

# Manual de Utilização do Gretl



Gnu Regression, Econometrics and Time-series

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# Conteúdo

<b>1</b>	<b>Introduction</b>	<b>1</b>
1.1	Features at a glance . . . . .	1
1.2	Acknowledgements . . . . .	1
1.3	Installing the programs . . . . .	2
<b>I</b>	<b>Use do programa</b>	<b>4</b>
<b>2</b>	<b>Getting started</b>	<b>5</b>
2.1	Let's run a regression . . . . .	5
2.2	Estimation output . . . . .	7
2.3	The main window menus . . . . .	7
2.4	Keyboard shortcuts . . . . .	10
2.5	The gretl toolbar . . . . .	11
<b>3</b>	<b>Modes of working</b>	<b>12</b>
3.1	Command scripts . . . . .	12
3.2	Saving script objects . . . . .	13
3.3	The gretl console . . . . .	14
3.4	The Session concept . . . . .	14
<b>4</b>	<b>Data files</b>	<b>17</b>
4.1	Native format . . . . .	17
4.2	Other data file formats . . . . .	17
4.3	Binary databases . . . . .	17
4.4	Creating a data file from scratch . . . . .	18
4.5	Structuring a dataset . . . . .	20
4.6	Missing data values . . . . .	23
4.7	Maximum size of data sets . . . . .	24
4.8	Data file collections . . . . .	25
<b>5</b>	<b>Special functions in genr</b>	<b>27</b>
5.1	Introduction . . . . .	27
5.2	Long-run variance . . . . .	27
5.3	Time-series filters . . . . .	27
5.4	Panel data specifics . . . . .	29
5.5	Resampling and bootstrapping . . . . .	30

5.6	Cumulative densities and p-values . . . . .	31
5.7	Handling missing values . . . . .	32
5.8	Retrieving internal variables . . . . .	32
5.9	Numerical maximization . . . . .	33
5.10	The discrete Fourier transform . . . . .	35
<b>6</b>	<b>Sub-sampling a dataset</b>	<b>38</b>
6.1	Introduction . . . . .	38
6.2	Setting the sample . . . . .	38
6.3	Restricting the sample . . . . .	39
6.4	Random sampling . . . . .	40
6.5	The Sample menu items . . . . .	40
<b>7</b>	<b>Graphs and plots</b>	<b>41</b>
7.1	Gnuplot graphs . . . . .	41
7.2	Boxplots . . . . .	42
<b>8</b>	<b>Discrete variables</b>	<b>44</b>
8.1	Declaring variables as discrete . . . . .	44
8.2	Commands for discrete variables . . . . .	45
<b>9</b>	<b>Loop constructs</b>	<b>49</b>
9.1	Introduction . . . . .	49
9.2	Loop control variants . . . . .	50
9.3	Progressive mode . . . . .	51
9.4	Loop examples . . . . .	52
<b>10</b>	<b>User-defined functions</b>	<b>56</b>
10.1	Defining a function . . . . .	56
10.2	Calling a function . . . . .	57
10.3	Function programming details . . . . .	58
10.4	Function packages . . . . .	60
<b>11</b>	<b>Named lists and strings</b>	<b>64</b>
11.1	Named lists . . . . .	64
11.2	Named strings . . . . .	66
<b>12</b>	<b>Matrix manipulation</b>	<b>69</b>
12.1	Introduction . . . . .	69
12.2	Creating matrices . . . . .	69
12.3	Selecting sub-matrices . . . . .	70
12.4	Matrix operators . . . . .	71
12.5	Matrix-scalar operators . . . . .	72

12.6	Matrix functions . . . . .	72
12.7	Matrix accessors . . . . .	78
12.8	Namespace issues . . . . .	80
12.9	Creating a data series from a matrix . . . . .	80
12.10	Matrices and lists . . . . .	81
12.11	Deleting a matrix . . . . .	81
12.12	Printing a matrix . . . . .	82
12.13	Example: OLS using matrices . . . . .	82
<b>13</b>	<b>Cheat sheet</b>	<b>84</b>
13.1	Dataset handling . . . . .	84
13.2	Creating/modifying variables . . . . .	85
13.3	Neat tricks . . . . .	86
<b>II</b>	<b>Métodos econométricos</b>	<b>87</b>
<b>14</b>	<b>Robust covariance matrix estimation</b>	<b>88</b>
14.1	Introduction . . . . .	88
14.2	Cross-sectional data and the HCCME . . . . .	89
14.3	Time series data and HAC covariance matrices . . . . .	90
14.4	Special issues with panel data . . . . .	94
<b>15</b>	<b>Panel data</b>	<b>95</b>
15.1	Estimation of panel models . . . . .	95
15.2	Dynamic panel models . . . . .	99
15.3	Illustration: the Penn World Table . . . . .	100
<b>16</b>	<b>Nonlinear least squares</b>	<b>102</b>
16.1	Introduction and examples . . . . .	102
16.2	Initializing the parameters . . . . .	102
16.3	NLS dialog window . . . . .	103
16.4	Analytical and numerical derivatives . . . . .	103
16.5	Controlling termination . . . . .	103
16.6	Details on the code . . . . .	104
16.7	Numerical accuracy . . . . .	104
<b>17</b>	<b>Maximum likelihood estimation</b>	<b>106</b>
17.1	Generic ML estimation with gretl . . . . .	106
17.2	Gamma estimation . . . . .	107
17.3	Stochastic frontier cost function . . . . .	109
17.4	GARCH models . . . . .	110
17.5	Analytical derivatives . . . . .	112

17.6	Debugging ML scripts . . . . .	113
<b>18</b>	<b>GMM estimation</b>	<b>114</b>
18.1	Introduction and terminology . . . . .	114
18.2	OLS as GMM . . . . .	115
18.3	TSLS as GMM . . . . .	117
18.4	Covariance matrix options . . . . .	117
18.5	A real example: the Consumption Based Asset Pricing Model . . . . .	118
18.6	Caveats . . . . .	120
<b>19</b>	<b>Model selection criteria</b>	<b>123</b>
19.1	Introduction . . . . .	123
19.2	Information criteria . . . . .	123
<b>20</b>	<b>Time series models</b>	<b>125</b>
20.1	ARIMA models . . . . .	125
20.2	Unit root tests . . . . .	129
20.3	ARCH and GARCH . . . . .	131
20.4	Cointegration and Vector Error Correction Models . . . . .	134
<b>21</b>	<b>Discrete and censored dependent variables</b>	<b>139</b>
21.1	Logit and probit models . . . . .	139
21.2	The Tobit model . . . . .	142
<b>III</b>	<b>Detalhes técnicos</b>	<b>145</b>
<b>22</b>	<b>Gretl and T<sub>E</sub>X</b>	<b>146</b>
22.1	Introduction . . . . .	146
22.2	T <sub>E</sub> X-related menu items . . . . .	146
22.3	Fine-tuning typeset output . . . . .	148
22.4	Character encodings . . . . .	150
22.5	Installing and learning T <sub>E</sub> X . . . . .	150
<b>23</b>	<b>Troubleshooting gretl</b>	<b>152</b>
23.1	Bug reports . . . . .	152
23.2	Auxiliary programs . . . . .	152
<b>24</b>	<b>O interface de linha de comandos (CLI)</b>	<b>153</b>
24.1	Gretl em modo de consola . . . . .	153
24.2	A sintaxe CLI . . . . .	153

<b>IV</b>	<b>Apêndices</b>	<b>154</b>
<b>A</b>	<b>Data file details</b>	<b>155</b>
A.1	Basic native format . . . . .	155
A.2	Traditional ESL format . . . . .	155
A.3	Binary database details . . . . .	156
<b>B</b>	<b>Building gretl</b>	<b>158</b>
B.1	Requirements . . . . .	158
B.2	Build instructions: a step-by-step example . . . . .	158
<b>C</b>	<b>Numerical accuracy</b>	<b>161</b>
<b>D</b>	<b>Related free software</b>	<b>162</b>
<b>E</b>	<b>Listing of URLs</b>	<b>163</b>
	<b>Bibliografia</b>	<b>164</b>

# Capítulo 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 B).

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

**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.

**Extendible** 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 C.

**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 or German, 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*); and Russell Davidson and James MacKinnon (*Econometric Theory and Methods*).

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), and Markus Hahn and Sven Schreiber (German).

**Gretl** has benefitted greatly from the work of numerous developers of free, open-source software: for specifics please see Appendix B. 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, and Dirk Eddelbuettel, who maintains the **gretl** package for Debian GNU/Linux.

### 1.3 Installing the programs

#### Linux

On the Linux<sup>1</sup> 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 (eg 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 B.

#### 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 (the default is `c:\userdata\gretl`).

#### 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

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<sup>1</sup>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.

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**.

## **Parte I**

# **Uso do programa**

## Capítulo 2

# Getting started

### 2.1 Let's run a regression

This introduction is mostly angled towards the graphical client program; please see Chapter 24 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.<sup>1</sup> 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.

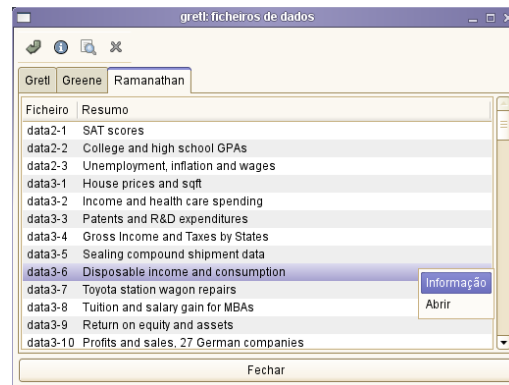


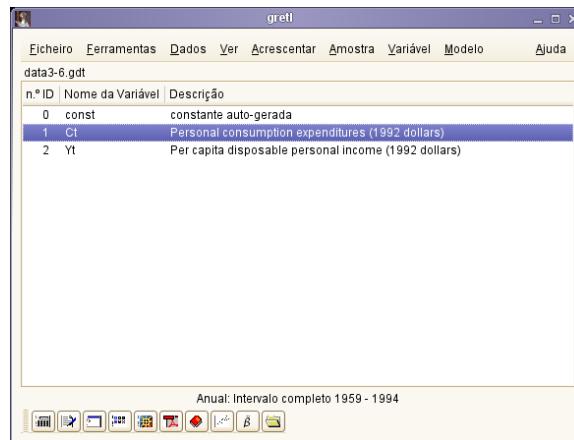
Figura 2.1: Practice data files window

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`.

<sup>1</sup> 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.

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.

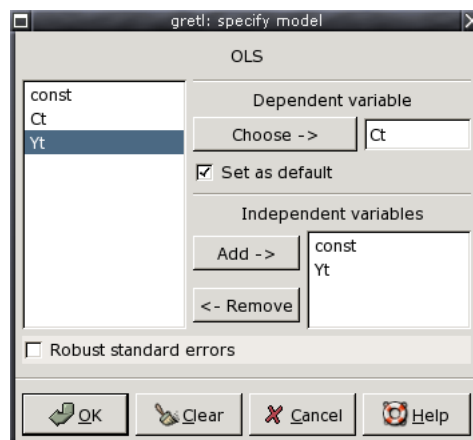
<sup>1</sup>For convenience I will refer to the graphical client program simply as `gretl` in this manual. Note, however, that the specific name of the program differs according to the computer platform. On Linux it is called `gretl_x11` while on MS Windows it is `gretlw32.exe`. On Linux systems a wrapper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



**Figura 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.



**Figura 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).

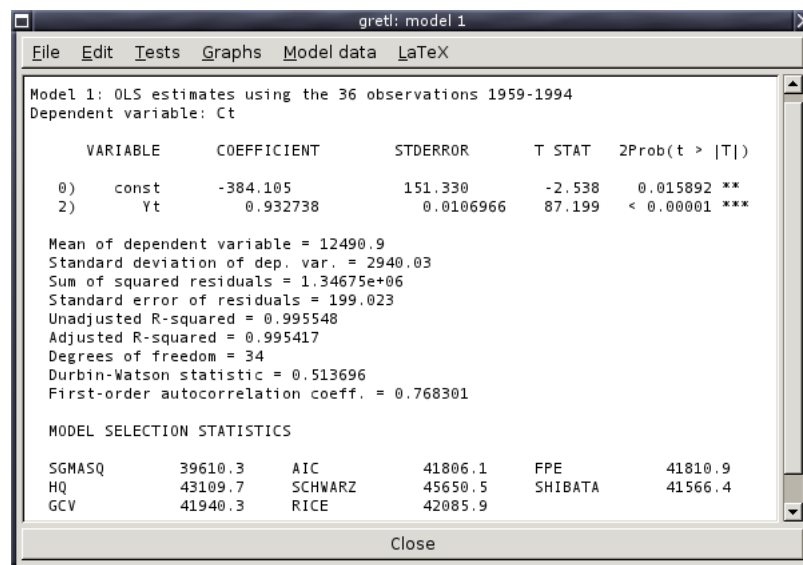


Figura 2.4: Model output window

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 L<sup>A</sup>T<sub>E</sub>X format. See Chapter 22 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 L<sup>A</sup>T<sub>E</sub>X. If you are pasting into a word processor, RTF may be a good option because the tabular formatting of the output is preserved.<sup>2</sup> 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.

## 2.3 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.

Eicheiro Ferramentas Dados Ver Acrescentar Amostra Variável Modelo Ajuda

<sup>2</sup>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.

