INTRODUCTION TO STATISTICAL MODELLING IN R

P.M.E.Altham, Statistical Laboratory, University of Cambridge.

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p.m.e.altham@statslab.cam.ac.uk

R is available as Free Software under the terms of the Free Software Foundation's GNU General Public License in source code form.
R is powerful and highly developed (and very similar in syntax to S-Plus).
The originators of R are R.Gentleman and R.Ihaca from New Zealand, and the R home page is at

`http://www.stat.auckland.ac.nz/rproj.html`

R runs on PC and UNIX systems and can be retrieved via anonymous ftp. If you want to get hold of R for yourself, go to

`http://www.ci.tuwien.ac.at/~hornik/R`

or use the link on my homepage.
Acknowledgements
Special thanks must go to Professor Jim Lindsey for launching me into R, to Dr R.J.Gibbens for his help in introducing me to S-plus, and also to Professor B.D.Ripley for access to his S-plus lecture notes. Several generations of keen and critical students for the Cambridge University Diploma in Mathematical Statistics (a 1-year graduate course, which from October 1998 was replaced by the MPhil in Statistical Science) have made helpful suggestions which have improved these worksheets. Readers are warmly encouraged to tell me of any further corrections or suggestions for improvements.
These worksheets may be used for any educational purpose provided their authorship (P.M.E.Altham) is acknowledged.
Note that throughout these notes, which were constructed for Part IIC of the Mathematical Tripos in Lent 2005, we will be using R as a free, 'look-alike' version of S-plus. You may find references to 'S-plus', which you can usually take to be references to 'R'.
There are subtle and important differences between the languages R and S-plus; these differences will not be explained in the following notes, except where they are strictly relevant to our worksheets.

`http://www.stats.ox.ac.uk/pub/R`

gives a careful description of the differences between R and S-Plus, in 'R' Complements to the text-book Modern Applied Statistics with S-plus, by W.N.Venables and B.D.Ripley, pub Springer.

`http://www.statslab.cam.ac.uk/~pat/notes.ps`

gives you the corresponding lecture notes for this course, with a fuller version of these notes at

`http://www.statslab.cam.ac.uk/~pat/All.ps`

My R/Splus worksheets for multivariate statistics, and other examples, may be seen at

`http://www.statslab.cam.ac.uk/~pat/misc.ps`

A word of reassurance about the Tripos questions for this course: I would not expect you to be able to remember a lot of R commands and R syntax. But I do think it's important that you are able to interpret R output for linear models and glm's, and that you can show that you understand the underlying theory. Of course you may find it convenient to use R for your Computational Projects.
Since I retired at the end of September 2005, I have added extra datasets (and graphs) from time to time, as you will see in the Table of Contents.

Table of Contents

1. Ways of reading in data, tables, text, matrices. Linear regression and basic plotting.
The datasets include welding, student funding, annual increases in CO_2, and EU receipts (etc) from the Common Agricultural Policy, for the 25 member states.
2. A fun example showing the use of 'identify()'
3. A oneway analysis of variance, and qqnorm plot of residuals. (potash data)
4. A twoway analysis of variance, setting up factor levels, and boxplots (occupations and countries data).
5. A 2-way layout with missing values (bookprices data).
6. Logistic regression for binomial data (alloyfasteners data).
Various 'links', comparison of normal and logistic curves.
7. The space shuttle temperature data: a cautionary tale.
8a. Binomial and Poisson regression. (The Missing Persons data).
New for 2008, Survival of extremely premature babies.
New for 2009, Scores for the UK team in the 2007 International Mathematical Olympiad.
8b. Simple 2-way contingency tables, use of chisq.test(). New data on the Sheffield flood of 1864.
9. The Poisson 'error' function; Poisson regression. (Aids data, and ministerial resignations).
New for August 2008: predicting the Total medals for Team GB at the Beijing Olympics.
An extra added in March 2008: Fitting a non-linear quasi-Poisson model to actuarial data. This uses Firth and Turner's gnm() package to fit the Lee-Carter model.
10. Contingency tables, 'Simpson's paradox'.
11. Plotting the contours of a log-likelihood: how to define a function.(for enthusiasts only)
12. A cleverly constructed data-set, due to the late Frank Anscombe.
THE REMAINING WORKSHEETS ARE DESIGNED AS INTERESTING OPTIONAL EXTRAS.
13. New for 2002: football arrests data, the Poisson and the negative binomial.
Similar data for 2002-3.
14. New for 2005: Prof Pippa Norris's data on UK elections turnout and Poll-Leads, from 1945 to 2001.
15. New for 2005: glm() and the gamma distribution.
16. Supplementary worksheet: CRIME, UNEMPLOYMENT and a case-control study.
17. Supplementary worksheet: maximising a multi-parameter log-likelihood, an example (from genetics) on a square contingency table.
18. New for 2006:
(i) cannabis and psychosis data
(ii) the Harry Potter effect?
(iii) life is a risky business if you are in a TV soap opera.
19. The results of the 2006 Corus Chess tournament (14 players), and the same paired comparison model applied to the World Cup Football tournament 2006, Group B results.

New for 2008, paired comparison results for Group A results.
20. New for 2007: what is the median lifetime of a President of the Royal Statistical Society?

References
For R/S-plus material
Maindonald, J. and Braun, J. (2007) Data Analysis and Graphics using R - an Example-Based Approach. Cambridge University Press.
Venables, W.N. and Ripley, B.D.(2002) Modern Applied Statistics with S-plus. New York: Springer-Verlag.
For statistics text books
Agresti, A.(2002) Categorical Data Analysis. New York: Wiley.
Collett, D.(1991) Modelling Binary Data. London: Chapman and Hall.
Dobson, A.J.(1990) An introduction to Generalized Linear Models. London: Chapman and Hall.
Pawitan, Y. (2001) In all likelihood: statistical modelling and inference using likelihood. Oxford Science Publications. (see also

```
http://www.meb.ki.se/~yudpaw
```

for a really helpful suite of R programs and datasets related to his book.)
The main purpose of the small index is to give a page reference for the *first* occurrence of each of the R commands used in the worksheets. Of course, this is only a small fraction of the total of R commands available, but it is hoped that these worksheets can be used to get you started in R.
Note that R has an excellent help system : try, for example

```
?lm
```

You can always inspect the CONTENTS of a given function by, eg

```
lm
```

A problem with the help system for inexperienced users is the sheer volume of information it gives you, in answer to what appears to be a quite modest request, eg

```
?scan
```

But you quickly get used to skimming through and/or ignoring much of what 'help' is telling you.
At the present time the help system still does not QUITE make the university teacher redundant, largely because (apart from the obvious drawbacks such as lacking the personal touch of the university teacher) the help system LOVES words, to the general exclusion of mathematical formulae and diagrams. But the day will presumably come when the help system becomes a bit more friendly. Thank goodness it does not yet replace a good statistical textbook, although it contains a wealth of scholarly information.

Many many useful features of S-plus/R may NOT been prominently illustrated in the worksheets that follow. The keen user of lm() and glm() in particular should be aware of the following
i) use of 'subset' for regression on a subset of the data, possibly defined by a logical variable (eg sex=="male")
ii) use of 'update' as a quick way of modifying a regression
iii) 'predict' for predicting for (new) data from a fitted model
iv) poly(x,2) (for example) for setting up orthogonal polynomials
v) summary(glm.example,correlation=T)
which is useful if we want to display the parameter estimates and se's, and also their correlation matrix.
vi)summary(glm.example,dispersion=0)
which is useful for a glm model (eg Poisson or Binomial) where we want to ESTIMATE the scale parameter ϕ, rather than force it to be 1. (Hence this is useful for data exhibiting overdispersion.)

Here is a tiny example of using R as a calculator to check Stirling's formula, which as you will know is

$$n! \sim \sqrt{2\pi} n^{n+1/2} \exp -n \ .$$

We take logs, and use the lgamma function in R.

```
n <- 1:100 ; y <- lgamma(n+1)
x <- (1/2) * log(2 * pi) + (n+ .5)* log(n) - n
plot(x,y)
q()
```

For the record, here are 2 little examples of loops in R.

```
 x <- .3 #  starting value
> for (i in 1:4){
+ x <- x+1
+ cat("iteration = ", i,"x=",x,"\n")
+ }
x <- .4 #starting value
 while (x^2 <90)
{
+ cat("x=",x,"\n")
+ x <- x+.9
+ }
```

But, one of the beauties of R/S-Plus is that you very rarely need to write explicit loops, as shown above. Because most straightforward statistical calculations can be *vectorised*, we can just use a built-in function instead of a loop, eg

```
sum(a*x)
```

for $\Sigma a_i x_i$ as you will see in the worksheets that follow.
Note: R/S-plus is case-sensitive.
Note: to abandon any command, press 'Control C' simultaneously.

Worksheet 1.

R and S-plus have very sophisticated reading-in methods and graphical output.
Here we simply read in some data, and follow this with linear regression and quadratic regression, demonstrating various special features of R as we go.
Note: S-Plus, and old versions of R, allowed the symbol $<-$ to be replaced by the underscore sign _ in all the commands. Note that $<-$ should be read as an arrow pointing from right to left; similarly $->$ is understood by R as an arrow pointing from left to right.
R and S-plus differ from other statistical languages in being 'OBJECT-ORIENTED'. This takes a bit of getting used to, but there are advantages in being Object-Oriented.

Catam users:

```
mkdir practice
cd practice
dir
copy X:\catam\stats\bigdata bigdata
copy bigdata weld
```

This will make the directory 'practice' and put in it the data-file 'bigdata', which you then copy to 'weld'.
Now use notepad to edit 'weld' to be exactly the numbers needed for the first worksheet. (Feel free to do this operation by another means, if you want to.)
To start R:
Open a Command Prompt window from the start button.
type

```
X:\catam\r
```

Statslab users:
just type

```
R
```

warning: the Catam version of R is not necessarily exactly the same as the the Statslab version.
Note that in the sequences of R commands that follow, anything following a # is a comment only, so need not be typed by you.
Note also that within most implementations of R you can use the ARROW KEYS to retrieve, and perhaps edit, your previous commands.

```
# reading data from the keyboard
x <- c(7.82,8.00,7.95) #"c" means "combine"
x
# a slightly quicker way is to use scan( try help(scan))
x <- scan()
```

```
7.82 8.00 7.95
                      # NB blank line shows end of data
x
# To read a character vector
x <- scan(,"")
 A B C
 A C B

x
demo(graphics)        # for fun
```

But mostly, for proper data analysis, we'll need to read data from a separate data file. Here are 3 methods, all doing things a bit differently from one another.

```
# scan() is the simplest reading-in function
data1 <- scan("weld", list(x=0,y=0))
data1 # an object, with components data1$x, data1$y
names(data1)
x<- data1$x ; y <- data1$y
# these data came from The Welding Institute, Abington, near Cambridge
x;y # x=current(in amps) for weld,y= min.diam.of resulting weld
summary(x)
# catam Windows automatically sets up the R graphics window for you
# but if you lose it, just type windows()
hist(x)
X <- matrix(scan("weld"),ncol=2,byrow=T) # T means "true"
X
```

Here is the nicest way to read a table of data.

```
weldtable <- read.table("weld",header=F) # F means "false"
weldtable
x <- weldtable[,1] ; y <- weldtable[,2]
```

For the present we make use only of x, y and do the linear regression of y on x, followed by that of y on x and x^2.

```
plot(x,y)
teeny <- lm(y~x) # the choice of name 'teeny' is mine!
```

This fits $y_i = \alpha + \beta x_i + \epsilon_i,\ 1 \leq i \leq n$, with the usual assumption that $\epsilon_i,\ 1 \leq i \leq n$ is assumed to be a random sample from $N(0, \sigma^2)$.

```
teeny     # This is an "object" in R terminology.
summary(teeny)
anova(teeny)
names(teeny)
fv1 <- teeny$fitted.values
fv1
par(mfrow=c(2,1)) # to have the plots in 2 rows, 1 column
```

```
plot(x,fv1)
plot(x,y)
abline(teeny)
par(mfrow=c(1,1)) # to restore to 1 plot per screen
Y <- cbind(y,fv1) # "cbind"is "columnbind"
# Y is now a matrix with 2 columns
matplot(x,Y,type="pl") # "matplot" is matrix-plot
res <- teeny$residuals
plot(x,res)
```

The plot shows a marked quadratic trend. So now we fit a quadratic, ie we fit $y_i = \alpha + \beta x_i + \gamma {x_i}^2 + \epsilon_i,\ 1 \leq i \leq n$

```
xx<- x*x
teeny2 <- lm(y~x +xx ) # there's bound to be a slicker way to do this
summary(teeny2)
```

This shows us that the quadratic term is indeed significant.
We may want more information, so the next step is

```
summary(teeny2, cor=T)
```

This gives us the correlation matrix of the parameter estimates.

```
vcov(teeny2) # for comparison, the corresponding covariance matrix.
fv2 <- teeny2$fitted.values
plot(x,y)
lines(x,fv2,lty=2) # adds 'lines' to the current plot
```

Now let us work out the 'confidence' interval for y at a new value of x, say $x = 9$ thus $x^2 = 81$. We will also find the corresponding 'prediction' interval. Why are they different? What happens to the width of the prediction interval if you replace $x = 9$ by a value of x further from the original data set, say $x = 20, x^2 = 400$? (and why is this rather a silly thing to do?)

```
 newdata <- data.frame(x=9, xx=81)
 predict.lm(teeny2, newdata, interval="confidence")
       fit      lwr      upr
1 5.582471 5.468468 5.696474
 predict.lm(teeny2, newdata, interval="prediction")
       fit      lwr     upr
1 5.582471 5.218793 5.94615

q()                    # to quit: say "yes" to ``save workspace image?"
```

The corresponding graph is shown as Figure 1. You have now come out of your R session. Try

```
type .Rhistory
```

to see the sequence of R commands that you used.
You have also generated the file

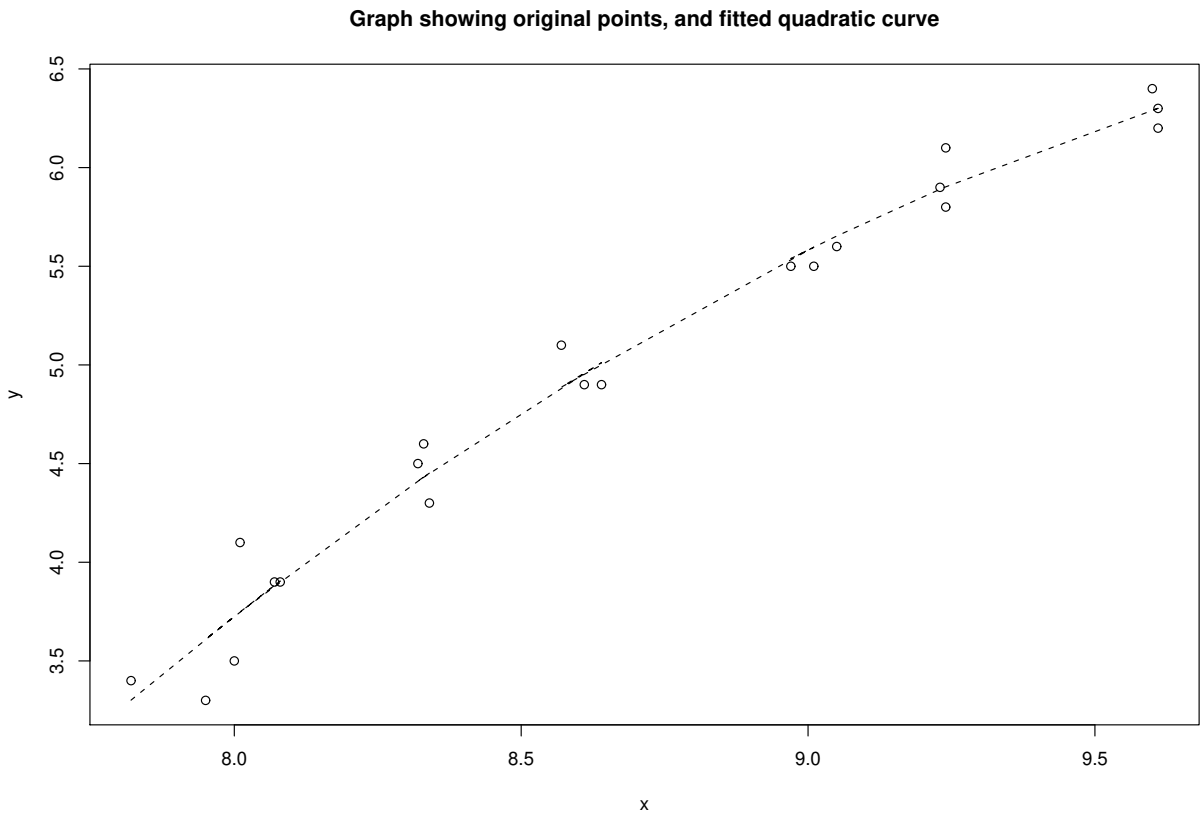

Figure 1: The fitted quadratic, and the original points, for the 'weld' data

`.Rdata`

Next time you go into R, you see what objects are in your current workspace, by

`ls()`

Here is the data-set "weld", with x, y as first, second column respectively.

```
7.82 3.4
8.00 3.5
7.95 3.3
8.07 3.9
8.08 3.9
8.01 4.1
8.33 4.6
8.34 4.3
8.32 4.5
8.64 4.9
8.61 4.9
8.57 5.1
9.01 5.5
8.97 5.5
9.05 5.6
```

```
9.23 5.9
9.24 5.8
9.24 6.1
9.61 6.3
9.60 6.4
9.61 6.2
```

Remember to END your R data-set with a BLANK line.
There is a substantial library of data-sets available on R, including the 'cherry-trees' data-set (see Examples sheet 2) and the 'Anscombe quartet' (see worksheet 13). Try

```
data()
```

And, lastly, how about the following datasets as examples for linear regression.
The Independent, November 28, 2003 gives the following data on UK Student funding, at 2001-2 prices (in pounds), under the headline **'Amid the furore, one thing is agreed: university funding is in a severe crisis'**.

```
        Funding per student  Students (000's)
1989-90    7916               567
1990-91    7209               622
1991-2     6850               695
1992-3     6340               786
1993-4     5992               876
1994-5     5829               944
1995-6     5570               989
1996-7     5204              1007
1997-8     5049              1019
1998-9     5050              1023
1999-00    5039              1041
2000-01    4984              1064
2001-02    5017              1087
2002-03*   5022              1101
* = provisional figures
```

Sometimes you may want to plot one variable (here Funding per student) against another (here year, from 1989 to 2002) with point size proportional to a third variable, here Students. An example is shown in Figure 2. It is achieved by

```
year <- 1989:2002
size <- Students/600 # some trial & error here, to see what works well
plot(Funding~ year, cex=size)
```

The Independent, October 11, 2004 gives the following CO_2 record (data collected by Dr Charles Keeling at Mauna Loa, an 11000 ft extinct volcano on the Big Island of Hawaii).

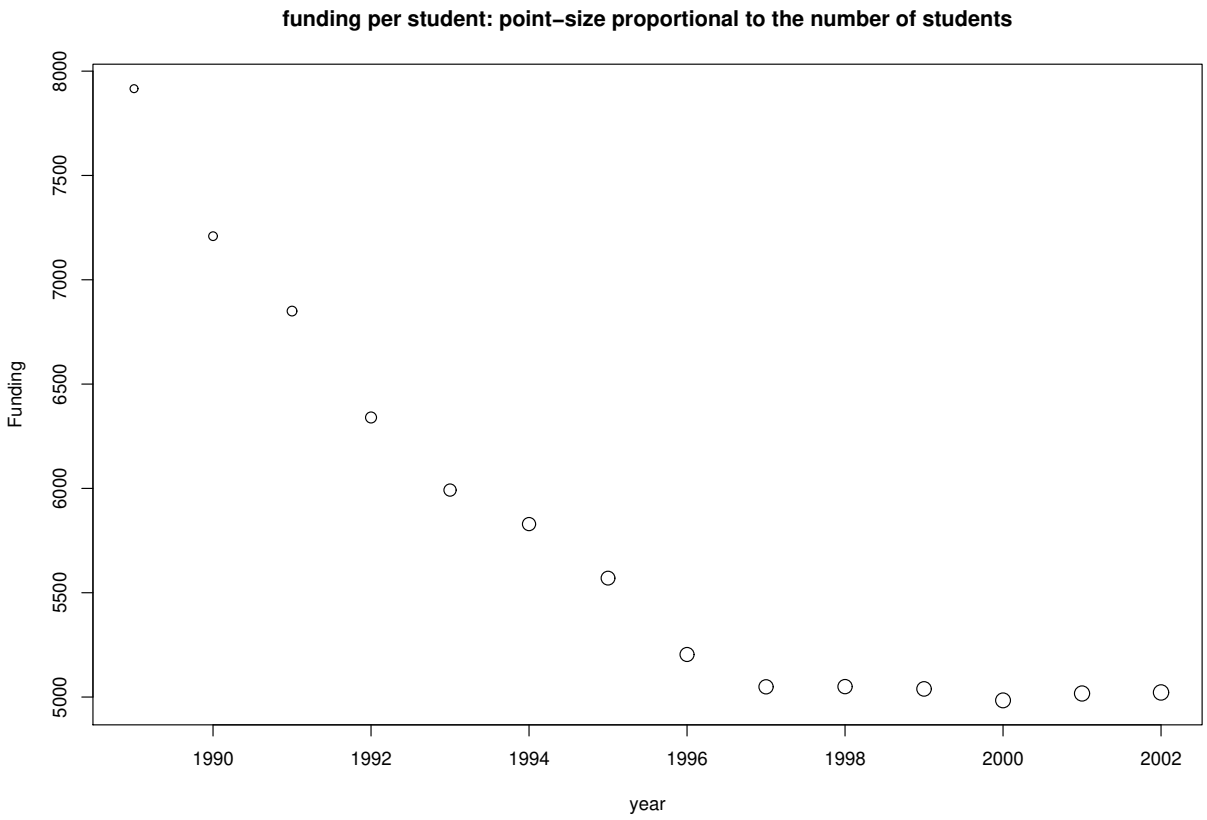

Figure 2: How funding per student has declined over time.

```
Year Level (in ppm, ie parts per million by volume)
 1958 315
 1959 315.98
 1960 316.91
 1961 317.65
 1962 318.45
 1963 318.99
 1964  NA
 1965 320.03
 1966 321.37
 1967 322.18
 1968 323.05
 1969 324.62
 1970 325.68
 1971 326.32
 1972 327.46
 1973 329.68
 1974 330.25
 1975 331.15
 1976 332.15
 1977 333.9
```

```
1978 335.5
1979 336.85
1980 338.69
1981 339.93
1982 341.13
1983 342.78
1984 344.42
1985 345.9
1986 347.15
1987 348.93
1988 351.48
1989 352.91
1990 354.19
1991 355.59
1992 356.37
1993 357.04
1994 358.88
1995 360.88
1996 362.64
1997 363.76
1998 366.63
1999 368.31
2000 369.48
2001 371.02
2002 373.1
2003 375.64
```

'as the graph shows, all of these (sharp peaks)-except the final one- can be explained by the fact that they occurred in the same year as El Nino... The sinister aspect of the most recent peak is that it does not coincide with an El Nino.....'. For a graph of the increase, see Figure 3.

