

glmLab

Using MATLAB for analysing
generalised linear models

Peter K. Dunn

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A Note on What You Read

Some small differences may exist between the figures that appear in this document and the figures that appear on your computer screen. Most of the figures that appear in this document are the figures as they appear in the UNIX or LINUX versions. Windows and Macintosh versions will produce figures that are similar, but different.

`gmlab` is often updated in small ways. Some of the most recent changes may not appear in the figures and output that is shown in this document (especially where dates are given).

This document was produced using \LaTeX and \TeX , with the pictures produced (obviously) using `MATLAB`.

Contact Information

There is no charge for using `gmlab`. However, if you find it useful, it would be greatly appreciated if you could contact the author and let him know how you are using `gmlab`, by emailing him at `dunn@sci.usq.edu.au`, or (preferred) writing to:

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You may also find it useful to visit the `gmlab` Home Page on the web at <http://www.sci.usq.edu.au/staff/dunn/gmlab/gmlab.html>.

Chapter 1

Introduction

1.1 Why `glm1ab`?

`glm1ab` was first written in 1995 to emulate some of the features of GLIM (Aitken *et al.* [1], Francis *et al.* [6]), industry standard software for analysing generalised linear models. However, GLIM is an expensive program to purchase (even student editions). Since MATLAB is inexpensive in student editions (especially considering its capabilities) and is a widely used numerical computation package, MATLAB was considered an ideal platform in which to perform the analyses performed in GLIM. `glm1ab` does not attempt to replace packages such as GLIM and S-PLUS (Statistical Sciences [9]), but rather to bring the world of generalised linear models to the MATLAB environment.

`glm1ab` uses a graphical user interface, which means very few additional commands need to be learnt to use `glm1ab`. This manual discusses some of the basic skills needed to use `glm1ab`. While it assumes some knowledge of MATLAB, there is an introduction to MATLAB in Chapter 2

1.2 What can `glm1ab` do?

MATLAB is a powerful computational tool that can be programmed to perform practically any numerical task. MATLAB has some basic statistical procedures built-in (for example, `hist`, `mean`, `median` and `std`). More statistical procedures are available—at extra cost—in the Statistics Toolbox. `glm1ab` extends MATLAB's statistical capabilities without needing the Statistics Toolbox, allowing the user to perform tasks such as:

- simple linear regression;
- multiple regression;
- weighted regression;
- log-linear models;
- logistic regression;
- other generalised linear modelling techniques; and
- residual plotting.

`glm1ab` also allows the user to save models between sessions, and returns a number of variables to the workspace for further analysis (see Section 3.5).

```

matlabpath([...
'C:\MATLAB\toolbox\local',...
';C:\MATLAB\toolbox\matlab\datafun',...
';C:\MATLAB\toolbox\matlab\elfun',...
:
:
:
';C:\MATLAB\toolbox\local',...
';C:\gmlab',... ← A new line to be included
';C:\gmlab\fit',... ← A new line to be included
';C:\gmlab\fit\link',... ← A new line to be included
';C:\gmlab\fit\dist',... ← A new line to be included
';C:\gmlab\misc',... ← A new line to be included
';C:\gmlab\plotting',... ← A new line to be included
';C:\gmlab\data',... ← A new line to be included
';C:\gmlab\glmhelp',... ← A new line to be included
';C:\gmlab\glmlog',... ← A new line to be included
]);

```

Figure 1.1: The MATLAB Windows Path

1.3 Installing gmlab

gmlab is available from the MathWorks user contributed site at <http://www.mathworks.com/statsv5.html> as `gmlab.zip` (best for Windows or Macintosh users) or `gmlab.tar` (best for UNIX users).

When installing gmlab, you will need to have write access to the `gmlab/glmlog` directory/folder so that it can create a file of the fitting parameters and to place the log file. For this reason, it is suggested that gmlab be installed in your own directories. (This will make more sense after reading the rest of this section.)

Please consult your MATLAB documentation to help with setting the appropriate MATLAB path. The steps outlined below can change and are sometimes platform dependent.

1.3.1 The PC Version of MATLAB

If you have the file `gmlab.zip`, you will need to “unzip” the file using a program such as PKunZip or WinZip.

After loading gmlab onto the computer’s hard disk, MATLAB must be told where to find the gmlab files. There are two ways to do this: one is to use the PathTool that comes with MATLAB, by typing `pathtool` at the MATLAB prompt. The second method is to edit the file `matlabrc.m` (generally found in the `matlab` directory). Load this file using a text editor (such as `notepad` or `edit`, or even a word processor) and find the section that begins with

```
matlabpath([...
```

This section must be edited to include the gmlab directories. Use the editor to include some extra lines so that it ends up looking similar to Figure 1.1 (many lines have been omitted).

Type `help gmlab` at the MATLAB prompt next time MATLAB is started. If the message `gmlab.m not found` appears on the screen, then the installation did not work and will need to be repeated.

```
setenv MATLABPATH /home/myname/glmlab:/home/myname/glmlab/fit:/home/
myname/glmlab/plotting:/home/myname/glmlab/misc:/home/myname/glmlab/fit/
link:/home/myname/glmlab/fit/dist:/home/myname/glmlab/data:/home/myname/
glmlab/glmhelp:/home/myname/glmlab/glmlog
```

Figure 1.2: The MATLAB UNIX Path in `tc shell`

<code>/glmlab</code>	Contains general information and files used in starting <code>glmlab</code> .
<code>/glmlab/fit</code>	Contains numerous files for fitting the model and parsing the input.
<code>/glmlab/fit/dist</code>	Contains information about the distributions that can be used.
<code>/glmlab/fit/link</code>	Contains information about the link functions that can be used.
<code>/glmlab/plotting</code>	Contains plotting routines.
<code>/glmlab/misc</code>	Contains other miscellaneous files used in <code>glmlab</code> , including formatting and tricks.
<code>/glmlab/glmhelp</code>	Contains the <code>glmlab</code> help menu information.
<code>/glmlab/glmlog</code>	Contains log files and fitting parameters that come with <code>glmlab</code> .
<code>/glmlab/data</code>	Contains the data files that come with <code>glmlab</code> .

Figure 1.3: The Structure of `glmlab`

1.3.2 The UNIX and LINUX Versions of MATLAB

To use `glmlab` with UNIX, the file `.cshrc` (or its equivalent, depending on the shell you are using) needs to have a line directing MATLAB to `glmlab`. There should be a line in the `.cshrc` (or equivalent) file starting with `setenv MATLABPATH` (or equivalent). If not, then a line beginning with this will need to be created. The Systems Administrator will be of great assistance here. The appropriate section of the `.cshrc` file (or equivalent) should include a *single line* that looks like Figure 1.2 (it may include other MATLAB directories besides the `glmlab` directories).

You may have to log out and log in again. Type `help glmlab` at the MATLAB prompt next time MATLAB is started. If the message `glmlab.m not found` appears on the screen, then the installation did not work and will need to be repeated.

NOTE: `glmlab` needs to have write permission to the `glmlab/glmlog` directory so that it can create a file of the fitting parameters and to place the log file. For this reason, it is suggested that `glmlab` be installed in your own directories.

1.4 Directory Structure

`glmlab` consists of over 70 MATLAB files in a number of directories (or folders). They are structured as shown in Figure 1.3.

Chapter 2

Starting with MATLAB

This section discusses, very briefly, how to start using MATLAB. Only details important for using `glmlab` are discussed. A more thorough introduction is given in <http://www.math.utah.edu/lab/ms/matlab/matlab.html>. The MATLAB manual will also prove useful.

2.1 Basic Use of MATLAB

MATLAB is designed to work easily with matrices and vectors, and a number of methods exist to declare matrices and vectors. For example, an entire matrix can be entered on one line with rows separated by semicolons (`;`):

```
>> A = [ 1 3 2 ; -1 0 9 ]
A =
     1     3     2
    -1     0     9
```

The matrix can also be typed in row by row:

```
>> A = [ 1 3           2
        -1      0           9]
A =
     1     3     2
    -1     0     9
```

Notice that the spacing used has no effect. The *transpose* of a matrix can be found using the quote symbol (`'`):

```
>> B = [0 3 ; 3 4; 6 6];
>> B'
ans =
     0     3     6
     3     4     6
```

The *semicolon* (`;`) at the end of a line stops MATLAB from displaying the answer on the screen. Basic matrix operations can be performed:

```
>> A + B
??? Error using ==> +
Matrix dimensions must agree.
```

```

>> A + B'
ans =
     1     6     8
     2     4    15

>> A - B'
ans =
     1     0    -4
    -4    -4     3

>> A * B
ans =
    21    27
    54    51

>> inv( A * B )
ans =
   -0.1318    0.0698
    0.1395   -0.0543

```

There are other operations in MATLAB apart from the standard operations. Preceding an operation with a period (.) causes the operation to be applied on an element by element basis. For example, consider the following commands:

```

>> C = [0 -3 4; 5 -4 3]
C =
     0     -3     4
     5     -4     3

>> D = [1 1 9; -3 0 1]
D =
     1     1     9
    -3     0     1

>> C * D
??? Error using ==> *
Inner matrix dimensions must agree.

>> C .* D
ans =
     0     -3    36
    -15     0     3

```

Here's another example of MATLAB's element by element procedure:

```

>> E = [1:4]
E =
     1     2     3     4

>> E * E
??? Error using ==> *
Inner matrix dimensions must agree.

>> E ^2
                                     %E^2 is the same as E*E
??? Error using ==> ^
Matrix must be square.

>> E .^ 2
ans =
     1     4     9    16

```

As demonstrated above, *comments* can be included in MATLAB with the `%` character. MATLAB ignores any characters after this symbol. It is good practice in any programming to include comments to explain details that are not immediately obvious.