- 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 D.
- 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 10.4), which allow you to access functions written by other users and share the ones written by you.
- Exit: Quit the program. If expert mode is not selected 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: Open a window which enables you to look up p-values from the Gaussian,  $t$ , chi-square,  $F$ , gamma or binomial distributions. See also the `pvalue` command in the *Gretl Command Reference*.
- 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). See also the item “Bivariate tests” under the Model menu.
- 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 D.
- 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. Select or unselect “expert mode”. (If this mode is selected various warning messages are suppressed.) Activate or suppress `gretl`'s messaging about the availability of program updates. Configure or turn on/off the main-window toolbar. See the *Manual dos Comandos do Gretl* 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: Active only if two or more variables are selected; shows the pairwise correlation coefficients for the selected variables.
- Principal components: Active only if two or more variables are selected; produces a Principal Components Analysis of the selected variables.
- Mahalanobis distances: Active only if two or more variables are selected; computes the Mahalanobis distance of each observation from the centroid of the selected set of 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 pre-defined 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 *Manual dos Comandos do Gretl* 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.

<b>Return</b>	Opens a window displaying the values of the currently selected variables: it is the same as selecting “Data, Display Values”.
<b>Delete</b>	Pressing this key has the effect of deleting the selected variables. A confirmation is required, to prevent accidental deletions.
<b>e</b>	Has the same effect as selecting “Edit attributes” from the “Variable” menu.
<b>F2</b>	Same as “e”. Included for compatibility with other programs.
<b>g</b>	Has the same effect as selecting “Define new variable” from the “Variable” menu (which maps onto the <b>genr</b> command).
<b>h</b>	Opens a help window for gretl commands.
<b>F1</b>	Same as “h”. Included for compatibility with other programs.
<b>r</b>	Refreshes the variable list in the main window: has the same effect as selecting “Refresh window” from the “Data” menu.
<b>t</b>	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 the gretl website in your web browser. This will work only if you are connected to the Internet and have a properly configured browser.
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.

If you don’t care to have the toolbar displayed, you can turn it off under the “Tools, Preferences, General” menu. Go to the Toolbar tab and uncheck the “show gretl toolbar” box.

## Capítulo 3

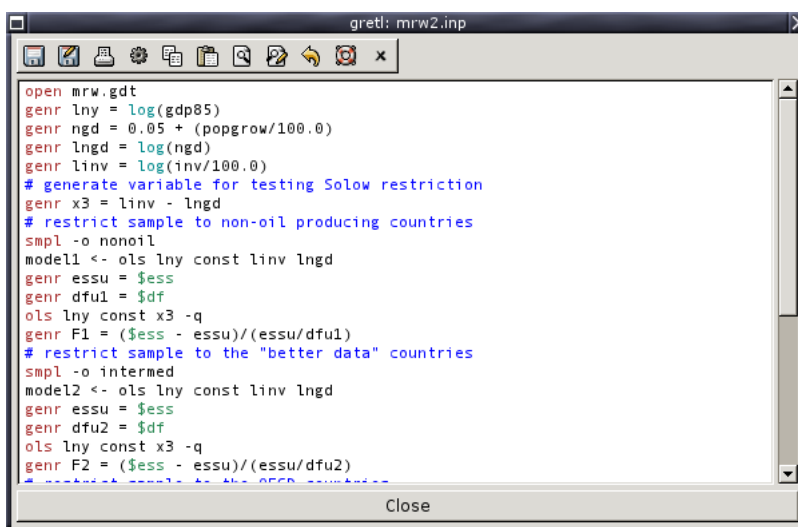
# Modes of working

### 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).



**Figura 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 (under Windows or the gnome desktop only); (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, all output is directed to a single window, where it can be edited, saved or copied to the clipboard. You can launch the script by clicking on the Execute icon or by pressing Ctrl-r. 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 *Manual dos Comandos do Gretl*.

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.<sup>1</sup>

In addition, 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 *Manual dos Comandos do Gretl*). 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.

## 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:

```
Model11 <- 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:

```
Model11.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:

---

<sup>1</sup>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.

```
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

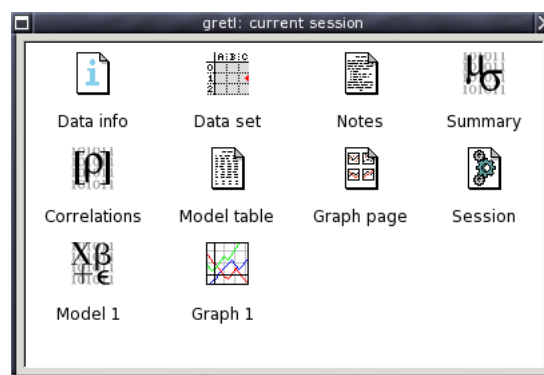
A further option is available for your computing convenience. Under gretl’s “Tools” menu you will find the item “Gretl console” (there is also an “open gretl console” button on the toolbar in the main window). This opens up a window in which you can type commands and execute them one by one (by pressing 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) as 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.



**Figura 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 redisplay 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,  $\text{\LaTeX}$  or Rich Text Format). Here is how to do it:<sup>2</sup>

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.

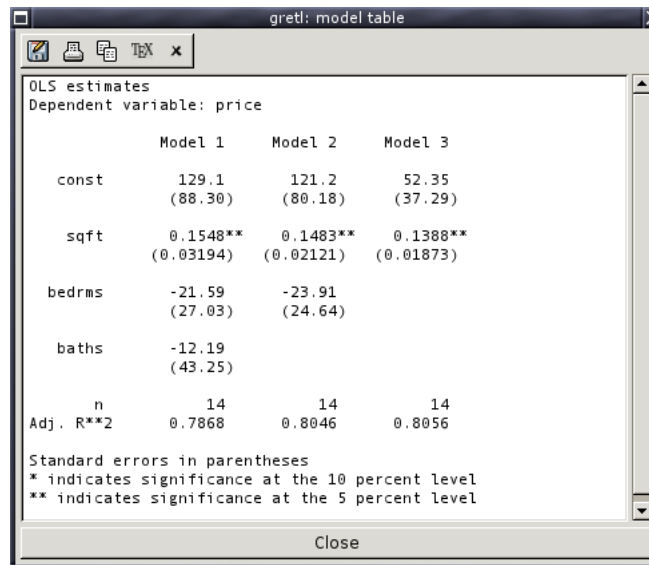
A simple instance of **gretl**’s model table is shown in Figure 3.3.

### 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  $\text{\LaTeX}$  typesetting system installed, and are able to generate and view either PDF or PostScript output.<sup>3</sup>

<sup>2</sup>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*.

<sup>3</sup>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`.



	Model 1	Model 2	Model 3
const	129.1 (88.30)	121.2 (80.18)	52.35 (37.29)
sqft	0.1548** (0.03194)	0.1483** (0.02121)	0.1388** (0.01873)
bedrms	-21.59 (27.03)	-23.91 (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

Close

**Figura 3.3:** Example of model table

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.

## Capítulo 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.
- Worksheets in the format of either MS Excel or Gnumeric. 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`).
- Eviews workfiles (`.wf1`).<sup>1</sup>

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.

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 and GNU Octave (see Appendix D). 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 flag `-r` (R) or `-m` (Octave).

### 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 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.

---

<sup>1</sup>This is somewhat experimental. See [http://www.ecn.wfu.edu/eviews\\_format/](http://www.ecn.wfu.edu/eviews_format/).



### RATS 4 databases

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 also handle such databases. Well, actually, a subset of same: I have only worked on time-series databases containing monthly and quarterly series. My university has the RATS G7 database containing data for the seven largest OECD economies and **gretl** will read that OK.

🌐 Visit the [gretl data page](#) for details and updates on available data.

## 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 program is MS Excel or Gnumeric), then use one of **gretl**'s "Import" options (CSV, Excel or Gnumeric, as the case may be).
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 create a 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. *Gretl* comes with a database of US macroeconomic time series and, as mentioned above, the program will reads RATS 4 databases.

Begin with *gretl*’s “File, Databases” menu item. This has three forks: “Gretl native”, “RATS 4” and “On database server”. You should be able to find the file `fedst1.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.<sup>2</sup> 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).

---

<sup>2</sup>See [www.estima.com](http://www.estima.com)

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 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 expanding 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`,<sup>3</sup> 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 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)
```

---

<sup>3</sup>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.

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 there 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.<sup>4</sup>

## 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.

---

<sup>4</sup>**genr** also offers the inverse function to **misszero**, namely **zeromiss**, which replaces zeros in a given series with the missing observation code.

## 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.
- 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.)

	<i>Linux</i>	<i>MS Windows</i>
system data dir	<code>/usr/share/gretl/data</code>	<code>c:\userdata\gretl\data</code>
system script dir	<code>/usr/share/gretl/scripts</code>	<code>c:\userdata\gretl/scripts</code>
user dir	<code>/home/me/gretl</code>	<code>c:\userdata\gretl\user</code>

**Tabela 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 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, I would encourage you to submit the collection for packaging as a `gretl` optional extra.

## Capítulo 5

# Special functions in genr

### 5.1 Introduction

The **genr** command provides a flexible means of defining new variables. It is documented in the *Manual dos Comandos do Gretl*. 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  $x_1, x_2, \dots, x_T$  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

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

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 and the Baxter–King bandpass filter.

#### 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

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

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

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

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  $c_t$ .

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

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

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

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  $y_t$ :

$$y_t = \int_{-\pi}^{\pi} e^{i\omega} dZ(\omega)$$

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

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

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 `gretcli`.

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

The functions `pmean()` and `psd()` can be used to generate basic descriptive statistics (mean and standard deviation) for a given variable, on a per-group basis.

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 do

```
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).

**Exemplo 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 *Manual dos Comandos do Gretl*; 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 *Manual dos Comandos do Gretl*; 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 maximization

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 string specifying 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_tol` (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:

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

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).

#### Exemplo 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
```

---

### Computing the Jacobian

To construct a covariance matrix for estimates produced via `BFGS_max`, you may wish to calculate a numerical approximation to the relevant Jacobian.

The `fdjac` function again takes two arguments: an  $n \times 1$  matrix holding initial parameter values and a string specifying a call to a function that calculates and returns an  $m \times 1$  matrix ( $n \leq m$ ), 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
```

## 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<sup>1</sup> 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)
```

---

<sup>1</sup>See chapter 12.

yields

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

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 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 polynomials:

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

The coefficients of the polynomial  $c(x)$  are the convolution of the coefficients 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 transform in econometrics has been mostly used in time-series analysis, the periodogram being the best known example. Example script [5.3](#) shows how to compute the periodogram of a time series via the `fft` function.

**Exemplo 5.3:** 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
```

---

## Capítulo 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.<sup>1</sup>

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”.

---

<sup>1</sup>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,

```
smp1 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 `smp1`. 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 `smp1` 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).

## Capítulo 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](http://www.gnuplot.info) (but note that a copy of gnuplot is bundled with the MS Windows version of `gretl`). `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.<sup>1</sup>
- **Edit:** Opens a controller for the plot which lets you adjust various 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).<sup>2</sup> 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.
- 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.

---

<sup>1</sup>For best results when pasting graphs into MS Office applications, choose the application's “Edit, Paste Special...” menu item, and select the option “Picture (Enhanced Metafile)”.

<sup>2</sup>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 remove labels that have been affixed in either of these ways, select “Edit” from the graph pop-up and uncheck “Show all data labels”.

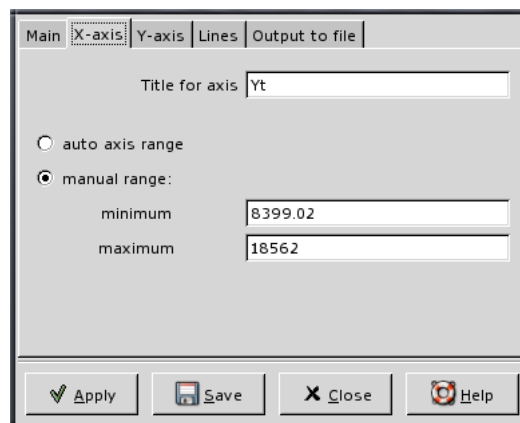
### Advanced options

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), you have two further options.

- Once the graph is saved as a session icon, you can right-click on its icon for a further pop-up menu. One of the options here is “Edit plot commands”, which 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** (with the Execute icon on the toolbar in the plot commands editing window).
- Another way to save the plot commands (or to save the displayed plot in formats other than EPS or PNG) is to use “Edit” item on a graph’s pop-up menu to invoke the graphical controller, then click on the “Output to file” tab in the controller. You are then presented with a drop-down menu of formats in which to save the graph.

To find out more about **gnuplot** see the [online manual](#) or [www.gnuplot.info](http://www.gnuplot.info).

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



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

## 7.2 Boxplots

Boxplots are not generated using **gnuplot**, but rather by **gretl** itself.

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.

In the case of notched boxes, the notch shows the limits of an approximate 90 percent confidence interval. This is obtained by the bootstrap method, which can take a while if the data series is very long.

Clicking the mouse in the boxplots window brings up a menu which enables you to save the plots as encapsulated postscript (EPS) or as a full-page postscript file. Under the X window system you can also save the window as an XPM file; under MS Windows you can copy it to the clipboard as a bitmap. The menu also gives you the option of opening a summary window which displays five-number summaries (minimum, first quartile, median, third quartile, maximum), plus a confidence interval for the median if the “notched” option was chosen.