The Independent, July 4, 2008 has the following headline
'Inflation worries prompt ECB to hike rates' (the ECB is the European Central Bank). This is accompanied by a graph showing the GDP annual growth, as a percentage, together with Inflation, also as a percentage, for each of 15 'European single currency member states'. These are given in the Table below.

```
          GDPgrowth Inflation
Ireland     3.8       3.3
UK          2.3       3.0
Bel         2.1       4.1
Neth        3.4       1.7
Lux         3.4       4.3
Ger         2.6       2.6
Slovenia    4.6       6.2
Austria     2.9       3.4
Portugal    2.0       2.5
```

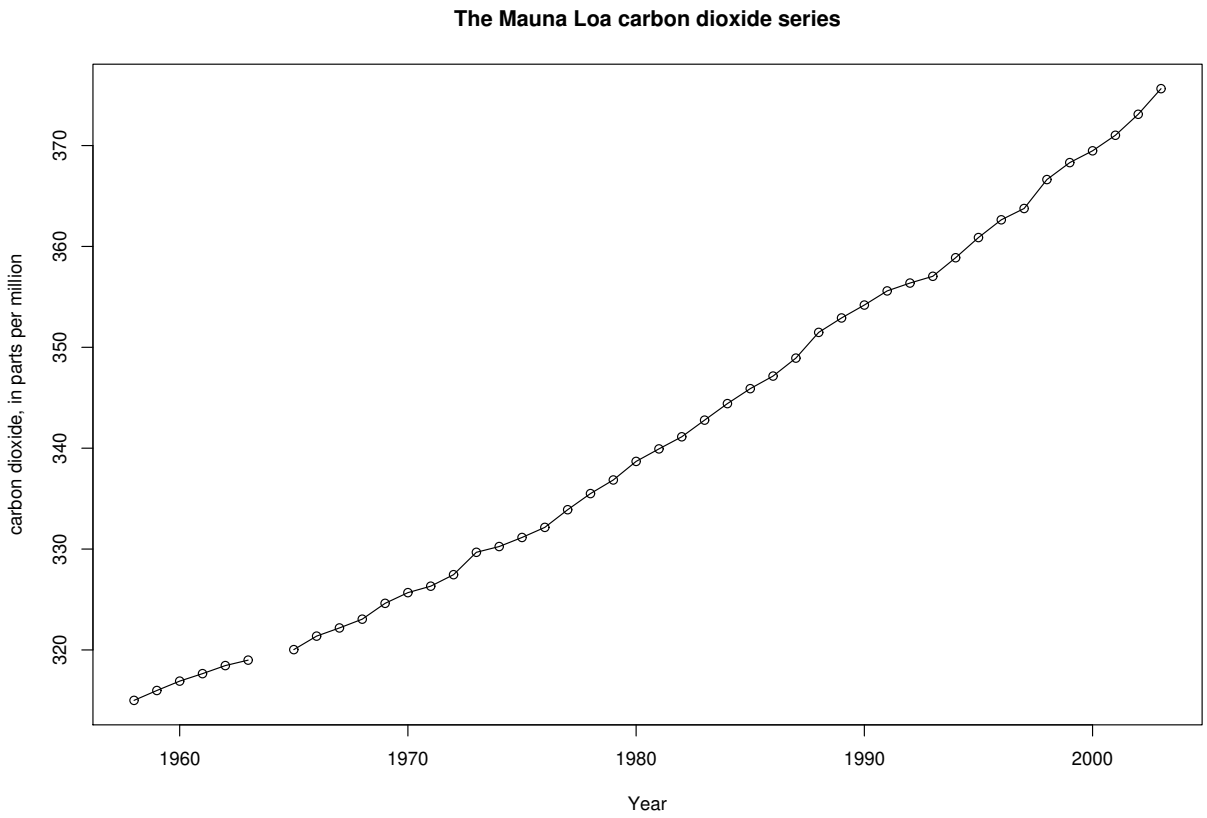

Figure 3: Global warming? The Mauna Loa carbon dioxide series

```
Spain     2.7    4.2
France    2.2    3.4
Malta     3.7    4.1
Italy     0.2    3.6
Greece    3.6    4.4
Cyprus    4.3    4.3
```

Note: the GDPgrowth figures are for the annual growth to the end of the first quarter of 2008, except for Ireland, Luxembourg, Slovenia, Portugal, Malta and Cyprus, in which case they are for the annual growth to the end of the fourth quarter of 2007. The inflation figures are for April 2008. Here is a suggestion for plotting a graph, shown here as Figure 4.

```
ED <- read.table("Europes.dilemma.data", header=T) ; attach(ED)
country = row.names(ED)
attach(ED)
 plot(GDPgrowth, Inflation, type="n")
 text(GDPgrowth, Inflation,country)
 points(GDPgrowth, Inflation, cex = 4, pch = 5)
# cex controls the SIZE of the plotting character
# pch determines the CHOICE of the plotting character, here diamonds
```

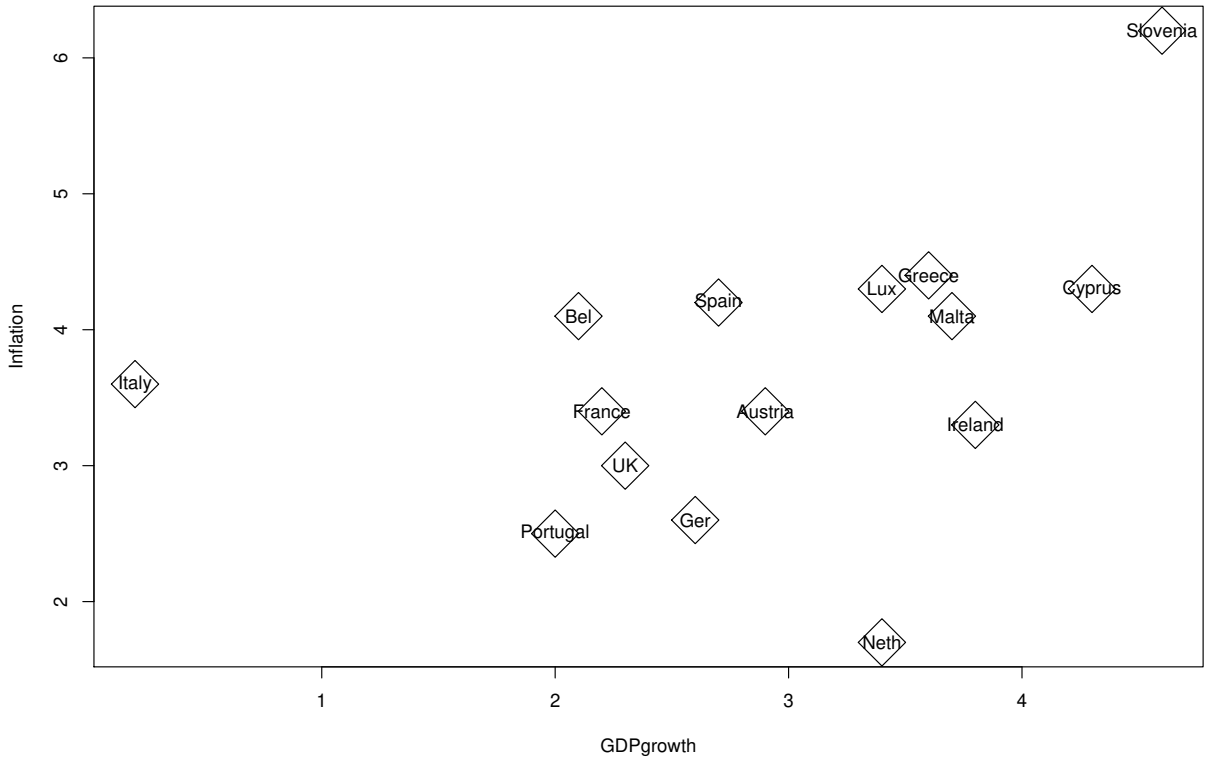

Figure 4: Annual Inflation against Annual GDP growth for 15 Eurozone countries, July 2008

The Independent, June 13, 2005, says 'So who really pays and who really benefits? A guide through the war of words over the EU rebate and the Common Agricultural Policy' and
'The annual income of a European dairy cow exceeds that of half the world's human population' to quote Andreas Whittam Smith.
The EU member countries are
Luxembourg, Belgium, Denmark, Netherlands, Ireland, Sweden, Finland, France, Austria, Germany, Italy, Spain, UK, Greece, Portugal, Cyprus, Slovenia, Malta, Czech Republic, Hungary, Estonia, Slovakia, Lithuania, Poland, Latvia.
In the same order of countries, we have
the per capita contribution to the EU, in $£$
466 362 358 314 301 289 273 266 256 249 228 187 186 154 128 110 88 83 54 54 45 41 35 32 28
and, the total contribution, in $£m$
218 3734 1933 5120 1205 2604 1420 15941 2098 20477 13208 8077 11133 1689 1326 84 176 33 554 548 58 223 125 1239 64
and, 'how the UK's rebate is paid, in $£m$
20 259 177 56 108 34 135 1478 27 302 1224 719 -5097 151 121 7 16 3 50 47 5 20 11 116 6

and, Receipts from Common Agricultural Policy, in $£m$
29 686 818 934 1314 580 586 6996 754 3930 3606 4336 2612 1847 572 NA NA NA NA NA NA NA NA NA NA
It's easiest to read the data set via read.table() from the table below

	per_cap_cont	total_cont	howUKrebate_pd	Rec_from_CAP
Luxembourg	466	218	20	29
Belgium	362	3734	259	686
Denmark	358	1933	177	818
Netherlands	314	5120	56	934
Ireland	301	1205	108	1314
Sweden	289	2604	34	580
Finland	273	1420	135	586
France	266	15941	1478	6996
Austria	256	2098	27	754
Germany	249	20477	302	3930
Italy	228	13208	1224	3606
Spain	187	8077	719	4336
UK	186	11133	-5097	2612
Greece	154	1689	151	1847
Portugal	128	1326	121	57
Cyprus	110	84	7	NA
Slovenia	88	176	16	NA
Malta	83	33	3	NA
Czech_Republic	54	554	50	NA
Hungary	54	548	47	NA
Estonia	45	58	5	NA
Slovakia	41	223	20	NA
Lithuania	35	125	11	NA
Poland	32	1239	116	NA
Latvia	28	64	6	NA

Worksheet 2.
A Fun example using data from Venables and Ripley showing you some plotting and regression facilities.
This includes some 'diagnostic plots' to check whether the residuals could have come from an $N(0, \sigma^2)$ distribution: the theory behind these 'qqplots' will be explained later in the course.
NB: we use a 'built-in' dataset from the Venables and Ripley library(MASS).

```
library(MASS)
data(mammals)
attach(mammals) # to 'attach' the column headings
species <- row.names(mammals) ; species
x <- body ; y <- brain
plot(x,y)
identify(x,y,species) # find man, & the Asian elephant
                      # click middle button to quit
plot(log(x),log(y))
identify(log(x),log(y),species) # again, click middle button to quit
species.lm <- lm(y~x)  # linear regression, y "on" x
summary(species.lm)
par(mfrow=c(2,2))     # set up 2 columns & 2 rows for plots
plot(x,y) ; abline(species.lm) # plot line on scatter plot
r <- species.lm$residuals
f <- species.lm$fitted.values # to save typing
qqnorm(r) ; qqline(r)
```

This is an eyeball check on whether the residuals are $NID(0, \sigma^2)$: they pretty obviously are NOT: can you see why?

```
lx<- log(x) ; ly <- log(y)
species.llm <- lm(ly~lx) ; summary(species.llm)
plot(lx,ly) ; abline(species.llm)
rl <- species.llm$residuals ;fl <- species.llm$fitted.values
qqnorm(rl) ; qqline(rl)  # a better straight line plot
plot(f,r)  ; hist(r)
plot(fl,rl); hist(rl)    # further diagnostic checks
 # Which of the 2 regressions do you think is appropriate ?
mam.mat <- cbind(x,y,lx,ly)    # columnbind to form matrix
cor(mam.mat)                   # correlation matrix
round(cor(mam.mat),3)          # easier to read
par(mfrow=c(1,1))              # back to 1 graph per plot
pairs(mam.mat)
```

Suppose we want a hard copy of this final graph. Here's how to proceed.

```
postscript("file.ps", height=4)
```

This will send the graph to the postscript file called 'file.ps'. It will contain the PostScript code for a figure 4 inches high, perhaps for inclusion by you in a later document. Warning: if 'file.ps' already exists in your files, it will be overwritten.

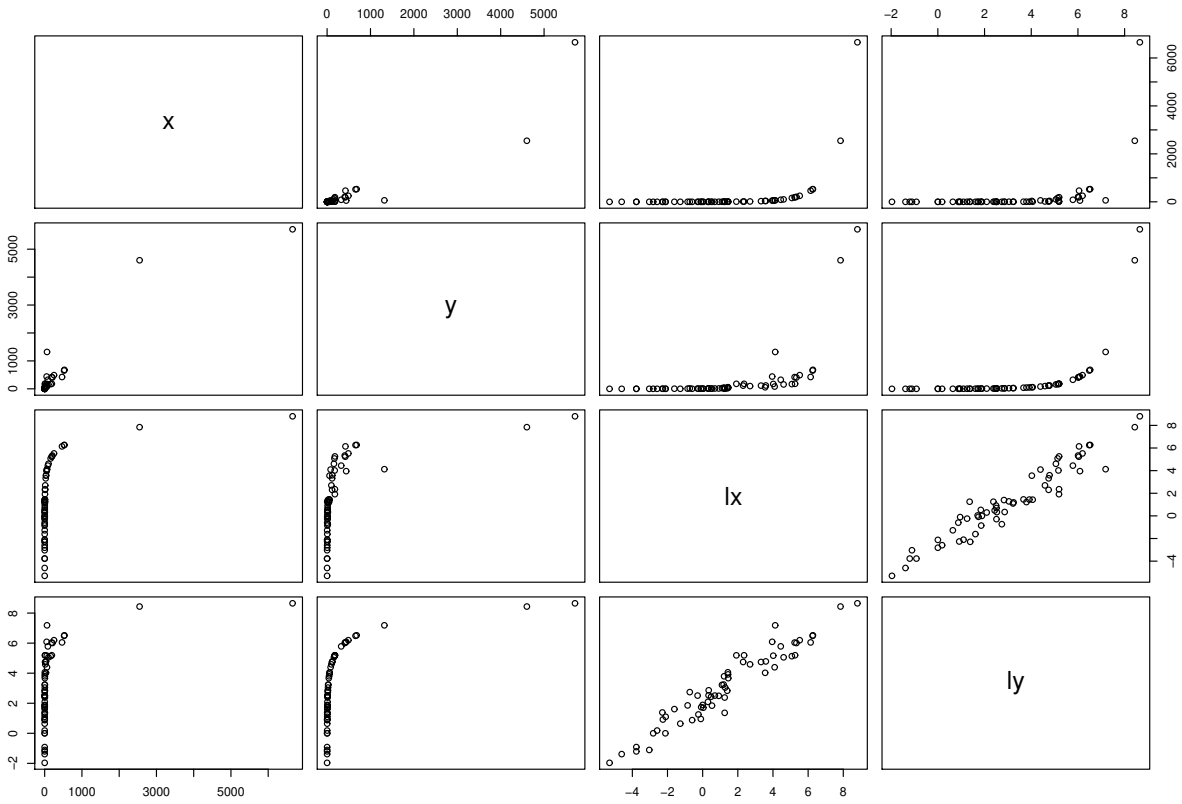

Figure 5: A pairs plot of bodyweight=x, brainweight=y, and their logs

```
pairs(mam.mat)  # will now put the graph into file.ps
dev.off() # will turn off the 'current device', so that
plot(x,y) # will now appear on the screen
q()
```

unix users:
ls
should show you that you have created file.ps
ghostview file.ps
enables you to look at this file on the screen
lp file.ps
enables you to print out the corresponding graph.

catam users:

You can also see file.ps via ghostview

Please await instructions in the practical class if you want to obtain a hard copy of this graph, via Postscript printer (But you may be able to work out this printing-out step for yourself. Use title(main="Posh Spice") for example, to put your name on the graph before you click on 'print'.) R-graphs can also be put into a Word document.

Here is the data-set 'mammals', from Weisberg (1985, pp144-5). It is in the Venables and Ripley (1994) library of data-sets.

	body	brain
Arctic fox	3.385	44.50
Owl monkey	0.480	15.50
Mountain beaver	1.350	8.10
Cow	465.000	423.00
Grey wolf	36.330	119.50
Goat	27.660	115.00
Roe deer	14.830	98.20
Guinea pig	1.040	5.50
Verbet	4.190	58.00
Chinchilla	0.425	6.40
Ground squirrel	0.101	4.00
Arctic ground squirrel	0.920	5.70
African giant pouched rat	1.000	6.60
Lesser short-tailed shrew	0.005	0.14
Star-nosed mole	0.060	1.00
Nine-banded armadillo	3.500	10.80
Tree hyrax	2.000	12.30
N.A. opossum	1.700	6.30
Asian elephant	2547.000	4603.00
Big brown bat	0.023	0.30
Donkey	187.100	419.00
Horse	521.000	655.00
European hedgehog	0.785	3.50
Patas monkey	10.000	115.00
Cat	3.300	25.60

Galago	0.200	5.00
Genet	1.410	17.50
Giraffe	529.000	680.00
Gorilla	207.000	406.00
Grey seal	85.000	325.00
Rock hyrax-a	0.750	12.30
Human	62.000	1320.00
African elephant	6654.000	5712.00
Water opossum	3.500	3.90
Rhesus monkey	6.800	179.00
Kangaroo	35.000	56.00
Yellow-bellied marmot	4.050	17.00
Golden hamster	0.120	1.00
Mouse	0.023	0.40
Little brown bat	0.010	0.25
Slow loris	1.400	12.50
Okapi	250.000	490.00
Rabbit	2.500	12.10
Sheep	55.500	175.00
Jaguar	100.000	157.00
Chimpanzee	52.160	440.00
Baboon	10.550	179.50
Desert hedgehog	0.550	2.40
Giant armadillo	60.000	81.00
Rock hyrax-b	3.600	21.00
Raccoon	4.288	39.20
Rat	0.280	1.90
E. American mole	0.075	1.20
Mole rat	0.122	3.00
Musk shrew	0.048	0.33
Pig	192.000	180.00
Echidna	3.000	25.00
Brazilian tapir	160.000	169.00
Tenrec	0.900	2.60
Phalanger	1.620	11.40
Tree shrew	0.104	2.50
Red fox	4.235	50.40

Here is the data-set 'Japanese set the pace for Europe's car makers', from The Independent, August 18, 1999. The 3 columns of numbers are Vehicles produced in 1998, and the Productivity, in terms of vehicle per employee, in 1997, 1998 respectively. Can you construct any helpful graphs?

	veh1998	prod97	prod98
Nissan(UK)	288838	98	105
Volkswagen(Spain)	311136	70	76
GM(Germany)	174807	77	76
Fiat(Italy)	383000	70	73

Toyota(UK)	172342	58	72
SEAT(Spain)	498463	69	69
Renault(France)	385118	61	68
GM(Spain)	445750	67	67
Renault(Spain)	213590	59	64
Honda(UK)	112313	62	64
Ford(UK)	250351	62	61
Fiat(2Italy)	416000	54	61
Ford(Germany)	290444	59	59
Ford(Spain)	296173	57	58
Vauxhall(UK)	154846	39	43
Skoda(CzechR)	287529	33	35
Rover(UK)	281855	33	30

An interesting modern example of multiple regression, complete with the full dataset, is given in
'Distance from Africa, not climate, explains within-population phenotypic diversity in humans'
by Betti, Balloux, Amos, Hanihara and Manica, *Proc. R.Soc. B* (2009) **276**, 809–814.

Finally, here is a classic dataset for you to play with. I think I originally took this dataset from the 2001 book by Brian Everitt "A handbook of Statistical Analyses using S PLUS".
Sulphur dioxide is one of the major air pollutants. A data-set presented by Sokal and Rohlf (1981) was collected on 41 US cities in 1969-71, corresponding to the following variables:
so2 = Sulphur dioxide content in micrograms per cubic metre
temp = average annual temperature in degrees Fahrenheit
manuf = number of manufacturing enterprises employing 20 or more workers
pop = population size (1970 census) in thousands
wind = Average annual wind speed in miles per hour
precip = Average annual precipitation (ie rainfall) in inches
days= Average annual number of days with precipitation per year.

region	so2	temp	manuf	pop	wind	precip	days
"Phoenix"	10	70.3	213	582	6.0	7.05	36
"Little Rock"	13	61.0	91	132	8.2	48.52	100
"San Francisco"	12	56.7	453	716	8.7	20.66	67
"Denver"	17	51.9	454	515	9.0	12.95	86
"Hartford"	56	49.1	412	158	9.0	43.37	127
"Wilmington"	36	54.0	80	80	9.0	40.25	114
"Washington"	29	57.3	434	757	9.3	38.89	111
"Jackson"	14	68.4	136	529	8.8	54.47	116
"Miami"	10	75.5	207	335	9.0	59.80	128

"Atlanta"	24	61.5	368	497	9.1	48.34	115
"Chicago"	110	50.6	3344	3369	10.4	34.44	122
"Indiana"	28	52.3	361	746	9.7	38.74	121
"Des Moines"	17	49.0	104	201	11.2	30.85	103
"Wichita"	8	56.6	125	277	12.7	30.58	82
"Louisvlle"	30	55.6	291	593	8.3	43.11	123
"New Orleans"	9	68.3	204	361	8.4	56.77	113
"Baltimore"	47	55.0	625	905	9.6	41.31	111
"Detroit"	35	49.9	1064	1513	10.1	30.96	129
"Minnesota"	29	43.5	699	744	10.6	25.94	137
"Kansas"	14	54.5	381	507	10.0	37.00	99
"St. Louis"	56	55.9	775	622	9.5	35.89	105
"Omaha"	14	51.5	181	347	10.9	30.18	98
"Albuquerque"	11	56.8	46	244	8.9	7.77	58
"Albany"	46	47.6	44	116	8.8	33.36	135
"Buffalo"	11	47.1	391	463	12.4	36.11	166
"Cincinnati"	23	54.0	462	453	7.1	39.04	132
"Cleveland"	65	49.7	1007	751	10.9	34.99	155
"Columbia"	26	51.5	266	540	8.6	37.01	134
"Philadelphia"	69	54.6	1692	1950	9.6	39.93	115
"Pittsburgh"	61	50.4	347	520	9.4	36.22	147
"Providence"	94	50.0	343	179	10.6	42.75	125
"Memphis"	10	61.6	337	624	9.2	49.10	105
"Nashville"	18	59.4	275	448	7.9	46.00	119
"Dallas"	9	66.2	641	844	10.9	35.94	78
"Houston"	10	68.9	721	1233	10.8	48.19	103
"Salt Lake City"	28	51.0	137	176	8.7	15.17	89
"Norfolk"	31	59.3	96	308	10.6	44.68	116
"Richmond"	26	57.8	197	299	7.6	42.59	115
"Seattle"	29	51.1	379	531	9.4	38.79	164
"Charleston"	31	55.2	35	71	6.5	40.75	148
"Milwaukee"	16	45.7	569	717	11.8	29.07	123

Worksheet 3.