2.2 Obtaining Help from MATLAB

General help can be found by using the *Help Desk*, which can be started by typing `helpdesk` at the MATLAB prompt. This opens a Web browser (Netscape or Internet Explorer, for example) that enables the user to search for help on topics.

In general, finding functions for a particular purpose in MATLAB is achieved typing `lookfor` and then a relevant word. MATLAB will then display any functions that may be relevant. For example, try typing `lookfor cos` at the MATLAB prompt. My computer produces the following (some has been omitted):

```
>> lookfor cos
ACOS      Inverse cosine.
ACOSH     Inverse hyperbolic cosine.
ACSC      Inverse cosecant.
.
.
.
LQGCOST Function which returns the difference between the
```

The MATLAB functions are displayed on the left, with a brief description of their purpose on the right. Sometimes the information to be displayed will be too much to fit on the screen. If this happens, type `more on` at the MATLAB prompt so that MATLAB will display only one screen at a time. Type `more off` to turn off this feature.

If information scrolls off the screen, type `more on` at the MATLAB prompt. This will present information one screen at a time. Pressing the space bar presents a new screen of information; pressing RETURN or ENTER will present one more line.

The MATLAB function `help` can then be used to explain how to use the function. For example,

```
>> help cos

COS      Cosine.
         COS(X) is the cosine of the elements of X.

>> help acosh

ACOSH    Inverse hyperbolic cosine.
         ACOSH(X) is the inverse hyperbolic cosine of...
```

Although it doesn't say, MATLAB always assumes the values are in radians when using trigonometric functions. MATLAB commands need to be entered in lower case. While the `help` places the commands in upper case to distinguish commands from the text, this can be confusing.

Always use lower case for MATLAB commands.

Here is an example of using `cos`:

```

>> cos(2)
ans =
    -0.4161

>> cos(pi)           %Notice that pi is used for 3.141592...
ans =
    -1

>> x=[0, pi/6, pi/4, pi/3, pi/2];

>> cos(x)
ans =
    1.0000    0.8660    0.7071    0.5000    0.0000

```

2.3 Using Data Files

In MATLAB, data can easily be loaded from a data file. This has many advantages: It is quicker to load a data file than to type in all the numbers; loading data at the keyboard is likely to introduce typing errors; if there *are* errors in the data, it is easier to alter the file than to re-enter all the data again.

A data file called `tester.txt` in the data subdirectory of `glm1ab` contains the following data:

```

1 2 -1 0
1 3 4 5
-1 -2 3 1

```

Here is an example of how to load the file, play with it, and save another file:

```

>> %LOAD THE FILE tester.txt
>> load tester.txt

```

The data is now loaded as a matrix called `tester`:

```

>> tester

tester =
     1     2    -1     0
     1     3     4     5
    -1    -2     3     1

```

Let's play with this a little. First, call the first column of data `y`:

```

>> %PLAY WITH THE DATA
>> y=tester(:,1)
y =
     1
     1
    -1

```

Call the second column `x1`, the third `x2`, the fourth `x3`:

```

>> x1=tester(:,2); x2=tester(:,3); x3=tester(:,4);

```


Many commands can be placed on one line, separated by a semicolon or a comma. Notice, also, how to access particular columns of a matrix using a colon. Rows can be accessed in a similar way; `r=tester(1, :)` would place the first row of `tester` into row vector `r`.

In MATLAB, it is standard to define variables as column vectors. This standard is adopted by `glmLab`.

We can now manipulate the vectors:

```
>> x = x1 + x2 - 3 * x3
x =
     1
    -8
    -2
```

To save `y` and `x` in the file `prac.txt`, proceed as follows:

```
>> save prac.txt y x -ascii
```

That is,

```
save <filename>.<extension> <variables> -ascii
```

where the `-ascii` is so that humans can read it. However, the *best* way to save the file is to use `save <filename> <variables>`:

```
>> save prac2 y x
```

This creates a file called `prac2.mat` which MATLAB can use, but humans can't understand. To load the file `prac2.mat`, simply type `load prac2`. This will automatically create two variables (called `x` and `y`) without you having to declare them explicitly.

A file called `loadme.mat` should be in the `glmLab` data folder. First, clear all the current variables (using `clear`), and then load this file:

```
>> clear all
>> load loadme
```

By typing `who` at the MATLAB prompt, the variables that have been loaded can be seen (try typing `whos` also):

```
>> who
```

```
Your variables are:
```

```
x          y          z
```

Have a look at the variables (especially the variable called `x`) by typing variable names at the MATLAB prompt.

When saving data, the best method is to use the syntax:
`save <filename> <variables>`

2.4 Using MATLAB for Plotting

MATLAB has many features to produce high quality plots. This section in no way explains all the plotting capabilities of MATLAB, or discusses all the ways in which things can be changed. Hopefully it will supply you with enough information to be able to create plots that are near enough to what you want.

The basic plotting command is `plot`. If you have defined two vectors (of the same length) named `x` and `y`, then `plot(x,y)` will generate a plot of `y` versus `x`. A word of warning: By default, MATLAB joins the points with straight lines in the order in which they are given. To plot the points in other ways, use the following commands:

- `plot(x,y,'+')` will use only plus signs at the points;
- `plot(x,y,'x')` will use only crosses at the points;
- `plot(x,y,'.')` will use only dots at the points;

For both lines and points, try these:

- `plot(x,y,'+-')` will indicate the points with a plus sign, and join the points with straight unbroken lines.
- `plot(x,y,'o--')` will indicate the points with a circle sign, and join the points with dashed lines.

A full list of the available type of points and lines is available by typing `help plot` first at the MATLAB prompt. (You may need to type `more on` at the prompt to see all the information.)

The plots should be annotated with labels on the x -axis, the y -axis and with a title. To place a label on the x -axis, use `xlabel`; to place a label on the y -axis, use `ylabel`; and to place a title, use `title`.

Remember to always give pictures meaningful titles and axis labels.



Let's have a look at using some of this information. First, define some vectors to manipulate:

```
>> x=[1:10]';           %The numbers 1, 2, ... 10
>> y=randn(10,1);      %10 by 1 vector of normally
>> plot(x,y);
```

This gives a plot joining the points with lines, but crosses would be better:

```
>> plot(x,y,'x');
```

The plot and the axes should be labelled:

```
>> xlabel('x-values');
>> ylabel('y-values');
>> title('A plot of y versus x');
```

The following functions may be useful also:

- `axis`: For example, `axis([0 10 0 5])` sets the axes such that the x -axis ranges from 0 to 10, and the y -axis ranges from 0 to 5.
- `propedit`: The *property editor* allows the user to make many changes to plots. Type `propedit` at the MATLAB prompt, and then click on the Figure to be edited. Change some of the settings to see what happens.

To print the plots that are produced on the screen, the `print` command can be used, and usually the Print option from the File menu of the Figure works also. In some cases, it may be best to save the picture to a file, and then print the file. The `print` command is still used in this case, but in a different form. See the help for `print` for more information. (You may need to use `more on.`) According to the help for `print`, the command `print -depson` will print the current picture on an Epson or Epson compatible 9- or 24-pin printer. Also, `print -depson lookatme.prt` should produce a file called `lookatme.prt` that can be sent to an Epson printer. Type `help print` to see what other types of printers that MATLAB supports (like LaserJets, BubbleJets and colour printers).

2.5 Other Miscellaneous MATLAB Commands

In this section, some other useful MATLAB commands are discussed. For a full description, see the MATLAB help for the function.