Some details of gretl's boxplots can be controlled via a (plain text) file named `.boxplotrc` which is looked for, in turn, in the current working directory, the user's home directory (corresponding to the environment variable `HOME`) and the gretl user directory (which is displayed and may be changed under the "Tools, Preferences, General" menu). Options that can be set in this way are the font to use when producing postscript output (must be a valid generic postscript font name; the default is Helvetica), the size of the font in points (also for postscript output; default is 12), the minimum and maximum for the y-axis range, the width and height of the plot in pixels (default, 560 x 448), whether numerical values should be printed for the quartiles and median (default, don't print them), and whether outliers (points lying beyond 1.5 times the interquartile range from the central box) should be indicated separately (default, no). Here is an example:

```
font = Times-Roman
fontsize = 16
max = 4.0
min = 0
width = 400
height = 448
numbers = %3.2f
outliers = true
```

On the second to last line, the value associated with `numbers` is a "printf" format string as in the C programming language; if specified, this controls the printing of the median and quartiles next to the boxplot, if no `numbers` entry is given these values are not printed. In the example, the values will be printed to a width of 3 digits, with 2 digits of precision following the decimal point.

Not all of the options need be specified, and the order doesn't matter. Lines not matching the pattern "key = value" are ignored, as are lines that begin with the hash mark, `#`.

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)
```

## Capítulo 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.

For example, the following code

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

Tabela 8.1: Number of bins for various sample sizes

```

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 can 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 options `-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.

## Capítulo 9

# Loop constructs

### 9.1 Introduction

The command `loop` opens a special mode in which `gretl` accepts a block of commands to be repeated one 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 accepted in this context are shown in Table 9.1.

**Tabela 9.1:** Commands usable in loops

;	add	adf	append	ar	ar1	arbond	arch
arima	break	chow	coeffsum	coint	coint2	corr	criteria
dataset	diff	difftest	discrete	dummify	elif	else	end
endif	endloop	equation	estimate	fcast	foreign	freq	garch
genr	gmm	graph	hausman	hccm	heckit	help	hsk
if	info	kpss	labels	lad	lags	ldiff	lmtest
logistic	logit	logs	loop	mahal	meantest	mle	mpols
nls	normtest	ols	omit	orthdev	outfile	panel	pca
pergm	plot	poisson	print	printf	probit	pvalue	quantreg
quit	rename	reset	restrict	rhodiff	runs	sdiff	set
setinfo	shell	smpl	spearman	sprintf	square	sscanf	store
summary	system	testuhat	tobit	tsls	var	varlist	vartest
vecm	wls	xtab					

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 `ols`, `print` and `store` 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 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 scalar. If it is in fact a series, its first value is read. 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 an inequality: the left-hand term should be the name of a predefined variable; the right-hand side may be either a numerical constant or the name of another predefined variable. For example,

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

Execution of the commands within the loop will continue so long as the specified condition evaluates as true. If the right-hand term of the inequality is a variable, it is evaluated at the top of the loop at each iteration.

### Index loop

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

The index variable may be used within the loop body in one or both of two ways: you can access the 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 variables. In the latter case the variables are evaluated once, when the loop is set up. 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 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:

```
open greene22_2
open greene22_2
discrete Z8
v8 = values(Z8)
n = rows(v8)
n = rows(v8)
loop for 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`.

**For each loop**

The fourth form of loop control also uses the internal variable `i`, but in this case the variable ranges over 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.

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
```

**For loop**

The final form of loop control uses a simplified version of the `for` statement in the C programming language. The expression is composed of three parts, separated by semicolons. The first part specifies an initial condition, expressed in terms of a control variable; the second part gives a continuation condition (in terms of the same control variable); and the third part specifies an increment (or decrement) for the control variable, to be applied each time round the loop. The entire expression is enclosed in parentheses. For 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 0.9900000000000001.)

To expand on the rules for the three components of the control expression:

1. The initial condition must take the form `LHS1 = RHS1`. `RHS1` must be a numeric constant or a predefined variable. If the `LHS1` variable does not exist already, it is automatically created.
2. The continuation condition must be of the form `LHS1 op RHS2`, where `op` can be `<`, `>`, `<=` or `>=` and `RHS2` is a numeric constant or a predefined variable. If `RHS2` is a variable it is evaluated each time round the loop.
3. The increment or decrement expression must be of the form `LHS1 += DELTA` or `LHS1 -= DELTA`, where `DELTA` is a numeric constant or a predefined variable. If `DELTA` is a variable, it is evaluated only once, when the loop is set up.

**9.3 Progressive mode**

If the `--progressive` option is given for a command loop, the effects of the commands `ols`, `print` and `store` are modified as follows.

**ols:** The results from each individual iteration of the regression 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 single value at each iteration, for example the error sum of squares from a regression.

**store:** This command writes out the values of the specified variables, from each time round the loop, to a specified file. Thus it keeps a complete record of the variables 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.

**Exemplo 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.

### Exemplo 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
```

---

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*.

### Indexed loop examples

Example 9.4 shows an indexed loop in which the `smp1` 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.

**Exemplo 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

```

---

**Exemplo 9.4:** Panel statistics

---

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

---

**Exemplo 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
```

---

## Capítulo 10

# User-defined functions

### 10.1 Defining a function

Since version 1.3.3, `gretl` has contained a mechanism for defining functions in the context of a script. This functionality has been through some changes in search of a stable and extensible framework. We believe that the version present in `gretl` 1.6.1 should provide a good basis for future development.

Functions must be defined before they are called. 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
<code>bool</code>	scalar variable acting as a Boolean switch
<code>int</code>	scalar variable acting as an integer
<code>scalar</code>	scalar variable
<code>series</code>	data series
<code>list</code>	named list of series
<code>matrix</code>	named matrix or vector

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`, 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 [10.3](#)); it is related to the use of pointer arguments in the C programming language. In addition, parameters may be modified by the tag `const` (again, see [10.3](#)).

Besides these required elements, the specification of a `scalar` parameter may include up to three pieces of additional information: a minimum value, a maximum, and a default. These additional 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]
```

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)
```

When a function is called, the parameters are instantiated by arguments given by the caller. 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 *function body* is composed of `gretl` commands, or calls to user-defined functions (that is, functions 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.

## 10.2 Calling a function

A user function is called or invoked 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. 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 Function programming details

#### Scope of variables

All 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.

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. There is, however, a mechanism for allowing 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 method is (at least superficially) similar to the passing of the address of a variable in the C programming language. 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 should use `null` in place of a real argument:

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

### 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`, or it can be “unpacked” using a `foreach` loop construct. For example, suppose you have a list `X` and want to calculate the standard deviation of each variable in the list:

```

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

```

When a named list of variables is passed to a function, the function is provided with a copy of the list. The variables referenced in the list are, however, made directly accessible to the function, in a similar manner to the case where a scalar or series argument is passed in “pointer” form, as discussed above. Passing a list is therefore another means of allowing a function to do more in the way of modifying data at the level of the caller than simply offering a return value. If the variables will *not* be modified inside the function, it is a good idea to flag this fact using the `const` modifier in the listing of parameters:

```
function myfunc (scalar y, const list X)
```

When a list is marked `const`, any attempt to rename, delete or overwrite the original values of the variables in the list will generate an error.

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 then 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. (This mechanism can also be used to check whether a named, but empty, list was supplied as an argument.)

### Return values

Functions can return nothing (just printing a result, perhaps), or they can return a single variable — a scalar, series, list or matrix. 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 = $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.

### Printing of output

The usual mechanism whereby `gretl` echos commands, and reports on the creation of new variables, is suppressed by default when a function is being executed. If you want to turn this on (for example, for the purpose of debugging function code), you can issue one or both of the following commands inside the function:

```

set echo on
set messages on

```

## 10.4 Function packages

As of `gretl` 1.6.0, there is a mechanism to package functions and make them available to other users of `gretl`. This is currently experimental, but 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 foo = diff(y)/y(-1)
  return series foo
end function
```

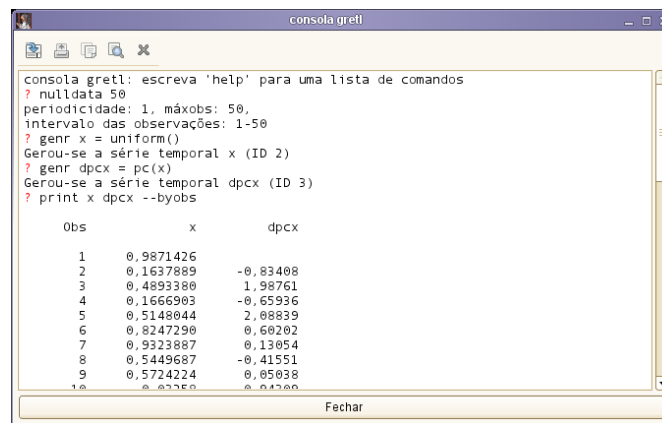


Figura 10.1: Output of function check

Now run your function. You may want to make sure your function 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
```

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

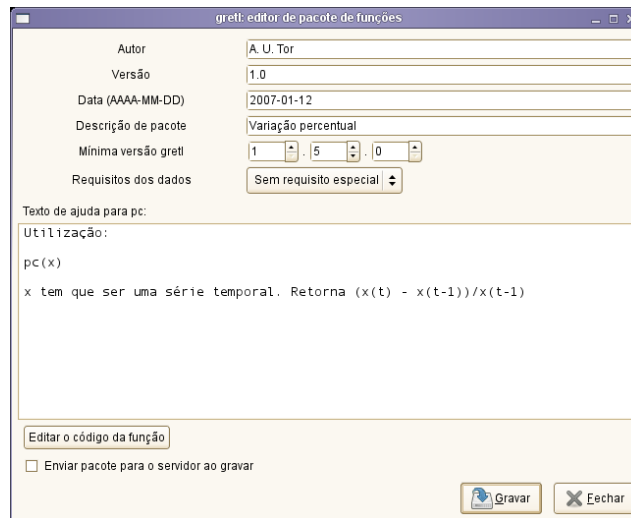
Start the GUI program and take a look at the “File, Function files” menu. This menu contains four items: “On local machine”, “On server”, “Edit package”, “New package”.

Select “New package” (the command will return 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 (currently, author, version, date, and a short description). You also get to enter help text



**Figura 10.2:** The package editor window

for the public interface. You have a further chance to edit the code of the functions to be packaged, by selecting them from the drop-down selector and clicking on “Edit function code”. Finally, you can choose to upload the package on gretl’s server as soon as it is saved, by checking the relevant checkbox.

Clicking “OK” 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 edit again a local function package.

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 functions are loaded into gretl, 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

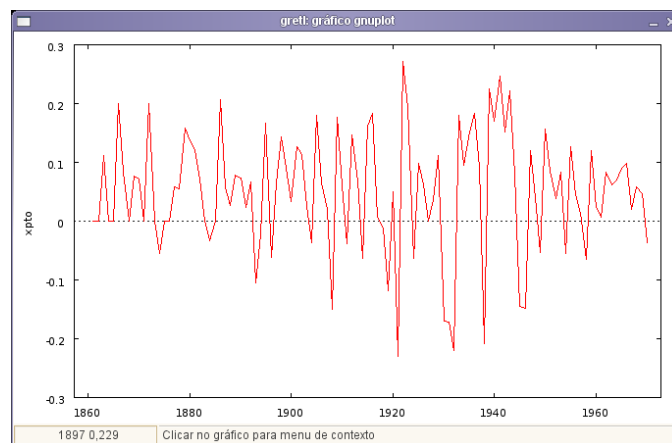
interface as described above, or by using the CLI, namely in a script or through the console. In the latter case, you load the function via the `include` command, specifying the package file as the argument, complete with the `.gfn` extension.



**Figura 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 `iproduct` 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. 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).



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

Alternatively, the same could have been accomplished by the script

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

## Capítulo 11

# Named lists and strings

### 11.1 Named lists

Many `gretl` commands take one or more lists of variables 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 either `null` (to create an empty list) or one or more variables to be placed on the list. For example,

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

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. When adding variables to a list, you can refer to them either by name or by their ID numbers.

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
```

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
list 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 simply make use of the fact that a named list can stand in for a “longhand” list. For example, we can do

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

#### Querying a list

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

```
series x11 = log(x1)
series x12 = log(x2)
list xlogs = x11 x12
genr is1 = islist(xlogs)
genr is2 = islist(x11)
```

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 `x11` 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
genr nl = nelem(xlist)
```

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

You can display the membership of a named list as illustrated in this interactive session:

```
? list xlist = x1 x2 x3
Added list 'xlist'
? list xlist print
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 a special form of the commands `logs`, `lags`, `diff`, `ldiff`, `sdiff` or `square`. In this context these keywords must be followed directly by a named list in parentheses. For example

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

When generating a list of *lags* in this way, you can 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 command will populate `laglist` with the specified number of lags of the variables in `xlist`. (As with the ordinary `lags` command, you can omit the order, in which case this is determined automatically based on the frequency of the data.) One further special feature is available when generating lags, namely, you can give the name of a single variable in place of a named list on the right-hand side, as in

```
series lx = log(x)
list laglist = lags(4, lx)
```

Note that the ordinary syntax for, e.g., `logs`, is just

```
logs x1 x2 x3
```

If `xlist` is a named list, you can also say

```
logs xlist
```

but this form will not save the logs as a named list; for that you need the form

```
list loglist = logs(xlist)
```



### Checking for missing values

Gretl offers several functions for recognizing and handling missing values (see the *Manual dos Comandos do Gretl* 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)
```

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.

## 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` 1.6.3 and higher.

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

```
string foo = "some stuff I want to save"
```

The first field after `string` is the name under which the string should be saved, then comes an equals sign, then comes the string to be saved, enclosed in double quotes. The latter can be represented as a sequence of sub-strings if need be, as in

```
string bits = "first " "and" " second"
```

See below for further variants of the `string` command, including use of `getenv`.

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 *retrieve the value* of a string variable, you give the name of the variable preceded by the “at” sign, `@`. In most contexts, the `@` 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 substituted 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 certain specific contexts, however, it is natural to treat `@`-variables as variables in their own right, and `gretl` does so. These contexts are:

- 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 `isstring` (see below).

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

```
? string vstr = "variance"
Saved string as 'vstr'
? printf "vstr: %12s\n", @vstr
vstr:      variance
```

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

```
? string 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 11.1.