This shows you how to construct a one-way analysis of variance and how to do a qqnorm-plot to assess normality of the residuals.
Here is the data in the file 'potash': nb, you may need to do some work to get the datafile in place before you go into R.

```
7.62 8.00 7.93
8.14 8.15 7.87
7.76 7.73 7.74
7.17 7.57 7.80
7.46 7.68 7.21
```

The origin of these data is lost in the mists of time; they show the strength of bundles of cotton, for cotton grown under 5 different 'treatments', the treatments in question being amounts of potash, a fertiliser. The design of this simple agricultural experiment gives 3 'replicates' for each treatment level, making a total of 15 observations in all. We model the dependence of the strength on the level of potash.
This is what you should do.

```
y <- scan("potash") ; y
```

Now we read in the experimental design.

```
x <- scan()      # a slicker way is to use the "rep" function.
36 36 36
54 54 54
72 72 72
108 108 108
144 144 144 #here x is treatment(in lbs per acre) & y is strength
            # blank line to show the end of the data
tapply(y,x,mean) # gives mean(y) for each level of x
plot(x,y)
regr <- lm(y~x) ; summary(regr)
```

This fits $y_{ij} = a + bx_{ij} + \epsilon_{ij}$, with $i = 1, \ldots, 5,\ j = 1, \ldots, 3$

```
potash <- factor(x) ; potash
plot(potash,y) # This results in a 'boxplot'
teeny <- lm(y~potash)
```

This fits $y_{ij} = \mu + \theta_i + \epsilon_{ij}$ with $\theta_1 = 0$ (the default setting in R)

```
anova(teeny)
names(teeny)
coefficients(teeny) # can you understand these ?
help(qqnorm)
qqnorm(resid(teeny))
qqline(resid(teeny))
plot(fitted(teeny),resid(teeny))
plot(teeny,ask=T) # for more of the  diagnostic plots
```

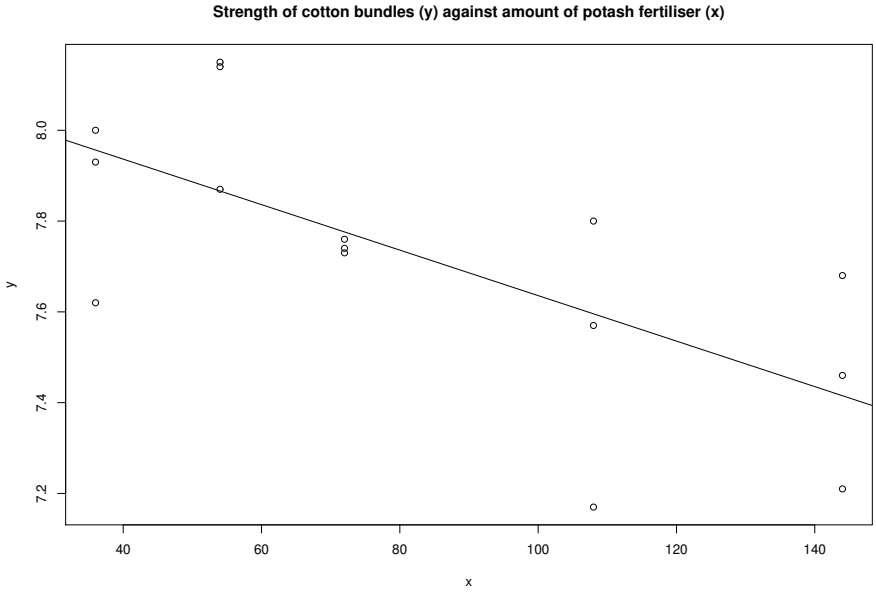

Figure 6: Strengths of cotton bundles against level of potash

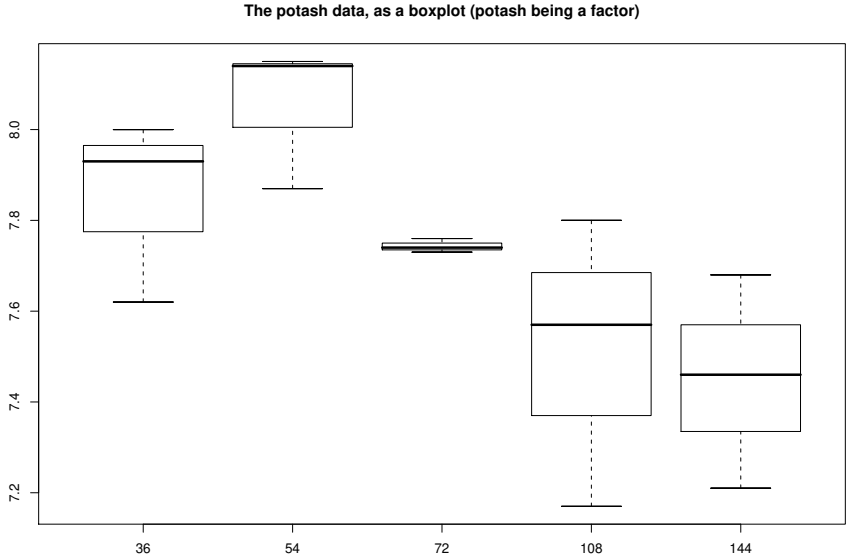

Figure 7: Boxplot for cotton bundles dataset

The original data, and the fitted regression line, are given in Figure 6. Figure 7 gives boxplot for this dataset.

Brief explanation of some of the diagnostic plots for the general linear model

With

$$Y = X\beta + \epsilon$$

and $\epsilon \sim N(0, \sigma^2 I)$, we see that $\hat{\beta} = (X^T X)^{-1} X^T Y$, and $\hat{Y} = HY$ and $\hat{\epsilon} = Y - \hat{Y} = (I - H)\epsilon$, where H is the usual 'hat' matrix.

From this we can see that $\hat{\epsilon}$, $\hat{Y}$, the residuals and fitted values, are independent, so

a plot of $\hat{\epsilon}$ against $\hat{Y}$ should show no particular trend.
If we **do** see a trend in the plot of $\hat{\epsilon}$ against $\hat{Y}$, for example if the residuals appear to be 'fanning out' as $\hat{Y}$ increases, then this may be a warning that the variance of Y_i is actually a function of $E(Y_i)$, and so the assumption $\text{var}(Y_i) = \sigma^2$ for all i may fail: we may be able to remedy this by replacing Y_i by $\log Y_i$, or some other transformation of Y, in the original linear model.
Further, $\hat{\epsilon}$ should be $N(0, (I - H)\sigma^2)$.
In order to check whether this is plausible, we find $F_n(u)$ say, the sample distribution function of the residuals. We would like to see whether

$$F_n(u) \simeq \Phi(u/\sigma)$$

for some σ (where Φ is as usual, the distribution function of $N(0, 1)$). This is hard to assess visually, so instead we try to see if

$$\Phi^{-1} F_n(u) \simeq u/\sigma.$$

This is what lies behind the qqplot. We are just doing a quick check of the linearity of the function $\Phi^{-1} F_n(u)$.
It's fun to generate a random sample of size 100 from the t-distribution with 5 df, and find its qqnorm, qqline plots, to assess the systematic departure from a normal distribution. To do this, try

```
y <- rt(100,5) ; hist(y) ; qqnorm(y); qqline(y)
```

Worksheet 4.

A two-way analysis of variance, first illustrating the R function gl() to set up the factor levels in a balanced design. The data are given below, and are in the file 'IrishIt'.
Under the headline
" Irish and Italians are the 'sexists of Europe'" The Independent, October 8, 1992, gave the following table.

```
The percentage having equal confidence in both sexes for various occupations

86 85 82 86  Denmark
75 83 75 79  Netherlands
77 70 70 68  France
61 70 66 75  UK
67 66 64 67  Belgium
56 65 69 67  Spain
52 67 65 63  Portugal
57 55 59 64  W. Germany
47 58 60 62  Luxembourg
52 56 61 58  Greece
54 56 55 59  Italy
43 51 50 61  Ireland
```

Here the columns are the occupations bus/train driver, surgeon, barrister, MP.
Can you see that the French are out of line in column 1 ?
You will need to remove the text from the data before you can read it via scan().

```
p <- scan("IrishIt") ; p
occ <- scan(," ")               # now read in row & column labels
bus/train surgeon barrister MP
                                # remember blank line
country <- scan(, " ")
Den Neth Fra UK Bel Spa
Port W.Ger Lux Gre It Irl
                                # remember blank line
OCC <- gl(4,1,48,labels=occ)    # gl() is the 'generate level' command
COUNTRY <- gl(12,4,48,labels= country)
OCC ; COUNTRY
OCC <- factor(OCC) ; COUNTRY<- factor(COUNTRY) # factor declaration(redundant)
```

Now we try several different models. Study the output carefully and comment on the differences and similarities.

```
ex2 <-  lm(p~COUNTRY+OCC) ; anova(ex2)
```

This fits $p_{ij} = \mu + \alpha_i + \beta_j + \epsilon_{ij}$ for $i = 1, \ldots, 12$ and $j = 1, \ldots, 4$ and the usual assumption about the distribution of (ϵ_{ij}).

```
ex2 ; summary(ex2)
names(ex2)
ex2$coefficients
lex2 <- lm(p~OCC +COUNTRY) ; anova(lex2)
lex3 <- lm(p~ OCC) ; lex3 ; summary(lex3)
lex4 <- lm(p~ COUNTRY); lex4 ; summary(lex4)
lex5 <- lm(p~  COUNTRY + OCC); lex5; anova(lex5)
summary(lex5,cor=T) # cor=T gives the matrix
          # of correlation coefficients of parameter estimates
tapply(p,OCC,mean)
tapply(p,COUNTRY,mean)
```

The default parametrisation for factor effects in R is different from the (rather awkward) default parametrisation used in S-Plus. If our model is

$$E(Y_{ij}) = \mu + \alpha_i + \beta_j$$

then R takes $\alpha_1 = 0,\ \beta_1 = 0$, so that effectively each of the 2nd, 3rd, ... etc factor level is being compared with the 1st such.
Now we'll demonstrate some nice graphics, starting with a multiple-comparisons test of the differences between the 4 occupations (hence $4 \times 3/2$ pairwise comparisons). The corresponding multiple-comparisons plot is given as Figure 8.

```
first.aov = aov(p~  COUNTRY + OCC) ; summary(first.aov)
TukeyHSD(first.aov, "OCC")
plot(TukeyHSD(first.aov, "OCC"))
```

```
boxplot(split(p,OCC)) # in fact same effect as plot(OCC,p)
boxplot(split(p,COUNTRY))
res <- ex2$residuals ; fv<- ex2$fitted.values
plot(fv,res)
hist(resid(ex2))
qqnorm(resid(ex2))   # should be approx straight line if errors normal
ls()     # opportunity to tidy up here,eg by
rm(ex2)
```

Here is another dataset with the same layout.
The Independent, 16 June 1999, under the headline 'Tourists get hidden costs warnings' gave the following table of prices in pounds, called 'How the resorts compared'.

```
Algarve      8.00  0.50  3.50  3.00  4.00  100.00
CostaDelSol  6.95  1.30  4.10 12.30  4.10  130.85
Majorca     10.25  1.45  5.35  6.15  3.30  122.20
Tenerife    12.30  1.25  4.90  3.70  2.90  130.85
Florida     15.60  1.90  5.05  5.00  2.50  114.00
Tunisia     10.90  1.40  5.45  1.90  2.75  218.10
```

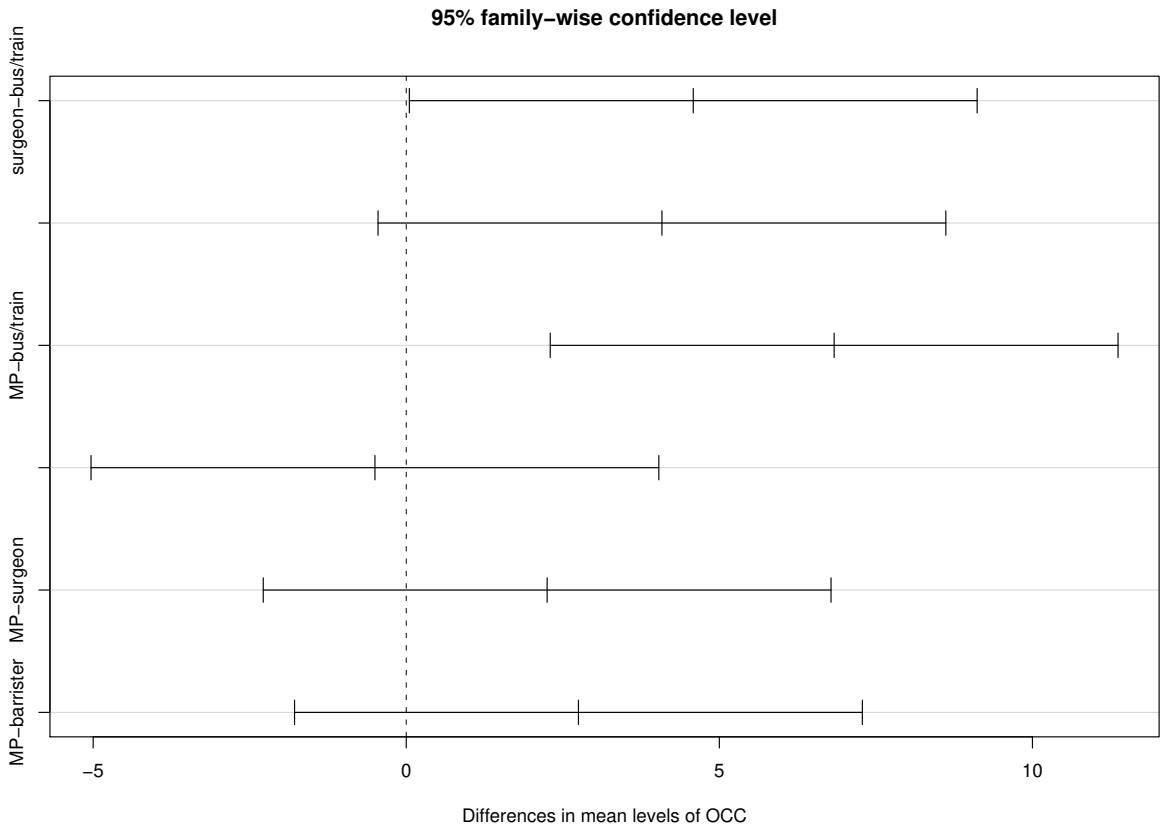

Figure 8: Multiple comparisons between occupations.

```
Cyprus      11.60  1.20  5.95  3.00  3.60  149.45
Turkey       6.50  1.05  6.50  4.90  2.85  263.00
Corfu        5.20  1.05  3.75  4.20  2.50  137.60
Sorrento     7.70  1.40  6.30  8.75  4.75  215.40
Malta       11.20  0.70  4.55  8.00  4.80   87.85
Rhodes       6.30  1.05  5.20  3.15  2.70  261.30
Sicily      13.25  1.75  4.20  7.00  3.85  174.40
Madeira     10.25  0.70  5.10  6.85  6.85  153.70
```

Here the column headings are, respectively,
Three-course meal, Bottle of Beer, Suntan Lotion, Taxi (5km), Film (24 exp), Car Hire (per week).
Fit the model

```
log(price) ~ place + item
```

and interpret the results. Note that this model is more appropriate than

```
price ~ place + item
```

can you see why? Which is the most expensive resort? How are your conclusions altered if you remove the final column (ie car-hire) in the Table?
Finally, for the racing enthusiasts:
for the Cheltenham Gold Cup, March 18, 2004, I computed the following table of

probabilities from the published Bookmakers' Odds:
thus, eg .6364 corresponds to odds of 4-7 (.6364 = 7/11).
In the event, BestMate was the winner, for the 3rd year in succession! (Note added November 3, 2005: sadly BestMate has just died.)

```
          Corals WmHills Ladbrokes Stanleys Tote
BestMate     .6364 .6364   .6364     .6000  .6000
TheRealBandit .125 .1111   .0909     .1111 .1111
KeenLeader    .0909 .0909  .0833     .0909 .0769
IrishHussar   .0667 .0909  .0909     .0833 .0833
BeefOrSalmon  .0909 .0769  .0909     .0769 .0667
FirstGold     .0833 .0769  .0909     .0769 .0769
HarbourPilot  .0588 .0667  .0588     .0588 .0588
TruckersTavern .0476 .0588 .0667     .0588 .0588
SirRembrandt  .0385  .0294 .0294     .0294 .0244
AlexB'quet    .0149  .0099 .0099     .0149 .0149
```

```
Suggestion:
 x <- read.table("BMData", header=T)
 y <- as.vector(t(x))
 horse <- row.names(x)
 Horse <- gl(10, 5, length=50, labels=horse)
 bookie <- scan(,"")
 Corals WmHills Ladbrokes Stanleys Tote

Bookie <- gl(5,1, length=50, labels=bookie)
first.lm <- lm(y ~ Horse + Bookie)
summary(first.lm); anova(first.lm)
```

What happens if we remove the BestMate row of the data-matrix?

Worksheet 5.

Analysis of an unbalanced two-way design
These data are taken from The Independent on Sunday for October 6,1991. They show the prices of certain best-selling books in 5 countries in pounds sterling. The columns correspond to UK, Germany, France, US, Austria respectively. The new feature of this data-set is that there are some MISSING values (missing for reasons unknown). Thus in the 10 by 5 table below, we use
NA to represent 'not available' for these missing entries.
We then use 'na.action...' to omit the missing data in our fitting, so that we will have an UNbalanced design. You will see that this fact has profound consequences: certain sets of parameters are NON-orthogonal as a result. Here is the data from

```
bookpr
```

```
14.99  12.68   9.00  11.00  15.95 S.Hawking,"A brief history of time"
14.95  17.53  13.60  13.35  15.95 U.Eco,"Foucault's Pendulum"
12.95  14.01  11.60  11.60  13.60 J.Le Carre,"The Russia House"
14.95  12.00   8.45   NA      NA  J.Archer,"Kane & Abel"
12.95  15.90  15.10   NA    16.00 S.Rushdie,"The Satanic Verses"
12.95  13.40  12.10  11.00  13.60 J.Barnes"History of the world in ..."
17.95  30.01   NA    14.50  22.80 R.Ellman,"Oscar Wilde"
13.99   NA     NA    12.50  13.60 J.Updike,"Rabbit at Rest"
 9.95  10.50   NA     9.85   NA   P.Suskind,"Perfume"
 7.95   9.85   5.65   6.95   NA   M.Duras,"The Lover"
```

'Do books cost more abroad?' was the question raised by The Independent on Sunday.

```
p <- scan("bookpr") ; p
 cou <- scan(,"")
 UK  Ger   Fra   US   Austria
                            # blank line
country <- gl(5,1,50,labels=cou)
author <-  gl(10,5,50)
plot.design(p~ country + author) # for a useful graphical summary
lmunb <- lm(p~ country + author,na.action=na.omit) ; summary(lmunb)
lmunb1<- lm(p~ country,na.action=na.omit) ; summary(lmunb1)
```

Observe that your least squares estimates for the 'country' parameters change from lmunb to lmunb1.

```
resid <- lmunb$residuals
resid
```

The results of 'plot.design' are given as Figure 9.
Note that resid is a vector with less than 50 elements. Thus,

```
plot(country,resid)
```

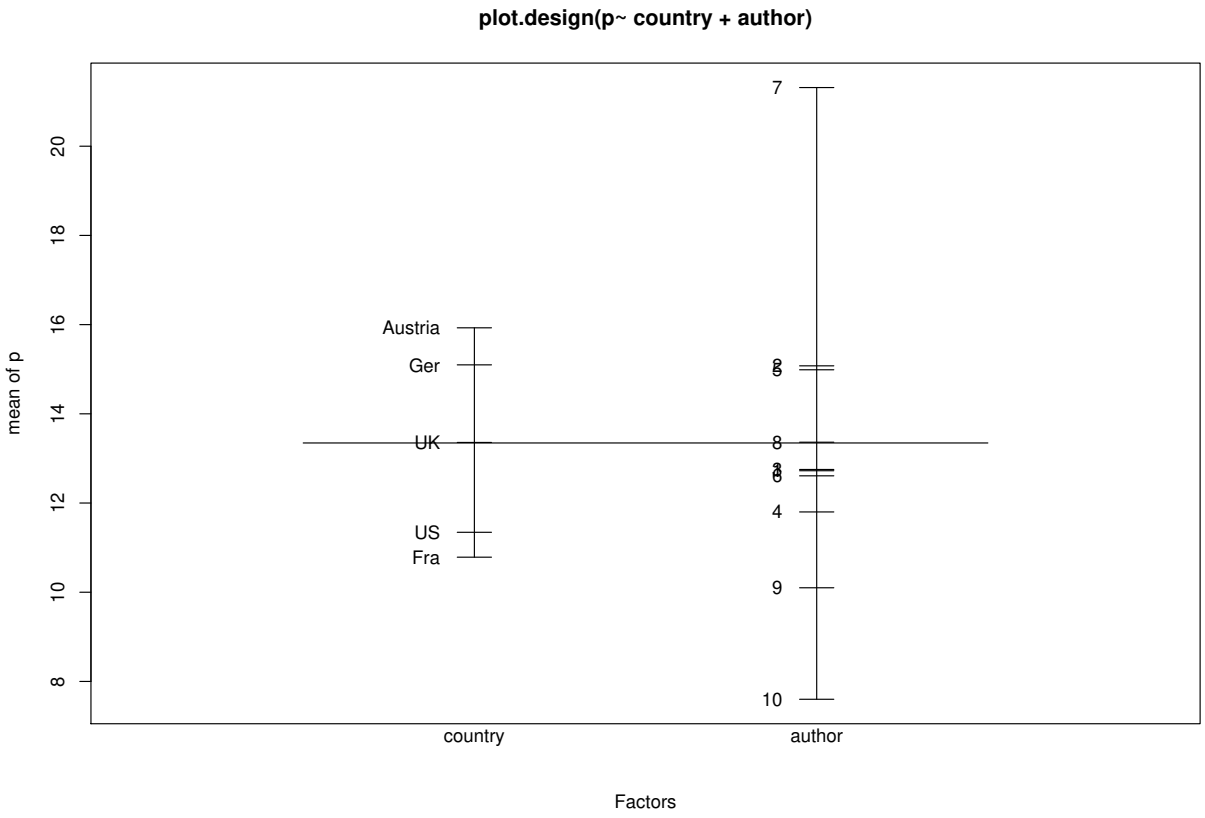

Figure 9: The 'design plot' for the countries, authors data

would give us an error message. To deal with this particular difficulty

```
plot(country[!is.na(p)],resid)  # Now do your 'unbalanced' anova
unbaov <- anova(lm(p~ country + author,na.action=na.omit)) ; unbaov
# Try lm(p~author +country,...)
# Try anova(lm(p~author + country,...))
# Try anova(lm(p~author,...))
```

Discuss carefully the consequences of non-orthogonality of the parameter sets country,author for this problem.
Was our model above on the correct scale? We try a log-transform.

```
lp <- log(p)
lmunblp <- lm(lp~ country+author,na.action=na.omit) ; summary(lmunblp)
qqnorm(resid(lmunb))
qqnorm(resid(lmunblp)) # which is best ?
q()
```

Problems involving MONEY should be attacked with multiplicative rather than additive models : discuss this provocative remark.
Here is another data-set with the same structure. Under the headline 'Afloat on a sea of alcohol, the booze cruisers bid last farewell to duty-free' The Independent of 28 June, 1999, gives the Table below.
'Booze and Fags: the relative cost'

200 Benson & Hedges special filter cigarettes	16.95	16.99	35.99	20.00	NA
1 litre Smirnoff vodka	9.99	10.74	10.39	11.00	10.25
1 litre Gordon's gin	10.25	8.29	10.69	11.35	9.99
5 X 50 gm Golden Virginia rolling tobacco	13.95	13.99	38.15	9.65	NA
24 X 440 cans Stella Artois	11.95	20.80	23.96	9.25	9.67
24 X 440 cans Guinness	15.75	22.95	22.74	11.90	15.83

Here the column headings (ie place of sale) are P&O Stena (on board ship), BAA (airport duty free), Tesco (UK, high street), Eastenders (Calais, cash & carry), and Wine & Beer Co (Calais, cash & carry).
And finally, just in case you want yet more data of this structure, 'Britons paying over the odds for designer goods' from The Independent, 27 April, 2001, gives the following table of prices in pounds sterling.

	UK	Sweden	France	Germany	US
U2CD	13.56	12.45	10.60	9.66	10.59
SPS2	299.99	312.43	272.99	266.17	226.76
Cl	24.45	28.84	24.48	24.35	14.66
Ca	305.36	346.83	316.43	312.83	248.62
Le	46.16	47.63	42.11	46.06	27.01
Do	58.00	54.08	47.22	46.20	32.22
TheMatrixDVD	19.26	15.61	17.93	15.29	15.75

```
Za            836.74 704.29  527.45 755.77  NA
Ti            111.00 104.12   89.43  93.36  75.42
Ikea          395.00 276.26  272.99 299.99 454.21
```

Key to row names,
U2CD, SPS2= Sony PlayStation 2, Cl= Clinique Moisturing lotion, Ca= Callaway golf club, Le= Levi's 501 (Red Tab), Do= Dockers "K1" khakis, TheMatrixDVD, Za= Zanussi ZF4Y refrigerator, Ti= Timberland women's boots, Ikea= Ikea "Nikkala" sofa.
(I'm not sure I would ever buy any of these, except Cl, in any country, but you might!)

Worksheet 6.

Logistic regression for the binomial distribution.