- `sort`: As the name suggests, `sort` sorts the data in ascending order. `-sort(-x)` sorts the data in x in *descending* order.
- `diary`: Typing `diary mine.txt` at the MATLAB prompt creates a file called `mine.txt` containing all the information printed in the MATLAB command window from the time the command is entered. To turn off this feature, type `diary off`. (This can be useful when submitting assignments to show what was happened at the computer.)
- `ones` and `zeros`: These commands create vectors of ones and zeros of given size.
- `eye`: This command create an identity matrix of a given size, usually called I .
- `size`: This command returns the number of rows and the number of columns of a given matrix.
- `ans`: Issuing this command at the MATLAB prompt recalls the last answer that wasn't assigned to another variable name.
- `...`: If the command line won't fit on one line, end the line with three dots. This tells MATLAB that the line that follows is a continuation of the previous line. For example, a large vector can be defined like this:

```
>> HPrices=[150000, 200000, 125000, 350000, 89000, 110000, ...
           110000, 150000, 120000, 100900, 93500, 97000, ...
           88000, 118500, 123300, 165000, 95000]';
```

When defining a long vector, it can be very useful to use the line continuation facility by ending the lines with the characters `...`



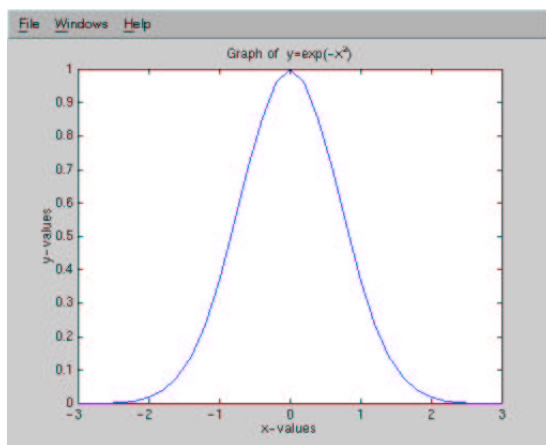


Figure 2.1: Graph of $y = \exp(-x^2)$.

Some Examples

Here are a few examples of using MATLAB, showing some important details (like how MATLAB deals uses `i` and `j` to represent one of the square roots of -1):

```
1. >> conj( [1+7i, 2-6j] )
ans =
    1.0000 - 7.0000i    2.0000 + 6.0000j

2. >> w = [-1 : 1 : 2]
w =
    -1     0     1     2
>> log(w)

Warning: Log of zero.
ans =
    0 + 3.1416i    -Inf         0         0.6931

3. >> x = [ -3 : 0.2 : 3 ];
>> y = exp( -x .* x ); %OR: y = exp( - x .^ 2 );
>> plot(x, y);
>> title('Graph of y=exp(-x^2)');
>> xlabel('x-values'); ylabel('y-values');
```

The final graph is shown in Figure 2.1.

Notice that the top of the graph is not very smooth. What can be done to make the graph smoother? It would also be good to have the graph not touching the top border. Have a look at the help for the function `axis`.

Chapter 3

glm1ab Reference

This section explains briefly most of the details of glm1ab, including all of the main menu items. Figure 3.1 shows the main glm1ab window.

3.1 The Main Window Items

There are eight drop-down menus on the main glm1ab screen. For a quick explanation, see Figure 3.2.

3.1.1 The File Menu

3.1.1.1 LOAD Data File

Allows the user to load a data file for use in glm1ab, using a graphical interface. A dialog box is issued confirming that the file has loaded correctly.

The dialog box initially defaults to the glm1ab data directory, but the default directory can be altered by moving the dummydata.m file to the required default folder/directory. See also Section 5.8.

3.1.1.2 Load glm1ab Model

Loads a previously saved glm1ab model, restoring details such as the error distribution, link function, scale parameter, residual type and variables entered.

3.1.1.3 Save glm1ab Model

Saves a glm1ab model, saving details such as the error distribution, link function, scale parameter, residual type and variables entered. A dialog box defaults to saving in the glmlog folder/directory, but this can be changed by moving the file dummylog.m to the desired directory.

3.1.1.4 QUIT glm1ab

Quits glm1ab and loses all information. The DETAILS.m file will retain its information until glm1ab is started again. This option is the same as pressing the QUIT button.

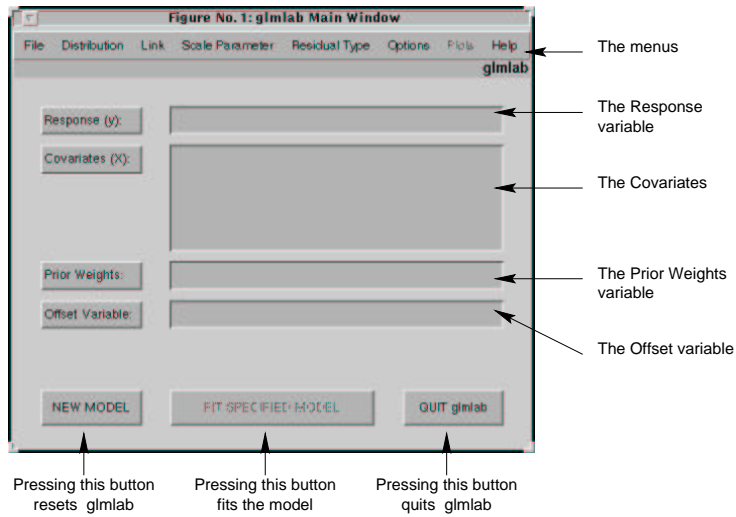


Figure 3.1: A Quick Tour of the *glm*lab Screen

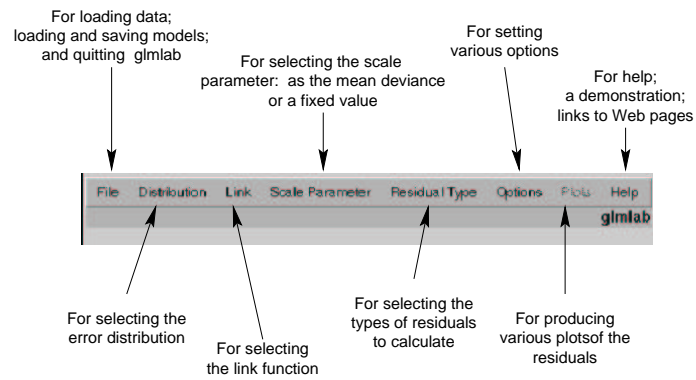


Figure 3.2: A Quick Tour of the Drop-Down Menus

3.1.1.5 EXIT matlab

Exits MATLAB and hence *glm1ab*. The `DETAILS.m` file will retain its information until *glm1ab* is started again.

3.1.2 The Distributions Menu

Alters the error distribution. The five choices are: normal, gamma, inverse Gaussian, binomial and Poisson. User defined distributions are also possible; see Section 5.6. Each distribution has its own set of default link functions and scale parameters as detailed in Table 5.1. User-defined distributions are also possible; see Section 5.6.

The binomial distribution requires two columns in the Response area; one for the observed counts and the other for the sample size. If only one column is given, it is assumed to be probabilities if all its elements are between 0 and 1, otherwise *glm1ab* issues a warning.

3.1.3 The Link Menu

Alters the link function. The choices are: identity, logarithm, reciprocal, square root, power, logit, probit, complementary log-log. The last three are only available when the binomial distribution is selected. User-defined link functions are also possible; see Section 5.6.

An edit box is presented for altering the power link function. If the power is given as 0, -1 , 0.5, the link function is automatically altered to identity, reciprocal or square root respectively. Each distribution has its own default link function (the distribution's canonical link) as shown in Table 5.1.

3.1.4 The Scale Parameter Menu

The user can chose to use the mean deviance as the scale parameter, or to use a fixed value. When choosing a fixed value, a input dialog box is presented that only allows positive values. Each distribution has its own default scale parameter as shown in Table 5.1.

3.1.5 The Residuals Type Menu

Sets the type of residual that is calculated. The user can choose from Pearson residual (the default), deviance residuals, quantile residuals (see Dunn and Smyth [4]), or the raw residuals (that is, $y - \mu$). Quantile residuals are only available for the distributions that come with *glm1ab* and not for user-defined distributions.

3.1.6 The Options Menu

There are several options that can be chosen as detailed below.

3.1.6.1 Declare New Model

After fitting models, this option should be selected to restore all options and reset *glm1ab*. After selecting this option, the `DETAILS.m` file will be overwritten. This is the same as pressing the NEW MODEL button.

3.1.6.2 Restore Default Settings

This option restores all the default settings. It can be selected if the user has become lost in setting the options elsewhere.

3.1.6.3 Warning Message Status

MATLAB often issues warnings. These warnings can be disabled or enabled in this menu. For more details, type `help warning`.

