971.00 | 447752.681800 | 362489.970500 |
| 1971.25 | 453553.860100 | 368313.558500 |
| 1971.50 | 460115.133100 | 372605.015300 |
| ... | | |

Table DATA

| | | | |
|---|---|---|---|
| 1970 | 1 | CAN | −517.9085000000 |
| 1970 | 2 | CAN | 662.5996000000 |
| 1970 | 3 | CAN | 1130.4155000000 |
| 1970 | 4 | CAN | 467.2508000000 |
| 1970 | 1 | COMPR | 18.4000000000 |
| 1970 | 2 | COMPR | 18.6341000000 |
| 1970 | 3 | COMPR | 18.3000000000 |
| 1970 | 4 | COMPR | 18.2663000000 |
| 1970 | 1 | D1 | 1.0000000000 |
| 1970 | 2 | D1 | 0.0000000000 |
| ... | | | |

**Table B.4**: Example AWM database — data

Example B.1 shows two elementary queries: first we set up an empty quarterly dataset. Then, we connect to the database by the `open` statement. Once the connection is established we retrieve, one column at a time, the data from the `Consump` table. In this case, no observation string is necessary because the data are already arranged in a matrix-like structure, so we only need to bring over the relevant columns.

In example B.2, on the contrary, we make use of the observation string, since we are drawing data from the `DATA` table, which is not rectangular. The SQL statement stored in the string `S` produces a table with three columns. The `ORDER BY` clause ensures that the rows will be in chronological order, although this is not strictly necessary in this case.

**Example B.1**: Simple query from a rectangular table

```
nulldata 160
setobs 4 1970:1 --time
open dsn=AWM user=Otto password=Bingo --odbc

string Qry1 = "SELECT consump FROM Consump"
data cons @Qry1 --odbc

string Qry2 = "SELECT income FROM Consump"
data inc @Qry2 --odbc
```

**Example B.2**: Simple query from a non-rectangular table

```
string S = "select year, qtr, xval from DATA \
       where varname=’WLN’ ORDER BY year, qtr"
data wln obs-format="%d:%d" @S --odbc
```

**Example B.3**: Handling of missing values for a non-rectangular table

```
string foo = "select year, qtr, xval from DATA \
       where varname='STN' AND qtr>1"
data bar obs-format="%d,%d" @foo --odbc
print bar --byobs
```

Example B.3 shows what happens if the rows in the outcome from the SELECT statement do not match the observations in the currently open gretl dataset. The query includes a condition which filters out all the data from the first quarter. The query result (invisible to the user) would be something like

```
  +------+------+---------------+
  | year | qtr  | xval          |
  +------+------+---------------+
  | 1970 |    2 |  7.8705000000 |
  | 1970 |    3 |  7.5600000000 |
  | 1970 |    4 |  7.1892000000 |
  | 1971 |    2 |  5.8679000000 |
  | 1971 |    3 |  6.2442000000 |
  | 1971 |    4 |  5.9811000000 |
  | 1972 |    2 |  4.6883000000 |
  | 1972 |    3 |  4.6302000000 |
  ...
```

Internally, gretl fills the variable bar with the corresponding value if it finds a match; otherwise, NA is used. Printing out the variable bar thus produces

```
         Obs           bar

    1970:1
    1970:2        7.8705
    1970:3        7.5600
    1970:4        7.1892
    1971:1
    1971:2        5.8679
    1971:3        6.2442
    1971:4        5.9811
    1972:1
    1972:2        4.6883
    1972:3        4.6302
  ...
```

# Appendix C

# Building gretl

## C.1 Requirements

Gretl is written in the C programming language, abiding as far as possible by the ISO/ANSI C Standard (C90) although the graphical user interface and some other components necessarily make use of platform-specific extensions.

The program was developed under Linux. The shared library and command-line client should compile and run on any platform that supports ISO/ANSI C and has the libraries listed in Table C.1. If the GNU readline library is found on the host system this will be used for gretcli, providing a much enhanced editable command line. See the readline homepage.

| *Library* | *purpose* | *website* |
|---|---|---|
| zlib | data compression | info-zip.org |
| libxml2 | XML manipulation | xmlsoft.org |
| LAPACK | linear algebra | netlib.org |
| FFTW3 | Fast Fourier Transform | fftw.org |
| glib-2.0 | Numerous utilities | gtk.org |

**Table C.1**: Libraries required for building gretl

The graphical client program should compile and run on any system that, in addition to the above requirements, offers GTK version 2.4.0 or higher (see gtk.org).[1]

Gretl calls gnuplot for graphing. You can find gnuplot at gnuplot.info. As of this writing the most recent official release is 4.2 (of March, 2007). The MS Windows version of gretl comes with a Windows version gnuplot 4.2; the gretl website also offers an rpm of gnuplot 3.8j0 for x86 Linux systems.