The data come from 'Modelling Binary Data', by D.Collett(1991). The compressive strength of an alloy fastener used in aircraft construction is studied. Ten pressure loads, increasing in units of 200psi from 2500 psi to 4300 psi, were used. Here
n= number of fasteners tested at each load
r= number of these which FAIL.
We assume that r_i is Binomial(n_i, π_i) for $i = 1, \ldots, 10$ and that these 10 random variables are independent. We model the dependence of π_i on $Load_i$, using graphs where appropriate.
The model assumed below is

$$log(\pi_i/(1-\pi_i)) = a + b \times Load_i.$$

[This is the LOGIT link in the glm, here the default link.] Note that we do the regression here with $p = r/n$ as the 'y-variable' , and n as 'weights'. See

```
help(glm)
```

for general syntax.
The corresponding data, given at the end of this sheet, is in the file called
alloyf
So, first set up the file 'alloyf'.

```
data6 <- read.table("alloyf",header=T)
attach(data6)  # BEWARE, this will not over-write variables already present.
p <- r/n
plot(Load,p)
ex6 <- glm(p~ Load,weights=n,family=binomial) #'weights' for sample sizes
```

Observe, we could put the above sequence of commands into a separate file, called,
eg "littleprog"
which we could then access, and execute, from within R, via the command

```
source("littleprog")
```

```
data6 ; names(data6); summary(data6)
plot(Load,p,type="l")  # note, l for 'line'
ex6 ; summary(ex6)
names(ex6)
plot(ex6,ask=T)    # for diagnostic plots
```

Now we'll see how to vary the link function. Previously we were using the default link, ie the logit(this is canonical for the binomial distribution)

```
ex6.l <- glm(p~Load,family=binomial(link=logit),weights=n)
ex6.p <- glm(p~Load,family=binomial(link=probit),weights=n)
ex6.cll <- glm(p~Load,binomial(link=cloglog),weights=n)
summary(ex6.l)
summary(ex6.p)   # the probit link
summary(ex6.cll) # the complementary loglog link
```

As you will see, all these three models fit very well (ex6.cll being slightly less good). The AIC is the Akaike information criterion; it is defined here as
$AIC = -2\times$maximized log likelihood $+2\times$ number of parameters fitted.
(The log-likelihood is of course defined only up to a constant depending on the data, so the same will be true of the AIC.) In all of the linear models (irrespective of the particular link function used) the number of parameters fitted is of course 2. In comparing different models, we look for the one with the smallest AIC.
Observe that for the fitted parameter estimates, the ratio a/b is about the same for the 3 link functions: this is a special case of a general phenomenon.
Which link function gives the best fit, ie the smallest deviance ? In practice the logit and probit will fit almost equally well.
We conclude by plotting a graph to show the fitted probability of failure under the logistic model: the 2 vertical lines are drawn to show the actual range of our data for Load. (Within this range, the link function is pretty well linear, as it happens.)

```
x = 15:55 ; alpha = ex6.l$coefficients[1]; beta= ex6.l$coefficients[2]
y = alpha + beta*x; Y= 1/(1+ exp(-y))
plot(x, Y, type="l",xlab="Load",ylab="Fitted Probability of failure")
abline(v=25); abline(v=43)
points(Load,p) # to put the original data-points on the graph
title("Fitting a logistic model")
```

The corresponding graph is shown in Figure 10. Here is the dataset "alloyf". (Warning: 'load' is a function in R, so we call the first column 'Load' rather than 'load'.)

```
Load  n  r
25   50  10
27   70  17
29  100  30
31   60  21
33   40  18
35   85  43
37   90  54
39   50  33
41   80  60
43   65  51
```

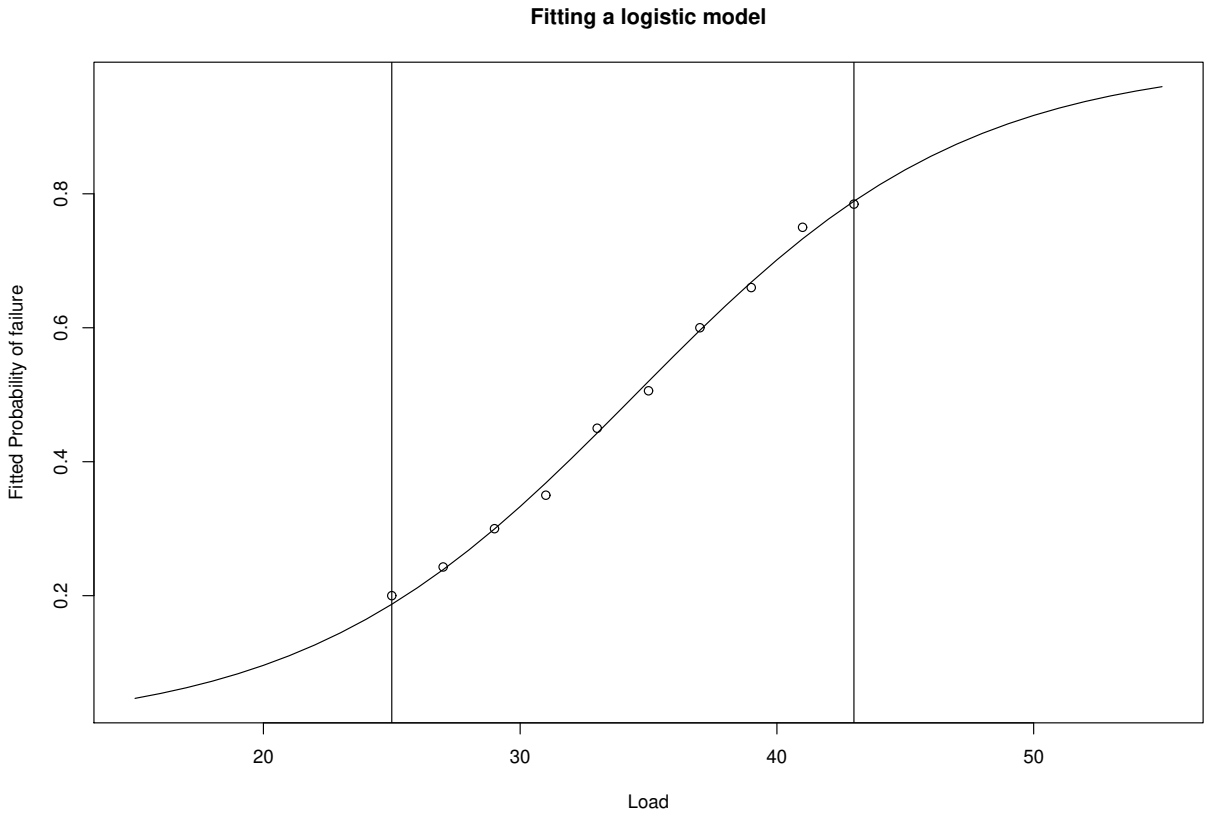

Figure 10: An example of a logistic curve

Worksheet 7.

Logistic regression and safety in space.
Swan and Rigby (GLIM Newsletter no 24,1995) discuss the data below, using binomial logistic regression. To quote from Swan and Rigby
'In 1986 the NASA space shuttle Challenger exploded shortly after it was launched. After an investigation it was concluded that this had occurred as a result of an 'O' ring failure. 'O' rings are toroidal seals and in the shuttles six are used to prevent hot gases escaping and coming into contact with fuel supply lines.
Data had been collected from 23 previous shuttle flights on the ambient temperature at the launch and the number of 'O' rings, out of the six, that were damaged during the launch. NASA staff analysed the data to assess whether the risk of 'O' ring failure damage was related to temperature, but it is reported that they excluded the zero responses (ie, none of the rings damaged) because they believed them to be uninformative. The resulting analysis led them to believe that the risk of damage was independent of the ambient temperature at the launch. The temperatures for the 23 previous launches ranged from 53 to 81 degreees Fahrenheit while the Challenger launch temperature was 31 degrees Fahrenheit (ie, -0.6 degrees Centigrade).'
Calculate $pfail = nfail/six$, where

```
six <- rep(6,times=23),
```

for the data below, so that $pfail$ is the proportion that fail at each of the 23 previous shuttle flights. Let *temp* be the corresponding temperature.
Comment on the results of

```
glm(pfail~ temp,binomial,weights=six)
```

and plot suitable graphs to illustrate your results.
Are any points particularly 'influential' in the logistic regression ?
How is your model affected if you omit all points for which $nfail = 0$?
Suggestion:

```
 glm(pfail~ temp,binomial,weights=six, subset=(nfail>0))
#note that here we are picking out a subset by using the 'logical condition'
#(nfail>0). Alternatively, for this example we could have used the condition
# subset=(nfail!=0).
# '!='  means 'not equal to' and is the negation of '=='
?"&"  # for full information on the logical symbols
```

Do you have any comments on the design of this experiment?
The data (read this by read.table("...",header=T)) follow.

nfail	temp
2	53
1	57
1	58
1	63
0	66
0	67
0	67
0	67
0	68
0	69
0	70
0	70
1	70
1	70
0	72
0	73
0	75
2	75
0	76
0	76
0	78
0	79
0	81

```
first.glm = glm(pfail~ temp, binomial, weights=six)
fv = first.glm$fitted.values
```

```
plot(temp, fv, type="l", xlim=c(30,85), ylim=c(0,1), xlab="temperature",
ylab="probability of failure")
points(temp, pfail)
title("The space shuttle failure data, with the fitted curve")
```

The corresponding logistic graph is shown in Figure 11. I took the temperature values from 30 degrees to 85 degrees (the x-axis) to emphasize the fact that we have **no data** in the range 30 degrees to 50 degrees.

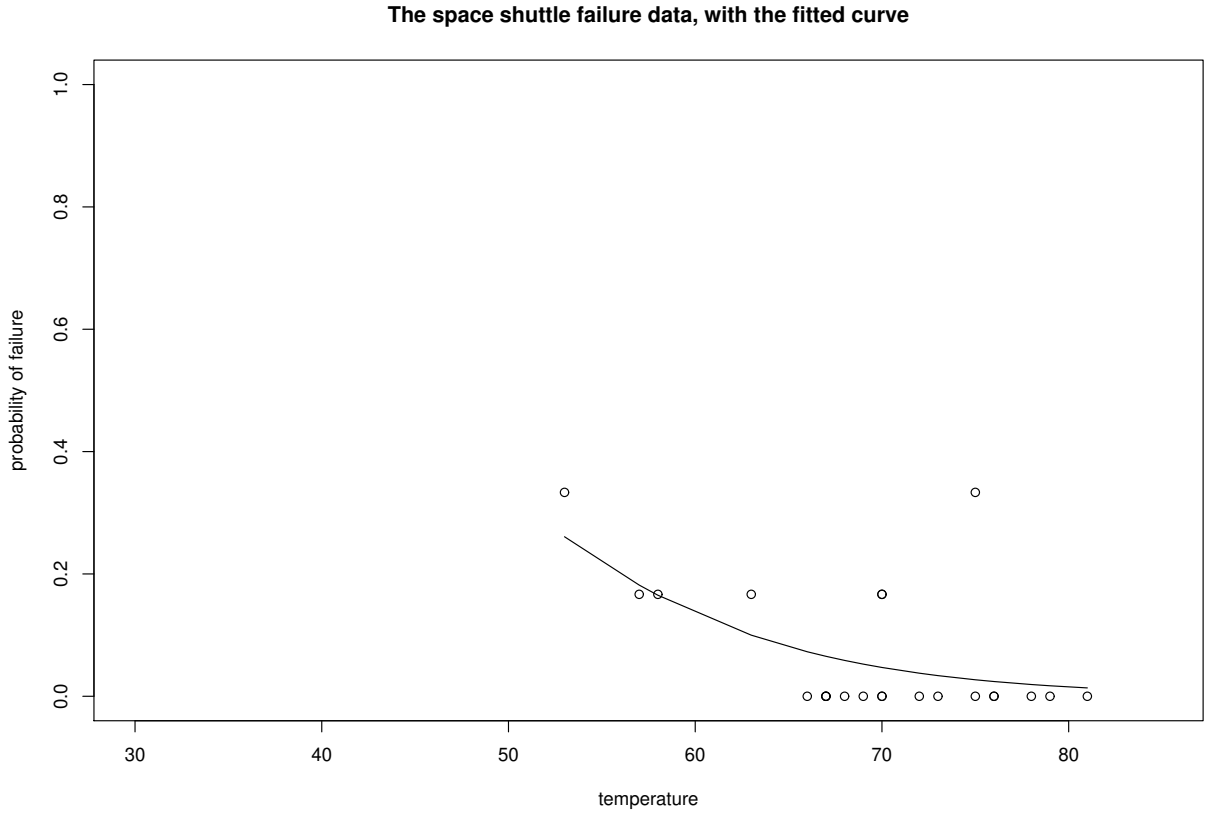

Figure 11: The logistic graph for the space shuttle data

Worksheet 8a.
Binomial and Poisson regression: the Missing Persons data.
Some rather gruesome data published on March 8, 1994 in The Independent under the headline
" Thousands of people who disappear without trace "
are analysed below,

```
s<- scan()
33 63 157
38 108 159
                              # nb, blank line
r<- scan()
3271  7256   5065
2486  8877   3520
                              # nb, blank line
```

Here,
r = number reported missing during the year ending March 1993, and
s = number still missing by the end of that year. These figures are from the Metropolitan police.

```
sex <- scan(,"")
m m m f f f

 age <- c(1,2,3,1,2,3)
# sex =m,f for males,females
# age=1,2,3 for 13 years  & under, 14-18 years, 19 years & over.
sex <- factor(sex) ; age <- factor(age)
bin.add <- glm(s/r ~ sex+age,family=binomial,weights=r)
summary(bin.add)
round(bin.add$fitted.values,3) # to ease interpretation
```

What is this telling us ?
The Binomial with large n, small p, is nearly the Poisson with mean (np). So we also try Poisson regression, using the appropriate "offset".

```
 l <- log(r)
Poisson.add <- glm(s~sex + age,family=poisson, offset=l)
summary(Poisson.add)
```

Describe and interpret these results, explaining the similarities.
Finally, we can show in Figure 12 a helpful plot.

```
Age = gl(3,1,length=6, labels=c("13&under", "14-18","19&over"))
interaction.plot(Age,sex,s/r, type="l")
```

New for 2008 Survival of extremely premature babies.
The data in Table 1 below is taken from the BMJ article 'Survival of extremely premature babies in a geographically defined population: prospective cohort study of

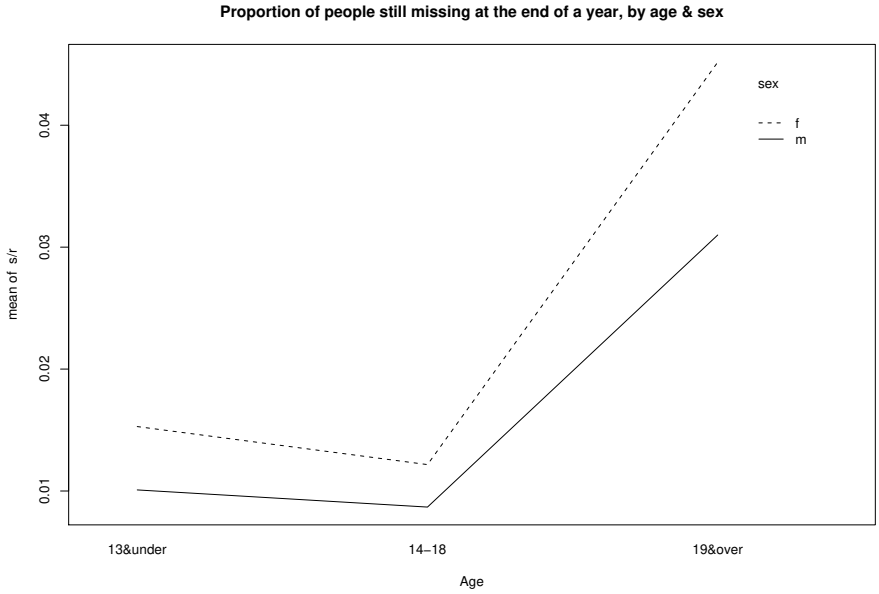

Figure 12: The interaction graph for age and sex

1994-9 compared with 2000-5' by Field, Dorling, Manktelow and Draper, BMJ2008; 336; 1221-1223.
As you will recall, the 'normal' length of gestation is 40 weeks. Table 1 shows r, the numbers of babies surviving to discharge from the hospital, out of n, the number admitted to neonatal intensive care, for babies born at gestational age of 23, 24 and 25 completed weeks respectively, firstly for the epoch 1994-9, and secondly for the epoch 2000-5. You will see from the raw data that happily most of the survival rates have improved from the first epoch to the second. For example, of babies born at gestational age 24 weeks, in the first epoch 24% survived to discharge, but in the second epoch 41% survived to discharge. Here is an extract from my R analysis of

Gestational Age, in completed weeks	23	23	24	24	25	25
	r	n	r	n	r	n
Epoch= 1994-9	15	81	40	165	119	229
Epoch= 2000-5	12	65	82	198	142	225

Table 1: Survival of extremely premature babies

these data for you to check and to interpret.

```
> first.glm <-  glm(r/n~ Epoch+GestationalAge,binomial,weights=n)
> summary(first.glm)
..........
Deviance Residuals:
      1        2        3        4        5        6
 0.8862  -0.8741   0.2657  -0.8856   0.7172  -0.2786
Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)       -1.7422     0.2265  -7.692 1.45e-14
```

```
Epoch2000-5         0.5320     0.1388   3.834 0.000126
GestationalAge24    0.7595     0.2420   3.139 0.001695
GestationalAge25    1.7857     0.2348   7.604 2.88e-14
---
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 109.1191  on 5  degrees of freedom
Residual deviance:   2.9963  on 2  degrees of freedom
AIC: 42.133
Number of Fisher Scoring iterations: 4
```

Although the above analysis shows a remarkably good fit to the model

$$\log(p_{ij}/(1-p_{ij})) = \mu + \alpha_i + \beta_j,\ i = 1, 2,\ j = 1, 2, 3$$

(using an obvious notation) we have so far taken no account of another possibly 'explanatory' variable, given in the BMJ paper. This is the mean number of days of care, per baby admitted, and this mean noticeably increases from Epoch 1 to Epoch 2. What happens if you include the data from Table 2 into your analysis?

Gestational Age, in completed weeks	23	24	25
	mean days	mean days	mean days
Epoch= 1994-9	22.9	45.0	52.6
Epoch= 2000-5	34.5	58.5	82.1

Table 2: Mean number of days of care, per admitted baby

New for July 2009. The dataset from the UK team in the 2007 International Mathematical Olympiad

There were 6 team members (whom I present anonymously as UK1, ..., UK6) and 6 questions, and the possible marks for each question ranged from 0 to 7. Here is the dataset

```
person   q1 q2 q3 q4 q5 q6
UK1       7  0  0  7  0  0
UK2       7  2  0  7  0  0
UK3       0  0  0  7  0  0
UK4       7  7  2  7  7  1
UK5       4  1  0  7  0  1
UK6       7  0  0  7  0  0
```

Setting up all the variables in the appropriate way, try

```
n <- rep(7, times=36)
first.glm <- glm(r/n ~ person + question, binomial, weights=n)
```

How is your analysis affected by the removal of question 4?
I took this dataset from the UK Mathematics Trust Yearbook, 2006-2007.

Worksheet 8b.

Analysis of a 4×2 contingency table : 3 ways of getting the same result.
Check from the log-likelihood function WHY these give the same result.
The data given in Table 3 were obtained by Prof I.M.Goodyer, as part of a study on 11-year-old children, to investigate the relationship between 'deviant behaviour' (no/yes) and several other variables. The results for the variable 'emotionality' are shown below (emo=1 meaning low emotionality,... emo=4 meaning high emotionality). Here are my suggestions for the analysis.

behaviour	no	yes
emo=1	51	3
emo=2	69	11
emo=3	28	22
emo=4	7	13

Table 3: Is there a link between emotionality and bad behaviour?

```
a <- c(51,69,28,7)  ; b <- c(3,11,22,13)
one <- c(1,1,1,1)
indepB <- glm(cbind(a,b)~ one ,binomial) # nb a ONE
summary(indepB)
x <- cbind(a,b)
chisq.test(x)
y <- c(a,b)
RR <- gl(4,1, length=8)  # or RR <- c(1,2,3,4,1,2,3,4)
CC <- gl(2,4, length=8)  # or CC <- c(1,1,1,1,2,2,2,2)
RR <- factor(RR) ; CC <- factor(CC) # is this necessary?
indepP <- glm(y~ RR + CC,poisson)
summary(indepP)
q()
```

All three tests are telling you the same thing: namely, behaviour is NOT independent of the level of emotionality, and of course you can just see by looking at the data that this is the case.
Other useful functions for contingency tables are

```
xtabs(),  mosaicplot(), fisher.test()
```

The last of these 3 functions relates to Fisher's 'exact' test, and makes use of the hypergeometric distribution. It is most often applied to 2×2 tables, but R has a version for an $r \times s$ table too.

An example added after the Sheffield floods in June 2007

The Sheffield flood of March 1864 was a disaster not easily forgotten, and an excellent description may be seen at

```
http://www2.shu.ac.uk/sfca
```

including the whole book 'A complete history of the great flood at Sheffield on March 11 and 12, 1864' by Samuel Harrison, and also details of the resulting insurance claims. (It is salutary to note that there was a total of 6987 claims, for a total of $£458,552$, of which $£273,988$ was paid out. This included $£123\ 11s\ 2d$ paid to my great great grandfather, who was a Saw Manufacturer on Kelham Island.) You may like to consider the contingency table given as Table 4, which shows Sheffield properties affected by the flood. The row names are respectively abbreviations of

	Totally Destroyed	Partially Destroyed	Flooded Only
Manufactories	12	25	80
Mills	4	17	22
Workshops	17	11	135
Shops	3	15	451
Dwellings	39	376	4096
Malthouses	2	22	162
Other	53	11	71

Table 4: Damage to property in the Sheffield flood of 1864

the following
Manufactories, tilts etc
Rolling, grinding, corn and other mills
Workshops, warehouses, store rooms etc,
Drapers', grocers' and other sale shops
Dwelling houses
Malt houses, breweries, public and beer houses
Other buildings.

Note added June 2006.
Julian Faraway's new book 'Extending the Linear Model with R: generalized Linear, Mixed Effects and Nonparametric Regression Models' (2006) contains the dataset

```
cmob
```

on Social class mobility from 1971 to 1981 in the UK.
This gives us the 6×6 contingency table describing Social class mobility from 1971 to 1981 for 42425 men from the United Kingdom census. The subjects were aged 45-64.
Key to data frame
y= Frequency of observation
class71= social class in 1971; this is a factor with levels 'I', professionals, 'II' semi-professionals, 'IIIN' skilled non-manual, 'IIIM' skilled manual, 'IV' semi-skilled, 'V' unskilled
class81= social class in 1981; also a factor, same levels as for 1971.
The source for these data was D. Blane and S. Harding and M. Rosato (1999) "Does social mobility affect the size of the socioeconomic mortality differential?: Evidence

from the Office for National Statistics Longitudinal Study" JRSS-A, 162 59-70.
Here is the dataframe 'cmob'.

```
         y class71 class81
1   1759       I       I
2    553       I      II
3    141       I    IIIN
4    130       I    IIIM
5     22       I      IV
6      2       I       V
7    541      II       I
8   6901      II      II
9    861      II    IIIN
10   824      II    IIIM
11   367      II      IV
12    60      II       V
13   248    IIIN       I
14  1238    IIIN      II
15  2562    IIIN    IIIN
16   346    IIIN    IIIM
17   308    IIIN      IV
18    56    IIIN       V
19   293    IIIM       I
20  1409    IIIM      II
21   527    IIIM    IIIN
22 12054    IIIM    IIIM
23  1678    IIIM      IV
24   586    IIIM       V
25   132      IV       I
26   419      IV      II
27   461      IV    IIIN
28  1779      IV    IIIM
29  3565      IV      IV
30   461      IV       V
31    37       V       I
32    53       V      II
33    88       V    IIIN
34   582       V    IIIM
35   569       V      IV
36   813       V       V
```

And here are some suggestions for the analysis. First construct the 6 by 6 contingency table

```
(x = xtabs(y ~ class71 + class81, data=cmob))
p = prop.table(x,1)
round(p,2) # to show the transition matrix, 1971- 1981
```

```
(p2 = p %*% p)
# this shows what happens after 2 jumps in the Markov chain.
p3 = p %*% p2 # and so on
```

Using repeated matrix multiplication, find the equilibrium probabilities of this assumed Markov chain.

Worksheet 9.

This exercise shows you use of the Poisson 'family' or distribution function for loglinear modelling.
Also it shows you use of the 'sink()' directive in R.
As usual, typing the commands below is a trivial exercise: what YOU must do is to make sure you understand the purpose of the commands, and that you can interpret the output.