3.1.6.4 Change Fitting Parameters

There are three parameters that the user can change:

- The number of iterations. This determines the maximum number of iterations used in the fitting algorithm. The default of 20 iterations will be sufficient for almost all cases.
- Parameter Tolerance. This parameter determines the accuracy of the parameter estimates.
- Ill-conditioning Tolerance. In general, this parameter determines the sensitivity of *glmmlab* to the singularity of the $X^T X$ matrix (where X is the covariate matrix). If $X^T X$ is singular (or close to singular), the parameter estimates can be inaccurate.

The parameter values are stored in the `PARVALS.mat` file in the same directory as the `DETAILS.m` file (usually the `glmlog` directory).

3.1.6.5 Include Constant Term

This options toggles the inclusion of the constant term in the fitting of the model. By default, the constant term is included in the fitting.

3.1.6.6 Output Display Information

The *glmmlab* output usually contains the parameter estimates and their standard errors; and the deviance, degrees of freedom and changes in them both. The user can decide not to display the parameter estimates and standard errors by disabling `Display Parameter Values`. The user can also display more information—such as the number of iterations to convergence—by selecting the `Display Fitting Information`.

3.1.6.7 Recycle Fitted Values

At the start of each fit, *glmmlab* usually uses an initial estimate such that $\mu = y$. In some cases, adjustments are made in case the response is zero. However, by selecting this option, *glmmlab* will use the previous fitted values for the initial estimate in the iterations.

3.1.7 The Plots Menu

Produces residual plots from the current fit. This menu item is unavailable until a model has been fitted, after changes have been made to the model structure (altering the distribution, link function, or scale parameter), and after changing the type of residual that is to be calculated.

These plots are plotted when the appropriate button is pressed. The type of residual used depends on the type of residual chosen in the Residuals Type menu, and some plots are unavailable for certain distributions and residuals types. *glm1ab* labels the plots as best as it is able. Apart from the plots listed below, *glm1ab* also has available the facility to plot histograms using MATLAB's `hist` command. The six options are:

- **Residuals vs Response (y):** This option plots the residuals against the response variable, y .
- **Residuals vs Covariates:** If there is more than one covariate, a window is displayed where the user can select the covariates against which to plot. The constant term is not an option. At present, only the first 40 covariates can be chosen, but this limit should be sufficient for almost all cases. If only a constant term is fitted, this option is disabled.
- **Normal Probability Plot of Residuals:** This option plots a normal probability plot of the residuals is given. It does *not* use the MATLAB function `normplot`.
- **Residuals vs Fitted Values:** This option plots the residuals against the fitted values.
- **Residuals vs Transformed Fitted Values:** This option plots the residuals versus the transformed fitted values as defined by the *constant information criterion* discussed by McCullagh and Nelder [7, page 398]. For the normal distribution, the transformation is simply an identity relationship and so this option is disabled in that case.
- **Fitted Values vs Quantile Equivalents:** The fitted values are plotted against the quantile equivalents of the residuals. For quantile residuals, this option is disabled.

3.1.8 The Help Menu

The help menu is far from thorough, but should be sufficient when used in conjunction with this manual and the on-line manual.

3.1.8.1 On-line Manual

Provided a Web Browser is running, this option takes you to the on-line version of the manual. This allows easy navigation around the manual.

3.1.8.2 Help with Main Window Items

This presents a screen of basic help concerning the items in the main area of the main *glm1ab* window.

3.1.8.3 Help with Menu Items

This presents a screen of basic help concerning the drop-down menu items.

3.1.8.4 Help with Interactions

glm1ab uses the @ symbol to specify that two (or more) variables interact. This help screen gives brief instructions on how to specify interactions.

3.1.8.5 Help with OUTPUT VARIABLES

A brief explanation is provided of all variables returned into the workspace by *glm1ab*. The variables returned are explained in Section 3.5.

3.1.8.6 Help with Residuals Items

This presents a screen of basic help for the Residuals window.

3.1.8.7 Run *glm1ab* Demo

This begins a small introductory demonstration of *glm1ab*. While the demonstration is running, the user is unable to fit models.

3.1.8.8 Where to get *glm1ab*

Places where *glm1ab* can be found are listed here.

3.1.8.9 Contact the Author

This option allows the user to email the author of *glm1ab*. The author encourages you to email him if you are using the program to let him know what you think, or to give suggestions for improvements, or how you are using *glm1ab*.

3.1.8.10 Initial Splash Screen

This option redisplay the splash screen that is displayed when *glm1ab* is first started.

3.1.8.11 Last Revision

This is only for information. The date of the latest change—even if a minor one—is given here.

3.2 The Main Window Edit Areas

3.2.1 The Response Area

The user types the name of the response variable (usually designated as y) in this area. Most legal MATLAB commands can be used (like `[1 2 3]'` or `randn(100,1)`) though *glm1ab* could complain if the commands become too complicated.

The binomial distribution requires two columns in the Response area; one for the observed counts and the other for the sample size. If only one column is given, it is assumed to be probabilities if all its elements are between 0 and 1, otherwise *glm1ab* issues a warning. See Section 5.5. No model is able to be fitted until a valid string is entered into the Response area.

3.2.2 The Covariates Area

The user types the name of the covariates (usually designated as X) in this area. It is possible to use most legal MATLAB commands (like `[1 2 3]' [3 0 1]'` or `randn(100,4)`) though *glmmlab* could complain if they become too complicated. In particular, *glmmlab* will become confused if a matrix is entered, or if some covariates are listed by variable name and others using legal MATLAB commands. *glmmlab* requires that each column of input into the Covariates window has its own MATLAB variable name (or command). For example, valid strings are:

```
[1 2 3]', [32 92 21]'
Wt, Ln
```

where `Wt` and `Ln` are valid MATLAB variables with *one column each*. Invalid entries are:

```
[1 2 3;3 4 5]
magic(8)
Msrments(:,1)
Msrments
```

where `Msrments` is a *matrix*.

It is best to define vector variables in the MATLAB workspace and enter the variable names in the *glmmlab* window. It is best not to use matrices.

Strings of variables can be separated by commas or spaces. *glmmlab* tries to sort out the string if it contains other characters, or double commas and so on, but it is certainly not foolproof. The constant term is included in fitting models by default, but can be controlled through the Options menu.

3.2.3 The Prior Weights Area

If prior weights are to be used, the variable name is entered here. Prior weights are used, for example, in weighted regression, log-linear models where there are structural zeroes, or when using the binomial distribution (see Section 5.5). If the variable consists of all zeroes, an error message is given. Valid MATLAB vectors are allowed.

3.2.4 The Offset Area

An offset is a variable with a known coefficient. The offset variable name is entered here. Valid MATLAB vectors are allowed.

3.3 The Main Window Buttons

3.3.1 QUIT

Quits *glmmlab* and loses all information. The `DETAILS.m` file will retain its information until *glmmlab* is started again. See Section 5.8. The option is the same as choosing Quit from the File menu.

3.3.2 FIT SPECIFIED MODEL

Pressing this button fits the model currently specified in the edit areas and in the pull-down menus. If there is no response variable defined, or there are no covariates defined (including a constant term), the button is dimmed since a model cannot be fitted.

3.3.3 NEW MODEL

This button prepares *glm1ab* for fitting a new model. It performs such tasks as restoring the default options and clearing the `DETAILS.m` file. It is the same as choosing the Options menu, and selecting Declare New Model.

3.4 Extra Commands

3.4.1 `fac`

The `fac` command indicates that the variable is a factor. Factors are also called *qualitative* variables or *categorical* variables. To fit a model using the factor `Gender`, use `fac(Gender)`.

3.4.2 `makefac`

`makefac` is used to generate a factor that has some regularity. (It is similar to the GLIM command `%gl.`) The general syntax of the `makefac` command is

```
makefac(length, number_of_levels, size_of_the_blocks)
```

For example, if the variable `Gender` in a data set was recorded as `M, M, M, M, F, F, F, F` then `makefac` could be used to generate the numeric equivalent. The vector would need to be of length 8; there are two levels (M and F), and they are repeated in block of size 4. The variable can be generated using `makefac(8, 2, 4)`. If `Gender` was recorded as `M, M, F, F, M, M, F, F`, then the variable would be generated using `makefac(8, 2, 2)`.

3.4.3 The @ Character

The @ character is used to specify interactions, and is usually obtained by holding down the SHIFT key while pressing 2. For example, to interact two variables called `Height` and `Gender` (which is a *factor*), use `Height@fac(Gender)`.