<code>@gretldir</code>	the <code>gretl</code> installation directory
<code>@userdir</code>	user's <code>gretl</code> directory
<code>@gnuplot</code>	path to, or name of, the <code>gnuplot</code> executable
<code>@tramo</code>	path to, or name of, the <code>tramo</code> executable
<code>@x12a</code>	path to, or name of, the <code>x-12-arma</code> executable
<code>@tramodir</code>	<code>tramo</code> data directory
<code>@x12adir</code>	<code>x-12-arma</code> data directory

**Tabela 11.1:** 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 `isstring`, as in

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

Note that `isstring` is really shorthand for “is a string that actually contains something”.

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

## Capítulo 12

# Matrix manipulation

### 12.1 Introduction

Since version 1.5.1, gretl has offered the facility of creating and manipulating user-defined matrices. There are a few changes in this respect in version 1.6.1.

### 12.2 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.

Please note: while gretl's built-in statistical functions 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 column-wise concatenation (see below), as in

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

You can create new matrices, or replace existing matrices, by means of various transformations just as with scalars and data series. The relevant mechanisms are discussed in the next several sections.

☞ 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.

### 12.3 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:

empty	selects all rows
a single integer	selects the single specified row
two integers separated by a colon	selects a range of rows
the name of a matrix	selects the specified rows

With regard to the second option, 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 last option, 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  $2 \times 3$  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)
.*	element-wise multiplication
./	element-wise division
.^	element-wise exponentiation
~	column-wise concatenation
	row-wise concatenation
**	Kronecker product
=	test for equality

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”,  $A/B$  is algebraically equivalent to  $B^{-1}A$  (pre-multiplication by the inverse of the “divisor”). Therefore the following two expressions are equivalent in principle:

```
matrix C = A / B
matrix C = inv(B) * A
```

where `inv` is the matrix inversion function (see below for more on matrix functions). The first form, however, may be more accurate than the second; the solution is obtained via LU decomposition, without the explicit calculation of the inverse.

In *element-wise multiplication* if we write

```
matrix C = A .* B
```

then the result depends on the dimensions of  $A$  and  $B$ . Let  $A$  be an  $m \times n$  matrix and let  $B$  be  $p \times q$ .

- If  $m = p$  and  $n = q$  then  $C$  is  $m \times n$  with  $c_{ij} = a_{ij} \times b_{ij}$ . This is known as the *Hadamard product*.
- Otherwise, if  $m = 1$  and  $n = q$ , or  $n = 1$  and  $m = p$ , then  $C$  is  $p \times q$  with  $c_{ij} = a_k \times b_{ij}$ , where  $k = j$  if  $m = 1$  else  $k = i$ .
- Otherwise, if  $p = 1$  and  $n = q$ , or  $q = 1$  and  $m = p$ , then  $C$  is  $m \times n$  with  $c_{ij} = a_{ij} \times b_k$ , where  $k = j$  if  $p = 1$  else  $k = i$ .
- If none of the above conditions are satisfied the product is undefined and an error is flagged.

For example, if  $A$  is a row vector with the same number of columns of  $B$ , then the columns of  $C$  are the columns of  $B$  multiplied by the corresponding element of  $A$ . 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  $V$ .

Element-wise division and element-wise exponentiation work in a manner exactly analogous to element-wise multiplication: simply replace  $\times$  by  $\div$ , or the exponentiation operation, in the account given for multiplication.

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  $C = \begin{bmatrix} A & B \end{bmatrix}$ .

*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  $C = \begin{bmatrix} A \\ B \end{bmatrix}$ .

## 12.5 Matrix–scalar operators

For matrix  $A$  and scalar  $k$ , the operators shown in Table 12.1 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  $k$ . (Note that the operator  $**$  cannot be used in place of  $^$  for this purpose because in a matrix context it is reserved for the Kronecker product.)

## 12.6 Matrix functions

Table 12.2 lists the matrix functions that `gretl` provides (an alphabetized version of the table is provided at the end of this chapter as Table 12.3). The following functions are available for *element-by-element transformations* of matrices: `log`, `exp`, `sin`, `cos`, `tan`, `atan`, `int`, `abs`, `sqrt`, `dnorm`, `cnorm`, `qnorm`, `gamma` and `lngamma`. These functions have the effects documented in relation to the `genr` command. For example, if a matrix  $A$  is already defined, then

<i>Expression</i>	<i>Effect</i>
<code>matrix B = A * k</code>	$b_{ij} = ka_{ij}$
<code>matrix B = A / k</code>	$b_{ij} = a_{ij}/k$
<code>matrix B = k / A</code>	$b_{ij} = k/a_{ij}$
<code>matrix B = A + k</code>	$b_{ij} = a_{ij} + k$
<code>matrix B = A - k</code>	$b_{ij} = a_{ij} - k$
<code>matrix B = k - A</code>	$b_{ij} = k - a_{ij}$
<code>matrix B = A % k</code>	$b_{ij} = a_{ij} \text{ modulo } k$

Tabela 12.1: Matrix-scalar operators

<b>Creation</b>						
	I	mnormal	muniform	ones	seq	zeros
<b>Shape/size</b>						
	cols	diag	dsort	mlag	mshape	rows
	sort	transp	unvech	vec	vech	
<b>Element by element</b>						
	abs	atan	cnorm	cos	dnorm	exp
	gamma	int	lngamma	log	qnorm	sin
	sqrt	tan				
<b>Matrix algebra</b>						
	cholesky	det	eigengen	eigensym	fft	ffti
	infnorm	inv	ldet	mexp	nullspace	onenorm
	qform	qrdecomp	rank	rcond	svd	tr
	cmult					
<b>Statistical</b>						
	cdemean	imaxc	imaxr	iminc	iminr	mcorr
	mcov	maxc	maxr	meanc	meanr	minc
	minr	princomp	sumc	sumr	values	

Tabela 12.2: Table of matrix functions by category

```
matrix B = sqrt(A)
```

generates a matrix such that  $b_{ij} = \sqrt{a_{ij}}$ . All of these functions require a single matrix as argument, or an expression which evaluates to a single matrix.

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`.

The functions `sort`, `dsort` and `values` are available for matrices as well as data series. In the matrix case the argument to these functions must be a vector ( $p \times 1$  or  $1 \times p$ ). For `sort` and `dsort` the return value is a vector containing the elements of the input vector sorted in ascending (`sort`) or descending (`dsort`) order of magnitude. For `values` the return is a vector containing the distinct values in the input vector, sorted in ascending order.

Several matrix-specific functions are available. These functions fall into five categories:

1. Those taking a single matrix as argument and returning a scalar.
2. Those taking a single matrix as argument (plus in some cases an additional parameter) and returning a matrix.
3. Those taking one or two dimensions as arguments and returning a matrix.



4. Those taking two matrices as arguments and returning a matrix.
5. Those taking one or more matrices as arguments and returning one or more matrices.

These sets of functions are discussed in turn below.

### Matrix to scalar functions

The functions which take a single matrix as argument and return a scalar are:

<b>rows</b>	number of rows
<b>cols</b>	number of columns
<b>rank</b>	rank
<b>det</b>	determinant
<b>ldet</b>	log-determinant
<b>tr</b>	trace
<b>onenorm</b>	1-norm
<b>infnorm</b>	infinity-norm
<b>rcond</b>	reciprocal condition number

The single matrix argument to these functions may be given as the name of an existing matrix or as an expression that evaluates to a single matrix. Note that the functions **det**, **ldet** and **tr** require a square matrix as input. The **rank** function is computed via the QR decomposition.

The functions **onenorm** and **infnorm** return, respectively, the 1-norm and the infinity-norm of a matrix. The former is the maximum across the columns of the matrix of the sums of the absolute values of the column elements, while the latter is the maximum across the rows of the matrix of the sums of the absolute values of the row elements. The function **rcond** returns the reciprocal condition number for a symmetric, positive definite matrix.

### Matrix to matrix functions

The functions which take a single matrix as argument and return a matrix are:

<b>sumc</b>	sum by column	<b>sumr</b>	sum by row
<b>meanc</b>	mean by column	<b>meanr</b>	mean by row
<b>mcov</b>	covariance matrix	<b>mcorr</b>	correlation matrix
<b>mexp</b>	matrix exponential	<b>inv</b>	inverse
<b>cholesky</b>	Cholesky decomposition	<b>diag</b>	extract principal diagonal
<b>transp</b>	transpose	<b>cdemean</b>	subtract column means
<b>vec</b>	elements as column vector	<b>vech</b>	vectorize lower triangle
<b>unvech</b>	undo <b>vech</b>	<b>mlag</b>	matrix lag or lead
<b>nullspace</b>	right nullspace	<b>princomp</b>	principal components
<b>maxc</b>	column maxima (values)	<b>maxr</b>	row maxima (values)
<b>imaxc</b>	column maxima (indices)	<b>imaxr</b>	row maxima (indices)
<b>minc</b>	column minima (values)	<b>minr</b>	row minima (values)
<b>iminc</b>	column minima (indices)	<b>iminr</b>	row minima (indices)
<b>fft</b>	discrete Fourier transform	<b>ffti</b>	discrete inverse Fourier transform

As with the previous set of functions, the argument may be given as the name of an existing matrix or as an expression that evaluates to a single matrix.

For an  $m \times n$  matrix  $A$ , **sumc**( $A$ ) returns a row vector holding the  $n$  column sums, and **sumr**( $A$ ) returns a column vector with the  $m$  row sums. **meanc**( $A$ ) returns a row vector with the  $n$  column means, and **meanr**( $A$ ) a column vector with the  $m$  row means.

Also for an  $m \times n$  matrix  $A$ , the **max** and **min** family of functions return either an  $m \times 1$  matrix (the **r** variants, which select the extremum of each row) or a  $1 \times n$  matrix (the **c** variants, which select the column extrema). The **max** vectors contain the values of the row or column maxima while the **min** ones hold the row or column minima. The variants with an **i** prefix (e.g. **imaxc**) return not the values but the (1-based) indices of the respective maxima or minima.

For a  $T \times k$  matrix  $A$ , **mcov**( $A$ ) and **mcorr**( $A$ ) both return  $k \times k$  symmetric matrices, in the first case containing the variances (on the diagonal) and covariances of the variables in the columns of  $A$ , and in the second, containing the correlations of the variables.

For an  $n \times n$  matrix  $A$ , **mexp**( $A$ ) returns an  $n \times n$  matrix holding the matrix exponential,

$$e^A = \sum_{k=0}^{\infty} \frac{A^k}{k!} = \frac{I}{0!} + \frac{A}{1!} + \frac{A^2}{2!} + \frac{A^3}{3!} + \dots$$

(This series is sure to converge.)

The **cholesky** function computes the Cholesky decomposition  $L$  of a symmetric positive definite matrix  $A$ :  $A = LL'$ ;  $L$  is lower triangular (has zeros above the diagonal).

The **diag** function returns the principal diagonal of an  $n \times n$  matrix  $A$  as a column vector — that is, an  $n$ -vector  $v$  such that  $v_i = a_{ii}$ .

The **cdemean** function applied to an  $m \times n$  matrix  $A$  returns an  $m \times n$  matrix  $B$  such that  $b_{ij} = a_{ij} - \bar{A}_j$ , where  $\bar{A}_j$  denotes the mean of column  $j$  of  $A$ .

The **vec** function applied to an  $m \times n$  matrix  $A$  returns a column vector of length  $mn$  formed by stacking the columns of  $A$ .

The **vech** function applied to an  $n \times n$  matrix  $A$  returns a column vector of length  $n(n+1)/2$  formed by stacking the elements of the lower triangle of  $A$ , column by column. Note that  $A$  must be square; for the operation to make sense  $A$  should also be symmetric. The **unvech** function performs the inverse operation, producing a symmetric matrix.

The **mlag** function requires two arguments, a matrix and a scalar lag order,  $m$ . Applied to an  $T \times k$  matrix  $A$ , this function returns a  $T \times k$  matrix  $B$  such that

$$b_{ij} = \begin{cases} a_{i-m,j} & 1 \leq i-m \leq T \\ 0 & \text{otherwise} \end{cases}$$

That is, the columns of  $B$  are lagged versions of the columns of  $A$ , with missing values replaced by zeros. The order  $m$  may be negative to generate leads instead of lags.

The **nullspace** function yields  $X$ , the right null space of a matrix  $A$  (it is assumed that  $A$  has full row rank):  $X$  satisfies  $A \cdot X = 0$ .

The function **princomp** requires two arguments, a  $T \times k$  matrix  $X$  and a scalar  $p$ ,  $0 < p \leq k$ . It is assumed that  $X$  contains  $T$  observations on each of  $k$  variables (series). The return value is a  $T \times p$  matrix  $P$  containing the first  $p$  principal components of  $X$ . The elements of  $P$  are computed as

$$P_{ij} = \sum_{t=1}^k Z_{ti} v_i^{(j)}$$

where  $Z_{ti}$  is the standardized value of variable  $i$  at observation  $t$ ,  $Z_{ti} = (X_{ti} - \bar{X}_i)/\hat{\sigma}_i$ , and  $v_i^{(j)}$  is the  $j$ th eigenvector of the correlation matrix of the  $X_i$ s, with the eigenvectors ordered by decreasing value of the corresponding eigenvalues.

The functions **fft** and **ffti** return the real discrete Fourier transform and its inverse, respectively. if  $X$  is an  $n \times k$  matrix, then **fft**( $X$ ) is an  $n \times 2k$  matrix containing the real part of the transform in the odd

columns and the complex part in the even ones. Conversely, `ffti` takes a  $n \times 2k$  argument and yields an  $n \times k$  result. See section 5.10 for some examples.