First. The total number of reported new cases per month of AIDS in the UK up to November 1985 are listed below(data from A.Sykes 1986).
We model the way in which y, the number of cases depends on i, the month number.

```
y <- scan()
0 0 3 0 1 1 1 2 2 4 2 8 0 3 4 5 2 2 2 5
4 3 15 12 7 14 6 10 14 8 19 10 7 20 10 19
               # nb, blank line
i<- 1:36
plot(i,y)
aids.reg <- glm(y~i,family=poisson) # NB IT HAS TO BE lower case p,
# even though Poisson was a famous French mathematician.
aids.reg          # The default link is in use here, ie the log-link
summary(aids.reg) # thus model is log E(y(i))=a + b*i
fv <- aids.reg$fitted.values
points(i,fv,pch="*") # to add to existing plot
lines(i,fv)      # to add curve to existing plot
sink("temp")      # to store all results from now on
# in the file called "temp". The use of
# sink(), will then switch the output back to the screen.
aids.reg          # no output to screen here
summary(aids.reg) # no output to screen here
sink()            # to return output to screen
names(aids.reg)
q()               # to QUIT R
type temp         # to read results of "sink"
```

(The deviance, $2\Sigma y_i \log(y_i/e_i)$, in the above example is large in comparison with the expected value of χ^2_{34}, but since we have so many cells with $e_i < 5$, the approximation to the χ^2_{34} distribution will be poor. We could improve matters here, say by pooling adjacent cells to give larger values of e_i for the combined cells, then recomputing the deviance, and reducing the degrees of freedom of χ^2 accordingly.)
Table 5 gives the Confirmed and probable vCJD patients reported to the end of December 2001, sorted into males (the first number given in each pair) and females (the second number of the pair), according to their Year of onset of the illness.
Can we use a Poisson model for these data?

Table 5: vCJD data

1994	1995	1996	1997	1998	1999	2000
3,5	5,5	4,7	7,7	8,9	20,9	12,11

Table 6: GM tree releases

1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998
1	1	0	2	2	2	1	1	6	3	5

Here is another data-set of similar structure for you to investigate (once again, a gloomy subject I'm afraid).
The Independent, November 10, 1999, published an article headed
"GM trees pose risk of 'superweed' calamity".
This article gave a table, headed 'Released into the environment', that showed the following figures for GM tree species released into the environment through field trials. This is summarised in Table 6. Thus, for example, in 1988 there was just one GM species (European aspen) released into the environment, and in 1998 five new GM species were released. (In total, 24 different GM tree species were released. These figures are taken from 'at least 116 GM tree trials in 17 countries, involving 24 species'.) You could try a Poisson regression for $1, 1, 0, ..., 5$.

Table 7 is yet another example of newspaper data for which we might try Poisson regression. On October 18, 1995, 'The Independent' gave the following Table 7 of the numbers of ministerial resignations because of one or more of the following:
Sex scandal, Financial scandal, Failure, Political principle, or Public criticism, which we abbreviate to Sex, Fin, Fai, Pol, Pub, respectively as the rows of Table 8. The years start in 1945, with a Labour government, and 7 Resignations.

Is there any difference between Labour and Conservative in the *rate* of resignations?
To answer this question, we will need to include $log(t)$ as an offset in the Poisson regression, where t is the length of time of that Government, which we only know from these data to the nearest year.
The Independent also gave the breakdown of the totals in Table 7, which of course results in a very sparse table. This is Table 8. The 11 columns correspond to the same sequence of $45-51, 51-55, \ldots, 90-95$ as before.

(The resignation which precipitated the newspaper article in October 1995 may in

Table 7: Ministerial resignations, and type of Government.

Date	45-51	51-55	55-57	57-63	63-64	64-70	70-74	74-76	76-79	79-90	90-95
Gov't	lab	con	con	con	con	lab	con	lab	lab	con	con
Res's	7	1	2	7	1	5	6	5	4	14	11

Table 8: Breakdown of resignations data

Sex	0	0	0	2	1	0	2	0	0	1	4
Fin	1	0	0	0	0	0	2	0	0	0	3
Fai	2	1	0	0	0	0	0	0	0	3	0
Pol	3	0	2	4	0	5	2	5	4	7	3
Pub	1	0	0	1	0	0	0	0	0	3	1

fact have been counted under two of the above headings.)

Extra data added November 3, 2005, following the resignation of David Blunkett

Abstracting the new data from today's Independent 'Those that have fallen: ministerial exits 1997-2005'

I decided not to attempt to give the 'reasons' for resignation (too controversial).

D.Foster May 1997
R.Davies Oct 1998
P.Mandelson Dec 1998
P.Mandelson Jan 2001
S.Byers May 2002
E.Morris Oct 2002
R.Cook March 2003
C.Short May 2003
A.Milburn June 2003
B.Hughes April 2004
D.Blunkett Dec 2004
D.Blunkett Nov 2005.

I still lack data for the period Oct 1995- April 1997, but here is an R program for you to try

```
Term  Gov Res years
45-51 lab  7  6
51-55 con  1  4
55-57 con  2  2
57-63 con  7  6
63-64 con  1  1
64-70 lab  5  6
70-74 con  6  4
74-76 lab  5  2
76-79 lab  4  3
79-90 con 14 11
90-95 con 11  5
97-05 lab 12  8
```

Having put this dataset in as the file "Resignations" given above, here's how we will analyse it. Note that this program also enables us to plot, in Figure 13
Res against log(years)
using different coloured points for the 2 levels of the factor Gov (blue for conservative,

and red for labour, unsurprisingingly).

```
 Resignations <- read.table("Resignations", header=T)
 attach(Resignations)
 plot(Res ~ log(years), pch=19, col=c(4,2)[Gov])
# Use palette() to find out which colour corresponds
# to which number
title("Ministerial Resignations against log(years)")
legend("topleft", legend= c("conservative", "labour"), col=c(4,2), pch=19)
# for onscreen location of legend box, you can replace
# "topleft" by locator(1)
# and use the mouse for positioning
first.glm <- glm(Res ~ Gov + log(years), poisson); summary(first.glm)
next.glm<- glm(Res ~ Gov + offset(log(years)), poisson); summary(next.glm)
last.glm <-  glm(Res ~log(years),poisson); summary(last.glm)
l <- (0:25)/10
fv <- exp(0.3168 + 0.9654*l)# to plot fitted curve under last.glm
lines(l,fv)
```

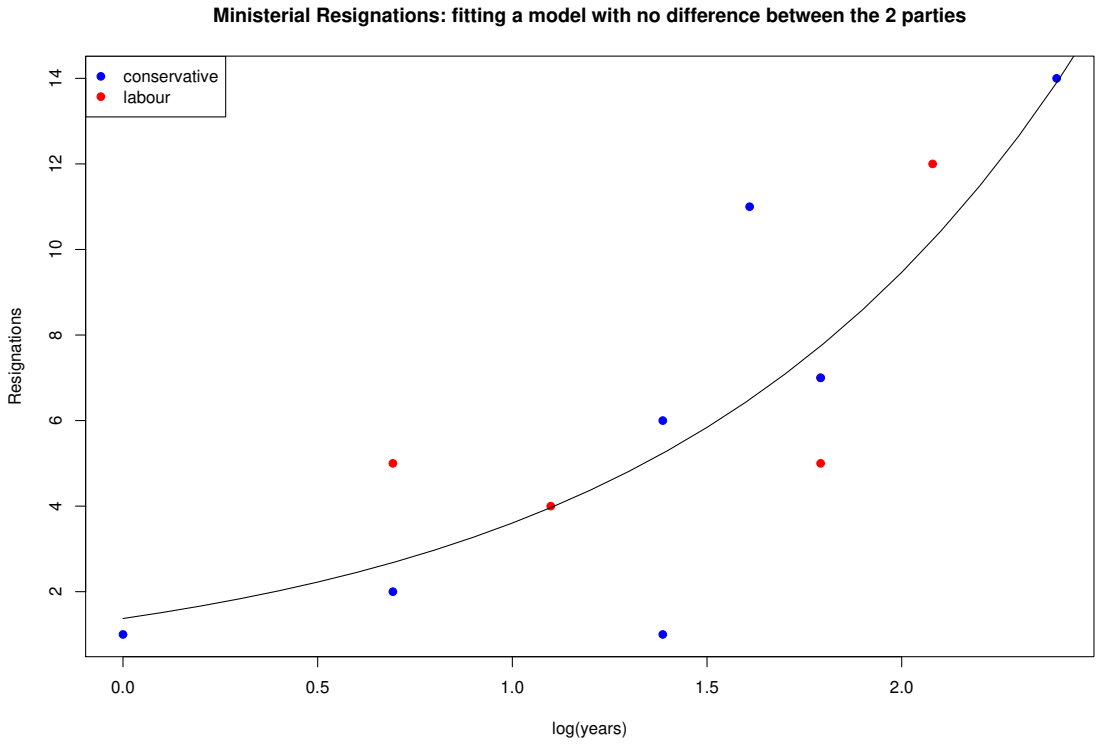

Figure 13: Ministerial resignations

And here's another dataset for Poisson regression. This is taken from the British Medical Journal, 2001;322:p460-463. The authors J.Kaye *et al* wrote 'Mumps,

measles, and rubella vaccine and the incidence of autism recorded by general practitioners: a time trend analysis' and produced the following table, for which the column headings are
Year of diagnosis, Number of cases, Number of person-years at risk, Estimated incidence per 10,000 person-years, median age (in years) of cases.

```
Diag  Cases Pyears  Inc  Age
1988     7  255771  0.3  6.0
1989     8  276644  0.3  5.6
1990    16  295901  0.5  5.0
1991    14  309682  0.5  4.4
1992    20  316457  0.6  4.0
1993    35  316802  1.1  5.8
1994    29  318305  0.9  4.6
1995    46  303544  1.5  4.3
1996    36  260644  1.4  4.7
1997    47  216826  2.2  4.3
1998    34  161664  2.1  5.4
1999    13   60502  2.1  5.9
```

These data are obtained from UK general practices.

Accidents for traffic into Cambridge, 1978-1981.
How does the number of accidents depend on traffic volume, Road and Time of day? We have data on the number of accidents y in this 3-year period, for Trumpington Rd, Mill Road, respectively, at 3 different times of day, 7-9.30 am,9.30am-3pm, 3-6.30 pm, respectively, with v as the corresponding estimate of traffic density. Naturally we expect the accident rate to depend on the traffic density, but we want to know whether Mill Rd is more dangerous than Trumpington Rd (it probably still is, but Trumpington Rd now has a cycle way) and whether one time of day is more dangerous than another. Our model is $y_{ij} \sim Po(\mu_{ij})$ with $log(\mu_{ij}) = \alpha + \beta_i + \gamma_j + \lambda log(v_{ij})$ for $i = 1, 2$ corresponding to Trumpington Rd, Mill Rd, respectively, and $j = 1, 2, 3$ corresponding to 7-9.30 am, 9.30am-3pm, 3-6.30 pm respectively. (As usual, $\beta_1 = 0$ and $\gamma_1 = 0$.)

```
y <- scan()
11 9 4 4 20 4

v <- scan()
2206 3276 1999 1399 2276 1417

rd  <- c(1,1,1,2,2,2)#rd=1 for Trumpington Rd,rd=2 for Mill Rd
ToD <- c(1,2,3,1,2,3)#ToD =1,2,3 for 7-9.30 am,9.30am-3pm,3-6.30 pm resp'ly
#but more elegantly,
rd  <- gl(2,3, length=6, labels=c("TrumpingtonRd","MillRd"))
ToD <- gl(3,1,length=6, labels=c("7-9.30am", "9.30am-3pm","3-6.30pm"))
plot.design(y/v ~ rd + ToD) # for quick eye-ball check
```

```
accidents<- glm(y~RD +ToD + log(v),family=poisson)
summary(accidents)
```

The resulting 'design plot' is given in Figure 14. The residual deviance of 1.88 on 1 df shows that the model fits well. We can see that Mill Rd is indeed more dangerous than Trumpington Rd, and the 9.30am-3pm time of day is less dangerous than the other two, which are about the same as each other.

```
drop.road <- update(accidents,.~. -RD) ; summary(drop.road)
drop.ToD  <- update(accidents,.~.-ToD) ;summary(drop.ToD)
new <- c(1,2,1, 1,2,1);NEW <- factor(new)
# or, more elegantly, as follows
NEW <- ToD; levels(NEW) <- c(1,2,1)
acc.new <- glm(y~RD+NEW+lv,poisson); summary(acc.new)
```

Can you see the point of the factor "NEW"?

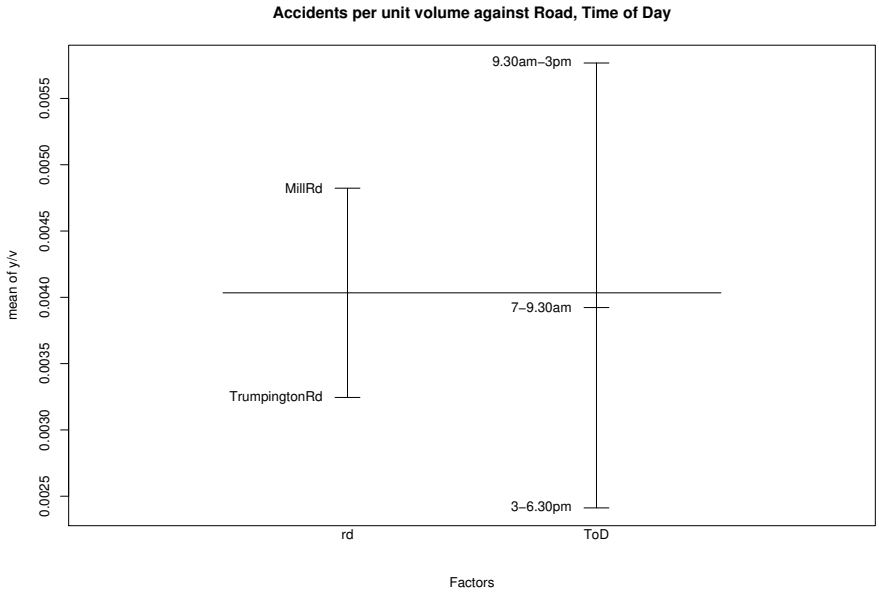

Figure 14: Mill Road and Trumpington Road, and Time of Day

Predicting the Beijing Olympics medals for Team GB, August 2008
The Independent, 6 August 2008, presents the dataset shown in Table 9 on 'British medal hauls at the past 10 Olympics'.

First of all we could look at this dataset as a 10×3 contingency table, to see if the distribution of Total medals into Gold, Silver and Bronze remains approximately homogeneous over these 10 sets of Games. (The sports enthusiasts will already know that the total number of Events, and the total number of competing countries both change considerably from 1968 to 2008.) However, if you just set up the table above as a suitable matrix, you will find that

```
chisq.test(x)
```

	Gold	Silver	Bronze
Athens 2004	9	9	12
Sydney 2000	11	10	7
Atlanta 1996	1	8	6
Barcelona 1992	5	3	12
Seoul 1988	5	10	9
Los Angeles 1984	5	11	21
Moscow 1980	5	7	9
Montreal 1976	3	5	5
Munich 1972	4	5	9
Mexico City 1968	5	5	3

Table 9: British Olympics medals from 1968 to 2004

results in a chisq statistic of 19.8 on 18 df. Hence in any given year, we expect the total number of medals to fall into the categories Gold, Silver, Bronze respectively with probabilities $0.242, 0.333, 0.425$ respectively.
Can we predict the total number of medals for Team GB in 2008?
Here is my suggestion.

```
Total <- Gold + Silver + Bronze ; Total
Year <- 10:1; first.glm = glm(Total~Year, poisson);summary(first.glm)
```

But this has residual deviance of 18.4 on 8 df, so the model fails to fit. Looking at it a bit harder, we can see the reason why: the Los Angeles 1984 games gives a large residual, and a surprisingly large Total of 31 medals. We can justify omitting this datapoint from our model, as 1984 was a 'strange' year in this context: almost all the Eastern Bloc countries boycotted these particular games. Thus our next model is

```
next.glm <- glm(Total[-6] ~ Year[-6], poisson)
```

Very satisfactorily, this brings the residual deviance right down: it is now 6.8 on 7 df.
Emboldened by this success, we will now predict the Team GB Total for 2008.

```
> library(MASS)
> new.data <-  data.frame(Year= 11)
> predict.glm(next.glm,newdata= new.data, type="response",se.fit=T)
$fit
       1
29.15959

$se.fit
       1
4.122133
> 29.15959- 2*4.122133 ; 29.15959 + 2*4.122133
[1] 20.91532
[1] 37.40386
```

So the predicted Total number of medals is 29.2, for which the confidence band is about $(20.9, 37.4)$, which I trust is wide enough for me to be proved correct in due course

August 25, 2008: Team GB has a Total of 47 medals, consisting of 19 Gold, 13 Silver and 15 Bronze. So the Team GB performance was much better than our past records led us to expect.

Note added March 2008: fitting a non-linear quasi-Poisson model to actuarial data

We may want to move outside the rather restricted framework of the Generalized Linear Model, and now R users may avail themselves of the powerful and flexible Generalized Nonlinear Model package, written by David Firth and Heather Turner of Warwick University.

For example, actuaries use the Lee-Carter model to describe the dependence of mortality on age and calendar year. Suppose we have data on the deaths D_{ay}, at age a which we will assume in our example takes values $20, 21, \ldots, 99, 100$ and during calendar year y. We will assume y takes values $1947, 1948, \ldots, 2003$. Let e_{ay} represent the 'exposure' corresponding to D_{ay} (for example this might be the number of person-years at risk in that particular category). Assume further that D_{ay} has expectation μ_{ay}, and variance $\phi\mu_{ay}$, for some unknown μ_{ay}, ϕ. We model the dependence of μ_{ay} on the age and the year. A Poisson model would have $\phi = 1$, but it makes sense to allow ϕ to be different from 1 (because we expect over-dispersion relative to the Poisson, in which case $\phi > 1$). The Lee-Carter model states that

$$\log(\mu_{ay}/e_{ay}) = \alpha_a + (\exp \beta_a)\gamma_y$$

for $a = 20, 21, \ldots, 99, 100$ and $y = 1947, 1948, \ldots, 2003$. (We have written the model in this form since it makes sense to have the multiplier $\exp \beta_a > 0$ always.)

For parameter identifiability, we will take

$$\alpha_{20} = 0, \beta_{20} = 0, \gamma_{1947} = 0.$$

Then, assuming we have read the data into R, and set up Age and Year as factors, the commands needed to fit the Lee-Carter model are

```
library(gnm)
first.gnm = gnm(Deaths ~ Age + Mult(Exp(Age),Year), constrain=c(82,163),
family="quasipoisson", offset=log(Exposure))
summary(first.gnm)
```

The 'constrain=c(82,163)' looks odd, but you'll find it's simply a matter of counting the number of parameters in the model. You can omit 'constrain=c(82,163)', and you will fitting an equivalent model, but I found the output harder to interpret as we no longer have the $\beta_{20} = 0, \gamma_{1947} = 0$ constraint.

Helpful plots are obtained, for example, by

```
library(relimp) ; library(qvcalc)
AgeContrasts = getContrasts(first.gnm, 82:162)
plot(AgeContrasts)
```

Worksheet 10.

Here we use the Poisson distribution for log-linear modelling of a two-way contingency table, and compare the results with the corresponding binomial formulation. We construct a fictitious 3-way table to illustrate Simpson's paradox.

The Daily Telegraph (28/10/88) under the headline 'Executives seen as DrinkDrive threat' presented the following data from breath-test operations at Royal Ascot and at Henley Regatta (these being UK sporting functions renowned for alcohol intake as well as racehorses and rowing respectively).

Are you more likely to be arrested, if tested, at R.A. than at H.R.?

You see below that a total of (24 + 2210) persons were breathalysed at R.A., and similarly a total of (5 + 680) were tested at H.R. Of these, 24 were arrested at R.A., and 5 at H.R. Hence the proportions arrested at R.A., H.R. respectively are $0.0107, 0.0073$. We wish to test whether these are significantly different. In other words, we wish to test whether the breath-test result (arrested or not arrested) is independent of the location (R.A. or H.R.).

```
 r <- scan()
24 2210 # Royal Ascot
5  680  # Henley Regatta

Row <- c(1,1,2,2) ; Col <- c(1,2,1,2);ROW <- factor(Row);COL <- factor(Col)
# Col= 1 for ARRESTED,Col= 2 for NOT arrested
   saturated <- glm(r~ ROW*COL,family=poisson)# for a perfect fit
independence <- glm(r~ ROW+COL,family=poisson)
summary(saturated)
```

This shows us that the ROW.COL term can be dropped: refer .39/.49 to $N(0,1)$.

```
summary(independence)
```

This shows us that the independence model fits well: refer the residual deviance of 0.67733 to χ^2 with 1 df.

Here is another way of answering the same question.

```
a <- c(24,2210) ; b<- c(5,680) ; tot <- a+b; p <- a/tot
Row <- c(1,2) ; ROW<- factor(Row)
indep <- glm(p~  1 ,family=binomial,weights=tot)
```

and you will see that this last model also has residual deviance of 0.67733 with 1 df. Recall that two independent Poisson random variables conditioned on their sum gives a binomial.

Telling the same story are

```
chisq.test(rbind(a,b)) # for an asymptotically equivalent result.
fisher.test(rbind(a,b)) # for Fisher's 'Exact' test
```

Now a little piece of fantasy, with a serious educational purpose (of course).

It can be very misleading to "collapse" a 3-way table, say Ascot/Henley × Arrest/NonArrest × Men/Women over one of the dimensions, say Men/Women. For example (pure invention) suppose the above 2×2 table was in fact

```
24=23,1   2210=2,2208
5 =3,2     680=340,340
```

the first number of each pair being the number of men, the second being the number of women. We analyse this 3-way table, again using a loglinear model, and the Poisson distribution.

```
r <- scan()
23  2  1  2208
3  340 2  340

Row <- c(1,1,1,1,2,2,2,2);Col <- c(1,2,1,2,1,2,1,2)
gender <- c(1,1,2,2,1,1,2,2)
ROW<- factor(Row) ; COL <- factor(Col) ; GENDER<- factor(gender)
sat <- glm(r~ROW*COL*GENDER ,poisson)  ; summary(sat)
```

Of course we have invented an example with a strong 3-way interaction. This means that the relation between any two of the factors, say rows and columns, depends on the level of the third factor, here the Gender. You should consider the following two questions.
How does the arrest rate for men vary between Ascot and Henley?
How does the arrest rate for women vary between Ascot and Henley?
This is an example of 'Yule's paradox'. (An historical note: G.U.Yule was a Fellow of St John's college, Cambridge at the start of the last century.) It must be admitted that most people outside Cambridge call it Simpson's paradox (Simpson wrote about 'his' paradox in 1951, whereas Yule had written about it about 50 years earlier.)
Here is another example of a 3-way table, with data collected by M.Raza (2003) on 50 recent famous movies. We look at the interdependence of the following 3 factors:
whether or not the movie gets a BAFTA award (1 if successful, 0 otherwise)
whether or not the movie gets a Golden Globe (1 if successful, 0 otherwise)
whether or not the movie gets an Academy Award (1 if successful, 0 otherwise).
This gives us Table10.

Thus, for example, there were 14 films that won a BAFTA, an Academy Award

bafta=0	aa=0	aa=1
gg=0	y=18	y=3
gg=1	y=1	y=4
bafta= 1	aa = 0	aa = 1
gg=0	y=6	y=2
gg=1	y=2	y=14

Table 10: Bafta, Academy and Golden Globe Awards for 50 famous films

and a Golden Globe, and 18 that won none of these.
By use of

```
y <- scan()
18 3 1 4 6 2 2 14
                # blank line
```

```
bafta <- gl(2,4), length=8, labels=c(0,1))
gg <- gl(2,2, length=8,labels=c(0,1)); aa <- gl(2,1,length=8,labels=c(0,1))
glm(y ~ bafta+ gg + aa, poisson)
```

show that these 3 binary variables are non-independent (refer 37.73 to χ^2_4). Find out what happens if you try

```
glm(y ~ (bafta+ aa)*gg, poisson)
xtabs(y ~gg + aa + bafta) # for presenting a 3-way table
```

This results in

```
, , bafta = 0

   aa
gg   0  1
  0 18  3
  1  1  4

, , bafta = 1

   aa
gg   0  1
  0  6  2
  1  2 14
```

Now try

```
ftable(xtabs(y ~gg + aa + bafta)) # ftable means 'flat table'
```

New for May 2010: Crime and temperature
Under the headline "Police feel the heat as crime rises along with temperature" The Independent of May 26, 2010, gives the following data on 'Calls to Greater Manchester Police: what a difference 12 deg C makes':
For the weekend of May 21-23, when the Manchester temperature had a high of 27 deg C, the number of calls to the GMP on Friday, Saturday, Sunday were $3702, 4193, 3825$ respectively. The corresponding figure for the weekend of May 14-17, when the Manchester temperature had a high of 15 deg C, were $3200, 3414, 3484$ respectively. Try the following program, and interpret the results.

```
n <- c(3702,3200,4193,3414,3825,3484)
Heat <- gl(2,1, length=6, labels = c("hot", "cool"))
Day <- gl(3,2, length=6, labels = c("Fri", "Sat","Sun"))
first.glm <- glm( n ~ Heat + Day, poisson)
summary(first.glm)
summary(glm(n ~ Heat + Day, family =quasipoisson))
```

Worksheet 11.