3.5 Returned Variables

glm1ab returns ten variables to the workspace for further manipulation. The variables are:

- `BETA`: The parameter estimates.
- `SERRORS`: The standard errors of the parameter estimates.
- `FITS`: The fitted values.
- `RESIDS`: The residuals calculated. The type of residual calculated is determined by the Residual Type menu item; see Section 3.1.5.
- `COVB`: The covariance matrix for the parameter estimates.
- `COVD`: The covariance matrix for the differences between the parameter estimates.
- `DEVLIST`: The deviance at each iteration of the fitting algorithm.
- `LINPRED`: the linear predictor, $\eta = X\beta$.

- `XMATRIX`: The X matrix used in the fitting.
- `XVARNAMES`: The names of the X variables as recorded in the `glm1ab` output.

Chapter 4

Examples Using `glmlab`

This section gives some examples of how to use `glmlab` for some basic tasks. `glmlab` can do more than is demonstrated here (see Chapter 5 for example).

4.1 Example: Multiple Regression

Table 4.1 shows (artificial) data recording the volume of a toxic chemical that is produced as a by-product in a certain industrial manufacturing process.

`glmlab` is started by typing `glmlab` at the MATLAB prompt, producing the initial `glmlab` screen given in Figure 4.1. The data is stored in the file `chemical.mat` in the `data` subdirectory of `glmlab`. This file can be loaded using the LOAD Data File option from the `glmlab` File menu. By default, the window opens in the `glmlab` data folder. To load the same file at the MATLAB prompt, type the following:

```
>> load chemical           %if not using the glmlab menu
```

After loading this file, check to see what variables have been loaded (using MATLAB's `who` command). Looking at the variable `Chemicalhelp` will also be useful—type `Chemicalhelp` at the MATLAB prompt.

Volume (in litres)	Temperature (in °C)	Weight of Catalyst (in kg)	Method
30	90	1.5	A
39	85	1.0	A
26	70	1.5	B
36	80	2.0	A
22	80	1.0	B
18	85	2.5	B
32	90	1.0	A
26	85	2.0	B

Table 4.1: Toxic Chemical Production Data

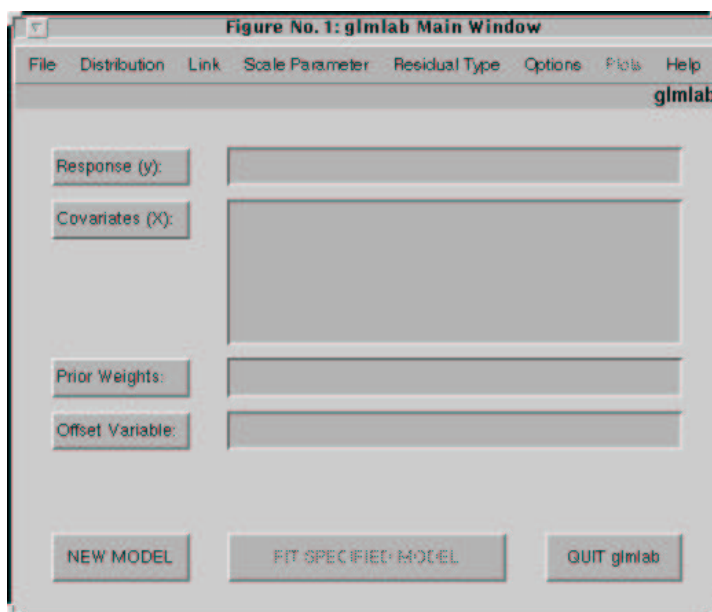


Figure 4.1: The Initial `gmlab` Screen

```
>> Chemicalhelp
Chemicalhelp =
The file chemical contains these variables:
Cat:    The weight of catalyst (in kg)
Method: The method used to produce the chemical (qualitative)
Temp:   The temperature of the manufacturing process
Vol:    The volume of toxic by-product produced.
```

Notice that variable names have been used with the first letter capitalised. This is a precaution against using names reserved by MATLAB or `gmlab`. (For example, `length` is a reserved word in MATLAB used for defining the length of a vector. If `length` was used as a variable name, any MATLAB code that used the function `length` would not work).

When defining variables, use names with capitalised first letters since most MATLAB commands contain all lower case letters.

Remember that `Method` is a *qualitative* (or *categorical*) variable. To represent `Method`, a '1' has been used for Method A and a '2' for Method B.

To begin fitting, start `gmlab`; the initial screen (Figure 4.1) should again appear. If `gmlab` is already running, `gmlab` needs to be told that a new model is to be fitted. To do this, choose `Declare New Model` from the `Options` menu.

If `gmlab` is running and a new model is to be fitted or new data is to be loaded, choose `Declare New Model` from the `Options` menu. This clears all the internal settings and resets the default options.

For demonstration purposes only, one variable at a time will be included in the model. The variables are then typed into their place: The response variable is `Vol` and the first covariate is `Temp`. When these are typed into the appropriate places in the `gmlab` Window, and the `FIT MODEL` button is pressed, the following parameter estimates appears on the screen:

```

-----
      Estimate      S.E.      Variable
-----
      12.000000     36.091550   Constant
       0.200000      0.433023    Temp
-----
Deviance:           334.000000          Link: ID
Residual df:                6   Distribution: NORMAL
Scale parameter (dispersion parameter):    55.666667

```

Variables names are listed in right column labelled `Variable` and the corresponding parameter estimates are given on the left (in the `Estimate` column). The column labelled `S.E.` contains the standard errors for the parameter estimates. The deviance listed under the parameter estimates is a measure of the goodness-of-fit of the model. For normal regression models only, the deviance is equivalent to the residual sum-of-squares. The scale parameter in the case of a normal distribution only is an estimate of the residual variance. The scale parameter is *always* found by dividing the residual deviance by the residual degrees of freedom.

Suppose that another variable is included, say `Cat`. This variable is then added to the covariate list, so that the `gmlmlab` screen will appear as in Figure 4.2. Pressing the `FIT MODEL` button produces the following parameter estimates:

```

-----
      Estimate      S.E.      Variable
-----
      22.404762     37.179998   Constant
       0.172619      0.430573    Temp
      -5.202381      4.980572    Cat
-----
Deviance:           274.172619   (change:   -59.827381)
Residual df:                5   (change:     -1)
Scale parameter (dispersion parameter):    54.834524

```

The deviance is given again, but also the *change* in the deviance. For normal distribution models, this change in the deviance (and corresponding change in the degrees of freedom) can be recorded in a analysis of variance table for testing. The change in deviance is equivalent to a change in the sum-of-squares for a normal distribution model only. The sign of the change in deviance is important: The negative sign implies that the deviance has become smaller than the last fitting (and therefore that the sum of the squared residuals are smaller¹).

The last variable to include is `Method`. This variable is qualitative and not quantitative (like `Vol`, `Temp` and `Cat`). So to indicate to `gmlmlab` that `Method` is qualitative, type `Method` in the covariate list using the `fac` command. The `fac` command indicates to `gmlmlab` that the variable is qualitative rather than quantitative (the `gmlmlab` default). See Figure 4.3.

When using qualitative variables, remember to use the `fac` command.



Pressing `FIT MODEL` again produces these estimates:

¹Some users may recognise this as the GLIM standard.

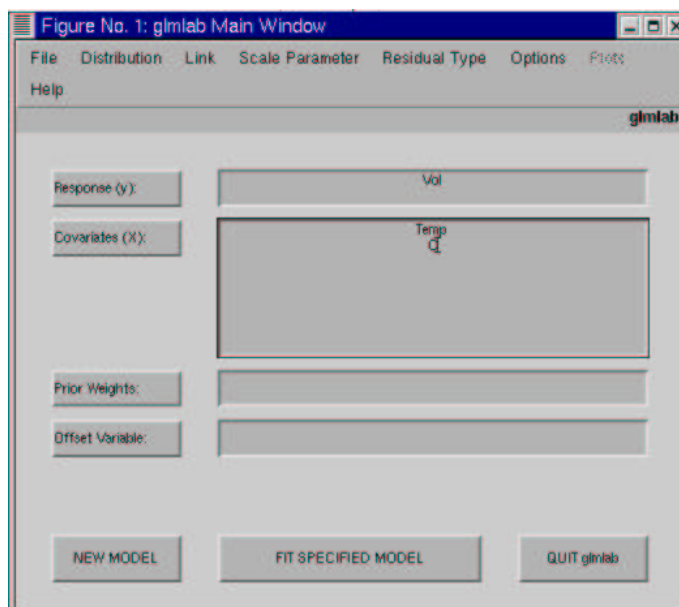


Figure 4.2: Variables Being Entered for Chemical Data

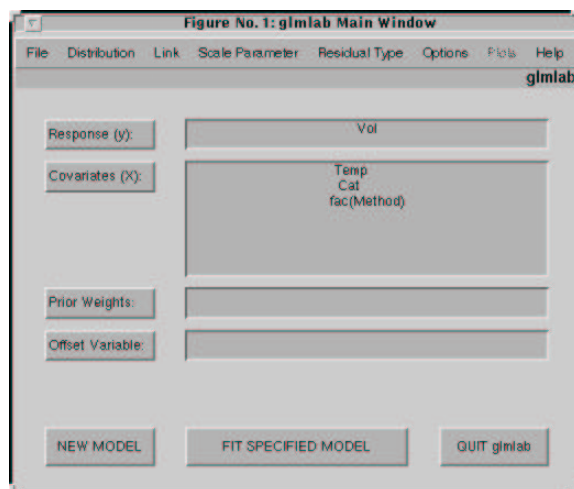


Figure 4.3: Entering Data Using the `fac` Command

```

-----
      Estimate      S.E.      Variable
-----
      66.452830    22.668419    Constant
      -0.354717     0.264890    Temp
      -1.169811     2.814611    Cat
      -13.028302     3.447181    Method(2)
-----
Deviance:                59.981132    (change:   -214.191487)
Residual df:                4    (change:    -1)
Scale parameter (dispersion parameter):    14.995283