### Matrix filling functions

The functions taking one or two integers as arguments and returning a matrix are:

<code>I(n)</code>	$n \times n$ identity matrix
<code>zeros(m,n)</code>	$m \times n$ zero matrix
<code>ones(m,n)</code>	$m \times n$ matrix filled with 1s
<code>uniform(m,n)</code>	$m \times n$ matrix filled with uniform random values
<code>mnormal(m,n)</code>	$m \times n$ matrix filled with normal random values
<code>seq(a,b)</code>	row vector containing the numbers from $a$ to $b$

The dimensions  $m$  and  $n$  — or in the case of `seq`, the limits  $a$  and  $b$  — may be given numerically, by reference to pre-existing scalar variables, or as expressions that evaluate to scalars.

The `uniform` and `mnormal` matrix functions fill the matrix with drawings from the uniform (0–1) distribution and the standard normal distribution respectively.

The `seq` function generates a sequence of integers from  $a$  to  $b$  inclusive, increasing if  $a < b$  or decreasing if  $a > b$ .

### Matrix reshaping

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
```

### Single-return two-matrix functions

The function `qform` constructs a quadratic form in a matrix  $A$  and a conformable symmetric matrix  $X$ . The command

```
B = qform(A, X)
```

calculates  $B = AXA'$ . This is computed more efficiently than the alternative command  $B = A*X*A'$ . In addition, the result is symmetric by construction.

The function `cmult` computes the complex product 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 product has no imaginary part, an  $n$ -vector.

### Multiple-return matrix functions

The functions that take one or more matrices as arguments and compute one or more matrices are:

<code>qrdecomp</code>	QR decomposition
<code>eigensym</code>	Eigen-analysis of symmetric matrix
<code>eigengen</code>	Eigen-analysis of general matrix
<code>svd</code>	Singular value decomposition (SVD)

The syntax for all but the last of these functions is of the form

```
matrix B = func(A, &C)
```

while for `svd` it is

```
matrix B = func(A, &C, &D)
```

The first argument,  $A$ , represents the input data, that is, the matrix whose decomposition or analysis is required.

The second argument (and in the case of `svd`, the third) 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 `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 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 `eigen` 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 `eigen` 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.

The function `svd` computes all or part of the singular value decomposition of the real  $m \times n$  matrix  $A$ . The decomposition is

$$A = U \Sigma V'$$

where  $\Sigma$  is an  $m \times n$  matrix which is zero except for its  $k = \min(m, n)$  diagonal elements,  $U$  is an  $m \times m$  orthogonal matrix, and  $V$  is an  $n \times n$  orthogonal matrix. 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  $\min(m, n)$  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.

## 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:

**Exemplo 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

```

---

<code>\$coeff</code>	vector of estimated coefficients
<code>\$stderr</code>	vector of estimated standard errors
<code>\$uhat</code>	vector of residuals
<code>\$yhat</code>	vector of fitted values
<code>\$vcv</code>	covariance matrix (see below)
<code>\$rho</code>	autoregressive coefficients for error process
<code>\$jalpha</code>	matrix $\alpha$ (loadings) from Johansen's procedure
<code>\$jbeta</code>	matrix $\beta$ (cointegration vectors) from Johansen's procedure
<code>\$jvbeta</code>	covariance matrix for the unrestricted elements of $\beta$ from Johansen's procedure

If these 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 is actually a system (a VAR or VECM, or system of simultaneous equations), `$uhat` retrieves the matrix of residuals (one column per equation) and `$vcv` gets the cross-equation covariance matrix; in the special case of a VAR or a VECM, `$coeff` returns the companion matrix. At present the other accessors are not available for equation systems.

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 20.4), 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 12.2 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 12.2 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 X1 = 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 12.2 illustrates the use of this sort of conversion to “normalize” a list, moving the constant (variable 0) to first position.

### Exemplo 12.2: 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 X1 = 2 3 0 4
matrix x = X1
normalize_list(&x)
list X1 = 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, you can simply give the name of the matrix in question on a line by itself, or you can use the `print` command:

```
matrix M = mnormal(100,2)
M
print M
```

### 12.13 Example: OLS using matrices

Example [12.3](#) shows how matrix methods can be used to replicate `gretl`'s built-in OLS functionality.

#### Exemplo 12.3: OLS via matrix methods

---

```
open data4-1
matrix X = { const, sqft }
matrix y = { price }
matrix b = inv(X'X) * X'y
printf "estimated coefficient vector\n"
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))
printf "estimated standard errors\n"
se
# compare with built-in function
ols price const sqft --vcv
```

---

abs	atan	cdemean	cholesky	cmult	cnorm
cols	cos	det	diag	dnorm	dsort
eigengen	eigensym	exp	fft	ffti	gamma
I	imaxc	imaxr	iminc	iminr	infnorm
int	inv	ldet	lngamma	log	mcorr
mcov	maxc	maxr	meanc	meanr	mexp
minc	minr	mlag	mnormal	mshape	muniform
nullspace	onenorm	ones	princomp	qform	qnorm
qrdecomp	rank	rcond	rows	seq	sin
sort	sqrt	sumc	sumr	svd	tan
tr	transp	unvech	values	vec	vech
zeros					

**Tabela 12.3:** Alphabetical listing of matrix functions

## Capítulo 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.

#### 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  $\varepsilon_t \sim NIID(0, 1)$ .

*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:

$$y_t = \begin{cases} x_t & \text{for } d_t = 1 \\ z_t & \text{for } d_t = 0 \end{cases}$$

*Solution:*

```
series y = d ? 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 `y = d*x + (1-d)*z`. 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.

### 13.3 Neat tricks

#### Interaction dummies

*Problem:* You want to estimate the model  $y_i = \mathbf{x}_i\beta_1 + \mathbf{z}_i\beta_2 + d_i\beta_3 + (d_i \cdot \mathbf{z}_i)\beta_4 + \varepsilon_i$ , 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`”).

## **Parte II**

# **Métodos econométricos**

## Capítulo 14

# Robust covariance matrix estimation

### 14.1 Introduction

Consider (once again) the linear regression model

$$y = X\beta + u \quad (14.1)$$

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

$$\hat{\beta} = (X'X)^{-1}X'y \quad (14.2)$$

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

$$\text{Var}(\hat{\beta}) = E\left((\hat{\beta} - \beta)(\hat{\beta} - \beta)'\right) = (X'X)^{-1}X'\Omega X(X'X)^{-1} \quad (14.3)$$

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,

$$\text{Var}(\hat{\beta}) = \sigma^2(X'X)^{-1} \quad (14.4)$$

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).<sup>1</sup> 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

$$\widehat{\text{Var}}_h(\hat{\beta}) = (X'X)^{-1}X'\hat{\Omega}X(X'X)^{-1} \quad (14.5)$$

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 HC-CME 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,  $\hat{u}_i^2$  — as HC<sub>0</sub>. (The associated standard errors are often called “White’s standard errors”.) The various refinements of White’s proposal share a 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

<sup>1</sup>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.



squared residuals,

$$\sum \hat{u}_t^2 = \sum (y_t - X_t \hat{\beta})^2$$

is minimized for given  $X$  and  $y$ . Suppose that  $\hat{\beta} \neq \beta$ . This is almost certain to be the case: even if 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 HC<sub>0</sub> take this point on board as follows:

- HC<sub>1</sub>: Applies a degrees-of-freedom correction, multiplying the HC<sub>0</sub> matrix by  $T/(T - k)$ .
- HC<sub>2</sub>: 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 diagonal elements of  $\hat{\Omega}$  and in general revises them upward.
- HC<sub>3</sub>: Uses  $\hat{u}_t^2/(1 - h_t)^2$ . The additional factor of  $(1 - h_t)$  in the denominator, relative to HC<sub>2</sub>, 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 under-estimated. 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 HC<sub>0</sub> 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, HC<sub>0</sub> is the default HCCME in `gretl`.

If you wish to use HC<sub>1</sub>, HC<sub>2</sub> or HC<sub>3</sub> 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 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

$$\begin{array}{ccccc} \hat{\Sigma} & = & X' & \hat{\Omega} & X \\ (k \times k) & & (k \times T) & (T \times T) & (T \times k) \end{array}$$

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,

$$w_j = \begin{cases} 1 - 6a_j^2 + 6a_j^3 & 0 \leq a_j \leq 0.5 \\ 2(1 - a_j)^3 & 0.5 < a_j \leq 1 \\ 0 & a_j > 1 \end{cases}$$

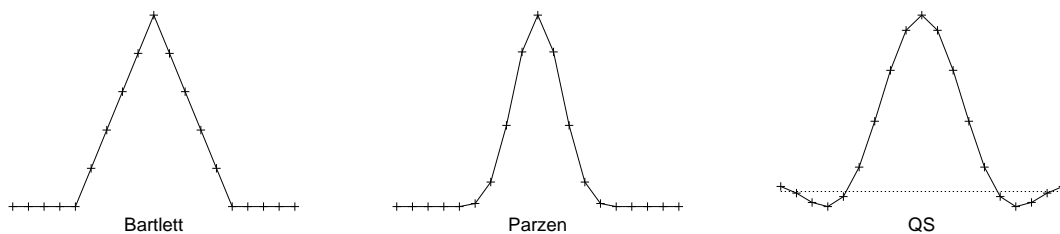
where  $a_j = j/(p+1)$ , and for the QS kernel,

$$w_j = \frac{25}{12\pi^2 d_j^2} \left( \frac{\sin m_j}{m_j} - \cos m_j \right)$$

where  $d_j = j/p$  and  $m_j = 6\pi d_j/5$ .

Figure 14.1 shows the weights generated by these kernels, for  $p = 4$  and  $j = 1$  to 9.

Figura 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.

You also have the option of specifying a fixed numerical value for  $p$ , as in

$T$	$p$ (nw1)	$p$ (nw2)
50	2	3
100	3	4
150	3	4
200	4	4
300	5	5
400	5	5

**Tabela 14.1:** HAC bandwidth: two rules of thumb

```
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  $\zeta_t = X_t \hat{u}_t$ . 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  $\zeta_t$ , but just to “mop up” a substantial part of the autocorrelation. Hence, the following VAR is estimated

$$\zeta_t = A\zeta_{t-1} + \varepsilon_t$$

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_prewhitened 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

$$\hat{\Sigma}_A = (X'X)^{-1} \left( \sum_{i=1}^n X_i' \hat{u}_i \hat{u}_i' X_i \right) (X'X)^{-1}$$

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

$$\hat{\Sigma}_{BK} = (X'X)^{-1} \left( \sum_{i=1}^n \sum_{j=1}^n \hat{\sigma}_{ij} X_i' X_j \right) (X'X)^{-1}$$

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.)

## Capítulo 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

$$y_{it} = X_{it}\beta + u_{it} \quad (15.1)$$

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

$$y_{it} = X_{it}\beta + \alpha_i + \varepsilon_{it} \quad (15.2)$$

That is, we decompose  $u_{it}$  into a unit-specific and time-invariant component,  $\alpha_i$ , and an observation-specific error,  $\varepsilon_{it}$ .<sup>1</sup> 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

$$\bar{y}_i = \frac{1}{T_i} \sum_{t=1}^{T_i} y_{it}$$

---

<sup>1</sup>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

$$\hat{\alpha}_i = \frac{1}{T_i} \sum_{t=1}^{T_i} (y_{it} - X_{it}\hat{\beta})$$

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

$$y_{it} = X_{it}\beta + v_i + \varepsilon_{it} \quad (15.3)$$

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  $\text{Var}(u_{is}) = \text{Var}(u_{it}) = \sigma_v^2 + \sigma_\varepsilon^2$ , 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

$$\mathbf{y}_i = \mathbf{X}_i\beta + \mathbf{u}_i \quad (15.4)$$

The vector  $\mathbf{u}_i$ , which includes all the disturbances for individual  $i$ , has a variance–covariance matrix given by

$$\text{Var}(\mathbf{u}_i) = \Sigma_i = \sigma_\varepsilon^2 I + \sigma_v^2 J \quad (15.5)$$

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

$$K_i \mathbf{y}_i = K_i \mathbf{X}_i \beta + K_i \mathbf{u}_i \quad (15.6)$$

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  $\sigma_\varepsilon^2 \rightarrow 0$ ,  $\theta \rightarrow 1$ , while for  $\sigma_v^2 \rightarrow 0$ ,  $\theta \rightarrow 0$ . 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,

$$\bar{\mathbf{y}}_i = \bar{\mathbf{X}}_i \beta + \mathbf{e}_i$$

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  $v_i$  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  $\text{Var}(\tilde{\beta} - \hat{\beta}) = \text{Var}(\tilde{\beta}) - \text{Var}(\hat{\beta}) = \Psi$ , where  $\text{Var}(\tilde{\beta})$  and  $\text{Var}(\hat{\beta})$  are estimated by the sample variance matrices of the fixed- and random-effects models respectively.<sup>2</sup>
- Compute  $H = (\tilde{\beta} - \hat{\beta})' \Psi^{-1} (\tilde{\beta} - \hat{\beta})$ .

Given the relative efficiencies of  $\tilde{\beta}$  and  $\hat{\beta}$ , the matrix  $\Psi$  “should be” positive definite, in which case  $H$  is

---

<sup>2</sup>Hausman (1978) showed that the covariance of the difference takes this simple form when  $\hat{\beta}$  is an efficient estimator and  $\tilde{\beta}$  is inefficient.