Here we plot the contours for the Poisson regression log-likelihood surface corresponding to the 'Aids' dataset used in Worksheet 10.

You will see how to define and use a function in R.

```
y <- scan("aids")          # same data as before.
i <- 1:36 ; ii<- i-mean(i) # to make the surface a better shape
aids.reg <- glm(y~ii,poisson)
summary(aids.reg, cor=T)
```

Our model is $y_i \sim Po(\mu_i)$, independent, with $log(\mu_i) = a + b * ii$. We see that our maximum likelihood estimates are $\hat{a} = 1.51 +/- .09$ and $\hat{b} = .08 +/- .008$. We now compute the loglikelihood function, in terms of the parameters a, b.

```
loglik <- function(a,b){
  loglik <- - sum(exp(a+b*ii)) + a*t1 +b*t2
  loglik
}
```

Here t1 and t2 are the sufficient statistics, thus

```
t1 <- sum(y) ; t2 <- sum(ii*y)
```

We plot the loglikelihood surface for $1.3 \leq a \leq 1.7$ and $.05 \leq b \leq .09$.

```
a <- 0:20 ; a <-  a*(.02) + 1.3
b <- 0:20 ; b <-  b*(.002) + 0.05
zz <- 1: (21*21) ; z <- matrix(zz,21,21) # to set up z as a matrix
for (x in 1:21){
 for (y in 1:21){
   z[x,y] <- loglik(a[x],b[y])
 }
}
z[1,] # to see the first row of the matrix
contour(a,b,z, xlab="a", ylab="b")
points(1.51, 0.08) # to put the mle on the graph
```

The elliptical contours are shown in Figure 15. Note that the elliptical contours show the negative correlation between the estimates of a and b.

```
image(a,b,z, col=terrain.colors(30))
persp(a,b,z,theta = 30, phi = 30, expand = 0.5, col = "lightblue")
```

also give nice plots, as shown in Figures 16, 17 respectively.

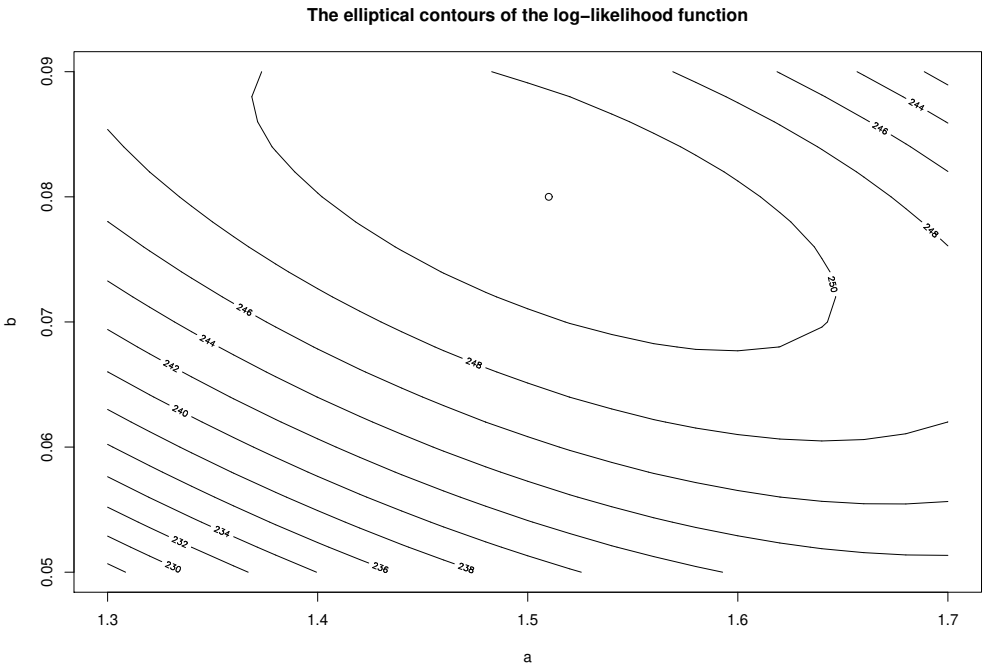

Figure 15: The contours of the log-likelihood function

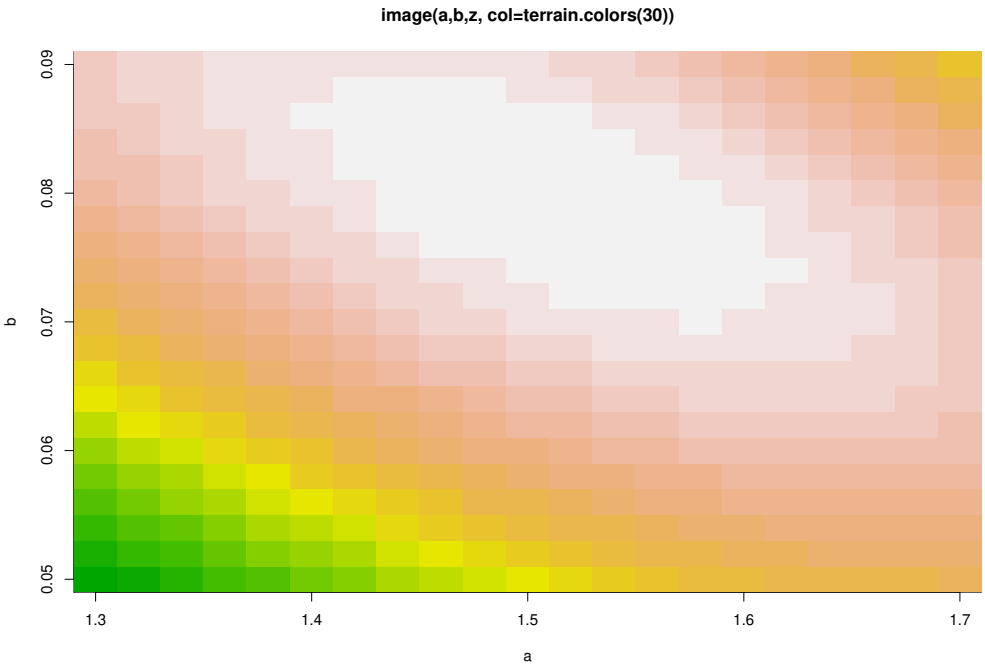

Figure 16: An image plot of the log-likelihood function

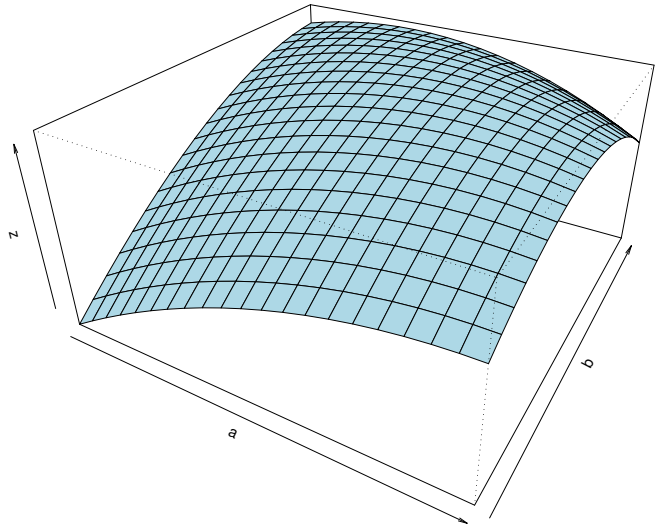

Figure 17: A perspective plot of the log-likelihood function (in Cambridge blue)

Worksheet 12.

More on Regression Diagnostics: the Hat matrix
First a very small simulation, to show you a point of high **leverage**.

```
set.seed(1.05) # to get same picture every time
x1 <- rnorm(10) ; y1 <- rnorm(10)
x <- c(x1,25) ; y <- c(y1,6)
plot(x,y)
big.lm <- lm(y~x) ; summary(big.lm) ; abline(big.lm, lty =1)
little.lm <- lm(y1~ x1) ; summary(little.lm) ; abline(little.lm, lty=2)
legend("topleft", lty = c(1, 2),
 legend = c("all points", "all but the point of high leverage"))
postscript("ws12.ps")
plot(x,y)
abline(big.lm, lty =1)
abline(little.lm, lty=2)
legend("topleft", lty = c(1, 2),
 legend = c("all points", "all but the point of high leverage"))
dev.off()
rm(x1,y1)# we use these as column headings in the next example
```

The corresponding graph is Figure 18. So you see that $(x1, y1)$ is a sort of 'cloud' of points, generated from the normal distribution, mean 0, variance 1, and so that there is no relation between $y1$ and $x1$. We should see that the resulting linear regression shows a rather low R^2.

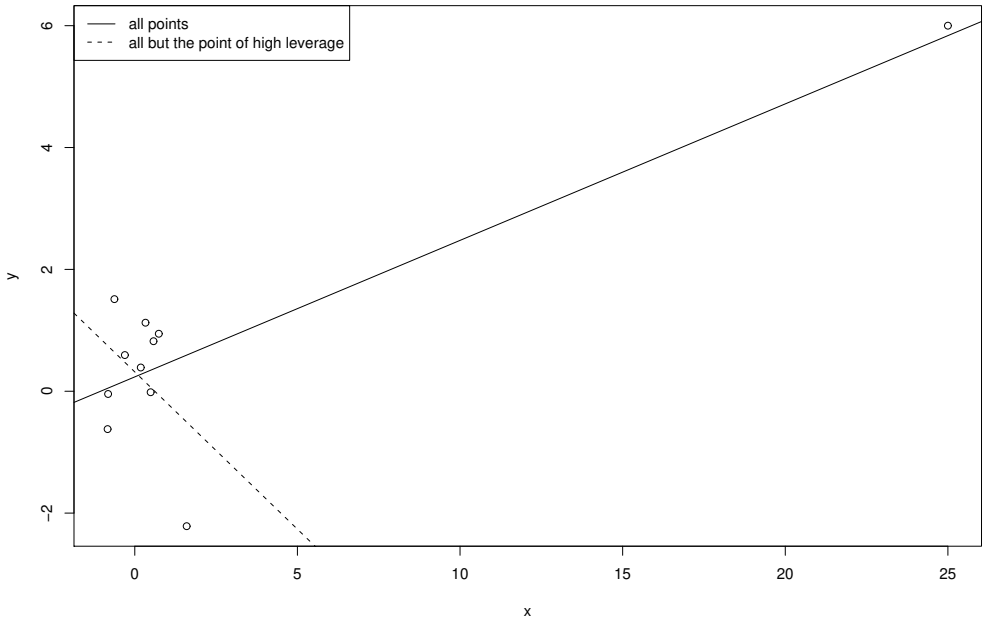

Figure 18: An example of a single point of high leverage

But when you augment this 'data' set by the 'special' point $(25, 6)$, the fit of the straight line is apparently much better, with R^2 much nearer to 1. Of course the graph shows you that the new fitted line is almost a perfect fit at this $(25, 6)$.

Table 11 shows a classic "data" set, cunningly constructed by the late F.J.Anscombe.
Read this data-set by

x1	y1	x2	y2	x3	y3	x4	y4
10.0	8.04	10.0	9.14	10.0	7.46	8.0	6.58
8.0	6.95	8.0	8.14	8.0	6.77	8.0	5.76
13.0	7.58	13.0	8.74	13.0	12.74	8.0	7.71
9.0	8.81	9.0	8.77	9.0	7.11	8.0	8.84
11.0	8.33	11.0	9.26	11.0	7.81	8.0	8.47
14.0	9.96	14.0	8.10	14.0	8.84	8.0	7.04
6.0	7.24	6.0	6.13	6.0	6.08	8.0	5.25
4.0	4.26	4.0	3.10	4.0	5.39	19.0	12.50
12.0	10.84	12.0	9.13	12.0	8.15	8.0	5.56
7.0	4.82	7.0	7.26	7.0	6.42	8.0	7.91
5.0	5.68	5.0	4.74	5.0	5.73	8.0	6.89

Table 11: Anscombe's cunning quartet

```
data(anscombe) # as it is already an R dataset
attach(anscombe)  # to put the column headings on
```

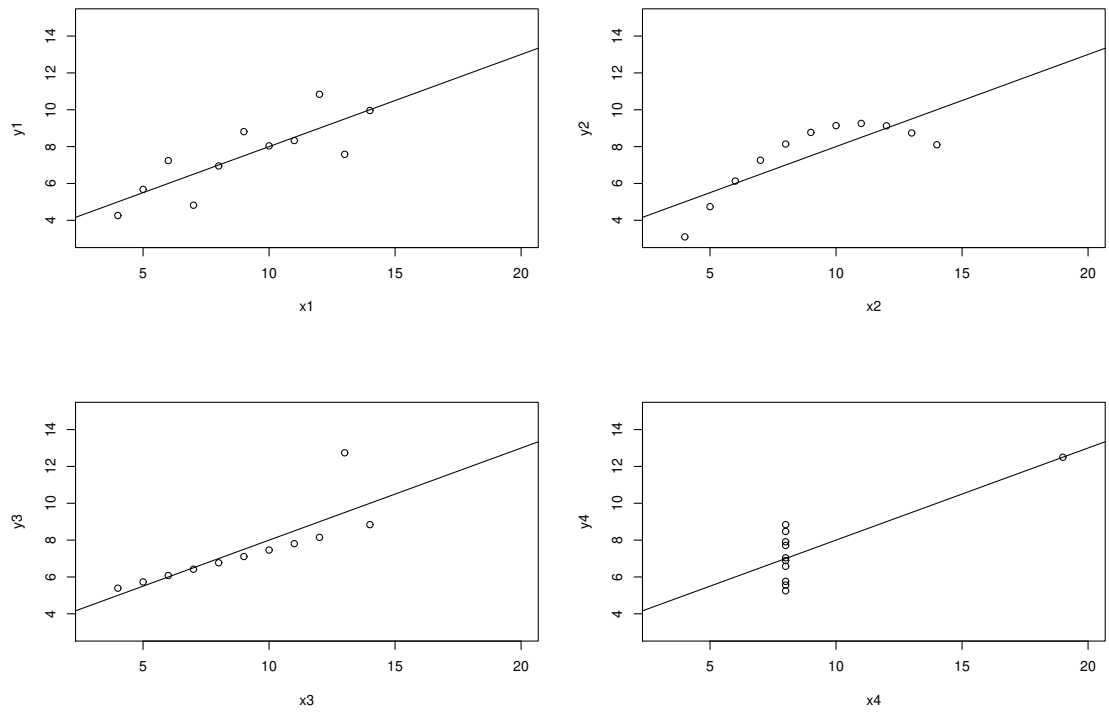

Figure 19: Four identical regression lines: which one do you trust?

```
par(mfrow=c(2,2))
plot(y1~x1, xlim=c(3,20), ylim=c(3,15))
abline(lm(y1~x1))
plot(y2~x2, xlim=c(3,20), ylim=c(3,15))
abline(lm(y2~x2))
plot(y3~x3, xlim=c(3,20), ylim=c(3,15))
abline(lm(y3~x3))
plot(y4~x4,xlim=c(3,20), ylim=c(3,15))
abline(lm(y4~x4))
summary(lm(y1 ~x1)) # .... and so on
```

The resulting 4 graphs are given as Figure 19.

We will now look at the Hat matrix, H. This will involve using R for some linear algebra.
Reminder, in the general linear model

$$Y_i = \beta^T x_i + \epsilon_i, \ 1 \leq i \leq n$$

equivalently

$$Y = X\beta + \epsilon,$$

where X is an $n \times p$ matrix, assumed to be of rank p, the Least Squares Estimator $\hat{\beta}$ of β is $\hat{\beta} = (X^T X)^{-1} X^T Y$, and so the fitted values $\hat{Y}$ may be written

$$\hat{Y} = X\beta = HY,$$

thus defining the matrix H as $H = X(X^TX)^{-1}X^T$. (You may check that $H = H^T$, and $HH = H$, further $tr(H) = p$.) Note that

$$\hat{Y}_i = \Sigma h_{ij} Y_j :$$

this shows you the special role of (h_{ii}), the diagonal elements of H, called the **leverages**. You could now try some influence or leverage plots: for example

```
X <- cbind(1,x1) # to construct the design matrix in lm(y1~x1)
H <- X %*% solve(t(X) %*% X) %*% t(X) # to construct the Hat matrix
# %*% is the symbol for matrix multiplication
# t() is the matrix transpose function
h <- diag(H) # to construct the vector of the diagonal els. of H
mean(h)     # must be (2/11), by general theory
index <- 1:11
plot(index,h) # for a plot of the leverages
hlarge <- (2*2)/11
abline(h=hlarge) # so that we can pick out points with large leverages
?hat
```

See E.R.Tufte, "The Visual Display of Quantitative Information".

Worksheet 13.

New for 2001: football arrests, the Poisson and the negative binomial. These data come from the National Criminal Intelligence Service, and represent Football- related arrest figures for 2000/2001, classified by 'Team Supported', for each of the four UK divisions. You can see the data for yourselves on

`http://www.ncis.gov.uk/press/29_01.html`

which also gives the names of the clubs, (Arsenal, Aston Villa etc) and further data giving the breakdown into types of offence (drink-related, ticket-touts etc). We use this dataset as an illustration of *over-dispersion* relative to the Poisson distribution, and how to fit an appropriate model.
Premiership, 1stDivision, 2ndDivision, 3rdDivision are the 4 columns of total arrests below, which you can read via

```
read.table(" ", header=T)
```

```
54  38 16  3
60  38  6 15
80  61 52 25
17  44 33 40
74  83  0 17
35   7  5  5
28  11  6 18
108 17 13 26
18  27 93 15
119 19 13  9
69  26  7 12
78  14 19 59
148 51 13  3
150 31 47 20
105 41 13 10
191 29 25  0
15  90 13 11
166 83 49  9
54  14 72  5
54  12 41 12
NA  20 10 20
NA  24 27 10
NA  11 24  1
NA  25  4  6
```

Here's a suggestion about how to proceed. Let us consider initially only the numbers from the first column: call these $y_1, \cdots, y_n$, say, where $n = 20$. First, we might try the model:
$y_1, \cdots, y_n$ is a random sample from the Poisson distribution, mean μ. Of course this is very quick to fit, via

```
summary(glm(y~1, poisson))
```

and what is perhaps hardly surprising, we find it fits VERY badly (deviance= 644.56, df = 19). The spread of the frequencies is much greater than we would expect from a Poisson distribution with mean 81.15 ($= \bar{y}$).
So, let's try something new. We will derive the negative binomial as a generalisation of the Poisson: this is often appropriate for 'accident' type data. Following the derivation given in Venables and Ripley's book, we assume
$Y|E = e$ is Poisson with mean μe
and θE is a gamma random variable, with parameter θ (ie θ is its *shape* parameter).
Hence E has mean 1, variance $1/\theta$, and
Y has mean μ, and variance $\mu + \mu^2/\theta$.
You may then check that the frequency function of Y is

$$f_Y(y; \mu, \theta) = \frac{\Gamma(\theta + y)\mu^y \theta^\theta}{\Gamma(\theta) y! (\mu + \theta)^{\theta + y}} \text{ for } y = 0, 1, \ldots .$$

As θ tends to ∞, this becomes an ordinary Poisson again. For finite θ, it is the negative binomial, with parameters μ, θ. Show that the resulting log-likelihood for the data above may be written as $L(\mu, \theta)$, which is

$$\Sigma[log\Gamma(\theta + y_i) + y_i log(\mu) + \theta log(\theta) - log\Gamma(\theta) - (\theta + y_i) log(\mu + \theta) - log\Gamma(y_i + 1)].$$

Now find the derivative of this with respect to μ, and hence show that

$$\hat{\mu} = \bar{y}.$$

Finding the mle of θ is more tricky: we cannot find a closed form expression for it. Here are 2 possible ways to find it numerically: both of them will teach you something:
i) Use an 'off-the-shelf' function, thus

```
library(MASS)
glm.nb(y~1)  # fitting the negative binomial, using a V&R function
```

This gives $\hat{\theta} = 2.328 (se = 0.717)$, and deviance= $21.354 (19 df)$.
To show you how different this negative binomial is from the Poisson with the same mean, namely 81.15, I have plotted the two frequency functions on the same graph, as shown in Figure 20. This is achieved by

```
x = 0:300
y1 = dpois(x,81.15)
y2 = dnbinom(x, size=2.33, mu=81.15)
matplot(x, cbind(y1,y2), type="l", ylab = "frequency function")
legend("topright", lty=c(1,2),
legend=c("Poisson with mean 81.15",
"negative binomial with mean 81.15, size=2.33"))
```

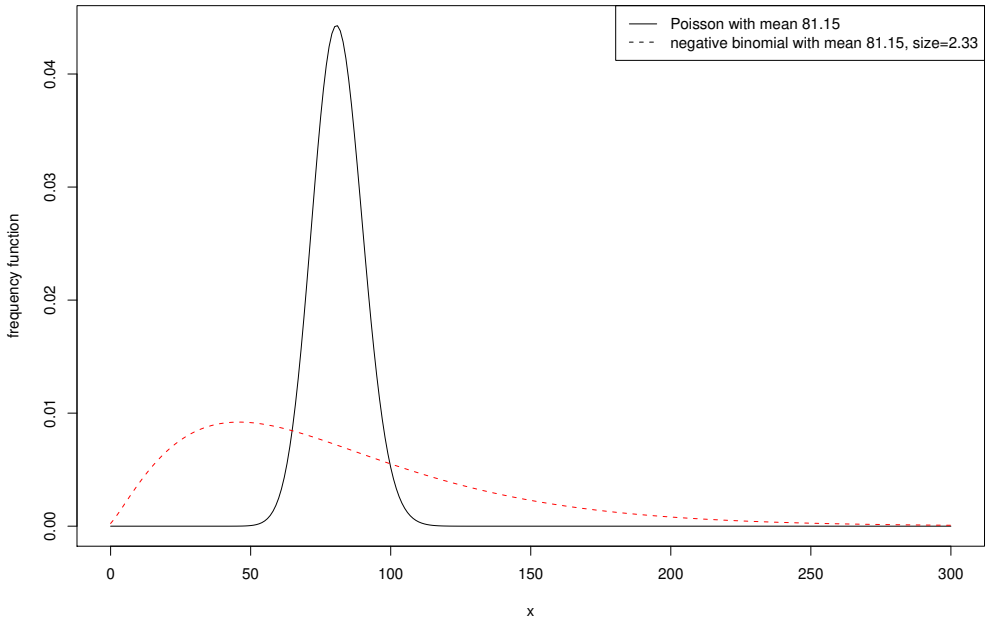

Figure 20: Comparing the Poisson and the negative binomial

ii) Set up the function $-L(\mu, \theta)$ in R, (see below) and minimise this 2-parameter function in R, finding also the matrix of 2nd derivatives at the same time, in order that you can then invert this to derive the asymptotic covariance matrix of the mle's, $(\hat{\mu}, \hat{\theta})$.

```
loglik <- function(p){
#actually this is minus log-lik, since nlm() MINIMISES
th <- p[1] ; mu <- p[2]
-(sum(lgamma(th+y)+y*log(mu/(mu+th))
+th*log(th/(mu+th))-lgamma(th)-lgamma(y+1)))
}
nlm(loglik,p=c(2,80), hessian=T)
```

When I repeated these calculations for the other 3 divisions, I found that my estimates of θ for each of the 4 divisions were, respectively

$$2.328(0.717), 2.525(0.745), 1.275(0.371), 1.51(0.48)$$

and I have to say that I am unable to interpret the fact that θ is around 2: perhaps YOU can offer an explanation for this? (Unfortunately total match attendance figures, which must surely be relevant, seem to be unavailable.) One thing you will notice is that while the Poisson distribution with mean 81.15 looks very symmetric (and Gaussian), the negative binomial with parameters $81.15, 2.33$ is highly skew, with a long tail to the right.
Go back to your expression for $\partial L/\partial \mu$: of course we know that this has expected value equal to zero. Take the derivative of this expression with respect to θ, and then take the expectation. Hence show that, asymptotically, $\hat{\mu}, \hat{\theta}$ are uncorrelated.