```

The output includes a term labelled `Method(2)`. This indicates that the parameter estimate corresponds to the second level of the variable `Method` (that is, Method B). We could therefore write the model as

$$\hat{V} = 66.45 - 0.35T - 1.17C - 13.03M,$$

where

- V = the volume of the toxic chemical produced;
- T = the temperature of the process;
- C = the amount of catalyst used;
- M = 1 if Method B is used (and is 0 otherwise).

All the variables are now fitted. To record all the important information, *glm1ab* produces a file called `DETAILS.m`. (On some Windows machines, the file name may be all lower case.) The file is stored in the `/glm1ab/glmlog` directory. The `DETAILS.m` file for this session should contain information similar to what follows:

```

>> type DETAILS

(Created at 3:06:44pm on 19-Apr-96.)
Deviance      Change    df  Change  Variables
334.000000    -59.827381  5   -1    [Vol];[Const,Temp]
274.172619    -59.827381  5   -1    [Vol];[Const,Temp,Cat]
59.981132    -214.191487  4   -1    [Vol];[Const,Temp,Cat, fac(Method)]

```

Whenever a new model is declared (in the Options menu) or whenever *glm1ab* is started, *glm1ab* determines if the file called `DETAILS.m` is in the appropriate directory. If so, it is *deleted without warning* so that a new `DETAILS.m` file can be created. This file must be copied to another file if the information needs to be kept.

Remember to copy the file `DETAILS.m` to another file if the information is to be kept, as `DETAILS.m` is overwritten whenever a new model is declared and whenever *glm1ab* is started.



Completing the analysis would include looking at some of the residual plots.

	Type of Counselling				
	Stress	Post Abortion Trauma	Relationship Breakdown	Loss of Loved One	Other Types
Male	65	n/a	21	20	39
Female	31	26	49	52	29
Total	96	26	70	72	68

Table 4.2: Counselling Service Data

4.2 Example: Log-Linear Models

Table 4.2 is a contingency table containing (fictitious) data of the patients at a local counselling service over the past year.

Suppose a log-linear model is to be fitted to the data. This problem concerns count data and can therefore be modelled by the Poisson distribution. We first define the variables in the problem:

```
>> Count=[65 31 0 26 21 49 20 52 39 29]';
```

The `makefac` command can be used to define `Gender` and `Type` (see Section 3.4.2). `Count` has been defined to contain the first column of the table, then the second column, then the third, etc. `Gender`, then, should be a variable of length 10 (the same size as `Count`). There are two levels of this variable (“male” and “female”) and they occur one at a time. (That is, according to the ordering of the variable `Count`, `Gender` is listed as “male”, “female”, “male”, “female”... so that each gender is listed as a block of size one.) Therefore, `Gender` can be specified as

```
>> Gender=makefac(10,2,1);
>> Gender'
ans =
     1     2     1     2     1     2     1     2     1     2
```

Similarly, `makefac` can be used for the type of counselling, `Type`.

```
>> Type=makefac(10,5,2);
>> Type'
ans =
     1     1     2     2     3     3     4     4     5     5
```

There is one further problem with the data: That males cannot be exposed to post-abortion trauma. This is called a *structural zero*. To circumvent this problem, define a vector of prior weights that effectively ignores the cell corresponding to male post abortion trauma:

```
>> Priorw=[1 1 0 1 1 1 1 1 1 1]';
```

The prior weights could also have been defined in this manner:

```
>> Priorw=ones(size(Count)); Priorw(3)=0;
```

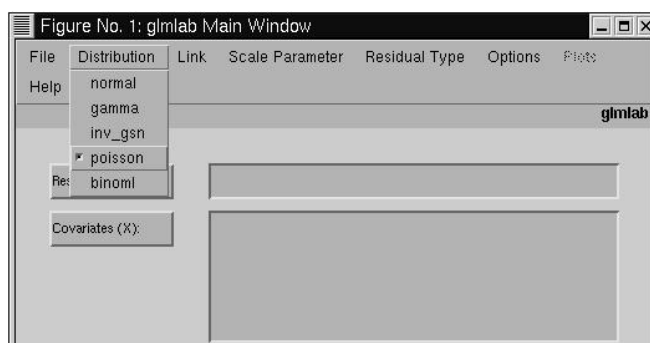


Figure 4.4: Selecting the Poisson Distribution

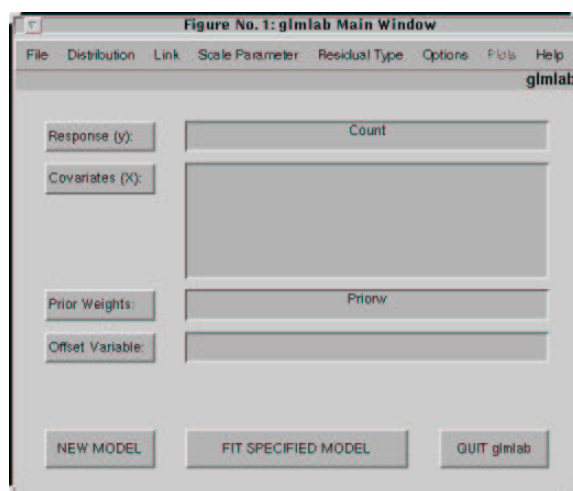


Figure 4.5: Response and Prior Weights Only Entered

Having defined the variables, *glmLab* can be started. As discussed before, if *glmLab* is already running, declare a new model (in the Options menu).

For this problem, the default normal distribution is no longer adequate. To change the distribution, press the Distribution menu item on the main *glmLab* window and choose `poisson`, as shown in Figure 4.4. This will cause the link function and the scale parameter to change (to the Poisson defaults), but no changes will be obvious in the *glmLab* window. Click on the Link menu item and the logarithm link should be selected; this is the default link function for the Poisson distribution.

The variables can now be typed into the main *glmLab* window. First, type the name of the response variable (`Count`) and the prior weights (`Priorw`) as shown in Figure 4.5. After pressing the FIT MODEL button, the following parameter estimates are produced:

```

-----
Estimate      S.E.      Variable
-----
3.607910     0.054882  Constant
-----
Scaled deviance:      50.434008      Link: LOG
Residual df:          8      Distribution: POISSON
Scale parameter (dispersion parameter):      1.000000

```

To add Gender to the covariate list, remember to use the `fac` command (as Gender is qualitative). Add `fac(Gender)` to the covariate list and press FIT MODEL again to produce new estimates:

```

-----
Estimate      S.E.      Variable
-----
3.590439     0.083044  Constant
0.031231     0.110653  Gender(2)
-----
Scaled Deviance:      50.354244      (change:      -0.079764)
Residual df:          7      (change:      -1)
Scale parameter (dispersion parameter):      1.000000

```

Now add the last variable, `Type`, to the covariate list so the list of variables in the Covariate area includes `fac(Gender)` and `fac(Type)`. Remember to use the `fac` command again because `Type` is qualitative. Press the FIT MODEL button to produces new estimates.

```

-----
Estimate      S.E.      Variable
-----
3.817497     0.118512  Constant
0.104671     0.114489  Gender(2)
-0.664071    0.227643  Type(2)
-0.315853    0.157170  Type(3)
-0.287682    0.155902  Type(4)
-0.344840    0.158501  Type(5)
-----
Scaled Deviance:      39.197423      (change:      -11.156820)
Residual df:          3      (change:      -4)
Scale parameter (dispersion parameter):      1.000000

```

The variable `Type` appears *four* times to indicate that there are *five* levels of this qualitative variable (only four variables are needed for a five level factor to maintain full rank). These four variables correspond to levels two, three, four and five of the `Type` variable.