Some features of gretl make use of portions of Adrian Feguin's gtkextra library. The relevant parts of this package are included (in slightly modified form) with the gretl source distribution.

A binary version of the program is available for the Microsoft Windows platform (Windows 98 or higher). This version was cross-compiled under Linux using mingw (the GNU C compiler, gcc, ported for use with win32) and linked against the Microsoft C library, `msvcrt.dll`. It uses Tor Lillqvist's port of GTK 2.0 to win32. The (free, open-source) Windows installer program is courtesy of Jordan Russell (jrsoftware.org).

## C.2 Build instructions: a step-by-step guide

In this section we give instructions detailed enough to allow a user with only a basic knowledge of a Unix-type system to build gretl. These steps were tested on a fresh installation of Debian Etch. For other Linux distributions (especially Debian-based ones, like Ubuntu and its derivatives) little should change. Other Unix-like operating systems such as MacOSX and BSD would probably require more substantial adjustments.

[1] Up till version 1.5.1, gretl could also be built using GTK 1.2. Support for this was dropped at version 1.6.0 of gretl.

In this guided example, we will build gretl complete with documentation. This introduces a few more requirements, but gives you the ability to modify the documentation files as well, like the help files or the manuals.

### Installing the prerequisites

We assume that the basic GNU utilities are already installed on the system, together with these other programs:

- some TEX/LATEXsystem (tetex or texlive will do beautifully)
- Gnuplot
- ImageMagick

We also assume that the user has administrative privileges and knows how to install packages. The examples below are carried out using the apt-get shell command, but they can be performed with menu-based utilities like aptitude, dselect or the GUI-based program synaptic. Users of Linux distributions which employ rpm packages (e.g. Red Hat/Fedora, Mandriva, SuSE) may want to refer to the dependencies page on the gretl website.

The first step is installing the C compiler and related utilities. On a Debian system, these are contained in a bunch of packages that can be installed via the command

```
apt-get install gcc autoconf automake1.9 libtool flex bison gcc-doc \
libc6-dev libc-dev libgfortran1 libgfortran1-dev gettext pkgconfig
```

Then it is necessary to install the "development" (dev) packages for the libraries that gretl uses:

| *Library* | *command* |
|---|---|
| GLIB | `apt-get install libglib2.0-dev` |
| GTK 2.0 | `apt-get install libgtk2.0-dev` |
| PNG | `apt-get install libpng12-dev` |
| XSLT | `apt-get install libxslt1-dev` |
| LAPACK | `apt-get install lapack3-dev` |
| FFTW | `apt-get install fftw3-dev` |
| READLINE | `apt-get install libreadline5-dev` |
| GMP | `apt-get install libgmp3-dev` |

(GMP is optional, but recommended.) The dev packages for these libraries are necessary to *compile* gretl — you'll also need the plain, non-dev library packages to *run* gretl, but most of these should already be part of a standard installation. In order to enable other optional features, like audio support, you may need to install more libraries.

### Getting the source: release or CVS

At this point, it is possible to build from the source. You have two options here: obtain the latest released source package, or retrieve the current CVS version of gretl (CVS = Concurrent Versions System). The usual caveat applies to the CVS version, namely, that it may not build correctly and may contain "experimental" code; on the other hand, CVS often contains bug-fixes relative to the released version. If you want to help with testing and to contribute bug reports, we recommend using CVS gretl.

To work with the released source:

1. Download the gretl source package from gretl.sourceforge.net.
2. Unzip and untar the package. On a system with the GNU utilities available, the command would be `tar xvfz gretl-N.tar.gz` (replace `N` with the specific version number of the file you downloaded at step 1).
3. Change directory to the gretl source directory created at step 2 (e.g. `gretl-1.6.6`).
4. Proceed to the next section, "Configure and make".

To work with CVS you'll first need to install the cvs client program if it's not already on your system. Relevant resources you may wish to consult include the CVS website at www.nongnu.org/cvs, general information on sourceforge CVS on the SourceForge CVS page, and instructions specific to gretl at the SF gretl CVS page.