Yudi Pawitan points out that although the deviance for the negative binomial cannot be interpreted as a goodness of fit test (the chi-sq distribution theory does not apply) we can do an 'eyeball' test of the goodness of fit as follows

```
yran <- rnbinom(20,mu=81.15, size=2.32)
# to generate a sample from this distribution
qqplot(y,yran) ; abline(0,1)
```

Note that for θ unknown, the negative binomial does NOT lie within the glm framework. But consider the following special case. Suppose θ is known, and $y_1, \ldots, y_n$ are independent negative binomial, with parameters $\mu_1, \ldots, \mu_n$ and common parameter θ. Consider the following link function

$$\mu_i/(\mu_i + \theta) = \exp \beta^T x_i$$

for given covariates $x_1, \ldots, x_n$. Show that this gives a glm with the canonical link, and obtain the equations for $\hat{\beta}$.

Finally, here's a recent set of data on soccer arrests, for the 4 divisions in England and Wales. Under the headline 'High-tech hooligans lure youths to football 'firms'', The Times, on August 19, 2003, gives the following data for the 2002-2003 season. The column headings are
totarr = total arrests, and viol= arrests for violent disorder.

```
Premiership
                totarr viol
ManchesterUtd    186   13
Sunderland       185    6
NewcastleUtd     139    2
BirminghamCity   138   27
Liverpool        133    8
Chelsea          122    5
Everton          119    3
ManchesterCity   110    6
LeedsUtd         104    5
AstonVilla       101   23
T'hamHotspur      88    9
Middlesborough    67    0
W,Brom.Albion     63    2
W.HamUtd          57    3
Arsenal           53    2
BlackburnRovers   51    0
BoltonWanderers   45    1
Southampton       40    3
Fulham            19    0
CharltonAthletic  17    1

Division One
```

```
                totarr viol
NottinghamForest  141   6
Burnley           121   7
SheffieldUtd      106  27
SheffieldWed      104  18
LeicesterCity      80  14
DerbyCo            72   6
StokeCity          69   4
Portsmouth         52   5
NorwichCity        43   5
Brighton&HoveAlb   35   6
CrystalPalace      35   2
PrstonNorthEnd     30   1
BradfordCity       28   3
CoventryCity       28   0
IpswichTown        28   1
RotherhamUtd       28   0
Reading            19   2
GrimsbyTown        18   0
Millwall           18   2
Gillingham          9   0

Division Two
                totarr viol
CardiffCity       149  11
PlymouthArgyle     91   3
BristolCity        70   6
Barnsley           59  24
QPR                53   5
HuddersfieldTown   52  17
SwindonTown        51   2
PortVale           46   3
LutonTown          42  13
WiganAthletic      41   3
MansfieldTown      32   2
OldhamAthletic     23   2
NorthamptonTown    21   5
TranmereRovers     15   0
Brentford          13   1
Chesterfield       10   0
Blackpool           9   0
PeterboroughUtd     9   0
CheltenhamTown      8   1
ColchesterUtd       8   0
NottsCounty         8   0
CreweAlexandra      7   0
StockportCounty     6   1
```

```
WycombeWanderers   3   1

 Division Three
                 totarr viol
LincolnCity       52  17
CarlisleUtd       42   9
SwanseaCity       32   2
ScunthorpeUtd     29   1
HartlepoolUtd     25   0
Wrexham           24   1
ShrewsburyTn      21   1
BristolRovers     18   3
CambridgeUtd      16   0
BostonUtd         15   3
Bournemouth       15   1
Darlington        14   0
ExeterCity        13   0
YorkCity          13   2
HullCity          12   0
OxfordUtd         10   0
Rochdale          10   0
Bury               8   2
LeytonOrient       7   1
SouthendUtd        7   0
Rushden&Diamonds   1   0
KidderminsterH's   0   0
Macclesfield       0   0
TorquayUtd         0   0
```

Note that you can very quickly fit negative binomials, in R, thus

```
library(MASS)
fitdistr(totarr,"Negative Binomial")
```

You might like to consider how the parameters θ change between the 4 divisions, and to see whether you can offer any interpretation.

Worksheet 14.
What happens when we model the data given by Prof Pippa Norris (Harvard University) in the Financial Times of April 20, 2005?
See 'Stirring up apathy?'
Here is her dataset, with my analysis in R.

```
>PN.data
   Year UKTurnout Poll_Lead
1  1945      72.8       6.0
2  1950      83.9       0.6
3  1951      82.6       4.5
4  1955      76.8       3.7
5  1959      78.7       2.8
6  1964      77.1       1.9
7  1966      75.8      10.4
8  1970      72.0       3.1
9  1974      78.8       3.6
10 1974      72.8       8.9
11 1979      76.0       5.3
12 1983      72.7      19.8
13 1987      75.3       8.0
14 1992      77.7       0.4
15 1997      71.4      16.0
16 2001      59.4      14.2
```

The linear regression of UKTurnout on Poll Lead has rather a poor fit, as shown below

```
> summary(lm(UKTurnout ~ Poll_Lead))

Call:
lm(formula = UKTurnout ~ Poll_Lead)


     Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  79.4492     1.7617  45.098  < 2e-16 ***
Poll_Lead    -0.6171     0.2006  -3.076  0.00822 **

Residual standard error: 4.434 on 14 degrees of freedom
Multiple R-Squared: 0.4032,     Adjusted R-squared: 0.3606
F-statistic:  9.46 on 1 and 14 DF,  p-value: 0.00822
```

but the dependence on Poll Lead is clearly significantly negative.

```
par(mfrow=c(2,1))
scatter.smooth(Year, UKTurnout)
```

```
# scatter.smooth() is used here without
# proper explanation, but you can see what it does.
scatter.smooth(Year, Poll_Lead)
```

This will plot two helpful graphs, as shown in Fig 21.
Many statisticians would prefer to work with a transform of UKTurnout and Poll

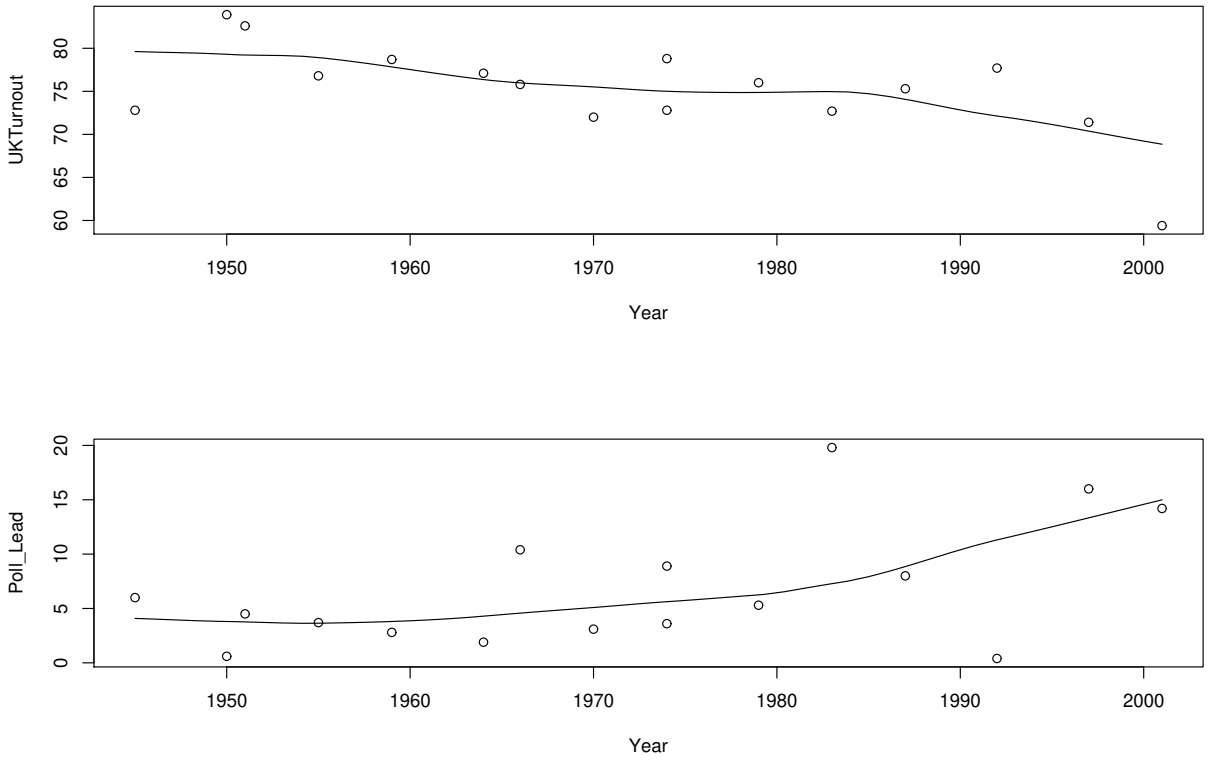

Figure 21: Scatter plots for UK election turnouts, and for Poll Leads

Lead, rather than the original variables, since each of UKTurnout and Poll Lead is constrained to be between 0 and 100. In this context it is natural to use the logit transform, and so we define the transformed variables x and y below, and repeat the linear regression, also including 'Year' as one of the independent variables. This greatly improves the fit, and shows that each of the terms x, Year in the regression equation is significant, with a negative coefficient.

```
>y <- log(UKTurnout/(100-UKTurnout))
>x <- log(Poll_Lead/(100-Poll_Lead))
>first.lm <- lm(y ~ x + Year)
Call:
lm(formula = y ~ x + Year)


Coefficients:
             Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept) 15.963014   6.282647   2.541   0.0246 *
x           -0.120186   0.047713  -2.519   0.0257 *
Year        -0.007708   0.003161  -2.439   0.0298 *

Residual standard error: 0.199 on 13 degrees of freedom
Multiple R-Squared: 0.5891,Adjusted R-squared: 0.5259
F-statistic:  9.32 on 2 and 13 DF,  p-value: 0.003083
library(lattice)
?cloud  # to find out about a 3-d scatter plot
```

We see that both x and Year have coefficients that are negative and significant.
But, study of standard regression 'diagnostics' shows that the 2001 row is highly 'influential' in the regression, so we repeat the linear model omitting that point: the results are then less dramatic.

```
>summary(lm(y ~ x + Year, subset = (Year != 2001)))
Call:
lm(formula = y ~ x + Year, subset = (Year != 2001))

Residuals:
     Min       1Q   Median       3Q      Max
-0.27468 -0.07640  0.03179  0.06444  0.29538

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 10.153553   5.597677   1.814   0.0948 .
x           -0.103097   0.039732  -2.595   0.0235 *
Year        -0.004719   0.002826  -1.670   0.1208

Residual standard error: 0.1636 on 12 degrees of freedom
Multiple R-Squared: 0.5084,Adjusted R-squared: 0.4265
F-statistic: 6.205 on 2 and 12 DF,  p-value: 0.01412
```

These analyses are a bit simple minded, since they make the the standard assumption that residuals are independent and identically normal: I have done a quick check for serial correlation, and it appears to be non-significant.
You could repeat this analysis including an extra row for 2005, for which UK-Turnout=61.3 % and Poll Lead =6 % (??)

Worksheet 15, for the new Part IIC course 'Statistical Modelling': using the gamma distribution.

We follow the notation of McCullagh and Nelder (1970), who define the density function of the gamma distribution with mean μ and shape parameter ν as

$$f(y|\mu,\nu) = \frac{1}{\Gamma(\nu)}(\nu y/\mu)^{\nu} e^{-\nu y/\mu}\ \frac{1}{y}$$

for $y > 0$.
You may check that this gives

$$E(Y) = \mu,\ var(Y) = (\mu^2)/\nu,$$

and the density is of standard glm form with $\phi = 1/\nu$, and canonical link $\eta = 1/\mu$. We simulate from two gamma distributions below, and use the glm fitting procedure, with canonical link (ie the inverse). See if you can work out what's going on.

```
 library(MASS)
 x <- (0:1000)/10
Y1  <- dgamma(x, shape=5, rate=0.1) # so true mean is 50
Y2  <- dgamma(x, shape=5, rate= 1)  # so true mean is 5
matplot(x, cbind(Y1,Y2), type = "l", xlab="x",
 ylab= "probability density function")
legend("topright", lty=c(1,2),
 legend=c("first gamma density", "second gamma density"))
```

Figure 22 shows us these two densities. Now we will generate 2 random samples, of sizes $100, 50$ respectively, from these two densities, and use glm() to fit the appropriate model.

```
 y1 = rgamma(100, shape=5, rate=0.1)
 y2 = rgamma(50, shape=5, rate= 1.0)
```

In this notation, μ =shape/rate, and ν = shape. (So shape = 1 will give us a negative exponential distribution.)

```
 par(mfrow=c(2,1))
 truehist(y1) ; truehist(y2) # graphs not shown here
summary(y1); summary(y2)
Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
4.817  30.770  43.770  48.360  59.730 114.300
Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
1.173   3.000   4.716   4.694   6.083  10.410

 x =c(rep("a", times=100), rep("b", times=50))
 is.factor(x) ; x = factor(x)
 y = c(y1,y2)
 plot(x,y)   # graphs not shown here
 first.glm = glm(y~x, Gamma) # nb, do not use "gamma"
```

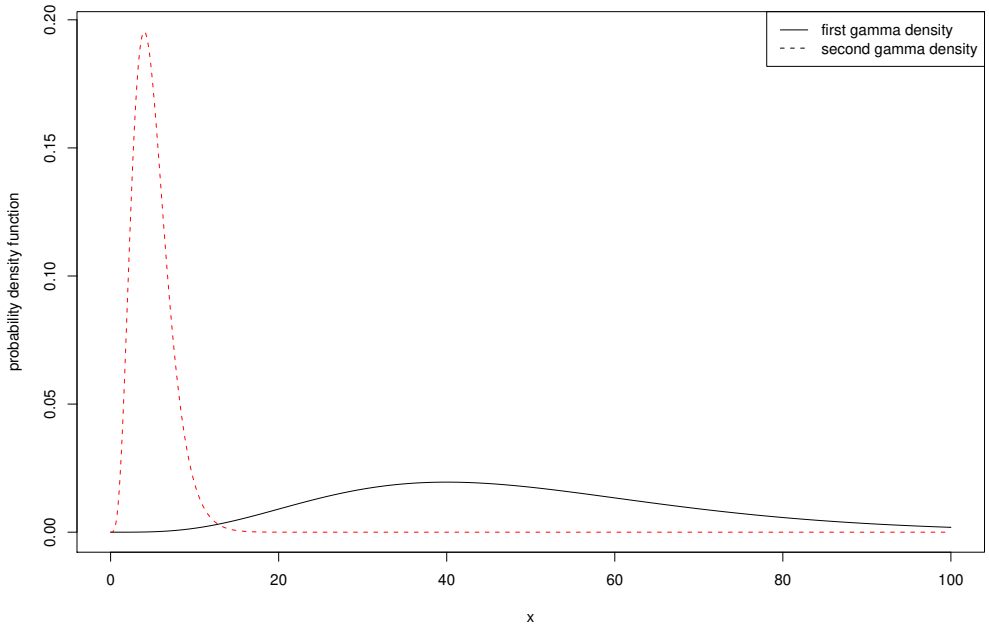

Figure 22: Two very different gamma densities

```
 summary(first.glm)
Call:
glm(formula = y ~ x, family = Gamma)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
     -1.21730  -0.33643  -0.09652   0.25573   1.10905

 Coefficients:
              Estimate Std. Error t value Pr(>|t|)
 (Intercept) 0.0209790  0.0009124   22.99   <2e-16 ***
 xb          0.1720752  0.0119088   14.45   <2e-16 ***
  ---
  Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

  (Dispersion parameter for Gamma family taken to be 0.1891440)

  Null deviance: 144.609  on 149  degrees of freedom
  Residual deviance:  28.430  on 148  degrees of freedom
    AIC: 1095.8
 dev = residuals(first.glm, type="deviance")
summary(dev) ; sum(dev^2)
```

This fits $1/\mu_i = \alpha$ for the first 100 observations, and $1/\mu_i = \alpha + \beta$ for the remaining 50 observations. What is $1/\hat{\alpha}$?
What is $1/(\hat{\alpha} + \hat{\beta})$?

Note that the estimate given for ν is the reciprocal of the dispersion parameter ϕ, and this dispersion parameter is estimated by

$$X^2/(n-p)$$

where n is the number of observations, and p is the number of parameters in the linear model (here $p = 2$) and

$$X^2 = \Sigma[(y_i - \hat{\mu}_i)/\hat{\mu}_i]^2$$

Thus we find for this example that $\hat{\nu} = 5.287$. This is actually a 'moments' estimator rather than the mle: as an exercise you can write down the equation for the maximum likelihood extimator. You will find that this gives an equation involving the function $\Gamma'(\nu)/\Gamma(\nu)$ (the digamma function), and there is no closed-form solution to this equation.
I must admit, I had difficulty working out where the AIC came from. It is, I believe, minus twice the maximised log-likelihood $+2 \times 3$, since we were fitting 3 parameters. Try

```
> nu <- 5.287 # your simulation may mean you have a different estimator here
> fv <- first.glm$fitted.value
> term= -lgamma(nu) + nu*log(nu * y/fv) - (nu*y/fv) - log(y)
> sum(term)
  -544.9114
```

and I trust you will see what I mean.

Reference
P.McCullagh and J.A.Nelder *Generalized Linear Models* Chapman and Hall (1990).

Supplementary worksheet:
CRIME, UNEMPLOYMENT and a case-control study

We reproduce 'matched-pairs' data first analysed in the GLIM Newsletter in 1987: the GLIM commands are easily translated into equivalent R commands. As part of a study on unemployment and crime, Farrington *et al* use the following data on 36 boys:

Boy	YearsinEmploy	OffE	YearsinUnemploy	OffU
1	1.21	3	0.68	1
2	1.47	0	1.28	1
3	1.02	0	0.89	8
4	2.97	2	0.36	0
5	3.37	2	0.30	0
6	2.65	8	0.60	0
7	3.16	1	0.67	1
8	3.07	1	0.27	0
9	2.51	2	0.40	0
10	1.58	2	1.08	0
11	2.21	1	1.37	4
12	2.45	1	0.47	0
13	1.52	2	0.64	2
14	2.64	1	0.70	0
15	2.46	2	0.57	0
16	1.54	1	0.85	0
17	2.83	1	0.37	0
18	1.50	2	1.25	0
19	2.37	1	0.55	0
20	2.25	0	0.75	1
21	2.84	1	0.75	0
22	1.66	4	0.61	1
23	2.39	2	0.44	1
24	2.42	3	0.78	0
25	1.17	0	2.50	2
26	3.15	2	0.43	0
27	1.75	1	0.25	0
28	0.83	1	0.88	3
29	2.22	0	0.28	1
30	1.25	4	0.96	2
31	1.31	2	0.69	1
32	2.91	2	0.67	0
33	2.67	1	0.67	0
34	3.28	4	0.45	0
35	3.00	1	0.34	0
36	2.14	0	0.46	1

We explain this dataset, using almost the same notation as in the 1987 paper. Let

$n_{1i},\ n_{2i}$ be the numbers of offences committed by the ith boy in Employment, Unemployment respectively, in times $t_{1i},\ t_{2i}$ years. We assume $n_{1i},\ n_{2i}$ are independent Poisson, with

$$logE(n_{1i}) = log\lambda_i + \alpha logt_{1i}$$
$$logE(n_{2i}) = log\theta + log\lambda_i + \alpha logt_{2i}$$

for $i = 1, \ldots, 36$. Here λ_i corresponds to the inherent 'criminality' of the ith boy, and θ to the extra (or reduced) propensity to commit offences while in Unemployment rather than Employment.
An important feature of this data set is that each boy is his own 'control': we must use the information on the pairing of $n_{1i},\ n_{2i}$ in our analysis.
We want to test the hypothesis $\theta = 1$ against the alternative $\theta > 1$, with $\lambda_1, \ldots, \lambda_{36}$ and α as nuisance parameters. (As usual, we take $log(\lambda_1) = 0$.) If the underlying offence process were exactly Poisson with constant rate over time, then we would have $\alpha = 1$. We can use glm() with a Poisson distribution and the log link to estimate the parameters in this model, as follows

```
>crimedata <- read.table("Fdata", header=T)
>attach(crimedata)
>N <- c(OffE,OffU) ; T <- c(YearsinEmploy,YearsinUnemploy)
>emp <- gl(2,36, length=72, labels= c("employed", "unemployed"))
>boy  <- gl(36,1, length=72)
>first.glm <- glm(N ~ boy + emp + log(T), poisson)
>summary(first.glm)
Call:
glm(formula = N ~ boy + emp + log(T), family = poisson)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-2.35751  -0.58849  -0.02662   0.20096   2.03317

Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.428032   0.525967   0.814   0.4158
boy2          -2.199690   1.140865  -1.928   0.0538 .
boy3           0.557188   0.617856   0.902   0.3672
boy4          -1.806815   0.933781  -1.935   0.0530 .
.......... we omit some parameter estimates
boy34         -1.310124   0.805664  -1.626   0.1039
boy35         -2.513290   1.173218  -2.142   0.0322 *
boy36         -1.973349   1.134956  -1.739   0.0821 .
empunemployed  0.884298   0.409491   2.160   0.0308 *
log(T)         1.860515   0.433602   4.291 1.78e-05 ***

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 126.872  on 71  degrees of freedom
Residual deviance:  45.918  on 34  degrees of freedom
```

```
AIC: 232.42

Number of Fisher Scoring iterations: 7
```

Hence $log\hat{\theta} = 0.884298$ with se= 0.409491: this is significant. Being out of a job appears to increase the crime-rate for the boys by a factor of about 2.42.
The fit of the model (compare 45.918 with χ^2 on 34 df) is not all that good, but very many of the fitted values for N are very small, < 1 in fact.
Now change the model so that we condition on OffE + OffU, for each boy.

```
>Tot <- OffE + OffU
>Timeratio <- YearsinUnemploy/YearsinEmploy
>next.glm <- glm(OffU/Tot ~ log(Timeratio), binomial, weights=Tot)
>summary(next.glm)
```

You can prove that the results must be equivalent to those for the Poisson.

```
>next.glm <- glm(OffU/Tot ~ log(Timeratio), binomial, weights = Tot)
>summary(next.glm)
Call:
glm(formula = OffU/Tot ~ log(Timeratio), family = binomial, weights = Tot)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.0024  -0.7038  -0.4057   0.6437   2.6130
Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)      0.8843     0.4095   2.160   0.0308 *
log(Timeratio)   1.8605     0.4336   4.291 1.78e-05 ***
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 72.778  on 35  degrees of freedom
Residual deviance: 45.918  on 34  degrees of freedom
AIC: 65.754
Number of Fisher Scoring iterations: 5
```

Here the intercept corresponds to $log(\theta)$, having an estimate identical to that obtained in the Poisson regression.
You could consider
i) how to allow for the over-dispersion
ii) is there a way of doing an *exact* test of $H_0 : log(\theta) = 0$?
iii) how to allow for the fact that we could not expect n_{1i}, n_{2i} to be truly Poisson: these 36 boys have been selected from the total of nearly 400 boys in the study as those who have committed at least 1 offence while in Employment or in Unemployment, **and** have had at least .25 years in each of Employment and Unemployment.

References

1. Altham, P.M.E. and Farrington, D.P. 'A Matched Pairs problem with discrete data: a comparison of offending rates under employment and unemployment' *GLIM Newsletter*, **14**, pp. 11-14, 1987.
2. Farrington, D.P. et al 'Unemployment, School Leaving and Crime' *British Journal of Criminology* **26**, pp. 335-356, 1986.

Worksheet 17.

Estimating the parameters in a model of quasi-independence in a square contingency table

Mary-Rose Wilkinson of Trinity College wrote her dissertation for the MPhil in Statistical Science, University of Cambridge, 2005 on 'Analysing the Frequencies of Loop Lengths of Genomic G-Quadruplex Structures' in which she analysed data (particularly square contingency tables) kindly provided by Dr Julian Huppert of the Sanger Centre.

Here is an extract from her dissertation.

'In this project I analyse data collected by Dr Julian Huppert on the loop lengths of putative G-quadruplex structures identified in the human genome. This analysis shows that there are statistical structures present in the data which indicate that at least some proportion of these putative G-quadruplex structures actually do form G-quadruplex structures under certain physiological conditions.'