It is common to want to fit interaction terms during modelling. To fit interaction terms, *glm*lab uses the character `@` (usually SHIFT-2 on the keyboard). See Section 3.4.3. In this problem, the interaction between the two qualitative variables `Gender` and `Type` could be included. This can be done in *glm*lab by entering the following string in the covariate section of the main *glm*lab window:

```
fac(Gender), fac(Type), fac(Gender)@fac(Type)
```

Notice that the `fac` command has been used again. Thus, interactions between variables can be specified by separating the variables with the character `@`.

To define the interaction between variables in *glm*lab, use the `@` character between the interacting variables. Remember to still use `fac` for qualitative variables.



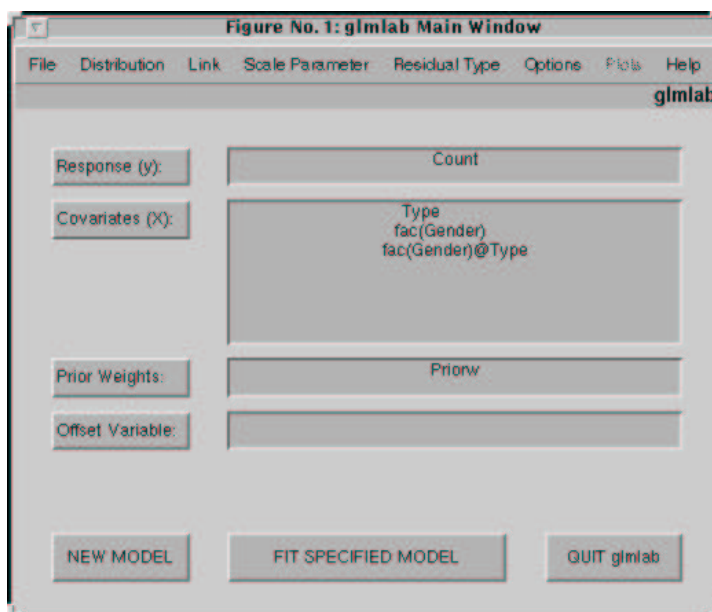


Figure 4.6: Including an Interaction Term

The interaction variable can be included in the *glmLab* Covariates area as shown in Figure 4.6.

Pressing the FIT MODEL button then gives the following parameter estimates:

```

-----
      Estimate      S.E.      Variable
-----
      4.174387      0.124035      Constant
     -0.740400      0.218272      Gender(2)
     -0.175891      0.265932      Type(2)
     -1.129865      0.251005      Type(3)
     -1.178655      0.255704      Type(4)
     -0.510826      0.202548      Type(5)
      0.000000      aliased      Gender(2)@Type(2)
      1.587698      0.340103      Gender(2)@Type(3)
      1.695912      0.341868      Gender(2)@Type(4)
      0.444134      0.328278      Gender(2)@Type(5)
-----
Scaled Deviance:      0.000000      (change:      -39.197423)
Residual df:          0      (change:      -3)
Scale parameter (dispersion parameter):      1.000000

```

Notice that the interaction between *Gender* and *Type* produces four terms in the model. There is no residual deviance or degrees of freedom as there are more parameters than there are observations to estimate. The presence of the term *aliased* indicates that the variable *Gender(2)@Type(2)* contains no new information.

Chapter 5

Advanced Topics and Examples

This section contains some topics more complicated than those previously discussed. Further examples are also given.

5.1 Offsets

Offsets are variables with known parameters. The name of the offset variable is listed in the Main `glmLab` window in the appropriate area. The output on the screen and in the output file `DETAILS.m` indicates the name of the offset variable used.

5.2 Default Settings for Distributions

The error distribution type can be altered in `glmLab` via the Distributions menu item (see Section 4.2). The distributions available are: normal; inverse Gaussian; Poisson; binomial and gamma. Likewise, the type of link function used can be changed in the Link menu. The link functions available are summarised in the Table 5.2. Each distribution has a default link function and scale parameter, as summarised in Table 5.1.

Only when the binomial distribution is chosen are the logit, probit and complementary log-log links available; at all other times, they appear are unavailable and dimmed in the Link menu.

5.3 Changing the Scale Parameter

Two types of scale parameter can be chosen: The mean deviance and a (positive) fixed value. The defaults are given in Table 5.1. When the scale parameter is estimated by the mean deviance, `glmLab` uses $D/(n-r)$ where D is the deviance, n is the number of data points, and r is the number of estimated parameters ($n-r$ is the number of degrees of freedom). The scale parameter can be fixed to any (positive) value; when the *Fixed Value* option is selected, the user is prompted for the value (whose default is 1).

Although the scale parameter is set to 1 by default for the binomial and Poisson distributions, it is not uncommon to use the mean deviance. This commonly occurs if under- or over-dispersion is present.

Error Distribution	Default Link Function	Default Scale Parameter
Normal	Identity $\eta = \mu$	Mean Deviance
Inverse Gaussian	Inverse Quadratic $\eta = 1/\mu^2$	Mean Deviance
Poisson	Logarithm $\eta = \log \mu$	Fixed (at 1)
Binomial	Logit $\eta = \log[\pi/(1 - \pi)]$	Fixed (at 1)
Gamma	Reciprocal $\eta = 1/\mu$	Mean Deviance

Table 5.1: Default Settings for Chosen Distributions
 η is the linear predictor and μ is the mean (π in the binomial case).

Link Function	Form
Identity	$\eta = \mu$
Logarithm	$\eta = \log \mu$
Reciprocal	$\eta = 1/\mu$
Square Root	$\eta = \sqrt{\mu}$
Power	$\eta = \mu^p$ (p non-zero)
Logit	$\eta = \log(\pi/(1 - \pi))$
Complementary log-log	$\eta = \log[-\log(1 - \pi)]$
Probit	$\eta = \Phi^{-1}(\pi)$

Table 5.2: Link Functions in `glmLab`
 η is the linear predictor and μ is the mean. (π in the binomial case).

AG Positive		AG Negative	
White Blood Count (WBC)	Survival Time (in weeks)	White Blood Count (WBC)	Survival Time (in weeks)
2300	65	4400	56
750	156	3000	65
4300	100	4000	17
2600	134	1500	7
6000	16	9000	16
10500	108	5300	22
10000	121	10000	3
17000	4	19000	4
5400	39	27000	2
7000	143	28000	3
9400	56	31000	8
32000	26	26000	4
35000	22	21000	3
100000	1	79000	30
100000	1	100000	4
52000	5	100000	43
100000	65		

Table 5.3: Feigl and Zelen's Leukemia Data

5.4 Example: A Generalised Linear Model

The data in Table 5.3 is taken from Feigl and Zelen [5]. The white blood cell counts for patients who died of acute myelogenous leukemia and their survival times were recorded. They were classified as AG positive or AG negative according to the absence or presence of a certain characteristic of white blood cells.

The data is analysed to determine if survival times can be predicted. The data can be loaded from the file `leuk.mat` in the `data` folder (using the MATLAB `load` command), or the `LOAD Data File` menu item.

```
>> who
```

```
Your variables are:
```

```
Ag      Time      Wbc
```

The variable `Ag` contains 1 if the patient is AG positive, and a 0 if AG negative; `Wbc` is the white blood cell count; `Time` is the survival time. The exponential distribution and reciprocal link function are used (though the original paper uses the identity link function). The exponential distribution is equivalent to the gamma distribution with the scale parameter set to 1. The first step is to alter the error distribution by selecting the `Distribution` menu item in the main `glmLab` window, and choosing the gamma distribution. The scale parameter is then altered by clicking on the `Scale Parameter` menu

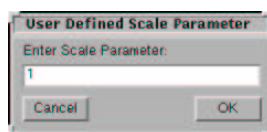


Figure 5.1: Entering a Fixed Value for the Scale Parameter

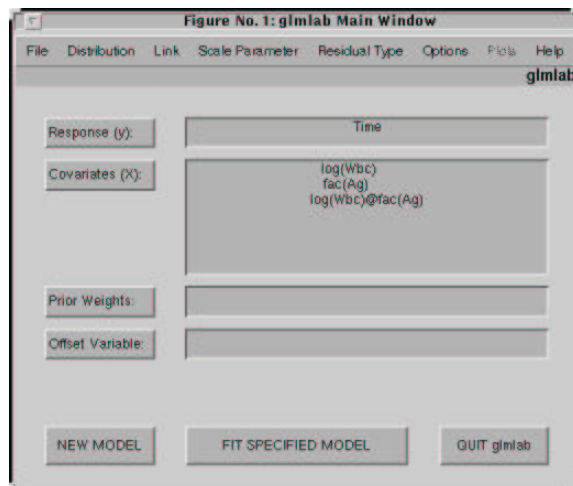


Figure 5.2: Variables Entered for Example 5.4

item in the main `gmlab` window, and selecting Fixed Value. A new window appears; enter in the fixed value of the scale parameter (in this case, 1); see Figure 5.1. This has effectively selected the exponential distribution.