When grabbing the CVS sources *for the first time*, you should first decide where you want to store the code. For example, you might create a directory called cvs under your home directory. Open a terminal window, cd into this directory, and type the following commands:

```
cvs -d:pserver:anonymous@gretl.cvs.sourceforge.net:/cvsroot/gretl login
cvs -z3 -d:pserver:anonymous@gretl.cvs.sourceforge.net:/cvsroot/gretl co -P gretl
```

After the first command you will be prompted for a password: just hit the Enter key. After the second command, cvs should create a subdirectory named `gretl` and fill it with the current sources.

When you want to *update the source*, this is very simple: just move into the `gretl` directory and type

```
cvs update -d -P
```

Assuming you're now in the CVS `gretl` directory, you can proceed in the same manner as with the released source package.

### Configure the source

The next command you need is `./configure`; this is a complex script that detects which tools you have on your system and sets things up. The `configure` command accepts many options; you may want to run

```
./configure --help
```

first to see what options are available. One option you way wish to tweak is `--prefix`. By default the installation goes under `/usr/local` but you can change this. For example

```
./configure --prefix=/usr
```

will put everything under the `/usr` tree. Another useful option refers to the fact that, by default, gretl offers support for the gnome desktop. If you want to suppress the gnome-specific features you can pass the option `--without-gnome` to `configure`.

In order to have the documentation built, we need to pass the relevant option to `configure`, as in

```
./configure --enable-build-doc
```

You will see a number of checks being run, and if everything goes according to plan, you should see a summary similar to that displayed in Example C.1.

☞ If you're using CVS, it's a good idea to re-run the `configure` script after doing an update. This is not always necessary, but sometimes it is, and it never does any harm. For this purpose, you may want to write a little shell script that calls `configure` with any options you want to use.

**Example C.1**: Output from `./configure --enable-build-doc`

```
Configuration:

  Installation path:                      /usr/local
  Use readline library:                   yes
  Use gnuplot for graphs:                 yes
  Use PNG for gnuplot graphs:             yes
  Use LaTeX for typesetting output:       yes
  Gnu Multiple Precision support:         yes
  MPFR support:                           no
  LAPACK support:                         yes
  FFTW3 support:                          yes
  Build with GTK version:                 2.0
  Script syntax highlighting:             yes
  Use installed gtksourceview:            yes
  Build with gnome support:               no
  Build gretl documentation:              yes
  Build message catalogs:                 yes
  Gnome installation prefix:              NA
  X-12-ARIMA support:                     yes
  TRAMO/SEATS support:                    yes
  Experimental audio support:             no

Now type 'make' to build gretl.
```

### Build and install

We are now ready to undertake the compilation proper: this is done by running the `make` command, which takes care of compiling all the necessary source files in the correct order. All you need to do is type

```
make
```

This step will likely take several minutes to complete; a lot of output will be produced on screen. Once this is done, you can install your freshly baked copy of gretl on your system via

```
make install
```

On most systems, the `make install` command requires you to have administrative privileges. Hence, either you log in as `root` before launching `make install` or you may want to use the `sudo` utility:

```
sudo make install
```

# Appendix D

# Numerical accuracy

Gretl uses double-precision arithmetic throughout — except for the multiple-precision plugin invoked by the menu item "Model, Other linear models, High precision OLS" which represents floating-point values using a number of bits given by the environment variable `GRETL_MP_BITS` (default value 256).

The normal equations of Least Squares are by default solved via Cholesky decomposition, which is highly accurate provided the matrix of cross-products of the regressors, $X'X$, is not very ill conditioned. If this problem is detected, gretl automatically switches to use QR decomposition.

The program has been tested rather thoroughly on the statistical reference datasets provided by NIST (the U.S. National Institute of Standards and Technology) and a full account of the results may be found on the gretl website (follow the link "Numerical accuracy").

To date, two published reviews have discussed gretl's accuracy: Giovanni Baiocchi and Walter Distaso (2003), and Talha Yalta and Yasemin Yalta (2007). We are grateful to these authors for their careful examination of the program. Their comments have prompted several modifications including the use of Stephen Moshier's `cephes` code for computing p-values and other quantities relating to probability distributions (see netlib.org), changes to the formatting of regression output to ensure that the program displays a consistent number of significant digits, and attention to compiler issues in producing the MS Windows version of gretl (which at one time was slighly less accurate than the Linux version).