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  $SSR_r$ .
- 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  $SSR_u$ .
- Compute  $H = n(SSR_r - SSR_u) / SSR_u$ , 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):

$$y_{it} = X_{it}\beta + \rho y_{it-1} + u_{it} \quad (15.7)$$

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  $T \rightarrow \infty$  (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:

$$\Delta y_{it} = \Delta X_{it}\beta + \rho \Delta y_{i,t-1} + \eta_{it} \quad (15.8)$$

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).<sup>3</sup>

**Exemplo 15.1:** The Anderson–Hsiao estimator for a dynamic panel model

---

```
# Penn World Table data as used by Nerlove
open pennngrow.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). There is provisional support for the Arellano–Bond method in current `gretl` — please see the documentation for the `arbond` command.

### 15.3 Illustration: the Penn World Table

The Penn World Table (homepage at [pwt.econ.upenn.edu](http://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).

---

<sup>3</sup>Also see Clint Cummins’ benchmarks page, <http://www.stanford.edu/~clint/bench/>.

**Exemplo 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
```

---

## Capítulo 16

# Nonlinear least squares

### 16.1 Introduction and examples

Gretl supports nonlinear least squares (NLS) using a variant of the Levenberg–Marquandt 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.

#### Exemplo 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
```

---

#### Exemplo 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.

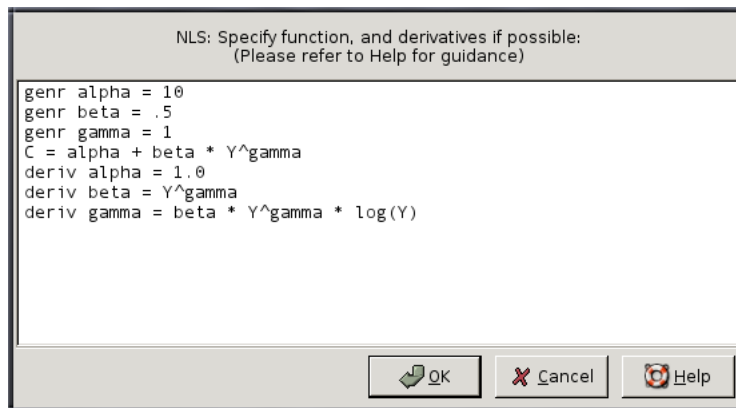


Figura 16.1: NLS dialog box

### 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  $3/4$ ,<sup>1</sup> but it can be adjusted using the `set` command with the parameter `nls_tol`. For example

```
set nls_tol .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](http://netlib.org). Specifically, the following `minpack` functions are called:

<code>lmder</code>	Levenberg–Marquandt algorithm with analytical derivatives
<code>chkder</code>	Check the supplied analytical derivatives
<code>lmdif</code>	Levenberg–Marquandt algorithm with numerical derivatives
<code>fdjac2</code>	Compute final approximate Jacobian when using numerical derivatives
<code>dmpar</code>	Determine the machine precision

On successful completion of the Levenberg–Marquandt 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.<sup>2</sup> For each dataset, two sets of starting values for the parameters 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.<sup>3</sup>

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–Marquandt 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

<sup>1</sup>On a 32-bit Intel Pentium machine a likely value for this parameter is  $1.82 \times 10^{-12}$ .

<sup>2</sup>For a discussion of `gretl`’s accuracy in the estimation of linear models, see Appendix C.

<sup>3</sup>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).

(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.<sup>4</sup>

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.

**Tabela 16.1:** Nonlinear regression: the NIST tests

	<i>Analytical derivatives</i>	<i>Numerical derivatives</i>
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 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.

---

<sup>4</sup>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).



## Capítulo 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<sup>1</sup> for the whole sample, namely the joint distribution of all the observations  $f(\mathbf{Y}; \theta)$ , where  $\mathbf{Y} = \{y_1, \dots, y_T\}$ . 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

$$\hat{\theta}(\mathbf{Y}) = \underset{\theta \in \Theta}{\text{Argmax}} \ell(\theta) \quad (17.1)$$

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  $k$ -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:

---

<sup>1</sup>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.

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 maximum 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_tol` (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,

$$\widehat{\text{Var}}_{\text{OPG}}(\hat{\theta}) = \left( G'(\hat{\theta}) G(\hat{\theta}) \right)^{-1}$$

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:

$$\widehat{\text{Var}}_{\text{QML}}(\hat{\theta}) = H(\hat{\theta})^{-1} G'(\hat{\theta}) G(\hat{\theta}) H(\hat{\theta})^{-1}$$

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

$$f(x_t) = \frac{\alpha^p}{\Gamma(p)} x_t^{p-1} \exp(-\alpha x_t) \quad (17.2)$$

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

$$\ell(\alpha, p) = \sum_{t=1}^T \log \left[ \frac{\alpha^p}{\Gamma(p)} x_t^{p-1} \exp(-\alpha x_t) \right] = \sum_{t=1}^T \ell_t \quad (17.3)$$

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

$$E(x_t) = p/\alpha \quad V(x_t) = p/\alpha^2$$

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  $v_i \sim |N(0, \sigma_v^2)|$ . 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:

$$f(\varepsilon_i) = \sqrt{\frac{2}{\pi}} \Phi\left(\frac{\lambda \varepsilon_i}{\sigma}\right) \frac{1}{\sigma} \phi\left(\frac{\varepsilon_i}{\sigma}\right) \quad (17.4)$$

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 from an irrelevant constant)

$$\ell_i = \log \Phi\left(\frac{\lambda \varepsilon_i}{\sigma}\right) - \left[ \log(\sigma) + \frac{\varepsilon_i^2}{2\sigma^2} \right]$$

Therefore, a Cobb–Douglas cost function with stochastic frontier is the model described by the following equations:

$$\begin{aligned} \log C_i &= \log C_i^* + \varepsilon_i \\ \log C_i^* &= c + \sum_{j=1}^m \beta_j \log y_{ij} + \sum_{j=1}^n \alpha_j \log p_{ij} \\ \varepsilon_i &= u_i + v_i \\ u_i &\sim N(0, \sigma_u^2) \\ v_i &\sim |N(0, \sigma_v^2)| \end{aligned}$$

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

$$\log C_i - \log p_{in} = c + \sum_{j=1}^m \beta_j \log y_{ij} + \sum_{j=2}^n \alpha_j (\log p_{ij} - \log p_{in}) + \varepsilon_i \quad (17.5)$$

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).

#### Exemplo 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
```

---

## 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

$$F_t = \{y_t, y_{t-1}, \dots\},$$

then the density of  $y_t$  conditional on  $F_{t-1}$  is normal:

$$y_t | F_{t-1} \sim N[\mu, h_t].$$

By means of the properties of conditional distributions, the joint density can be factorized as follows

$$f(y_t, y_{t-1}, \dots) = \left[ \prod_{t=1}^T f(y_t | F_{t-1}) \right] \cdot f(y_0)$$

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

$$\ell(\mu, \omega, \alpha, \beta) = \sum_{t=1}^T \ell_t \quad (17.6)$$

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

$$\frac{\partial \ell(\theta_1, \dots, \theta_n)}{\partial \theta_i} \simeq \frac{\ell(\theta_1, \dots, \theta_i + h, \dots, \theta_n) - \ell(\theta_1, \dots, \theta_i - h, \dots, \theta_n)}{2h}$$

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<sup>2</sup>:  $y_t$  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,  $y_t = 1$  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

$$\frac{\partial \ell}{\partial \beta_i} = \frac{\partial \ell}{\partial \pi_t} \cdot \frac{\partial \pi_t}{\partial \beta_i}$$

---

<sup>2</sup>Again, gretl does provide a native `probit` command (see section 21.1), but a probit model makes for a nice example here.

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 than 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
```



## Capítulo 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  $x_1, x_2, \dots, x_T$ . 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:

$$E[x_t - g(\theta)] = 0 \Leftrightarrow \theta = \theta_0, \quad (18.1)$$

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

$$\bar{X} = \frac{1}{T} \sum_{t=1}^T x_t \xrightarrow{p} g(\theta_0);$$

hence, since  $g(\cdot)$  is invertible, the statistic

$$\hat{\theta} = g^{-1}(\bar{X}) \xrightarrow{p} \theta_0,$$

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

$$F(\theta) = \left[ \frac{1}{T} \sum_{t=1}^T (x_t - g(\theta)) \right]^2 = [\bar{X} - g(\theta)]^2; \quad (18.2)$$

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

$$E[f_i(x_t, \theta)] = 0 \quad \text{for } i = 1 \dots m, \quad (18.3)$$

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

$$E[f_i(x_t, \theta) \cdot z_{j,t}] = E[f_{i,j,t}(\theta)] = 0 \quad \text{for } i = 1 \dots m \quad \text{and } j = 1 \dots p; \quad (18.4)$$

equation (18.4) is known as an *orthogonality condition*, or *moment condition*. The GMM estimator is defined as the minimum of the quadratic form

$$F(\theta, W) = \tilde{\mathbf{f}}' W \tilde{\mathbf{f}}, \quad (18.5)$$

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

$$\hat{\theta} = \underset{\theta}{\text{Argmin}} F(\theta, W) \quad (18.6)$$

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:

$$E[f(\beta)] = 0, \quad (18.7)$$

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  $(y_t - x_t\beta)x_t = u_tx_t$ ; 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.

**Exemplo 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`. 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. 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.<sup>1</sup>

### 18.4 Covariance matrix options

The covariance matrix of the estimated parameters depends on the choice of  $W$  through

$$\hat{\Sigma} = (J'WJ)^{-1}J'W\Omega WJ(J'WJ)^{-1} \quad (18.8)$$

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:

$$\hat{\Omega}_0(\theta) = \frac{1}{T} \sum_{t=1}^T f_t(\theta) f_t(\theta)' \quad (18.9)$$

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 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).

$$\hat{\Omega}_k(\theta) = \frac{1}{T} \sum_{t=k}^{T-k} \left[ \sum_{i=-k}^k w_i f_t(\theta) f_{t-i}(\theta)' \right], \quad (18.10)$$

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
```

---

<sup>1</sup>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](http://gretl.sourceforge.net/gretl_data.html).

**Exemplo 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 = taxes / cpi
# real average sales tax
genr rtaxso = rtaxs - rtax
# logs of consumption, price, income
genr lpackpc = log(packpc)
genr lavgprs = 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 lavgprs 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*lavgprs - b2*lperinc
    orthog e ; Z
    weights W
    params b0 b1 b2
end gmm

```

---

**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:

$$pU'(c_t) = \delta^k E[r_{t+k}U'(c_{t+k})|\mathcal{F}_t], \quad (18.11)$$

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.

**Exemplo 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 ***
lragvprs	-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\*lragvprs - 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

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  $j$ :

$$E \left[ \delta \frac{r_{j,t+1}}{p_{j,t}} \left( \frac{C_{t+1}}{C_t} \right)^{\alpha-1} \middle| \mathcal{F}_t \right] = 1, \quad (18.12)$$

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.

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

**Exemplo 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

```

---

greater than the number of estimated parameters (2), the choice of initial 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.



**Exemplo 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)

---

## Capítulo 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

$$\text{AIC} = -2\ell(\hat{\theta}) + 2k \quad (19.1)$$

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

$$\ell(\hat{\theta}) = -\frac{n}{2}(1 + \log 2\pi - \log n) - \frac{n}{2} \log \text{SSR} \quad (19.2)$$

Substituting (19.2) into (19.1) we get

$$\text{AIC} = n(1 + \log 2\pi - \log n) + n \log \text{SSR} + 2k$$

which can also be written as

$$\text{AIC} = n \log \left( \frac{\text{SSR}}{n} \right) + 2k + n(1 + \log 2\pi) \quad (19.3)$$

Some authors simplify the formula for the case of models estimated via least squares. For instance, William Greene writes

$$\text{AIC} = \log \left( \frac{\text{SSR}}{n} \right) + \frac{2k}{n} \quad (19.4)$$

This variant can be derived from (19.3) by dividing through by  $n$  and subtracting the constant  $1 + \log 2\pi$ . That is, writing  $\text{AIC}_G$  for the version given by Greene, we have

$$\text{AIC}_G = \frac{1}{n} \text{AIC} - (1 + \log 2\pi)$$

Finally, Ramanathan gives a further variant:

$$\text{AIC}_R = \left( \frac{\text{SSR}}{n} \right) e^{2k/n}$$

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

$$\text{BIC} = -2\ell(\hat{\theta}) + k \log n$$

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

$$\text{HQC} = -2\ell(\hat{\theta}) + 2k \log \log n$$

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.

## Capítulo 20

# Time series models

### 20.1 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

$$\phi(L)y_t = \theta(L)\epsilon_t \quad (20.1)$$

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

$$\phi(L)(y_t - x_t\beta) = \theta(L)\epsilon_t \quad (20.2)$$

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

$$\phi(L)y_t = z_t\gamma + \theta(L)\epsilon_t \quad (20.3)$$

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

$$\phi(L)(y_t - \mu) = \theta(L)\epsilon_t \quad (20.4)$$

and

$$\phi(L)y_t = \alpha + \theta(L)\epsilon_t \quad (20.5)$$

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

$$\alpha = (1 - \phi_1 - \dots - \phi_p) \mu$$

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:

$$y_t - x_t\beta = \phi_1(y_{t-1} - x_{t-1}\beta) + \dots + \phi_p(y_{t-p} - x_{t-p}\beta) + \epsilon_t + \theta_1\epsilon_{t-1} + \dots + \theta_q\epsilon_{t-q}$$

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:

$$y_t = x_t\gamma + \phi_1y_{t-1} + \dots + \phi_py_{t-p} + \epsilon_t + \theta_1\epsilon_{t-1} + \dots + \theta_q\epsilon_{t-q}$$

Ideally, the issue broached above could be made moot by writing a more general specification that nests the alternatives; that is

$$\phi(L)(y_t - x_t\beta) = z_t\gamma + \theta(L)\epsilon_t; \quad (20.6)$$

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

$$\phi(L)\Phi(L^s)y_t = \theta(L)\Theta(L^s)\epsilon_t. \quad (20.7)$$

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”.

### 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 20.2). 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  $\text{ARMA}(p, q)$  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 `arma` 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 = sdifff(y)
arma 1 0 ; 1 1 ; dsy
```

where we use the `sdifff` 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  $t_0, \dots, T$ . 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.