The original paper analyses the logarithm of the white blood cell counts, with the survival time, the AG factor, plus their interaction as covariates. The complete model can be fitted by typing in the variables in the main `gmlab` window as shown in Figure 5.2. Note the use of the `fac` command (because `Ag` is qualitative) and the `@` symbol.

Pressing the FIT MODEL button produces the following estimates:

Estimate	S.E.	Variable
8.478205	1.655453	Constant
-0.481829	0.173635	log(Wbc)
-4.137813	2.570290	Ag(2)
0.328110	0.266888	log(Wbc)@Ag(2)

Scaled Deviance:	38.554607	(change:	+0.000000)
Residual df:	29	(change:	+0)
Scale parameter (dispersion parameter):			1.000000

Dose (\log_{10} CS ₂ mg l ⁻¹)	Number of Beetles (n_i)	Number of Beetles Killed (r_i)
1.6907	59	6
1.7242	60	13
1.7552	62	18
1.7842	56	28
1.8113	63	52
1.8369	59	53
1.8610	62	60
1.8839	60	60

Table 5.4: Beetles Mortality Data

5.5 Example: Binomial Distributions

Because of the special nature of the binomial distribution, an small illustrative example will given. A binomial response variable consists of two columns: the first for the counts, and the second for the sample sizes. Alternatively, the counts can be given as the response data with the sample sizes as prior weights. When the data to be analysed is in the form of probabilities, only one column is needed.

The data comes from Bliss [2] (cited in Dobson [3]) and is shown in Table 5.4. The data involves counting the number of beetles killed after five hours of exposure to various concentration of gaseous carbon disulphide (CS₂). The analysis concerns estimating the proportion r_i/n_i of beetles killed by the gas.

The variables in MATLAB were named `Dose`, `Number` and `Killed` for the obvious variables. Dobson analyses the data using a logit link function. The data is entered into `glm` as shown in Figure 5.3. Note the entry for the response variable, which is entered as two columns. After choosing the binomial distribution and the logit link function from the menus, the results are given below:

```

=== INFO :-| =====
Response Variable:      [Killed,Number]
Covariates:            Dose
- fitting a constant term/intercept
-----
Estimate      S.E.      Variable
-----
-60.717455    5.180701   Constant
 34.270326    2.912134   Dose
-----
Scaled deviance:      11.232231      Link: LOGIT
Residual df:          6      Distribution: BINOML
Scale parameter (dispersion parameter):      1.000000
Output variables:     BETA SERRORS FITS RESIDS COVB COVD
                     DEVLIST LINPRED XMATRIX XVARNames

```

The results agree with those given in Dobson. An alternative method is to fit the model using the probabilities r_i/n_i as the response (that is, one column of probabilities), and use n_i as the prior weights. The parameter estimates are identical. The residual plotted against the fitted values shows a possible curvature. However, using the complementary log-log link function improves the fit greatly. Use this link and see the improvement yourself.



Figure 5.3: Variables Entered for the Beetle Mortality Example

5.6 User Defined Links and Distributions

glmLab allows the user to define link functions and error distributions that are not included with glmLab. This is a more difficult section, and requires some knowledge of vectorised programming in MATLAB. The files `dstyle` and `lstyle` give a template for the files to edit, and the files `dlist.m` and `llist.m` contain the list of files containing information about the distributions and the links respectively. To demonstrate how to include user-defined distributions in glmLab, see Example 5.7 (the next section).

5.7 Example: User Defined Distributions

Nelder and Pregibon [8] and McCullagh and Nelder [7, Chapter 9] discuss quasi-likelihood, where the complete error distribution need not be specified; all that is required is information about the first two moments (the mean and the variance). As an example, consider including a new distribution specified by the variance function

$$V(\mu) = \mu^4. \quad (5.1)$$

This variance function defines one of the Tweedie family of distributions (defined in Tweedie [10]), sometimes called a positive stable distribution.

To incorporate such a distribution in glmLab, proceed as follows:

1. The first step is to create a file that contains the pertinent information. Suppose that the file for the given variance function is called `dfourpwr.m`. (The `d` at the start of the file name is mandatory for defining new distributions; in a similar fashion, new link functions must be created in files that begin with an `l`.) The first step then is to create this file in the `dist` subdirectory of the `fit` directory (or the `link` subdirectory if a new link is being defined). The best way is to copy the file `dstyle.m` to `dfourpwr.m`. The file `dstyle.m` contains the template style for making new distributions (`lstyle.m` for new link functions).

- The second step is to edit the file named `dfourpwr.m` using any text editor. Near the end of the file is a section with the following information:

```
%Calculate
if strcmp(what,'varfn'),
    %%In here, you need lines to find the variance function
    %%from mu and y.
    %%The section should return the variance function as answ
elseif strcmp(what,'sdev');
    %%In here, you need lines to find the scaled deviance
    %%from mu and y.
    %%The section should return the scaled deviance as answ
end;
```

It should be clear that there are two sections to alter: One section requires information about the variance function, and the other about the deviance. For the variance function given in Equation (5.1), the MATLAB equivalent code is

```
answ = mu .^ 4;
```

This line should be entered into the section requiring information about the variance function. The deviance can be found from the integral

$$D(y,\mu) = -2 \int_y^\mu \frac{y-u}{V(u)} du,$$

which, for the given variance function, is

$$D = \frac{1}{6y^2} + \frac{y}{3\mu^3} - \frac{1}{2\mu^2}.$$

The equivalent MATLAB code is

```
answ=1/(6*y^2) + ( y./(3*mu.^3) ) - ( 1/(2*mu.^2) );
```

This line of code is placed in the section requiring the deviance. Now `glmLab` has the information that it requires; it now needs to know to use the file `dfourpwr.m`.

- In the `dist` directory, there is a file called `dlist.m` which lists all the files that contain information about distributions. (There is a corresponding file `llist.m` for the link functions.) Add a new line to the *end* of this file that says only


```
dfourpwr.m
```
- All the required tasks have been completed. Next time `glmLab` is started, there should be a distribution named `fourpwr` at the bottom of list of distributions.

A similar procedure is used for defining new link functions, but the corresponding files in the `link` subdirectory of the `fit` directory are used. Adding new distribution or link functions is not recommended unless the user knows the use of the distribution or link function, as odd results may eventuate otherwise.

5.8 The Default Data Directory

As discussed in sections 4.1 and 5.4, data can be loaded with the graphical interface by selecting LOAD Data File under the file menu. The default data directory is initially `glmLab/data`. This can,

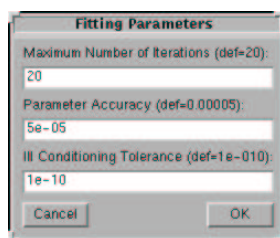


Figure 5.4: The Fitting Parameters Window

however, be easily changed. In the `glmLab/data` directory, there is a file named `dummydata.m` which contains basically nothing; the sole purpose of the file is to define the default data directory. To have a different default directory, simply move this file into the appropriate directory. Next time the graphical load data window appears, the default directory will be the directory where this file is located.

5.9 `npplot`

This function can be used to produce a normal probability plot (which is useful for checking the normality of the data). It is called by the `glmLab` plotting window, but can also be used outside of `glmLab`. The general form of the command is

```
npplot(y,s);
```

where `y` is the data and `s` is 0 to include a dotted line corresponding to the standard normal distribution, and is 1 too include a dotted line corresponding to a normal distribution with the same mean and variance as the given data, `y`.

The Statistics Toolbox of MATLAB has its own function for plotting a normal probability plot.

5.10 Changing the Fitting Parameters

There are three parameters in `glmLab` that are used when fitting models: the maximum number of iterations to use; the accuracy (tolerance) of the parameters; and the ill-conditioning tolerance which, in simple terms, refers to the sensitivity of `glmLab` to $X^T X$ being singular, where X is the covariate matrix. All of these can be changed from the Options menu by selecting Change Fitting Parameters. To change the parameters, the new values are entered into the input window shown in Figure 5.4. The default settings are: maximum number of iterations: 20; Parameter tolerance: 0.00001; ill-conditioning tolerance: 1e-10. The values of the parameters are stored in the file `PARVALS.mat` in the same directory as the file `DETAILS.m`.

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Index

Entries in typewriter font refer to MATLAB or glm-lab commands.

Symbols

@ *see* interaction
' *see* transpose
. *see* line continuation
. *see* period
: *see* colon
; *see* semicolon
^ *see* caret
* *see* asterisk
% *see* comments

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