Gretl now includes a "plugin" that runs the NIST linear regression test suite. You can find this under the "Tools" menu in the main window. When you run this test, the introductory text explains the expected result. If you run this test and see anything other than the expected result, please send a bug report to `cottrell@wfu.edu`.

All regression statistics are printed to 6 significant figures in the current version of gretl (except when the multiple-precision plugin is used, in which case results are given to 12 figures). If you want to examine a particular value more closely, first save it (for example, using the `genr` command) then print it using `print --long` (see the *Gretl Command Reference*). This will show the value to 10 digits (or more, if you set the internal variable `longdigits` to a higher value via the `set` command).

# Appendix E

# Related free software

Gretl's capabilities are substantial, and are expanding. Nonetheless you may find there are some things you can't do in gretl, or you may wish to compare results with other programs. If you are looking for complementary functionality in the realm of free, open-source software we recommend the following programs. The self-description of each program is taken from its website.

- **GNU R** r-project.org: "R is a system for statistical computation and graphics. It consists of a language plus a run-time environment with graphics, a debugger, access to certain system functions, and the ability to run programs stored in script files... It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS." Comment: There are numerous add-on packages for R covering most areas of statistical work.
- **GNU Octave** www.octave.org: "GNU Octave is a high-level language, primarily intended for numerical computations. It provides a convenient command line interface for solving linear and nonlinear problems numerically, and for performing other numerical experiments using a language that is mostly compatible with Matlab. It may also be used as a batch-oriented language."
- **JMulTi** www.jmulti.de: "JMulTi was originally designed as a tool for certain econometric procedures in time series analysis that are especially difficult to use and that are not available in other packages, like Impulse Response Analysis with bootstrapped confidence intervals for VAR/VEC modelling. Now many other features have been integrated as well to make it possible to convey a comprehensive analysis." Comment: JMulTi is a java GUI program: you need a java run-time environment to make use of it.

As mentioned above, gretl offers the facility of exporting data in the formats of both Octave and R. In the case of Octave, the gretl data set is saved as a single matrix, X. You can pull the X matrix apart if you wish, once the data are loaded in Octave; see the Octave manual for details. As for R, the exported data file preserves any time series structure that is apparent to gretl. The series are saved as individual structures. The data should be brought into R using the `source()` command.

In addition, gretl has a convenience function for moving data quickly into R. Under gretl's "Tools" menu, you will find the entry "Start GNU R". This writes out an R version of the current gretl data set (in the user's gretl directory), and sources it into a new R session. The particular way R is invoked depends on the internal gretl variable Rcommand, whose value may be set under the "Tools, Preferences" menu. The default command is `RGui.exe` under MS Windows. Under X it is `xterm -e R`. Please note that at most three space-separated elements in this command string will be processed; any extra elements are ignored.

Appendix F

# Listing of URLs

Below is a listing of the full URLs of websites mentioned in the text.

**Estima (RATS)** `http://www.estima.com/`

**FFTW3** `http://www.fftw.org/`

**Gnome desktop homepage** `http://www.gnome.org/`

**GNU Multiple Precision (GMP) library** `http://swox.com/gmp/`

**GNU Octave homepage** `http://www.octave.org/`

**GNU R homepage** `http://www.r-project.org/`

**GNU R manual** `http://cran.r-project.org/doc/manuals/R-intro.pdf`

**Gnuplot homepage** `http://www.gnuplot.info/`

**Gnuplot manual** `http://ricardo.ecn.wfu.edu/gnuplot.html`

**Gretl data page** `http://gretl.sourceforge.net/gretl_data.html`

**Gretl homepage** `http://gretl.sourceforge.net/`

**GTK+ homepage** `http://www.gtk.org/`

**GTK+ port for win32** `http://www.gimp.org/~tml/gimp/win32/`

**Gtkextra homepage** `http://gtkextra.sourceforge.net/`

**InfoZip homepage** `http://www.info-zip.org/pub/infozip/zlib/`

**JMulTi homepage** `http://www.jmulti.de/`

**JRSoftware** `http://www.jrsoftware.org/`

**Mingw (gcc for win32) homepage** `http://www.mingw.org/`

**Minpack** `http://www.netlib.org/minpack/`

**Penn World Table** `http://pwt.econ.upenn.edu/`

**Readline homepage** `http://cnswww.cns.cwru.edu/~chet/readline/rltop.html`

**Readline manual** `http://cnswww.cns.cwru.edu/~chet/readline/readline.html`

**Xmlsoft homepage** `http://xmlsoft.org/`

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