**Tabela 20.1:** ML and CML estimates

Parameter	ML		CML	
$\mu$	6.93042	(0.673202)	1.07322	(0.488661)
$\phi$	0.855360	(0.0512026)	0.852772	(0.0450252)
$\theta$	0.588056	(0.0809769)	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-arma`, as in

```
arma p q ; y --x-12-arma
```

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).<sup>1</sup> 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).

### Limitations

The structure of `gretl`’s `arma` command does not allow you to specify models with gaps in the lag structure, other than via the seasonal specification discussed above. For example, if you have a monthly time series, you cannot estimate an ARMA model with AR terms (or MA terms) at just lags 1, 3 and 5.

At a pinch, you could circumvent this limitation in respect of the AR part of the specification by the trick of including lags of the dependent variable in the list of “exogenous” variables. For example, the following command

```
arma 0 0 ; 0 1 ; y const y(-2)
```

on a quarterly series would estimate the parameters of the model

$$y_t - \mu = \phi(y_{t-2} - \mu) + \epsilon_t + \Theta\epsilon_{t-4}$$

However, this workaround is not really recommended: it should deliver correct estimates, but will break the existing mechanism for forecasting.

## 20.2 Unit root tests

### The ADF test

The ADF (Augmented Dickey-Fuller) test is, as implemented in `gretl`, the  $t$ -statistic on  $\varphi$  in the following regression:

$$\Delta y_t = \mu_t + \varphi y_{t-1} + \sum_{i=1}^p \gamma_i \Delta y_{t-i} + \epsilon_t. \quad (20.8)$$

<sup>1</sup>See in particular their “Program 4” on p. 505ff.



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

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:

$$\eta = \frac{\sum_{i=1}^T S_i^2}{T^2 \bar{\sigma}^2} \quad (20.9)$$

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.

### The Johansen tests

Strictly speaking, these are tests for cointegration. However, they can be used as multivariate unit-root tests since they are the multivariate generalization of the ADF test. See section 20.4 for more details.

## 20.3 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

$$u_t = \sigma_t \varepsilon_t; \quad \sigma_t^2 \equiv E(u_t^2 | \Omega_{t-1}) = \alpha_0 + \sum_{i=1}^q \alpha_i u_{t-i}^2$$

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

$$u_t = \rho u_{t-1} + \varepsilon_t; \quad -1 < \rho < 1$$

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:

$$y_t = X_t\beta + u_t \quad (20.10)$$

$$u_t = \sigma_t \varepsilon_t \quad (20.11)$$

$$\sigma_t^2 = \alpha_0 + \sum_{i=1}^q \alpha_i u_{t-i}^2 + \sum_{j=1}^p \delta_j \sigma_{t-j}^2 \quad (20.12)$$

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  $\delta_j$  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),<sup>2</sup> 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.)

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.

**Tabela 20.2:** Options for the GARCH covariance matrix

<i>command</i>	<i>effect</i>
<code>set garch_vcv hessian</code>	Use the Hessian
<code>set garch_vcv im</code>	Use the Information Matrix
<code>set garch_vcv op</code>	Use the Outer Product of the Gradient
<code>set garch_vcv qml</code>	QML estimator
<code>set garch_vcv bw</code>	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

$$\sigma_t^2 = \alpha_0 + \alpha_1 u_{t-1}^2 + \delta_1 \sigma_{t-1}^2 \quad (20.13)$$

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).

<sup>2</sup>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.

## 20.4 Cointegration and Vector Error Correction Models

### 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). Then, it is possible to write the  $n$ -variate process  $y_t$  as

$$y_t = \mu_t + A_1 y_{t-1} + A_2 y_{t-2} + \cdots + A_p y_{t-p} + \epsilon_t;$$

however, this model can be re-cast in a form more suitable to analyze the phenomenon of cointegration. Since  $y_t = y_{t-1} - \Delta y_t$  and  $y_{t-i} = y_{t-1} - (\Delta y_{t-1} + \Delta y_{t-2} + \cdots + \Delta y_{t-i+1})$ , the *Vector Error Correction* form of the previous model is given by

$$\Delta y_t = \mu_t + \Pi y_{t-1} + \sum_{i=1}^p \Gamma_i \Delta y_{t-i} + \epsilon_t, \quad (20.14)$$

where  $\Pi = \sum_{i=1}^p A_i$  and  $\Gamma_k = -\sum_{i=k}^p A_i$ .

If the rank of  $\Pi$  is 0, the processes are all I(1); if the rank of  $\Pi$  is full, the processes are all I(0); in between,  $\Pi$  can be written as  $\alpha\beta'$  and you have cointegration.

The rank of  $\Pi$  is investigated by computing the eigenvalues of a closely related matrix (call it  $M$ ) whose rank is the same as  $\Pi$ : however,  $M$  is by construction symmetric and positive semidefinite. As a consequence, all its eigenvalues are real and non-negative; tests on the rank of  $\Pi$  can therefore be carried out by testing how many eigenvalues of  $M$  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. On the other extreme, if no eigenvalues are significantly different from 0, then not only the process  $y_t$  is non-stationary, but the same holds for any linear combination  $\beta' y_t$ ; in other words, no cointegration occurs.

The two Johansen tests are the “ $\lambda$ -max” test, for hypotheses on individual eigenvalues, and the “trace” test, for joint hypotheses. The `gretl` command `coint2` performs these two tests.

As in the ADF test, the asymptotic distribution of the tests varies with the deterministic kernel  $\mu_t$  one includes in the VAR. `gretl` provides the following options (for a short discussion of the meaning of the five options, see section 20.4 below):

$\mu_t$	command option
0	<code>--nc</code>
$\mu_0, \alpha'_{\perp} \mu_0 = 0$	<code>--rc</code>
$\mu_0$	default
$\mu_0 + \mu_1 t, \alpha'_{\perp} \mu_1 = 0$	<code>--crt</code>
$\mu_0 + \mu_1 t$	<code>--ct</code>

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).

The following code uses the `denmark` database, 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 (20.14) comprises the four variables LRM, LRY, IBO, IDE. The number of lags equals  $p$  in (20.14) plus one. 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]

Since both the trace and  $\lambda$ -max accept the null hypothesis that the smallest eigenvalue is in fact 0, we may conclude that the series are in fact non-stationary. However, some linear combination may be  $I(0)$ , as indicated by the rejection of the  $\lambda$ -max of the hypothesis that the rank of  $\Pi$  is 0 (the trace test gives less clear-cut evidence for this).

### The Johansen cointegration test

The Johansen test for cointegration is used to establish the rank of  $\beta$ ; in other words, how many cointegration vectors the system has. This test has to take into account what hypotheses one is willing to make on the deterministic terms, which leads to the famous “five cases.” A full and general illustration of the five cases requires a fair amount of matrix algebra, but 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. As is easy to show,  $x_t$  is a random walk which fluctuates around a deterministic trend with slope  $m$ . In the special case  $m = 0$ , the deterministic trend 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 in a position 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 distance  $k$  from  $x_t$ . The vector  $\mu_0$  is unrestricted. This case is the default for gretl’s `vecm` command.
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; it may be specified in gretl’s `vecm` command using the option flag `--rc`.

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.” This case is specified using the option flag `--nc` with `vecm`.

In most cases, the choice between the 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). These two cases are specified by the option flags `--crt` and `--ct`, respectively, with the `vecm` command.

**Identification of the cointegration vectors****FIXME: this is but a stub**

Maximum likelihood estimation of  $\beta$  can be shown to be equivalent to solving an eigenvector problem. In practice, if the cointegration rank is known to be  $r$ , the  $n \times r$  matrix  $\beta$  is estimated as the solution to the following matrix equation:

$$M\beta = \beta\langle\lambda\rangle$$

where  $\langle\lambda\rangle$  is a diagonal matrix containing the eigenvalues. Notice, however, that if all columns of  $\beta$  are cointegration vectors, then any arbitrary linear combinations of those is a cointegration vector too. This means that the matrix  $\beta$  is under-identified. As a consequence, its elements do not have a proper covariance matrix, but this difficulty can be circumvented by imposing an appropriate number of restrictions. The method `gretl` uses is known as the “Phillips normalization”. The starting point is writing  $\beta$  in partitioned form as in

$$\beta = \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix},$$

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

$$\hat{\beta} = \begin{bmatrix} I \\ \beta_2\beta_1^{-1} \end{bmatrix} = \begin{bmatrix} I \\ \hat{\beta}_2 \end{bmatrix},$$

The coefficients that `gretl` produces are  $\hat{\beta}$ , with  $\hat{\beta}_2$  known as the matrix of unrestricted coefficients.



**Exemplo 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

## Capítulo 21

# Discrete and censored dependent variables

### 21.1 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,

$$y_i \begin{cases} 1 & P_i \\ 0 & 1 - P_i \end{cases} \quad (21.1)$$

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

$$\text{probit} \quad P_i = F(z_i) = \Phi(z_i) \quad (21.2)$$

$$\text{logit} \quad P_i = F(z_i) = \Lambda(z_i) = \frac{1}{1 + e^{-z_i}} \quad (21.3)$$

$$z_i = \sum_{j=1}^k x_{ij} \beta_j \quad (21.4)$$

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:

$$y_i^* = \sum_{j=1}^k x_{ij} \beta_j + \varepsilon_i = z_i + \varepsilon_i \quad (21.5)$$

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; 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.

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 21.1 gives the following output:

**Exemplo 21.1:** Estimation of simple logit and probit models

---

```
open greene19_1
```

```
logit GRADE const GPA TUCE PSI
probit GRADE const GPA TUCE PSI
```

---

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  $\varepsilon_i$ . These are defined as

$$u_i = \begin{cases} y_i - \hat{P}_i & \text{for the logit model} \\ y_i \cdot \frac{\phi(\hat{z}_i)}{\Phi(\hat{z}_i)} - (1 - y_i) \cdot \frac{\phi(\hat{z}_i)}{1 - \Phi(\hat{z}_i)} & \text{for the probit model} \end{cases} \quad (21.6)$$

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 21.2 shows how to perform a variable addition test.

**Exemplo 21.2:** 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)
```

---

### Ordered models

These models are simple variations of ordinary logit/probit models, and are usually applied in case the dependent variable is a discrete and ordered measurement, not necessarily quantitative. For example, this sort of model can be applied when the dependent variable is a qualitative assessment like “Good”, “Average” and “Bad”. Assuming we have  $p$  categories, the probability that individual  $i$  falls in the  $j$ -th category is given by

$$P(y_i = j|x_i) = \begin{cases} F(z_i + \mu_0) & \text{for } j = 0 \\ F(z_i + \mu_j) - F(z_i + \mu_{j-1}) & \text{for } 0 < j < p \\ 1 - F(z_i + \mu_{p-1}) & \text{for } j = p \end{cases} \quad (21.7)$$

The unknown parameters  $\mu_j$  are called the “cutoff points” and are estimated together with the  $\beta$ s. For identification purposes,  $\mu_0$  is assumed to be 0. In terms of the unobserved variable  $y_i^*$ , the model can be equivalently cast as  $P(y_i = j|x_i) = P(\mu_{j-1} \leq y_i^* < \mu_j)$ .

In order to apply these models, the dependent variable must be marked as discrete and its lowest value must be 0. Example 21.3 reproduces the estimation given in chap. 15 of Wooldridge (2002a). 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 not binary (provided it has already been marked as discrete).

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.

**Exemplo 21.3:** Ordered probit model

---

```
open pension.gdt
series pctstck = pctstck/50
discrete pctstck
probit pctstck const choice age educ female black married finc25 finc35 \
    finc50 finc75 finc100 finc101 wealth89 prftshr
```

---

**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 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  $0, 1, \dots, p$ . 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 21.4 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.

**21.2 The Tobit model**

The Tobit model is used when the dependent variable of a model is *censored*.<sup>1</sup> 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

$$y_i \begin{cases} y_i^* & \text{for } y_i^* > 0 \\ 0 & \text{for } y_i^* \leq 0 \end{cases} \quad (21.8)$$

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

---

<sup>1</sup>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. The more general case of two-sided censoring is not handled by `gretl` via a native command yet, but it is possible to estimate such models using the `mle` command (see chapter 17).

**Exemplo 21.4:** 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

```

---

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.

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) test for normality by default.

**Generalized Tobit model**

In the so-called “Tobit II” model, there are two latent variables:

$$y_i^* = \sum_{j=1}^k x_{ij} \beta_j + \varepsilon_i \quad (21.9)$$

$$s_i^* = \sum_{j=1}^p z_{ij} \gamma_j + \eta_i \quad (21.10)$$

and the observation rule is given by

$$y_i \begin{cases} y_i^* & \text{for } s_i^* > 0 \\ 0 & \text{for } s_i^* \leq 0 \end{cases} \quad (21.11)$$

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 (21.9); otherwise, OLS does not yield consistent estimates of the parameters  $\beta_j$ .

A widely used estimator is 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 (21.10); next, the generalized residuals are inserted in equation (21.9) to correct for the effect of sample selection.

Example 21.5 shows two estimates from the dataset used in Mroz (1987): the first one replicates Table 22.7 in Greene (2003), while the second one replicates table 17.1 in Wooldridge (2002a). Note that the `heckit.inp` script (provided with `gretl` as an example script) is invoked.

#### Exemplo 21.5: Heckit model

---

```
open mroz.gdt
include heckit.inp

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)

# 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)
```

---

## **Parte III**

# **Detalhes técnicos**



## Capítulo 22

# Gretl and T<sub>E</sub>X

### 22.1 Introduction

T<sub>E</sub>X — 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 T<sub>E</sub>X engine, and to save output in a form suitable for further processing with T<sub>E</sub>X.

This chapter explains the finer points of gretl’s T<sub>E</sub>X-related functionality. The next section describes the relevant menu items; section 22.3 discusses ways of fine-tuning T<sub>E</sub>X output; section 22.4 explains how to handle the encoding of characters not found in English; and section 22.5 gives some pointers on installing (and learning) T<sub>E</sub>X if you do not already have it on your computer. (Just to be clear: T<sub>E</sub>X 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 T<sub>E</sub>X. 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 scenes 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.<sup>1</sup>

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.

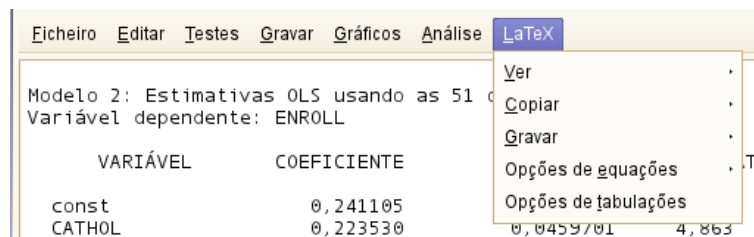
### 22.2 T<sub>E</sub>X-related menu items

#### The model window

The fullest T<sub>E</sub>X 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 22.1).

---

<sup>1</sup>Experts will be aware of something called “plain T<sub>E</sub>X”, which is processed using the program `tex`. The great majority of T<sub>E</sub>X users, however, use the L<sup>A</sup>T<sub>E</sub>X macros, initially developed by Leslie Lamport. Gretl does not support plain T<sub>E</sub>X.

Figura 22.1: L<sup>A</sup>T<sub>E</sub>X menu in model window

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 22.1 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).

Tabela 22.1: Example of L<sup>A</sup>T<sub>E</sub>X tabular output

Model 1: OLS estimates using the 51 observations 1–51  
Dependent variable: ENROLL

Variable	Coefficient	Std. Error	<i>t</i> -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:

$$\widehat{\text{ENROLL}} = 0.241105 + 0.223530 \text{ CATHOL} - 0.00338200 \text{ PUPIL} - 0.152643 \text{ WHITE}$$

$(0.066022) \quad (0.04597) \quad (0.0027196) \quad (0.040706)$   
 $T = 51 \quad \bar{R}^2 = 0.4462 \quad F(3, 47) = 14.431 \quad \hat{\sigma} = 0.038856$   
 (standard errors in parentheses)

The distinction between the “Copy” and “Save” options (for both tabular and equation) is twofold. First, “Copy” puts the T<sub>E</sub>X 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 T<sub>E</sub>X 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 T<sub>E</sub>X 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 T<sub>E</sub>X preview, copy and save enabled. In the case of windows having a graphical toolbar, look for the T<sub>E</sub>X button. Figure 22.2 shows this icon (second from the right on the toolbar) along with the dialog that appears when you press the button.

Figura 22.2: T<sub>E</sub>X icon and dialog



One aspect of gretl’s T<sub>E</sub>X 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 22.2.

## 22.3 Fine-tuning typeset output

There are three aspects to this: adjusting the appearance of the output produced by gretl in L<sup>A</sup>T<sub>E</sub>X 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 T<sub>E</sub>X 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 T<sub>E</sub>X source. The default value of the preamble is as follows:

```
\documentclass[11pt]{article}
\usepackage[latin1]{inputenc}
\usepackage{amsmath}
\usepackage{dcolumn,longtable}
\begin{document}
\thispagestyle{empty}
```

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 modified if gretl finds itself running on a system where UTF-8 is the default character encoding — see section 22.4 below.

**Tabela 22.2:** Example of model table output

OLS estimates			
Dependent variable: ENROLL			
	Model 1	Model 2	Model 3
const	0.2907** (0.07853)	0.2411** (0.06602)	0.08557 (0.05794)
CATHOL	0.2216** (0.04584)	0.2235** (0.04597)	0.2065** (0.05160)
PUPIL	-0.003035 (0.002727)	-0.003382 (0.002720)	-0.001697 (0.003025)
WHITE	-0.1482** (0.04074)	-0.1526** (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

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 T<sub>E</sub>X 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 T<sub>E</sub>X 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 *Manual dos Comandos do Gretl*.

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 T<sub>E</sub>X 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 T<sub>E</sub>X 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 L<sup>A</sup>T<sub>E</sub>X document classes, the only files needed are, as noted above, the `amsmath`, `dcolum` and `longtable` packages. These should be included in any reasonably full T<sub>E</sub>X implementation.

## 22.4 Character encodings

People using `gretl` in English-speaking locales are unlikely to have a problem with this, but if you're generating T<sub>E</sub>X output in a locale where accented characters (not in the ASCII character set) are employed, you may want to pay attention here.

`Gretl` generates T<sub>E</sub>X 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 without 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 T<sub>E</sub>X system can handle UTF-8 input, which requires use of the `latex-ucs` package. So: if you are using `gretl` to generate T<sub>E</sub>X 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 T<sub>E</sub>X.

For reference, if `gretl` detects a UTF-8 environment, the following lines are used in the T<sub>E</sub>X preamble:

```
\usepackage{ucs}
\usepackage[utf8x]{inputenc}
```

## 22.5 Installing and learning T<sub>E</sub>X

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 T<sub>E</sub>X, and in fact these are likely to be installed by default. Check the documentation for your distribution. For MS Windows, several packaged versions of T<sub>E</sub>X are available: one of the most popular is MiK<sub>T</sub>E<sub>X</sub> at <http://www.miktex.org/>. For Mac OS X a nice implementation is i<sub>T</sub>E<sub>X</sub>Mac, at <http://itexmac.sourceforge.net/>. An essential starting point for online T<sub>E</sub>X resources is the Comprehensive T<sub>E</sub>X Archive Network (CTAN) at <http://www.ctan.org/>.

As for learning T<sub>E</sub>X, many useful resources are available both online and in print. Among online guides, Tony Roberts' "L<sup>A</sup>T<sub>E</sub>X: 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 L<sup>A</sup>T<sub>E</sub>X Companion* (Goossens *et al.*, 2004).

## Capítulo 23

# Troubleshooting gretl

### 23.1 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?

### 23.2 Auxiliary programs

As mentioned above, `gretl` calls some other programs to accomplish certain tasks (gnuplot for graphing, L<sup>A</sup>T<sub>E</sub>X 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.<sup>1</sup> Thus if a given program fails, try the experiment of typing the program name at the command prompt, as shown below.

	<i>Graphing</i>	<i>Typesetting</i>	<i>GNU R</i>
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.

---

<sup>1</sup>The exception to this rule is the invocation of `gnuplot` under MS Windows, where a full path to the program is given.

## Capítulo 24

# O interface de linha de comandos (CLI)

### 24.1 Gretl em modo de consola

A aplicação `gretl` inclui o programa de linha de comandos `gretlcli`. Em Linux pode ser iniciado a partir de uma janela de terminal (`xterm`, `rxvt`, ou semelhante), ou de uma consola de texto. No MS Windows pode ser executado numa janela de linha de comandos (algumas vezes incorrectamente chamada de “janela MS DOS”). `gretlcli` tem o seu próprio ficheiro de ajuda, que pode ser acedido escrevendo o comando “help” no interface CLI. Pode ser executado em modo de sequência de comandos, enviando os resultados directamente para um ficheiro (ver também o *Manual dos Comandos do Gretl*).

Se `gretlcli` tiver sido ligado no momento da compilação à biblioteca de programas `readline` (o que acontece sempre no caso da versão MS Windows; ver também Apêndice B), é possível repetir e editar as linhas de comandos, e também completar comandos automaticamente. Você pode usar as teclas seta-Acima e seta-Abaixo para percorrer os comandos anteriormente executados. Numa dada linha de comando, você pode usar as setas para mover o cursor, em conjunto com as combinações de teclas do editor Emacs.<sup>1</sup> As mais comuns são:

<i>Combinação</i>	<i>Efeito</i>
<b>Ctrl-a</b>	ir para o início da linha
<b>Ctrl-e</b>	ir para o fim da linha
<b>Ctrl-d</b>	apagar o carácter à direita

onde “**Ctrl-a**” significa premir a tecla “a” ao mesmo tempo que a tecla “**Ctrl**” é premida. Assim, se você quiser alterar algo no início de um comando, você *não* precisa de apagar carácter a carácter na linha toda. Basta saltar para o início e acrescentar ou apagar caracteres. Se você escrever as primeiras letras de um comando e pressionar a tecla Tab, o sistema `readline` vai tentar completar o comando por você. Se houver uma única possibilidade, o comando é automaticamente completado. Se houver mais que uma, pressionando Tab uma segunda vez faz aparecer uma lista.

### 24.2 A sintaxe CLI

Provavelmente o modo mais produtivo para análises intensivas com o `gretlcli` é em modo de sequência de comandos (não-interactivo), no qual o programa lê e processa um ficheiro de sequência de comandos, e envia a saída para um ficheiro. Por exemplo

```
gretlcli -b ficheirodecomandos > ficheiroderesultados
```

O *ficheirodecomandos* é tratado como um argumento de programa; ele deve especificar um ficheiro para ser usado internamente, usando a sintaxe `open ficheirodedados`. Não esquecer a opção `-b` (*batch=lote*), de outro modo o programa ficará a aguardar comandos do utilizador após a execução da sequência de comandos.

---

<sup>1</sup>Na realidade, as combinações de teclas referidas abaixo são apenas as definidas por omissão; elas poderão ser personalizadas por si. Ver o [manual do readline](#).



## **Parte IV**

# **Apêndices**

## Apêndice 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:

```
GOM910 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.

## Apêndice B

# Building gretl

### B.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 B.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](#).

<i>Library</i>	<i>purpose</i>	<i>website</i>
zlib	data compression	<a href="#">info-zip.org</a>
libxml2	XML manipulation	<a href="#">xmlsoft.org</a>
LAPACK	linear algebra	<a href="#">netlib.org</a>
FFTW3	Fast Fourier Transform	<a href="#">fftw.org</a>
glib-2.0	Numerous utilities	<a href="#">gtk.org</a>

**Tabela B.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](#)).<sup>1</sup>

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](#)).

### B.2 Build instructions: a step-by-step example

In this section we give instructions detailed enough to allow a user with only a basic knowledge of a Unix 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.

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.

---

<sup>1</sup>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`.

We assume that the basic GNU utilities are already installed on the system, together with these other programs:

- some  $\text{T}_{\text{E}}\text{X}/\text{L}^{\text{A}}\text{T}_{\text{E}}\text{X}$  system (`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:

<i>Library</i>	<i>command</i>
GLIB	<code>apt-get install libglib2.0-dev</code>
GTK 2.0	<code>apt-get install libgtk2.0-dev</code>
PNG	<code>apt-get install libpng12-dev</code>
XSLT	<code>apt-get install libxslt1-dev</code>
LAPACK	<code>apt-get install lapack3-dev</code>
FFTW	<code>apt-get install fftw3-dev</code>
GMP	<code>apt-get install libgmp3-dev</code>

(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.

At this point, it is possible to build from the source.

1. Download the latest gretl source package from [gretl.sourceforge.net](http://gretl.sourceforge.net). The released versions are guaranteed to build correctly. However, if you like to live dangerously, you may download the CVS version, which contains the work in progress towards the next release. For instructions on how to download the CVS version, please refer to the appropriate [SourceForge page](#).
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-1.6.2`).

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 may 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 B.1.

**Exemplo B.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.

---

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
```

## Apêndice C

# 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 accurate enough for most purposes (with the option of using QR decomposition instead). 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”).

Giovanni Baiocchi and Walter Distaso published a review of gretl in the *Journal of Applied Econometrics* (2003). We are grateful to Baiocchi and Distaso for their careful examination of the program, which prompted the following modifications.

1. The reviewers pointed out that there was a bug in gretl’s “p-value finder”, whereby the program printed the complement of the correct probability for negative values of  $z$ . This was fixed in version 0.998 of the program (released July 9, 2002).
2. They also noted that the p-value finder produced inaccurate results for extreme values of  $x$  (e.g. values of around 8 to 10 in the  $t$  distribution with 100 degrees of freedom). This too was fixed in gretl version 0.998, with a switch to more accurate probability distribution code.
3. The reviewers noted a flaw in the presentation of regression coefficients in gretl, whereby some coefficients could be printed to an unacceptably small number of significant figures. This was fixed in version 0.999 (released August 25, 2002): now all the statistics associated with a regression are printed to 6 significant figures.
4. It transpired from the reviewer’s tests that the numerical accuracy of gretl on MS Windows was less than on Linux. For example, on the Longley data — a well-known “ill-conditioned” dataset often used for testing econometrics programs — the Windows version of gretl was getting some coefficients wrong at the 7th digit while the same coefficients were correct on Linux. This anomaly was fixed in gretl version 1.0pre3 (released October 10, 2002).

The current version of gretl 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](mailto:cottrell@wfu.edu).

As mentioned above, all regression statistics are printed to 6 significant figures in the current version of gretl (except when the multiple-precision plugin is used, then 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).



## Apêndice D

# 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](http://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](http://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](http://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.

## Apêndice E

# 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](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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