DNA is a long polymer made up of a series of units called nucleotides. Each nucleotide consists of a sugar, a phosphate group and an organic molecule (a heterocycle) called a base which is one of adenine (A), cytosine (C), guanine (G) or thymine (T). It is well known that the usual structure of DNA is the double-helix (like a spiral staircase, with the sugar-phosphate backbone forming the 'railing' and the bases of the nucleotides being the 'steps'). However, sequences of bases of certain patterns can form other structures, and one structure which can be formed by guanine rich sequences is the G-quadruplex.

The G-quadruplex structure has a core of stacked tetrads linked by three loops. These loops are sequences of between one and seven bases, and the combination of lengths of the three loops affects the stability and shape of the G-quadruplex. These loops are the focus of this dissertation.

Dr Huppert developed a 'quadruplex folding rule' which says that sequences of bases of a particular form will form a G-quadruplex structure under certain physiological conditions. Dr Huppert also developed an algorithm called 'Quadparser' which he used to search the whole of the human genome for sequences which satisfy this rule. Although Dr Huppert had identified that sequences of this form could form G-quadruplexes, it was not known how many of them actually do form G-quadruplex structures physiologically in the genome.

For each putative G-quadruplex structure identified by Quadparser, the three lengths of the loops that would be formed if the sequence formed a G-quadruplex physiologically were recorded. As these loops are of between one and seven bases in length, this gave a $7 \times 7 \times 7$ contingency table, each dimension of the contingency table giving the length of one of the loops.

The aim of this project was to analyse the contingency table, investigating whether there were statistical structures present. Presence of statistical structures would indicate that the sequences identified show evidence of evolutionary selection, and hence that they may actually form G-quadruplexes physiologically in the genome.'

The three loop-lengths are very definitely non-independent: there is a predominance of frequencies in the diagonal cells.

'Further analysis of the three-way contingency table did not initially lead in a particular direction for further work, so I collapsed the table by summing over the lengths of loop two to give a 7×7 contingency table showing the lengths of loops one and

three. It was natural to consider loops one and three together as they have a similar position in the G-quadruplex structure.
This two-way contingency table had three interesting features. Firstly it was almost exactly symmetric, secondly there were a large number of counts where one or both of loops one or three were only one base long, and thirdly, there were a large number of counts on the diagonal, where the lengths of the two loops are the same. As the first row and column of this table had such a dominating effect I excluded them from the next section of the analysis, and fitted a quasi-independence model to the remaining 6×6 table, which would model the excess of counts on the diagonal and the symmetry.' The quasi-independence model is a probability mixture model, given by

$$p_{ij} = \begin{cases} \alpha\theta_i + (1-\alpha)\beta_i^2 & \text{for } i = j; \\ (1-\alpha)\beta_i\beta_j & \text{for } i \neq j \end{cases}$$

where all parameters $\alpha, (\theta_i), (\beta_i)$ are between 0 and 1, and $\Sigma\theta_i = 1 = \Sigma\beta_i$.
Here the parameter of interest is the probability α, and we wish to estimate α and in addition to give Dr Huppert an idea of how precise this estimate is: in other words we seek $\hat{\alpha}$, the mle, together with its standard error.
In her project, Mary-Rose uses 3 distinct methods to tackle this problem:
i) approximating α to Cohen's Kappa statistic,
ii) by numerically maximising the profile log-likelihood, and
iii) by Markov Chain Monte Carlo.
The three estimates that were obtained agree very closely, the latter two methods agreeing to give $\hat{\alpha} = 0.098$ to three decimal places, with a very tight confidence interval of $(0.096, 0.010)$.
She also modified her programs to run on the 7 x 7 contingency table, to include the counts where one or both of the loops were just one base long; this gave slightly higher estimates. Those obtained through the profile log-likelihood and Markov Chain Monte Carlo methods were both 0.129 with confidence interval $(0.128, 0.131)$.
The 7×7 table of frequencies (which is obtained by summing over the Loop 2 positions) is given below:

		Loop 1						
		1	2	3	4	5	6	7
	1	94210	28196	18861	18049	17700	12899	11441
	2	28158	23102	11062	10564	8283	7732	8045
	3	19051	11033	16463	8229	6565	6453	6627
Loop 3	4	18007	10485	8513	11766	6676	6068	5737
	5	17829	8389	6518	6672	9044	5231	4624
	6	12981	7915	6530	5973	5217	6177	4325
	7	11371	7603	6594	5670	4549	4326	6095

Table 12: The data given in a 7×7 contingency table.

Dividing the frequencies by their total gives the following table of probabilities: The table is almost exactly symmetric. You may easily check that a standard glm()

		Loop 1						
		1	2	3	4	5	6	7
	1	0.159	0.047	0.032	0.030	0.030	0.022	0.019
	2	0.047	0.039	0.019	0.018	0.014	0.013	0.014
	3	0.032	0.019	0.028	0.014	0.011	0.011	0.011
Loop 3	4	0.030	0.018	0.014	0.020	0.011	0.010	0.010
	5	0.030	0.014	0.011	0.011	0.015	0.009	0.008
	6	0.022	0.013	0.011	0.010	0.009	0.010	0.007
	7	0.019	0.013	0.011	0.010	0.008	0.007	0.010

Table 13: Table of empirical probabilities for the number of bases in loops one and three.

test on the frequencies for fitting the null hypothesis of symmetry gives the residual deviance as 24.907 on 21 degrees of freedom.
But the first row and column of the table have a dominating effect (the probability of having at least one of the loops having one base is 0.519), so we now look at the 6×6 contingency table obtained by excluding the first row and column. (Apparently, reducing the dataset in this way makes sense scientifically: the dominating effect of the first row and column may be due to increased stability for shorter loop lengths or may be also partly due to the shortest possible loop assumption made by Quadparser.)
There are large counts on the diagonal (possibly due to the fact that a quadruplex structure has better stability when loops one and three are of similar length). Thus a simple model of independence of the numbers of bases in loops one and three totally fails to fit.
Therefore we next fit a quasi-independence model, which includes the symmetry:

$$p_{ij} = \begin{cases} \alpha\theta_i + (1-\alpha)\beta_i^2 & \text{for } i = j; \\ (1-\alpha)\beta_i\beta_j & \text{for } i \neq j \end{cases}$$

where p_{ij} is the probability of classification in the ith row and jth column of the table, that is the probability of having i bases on loop three and j bases on loop one.
This is a probability mixture model: with probability α the row and column classifications must be the same, and with probability $(1-\alpha)$ the row and column classes are independent, but each with the same distribution.
We are interested in estimating the probability α, as we believe that selective pressures may favour the first and third loops being of similar length.
Estimation of α
Mary-Rose estimated α using three different methods: by approximating α to Cohen's Kappa statistic, by numerically maximising the profile log-likelihood for α and by using Markov Chain Monte Carlo techniques.
i) Estimation of α through Cohen's Kappa (see Agresti, 2002, p453, ex 10.39.)
Make the simplifying assumption (which turns out to be not quite true, as it happens) that

$$\theta_i = \beta_i$$

for each i. Then we have

$$p_{ij} = \begin{cases} \alpha\theta_i + (1-\alpha)\theta_i^2 & \text{for } i = j; \\ (1-\alpha)\theta_i\theta_j & \text{for } i \neq j \end{cases}$$

so

$$p_{i+} = p_{+i} = \alpha\theta_i + (1-\alpha)\theta_i \sum_j \theta_j$$

which simplifies to give $\theta_i = p_{i+} = p_{+i}$. Also

$$\sum_i p_{ii} = \ldots = \alpha + (1-\alpha)\sum_i p_{i+}p_{+i}$$

giving $\alpha = (P_o - P_e)/(1 - P_e)$ where $P_o = \sum p_{ii}$ and $P_e = \sum p_{i+}p_{+i}$.
$(P_o - P_e)/(1 - P_e)$ is Cohen's Kappa. This was introduced by Cohen in 1960 to measure the agreement between ratings by two observers. Note that P_o is the probability the two observers agree and that P_e is the probability of agreement if the two observers' ratings are statistically independent, so $P_o - P_e$ is the excess of observer agreement over that expected purely by chance. Dividing this numerator by $(1-P_e)$ means that Kappa equals 0 when the agreement equals that expected by chance and equals 1 when there is perfect agreement. The stronger the agreement, the higher the value.
For multinomial sampling, the sample estimate of Kappa is approximately normal, with variance given by

$$\begin{aligned} \hat{\sigma}^2(\hat{\kappa}) &= \frac{1}{n}\left(\frac{P_o(1-P_o)}{(1-P_e)^2} + \frac{2(1-P_o)\big(2P_oP_e - \sum \hat{p}_{ii}(\hat{p}_{i+} + \hat{p}_{+i}\big)}{(1-P_e)^3} \right. \\ &+ \left. \frac{(1-P_o)^2\big(\sum\sum \hat{p}_{ij}(\hat{p}_{j+} + \hat{p}_{+i})^2 - 4P_e^2\big)}{(1-P_e)^4} \right) \end{aligned}$$

Mary-Rose found by using this method of calculating Cohen's Kappa , $\hat{\alpha} = 0.0947$ (to 4 d.p.) with standard error 0.0010 (to 4 d.p.).

Estimation of α through Classical Likelihood Theory
The above method makes the assumption $\beta_i = \theta_i \ \forall i$, which may not be correct. So we now consider other methods of estimating α which do not require this assumption. One method is to work with the profile log-likelihood.
The likelihood up to a constant is

$$\begin{aligned} \prod_{i,j} p_{ij}^{n_{ij}} &= \prod_i \big(\alpha\theta_i + (1-\alpha)\beta_i^2\big)^{n_{ii}} \prod_{i\neq j} \big((1-\alpha)\beta_i\beta_j\big)^{n_{ij}} \\ &= \prod_i \left(\frac{\alpha\theta_i + (1-\alpha)\beta_i^2}{(1-\alpha)\beta_i^2}\right)^{n_{ii}} \prod_{i,j} \big((1-\alpha)\beta_i\beta_j\big)^{n_{ij}} \end{aligned}$$

where n_{ij} is the number of counts in the (i,j) cell.
This gives the log-likelihood as

$$\begin{aligned} l(\alpha,\theta,\beta) &= \sum_i n_{ii}\log\left(\frac{\alpha\theta_i+(1-\alpha)\beta_i^2}{(1-\alpha)\beta_i^2}\right)+\sum_{i,j} n_{ij}\log\big((1-\alpha)\beta_i\beta_j\big) \\ &= \sum_i n_{ii}\log\left(\frac{\alpha\theta_i+(1-\alpha)\beta_i^2}{(1-\alpha)\beta_i^2}\right)+\sum_i (n_{+i}+n_{i+})\log\beta_i + n\log(1-\alpha) \end{aligned}$$

where $n_{i+}=\sum_j n_{ij}$, $n_{+i}=\sum_j n_{ji}$ and $n=n_{++}$.
Mary-Rose maximised this log-likelihood with respect to θ and β for specified values of α between 0.045 and 0.145 subject to $\sum\theta_i, \sum\beta_i = 1$ and $\theta_i, \beta_i \geq 0$, using the R-function `constrOptim`. Thus she obtained $l_p(\alpha)$, the **profile** log-likelihood for α, for $0<\alpha<1$. She chose the range of α to be 0.045 to 0.145 because of the estimate 0.0947 obtained for α from Cohen's Kappa.
The maximum of the profile log-likelihood is at $\hat{\alpha}=0.0979$ (to 4 d.p.) with a confidence interval of $(0.0960, 0.0998)$ obtained from the asymptotic chi-squared distribution on one degree of freedom of the Wilk's Statistic. (We require the region $\{\alpha : l_p(\alpha) \geq l_p(\hat{\alpha}) - \frac{1}{2}\chi^2_{0.95,1}\}$ where $\chi^2_{0.95,1}$ is the 0.95 point of the χ^2_1 distribution.)
This estimate agrees fairly closely with the estimate obtained using Cohen's Kappa: subtracting twice the Cohen's Kappa standard error estimate from the Cohen's Kappa estimate gives 0.0967 (to 4 d.p.), which lies just inside the confidence interval obtained for α above. Also, the standard error is 0.00095, which agrees very closely with the estimate obtained using Cohen's Kappa, which was 0.00098.
Modifying her Program slightly to run for the 7 by 7 table so as to use the data from the first row and column gives an estimate of $\hat{\alpha}=0.1291$ (to 4 d.p.) with a confidence interval of $(0.1276, 0.1307)$, higher than the estimate obtained before when using the 6 by 6 table.
The corresponding calculations for Cohen's Kappa give $\hat{\alpha}=0.1093$ (to 4 d.p.) with standard error 0.0007 (to 4 d.p.). The estimate is higher due to the comparatively very large number of counts in cell (1,1).
The second two methods of the three considered agree to give $\hat{\alpha}=0.098$ (to 3 d.p.) for the 6×6 table, with 95% confidence interval $(0.096, 0.100)$ (to 3 d.p.). The estimates obtained through Cohen's Kappa do not agree so closely, but for this calculation we assumed $\beta_i=\theta_i\ \forall i$, which is only approximately true.

Method	6 by 6 data	7 by 7 data
Cohen's Kappa	0.0947 (0.0937,0.0957)	0.1093 (0.1086, 0.1100)
Profile log-likelihood	0.0979 (0.0960, 0.0998)	0.1291 (0.1276, 0.1307)
MCMC	0.0978 (0.0959, 0.0998)	0.1291 (0.1276, 0.1306)

Table 14: Estimates obtained for α.

While the methods used by Mary-Rose were interesting and certainly helped our understanding, a more straightforward method, shown below, is simply to maximise the log-likelihood function, and then to pick out $var(\hat{\alpha})$ from the appropriate term in the inverse of minus the matrix of second derivatives.
The worksheet that follows shows firstly the 6×6 table of frequencies, followed by a

rather simple method for estimating α, the parameter of interest, by straightforward maximisation of the log-likelihood function, using

`optim()`.

Here is the datafile "RJdata".

```
23102 11062 10564 8283 7732 8045
11033 16463 8229 6565 6453 6627
10485 8513 11766 6676 6068 5737
8389 6518 6672 9044 5231 4624
7915 6530 5973 5217 6177 4325
7603 6594 5670 4549 4326 6095
```

And here is the corresponding R program. It is designed to make use of the elegant matrix functions available in R.

```
original = scan("RJdata")
k=6 # here we fit the model for a 6 by 6 table
original = matrix(original, nrow=k, byrow=T)
one = rep(1, times=k)
one = matrix(one, nrow=k, byrow=T)
rn = original %*% one ; cn = t(original)%*% one
# Thus we have computed the row-sums and the column-sums
D = diag(original)
N = sum(original)
od = N -sum(D)#sum of off-diagonal terms
j = k-1# we fit (2*j + 1) parameters
th= rep(.1, times=k) ; beta = rep(.1, times=k)
# this sets up th & beta as vectors of the right length
# Now set up f as minus log-likelihood
f = function(x){
th[1:j] = x[1:j] ; th[k] = 1-sum(x[1:j])
beta[1:j] = x[k: (2*j)] ; beta[k] = 1- sum(x[k:(2*j)])
a=x[2*j +1]
-sum(D*log(a*th+(1-a)* beta^2))-sum((rn + cn-2*D)*log(beta))-od*log(1-a)
}
x = rep(.1,times=2*j+1)
f(x) # as a trial
x0 = rep(0.1, times=2*j +1) # starting value
first.opt = optim(x0, f, method="BFGS", hessian=T)
# we get a lot of error messages, but the method seems to be working ok
first.eigen = eigen(first.opt$hessian)
first.eigen$values # to check that hessian matrix is positive definite

x= first.opt$par
a = x[2*k -1] # this is our est of alpha
# I got alpha=0.09787283.
V = solve(first.opt$hessian)# to invert the Hessian matrix
```

```
se= sqrt(V[2*k -1,2*k -1]) # this is our se of the  est of alpha
# I got se = 0.000999305.
# Now we compute the expected frequencies
th[1:j] = x[1:j] ; th[k] = 1-sum(x[1:j])
beta[1:j] = x[k: (2*j)] ; beta[k] = 1- sum(x[k:(2*j)])
Beta = matrix(beta,nrow=k, byrow=T)
p = a*diag(th) + (1-a)* Beta %*% t(Beta)
sum(p) # to check these sum to 1
expected = p*N # fitted frequencies
dis = (original- expected)^2
(dis/expected) # to see contribution to chisq statistic
Chisq = sum(dis/expected) # here with 35-11=24 df
```

(i) You could experiment with other Optimization functions: see for example Venables and Ripley (2002) Chapter 16.
(ii) You could also readily adapt the program given above to estimate the mixing probability α when we **don't** assume that the table is symmetric, so that the model now becomes

$$p_{ij} = \begin{cases} \alpha\theta_i + (1-\alpha)\beta_i\gamma_i & \text{for } i = j; \\ (1-\alpha)\beta_i\gamma_j & \text{for } i \neq j \end{cases}$$

where all parameters $\alpha, (\theta_i), (\beta_i), (\gamma_i)$ are between 0 and 1, and $\Sigma\theta_i = 1 = \Sigma\beta_i = \Sigma\gamma_i$.
(iii) It should be possible, without much extra effort, to implement a version of the program given here in Splus. (You will need to replace

```
optim()
```

by

```
nlminb()
```

for example.) However, I had problems, so far unsolved, in getting the definition of the function

```
f()
```

to work in Splus.

18. New for 2006: cannabis use and psychosis, the 'Harry Potter' effect, and life is a risky business if you are in a TV soap opera.

i) The BMJ, December 1, 2004, published 'Prospective cohort study of cannabis, predisposition for psychosis, and Psychotic symptoms in young people' by C.Henquet and others. This included the following table of data (slghtly simplified here).

```
      cannabis use      Number with        Number without
      at baseline     psychosis outcome   psychosis outcome
p.no    none              294                 1642
p.no    some               59                  216

p.yes   none               47                  133
p.yes   some               23                   22
-----------------------------------------------------------
```

Here the first 2 rows of the table, 'p.no', correspond to those with *no* predisposition for psychosis at baseline, and the second 2 rows of the table, 'p.yes', correspond to those with predisposition for psychosis at baseline. Thus for example, there were $23 + 22$ persons who had both cannabis use at baseline, and predisposition for psychosis at baseline: of these 45, a total of 23 had a psychosis outcome. Note that of those without a predisposition for psychosis, 15% of those with no cannabis use had a psychosis outcome, compared with 21% of those with cannabis use. For those with a predisposition for psychosis, the difference was much more striking: 26% of those with no cannabis use had a psychosis outcome, compared with 51% of those with cannabis use. This suggests that there is a **3-way interaction** between the rows, columns and layers of the given $2 \times 2 \times 2$ table, and we show how to test this formally, in the following R analysis.

```
> cannabis <- read.table("cannabis", header=T);  cannabis
cannabis.use    with  without predisposition
none     294     1642     no
some      59      216     no
none      47      133    yes
some      23       22    yes
> attach(cannabis) ; tot <- with + without
> summary(glm(with/tot~cannabis.use*predisposition,binomial,weights=tot))
> interaction.plot(predisposition,cannabis.use, with/tot)
> title("Proportion with a psychosis outcome")
```

You can see that there is a **significant interaction** between cannabis.use and the baseline predisposition for psychosis in terms of their effect on whether or not the young person develops psychotic symptoms: refer $.66230/.37857 = 1.749$ to $N(0, 1)$. It's usually much easier to interpret an interaction by a graph: see the interaction plot Figure 23 given here.

What we have done above is to test the null hypothesis of no 3-way interaction in the original $2 \times 2 \times 2$ table. We can of course do this test in a much more straightforward way, which will be exactly equivalent, by considering **log crossratios**, as follows. The first table is

	cannabis use at baseline	Number with psychosis outcome	Number without psychosis outcome
p.no	none	294	1642
p.no	some	59	216

The log-crossratio for this table is say $m_1 = \log(294 * 216)/(1642 * 59)$, with corresponding estimated variance say $v_1 = (1/294) + (1/1642) + (1/59) + (1/216)$. Likewise, the second table is

	cannabis use at baseline	Number with psychosis outcome	Number without psychosis outcome
p.yes	none	47	133
p.yes	some	23	22

and the corresponding log-crossratio is say $m_2 = \log(47 * 22)/(133 * 23)$, with estimated variance say $v_2 = (1/47) + (1/133) + (1/23) + (1/22)$.
We assume the 2 tables are independent, and thus compute $(m_1 - m_2)/(v_1 + v_2)^{1/2}$. You will find this is 1.749, as above.

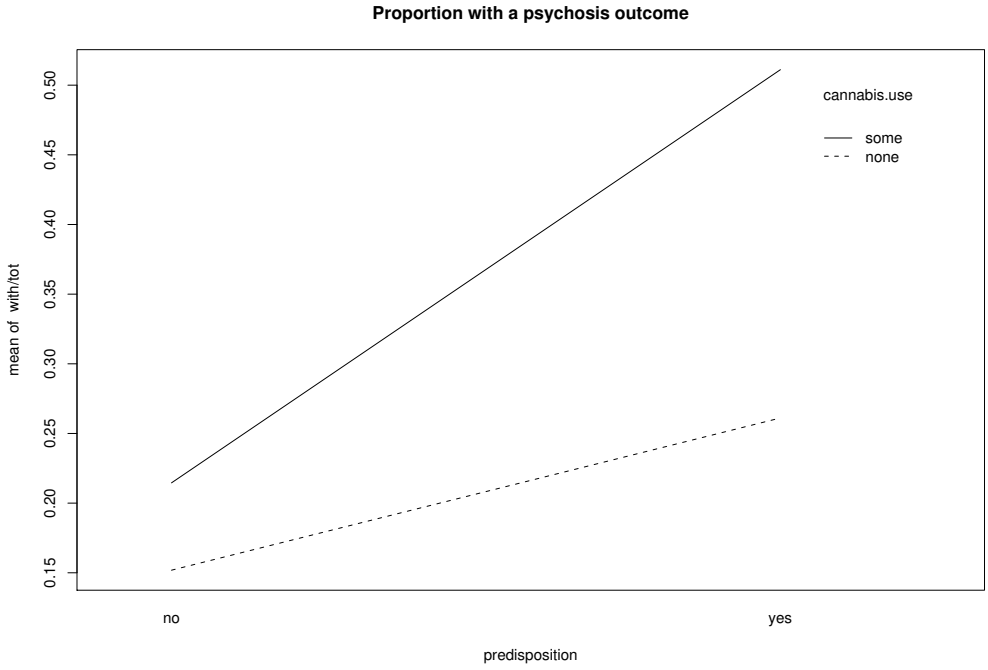

Figure 23: Cannabis use and predisposition to psychosis

ii) 'Harry Potter casts a spell on accident-prone children' was published by Gwilym, Howard, Davies and Willett in the BMJ on 23 December 2005. The data given below show the numbers of children aged 7-15 with musculoskeletal injuries who attended the emergency department of the John Radcliffe Hospital Oxford as weekend admissions (ie between 8am Saturday and 8am Monday) over the summer months of a 3-year period.
The launch dates of the two most recent Harry Potter books- *The Order of the*

Phoenix and *The Half-Blood Prince* were Saturday 21 June 2003 and Saturday 16 July 2005: these weekends are marked * in the 26 rows of data given below. (NB I had to read the data from the graph given on p1506 so my numbers may very slightly disagree with those actually used by Gwilym and his colleagues in the significance test they carried out.) Here is the dataset I used, which you may read via

```
read.table("  ", header=T)
```

```
Date    Year   N
7-8June 2003   62
15-15June 2003 78
21-22June 2003 36 *
28-29June 2003 62
5-6July 2003   77
12-13July 2003 70
19-20July 2003 60
26-27July 2003 51
5-6June 2004   80
12-13June 2004 82
19-20June 2004 70
26-30June 2004 78
3-4July 2004   81
10-11July 2004 59
17-18July 2004 64
24-25July 2004 61
4-5June 2005   50
11-12June 2005 81
18-19June 2005 61
25-26June 2005 66
2-3July 2005   75
9-10July 2005  77
16-17July 2005 37 *
23-24July 2005 43
30-31July 2005 67
6-7August 2005 60
```

The graph of the number of injuries against the weekend number is shown in Figure 24. Note that there appears to be a seasonal pattern to the number of injuries. For this reason we will use only the first 24 observations of the total of 26.

```
Year = Year[1:24] ; N= N[1:24] ; year<- factor(Year)
weekend <- gl(8,1, length=24) ; Weekend<- as.real(weekend)
plot(Weekend,N )
points(3,36, pch=4) ; points(7,37, pch=4)
# to mark the 'Harry Potter' weekends as special points on the graph
first.glm <- glm(N~  weekend + year, poisson)
```

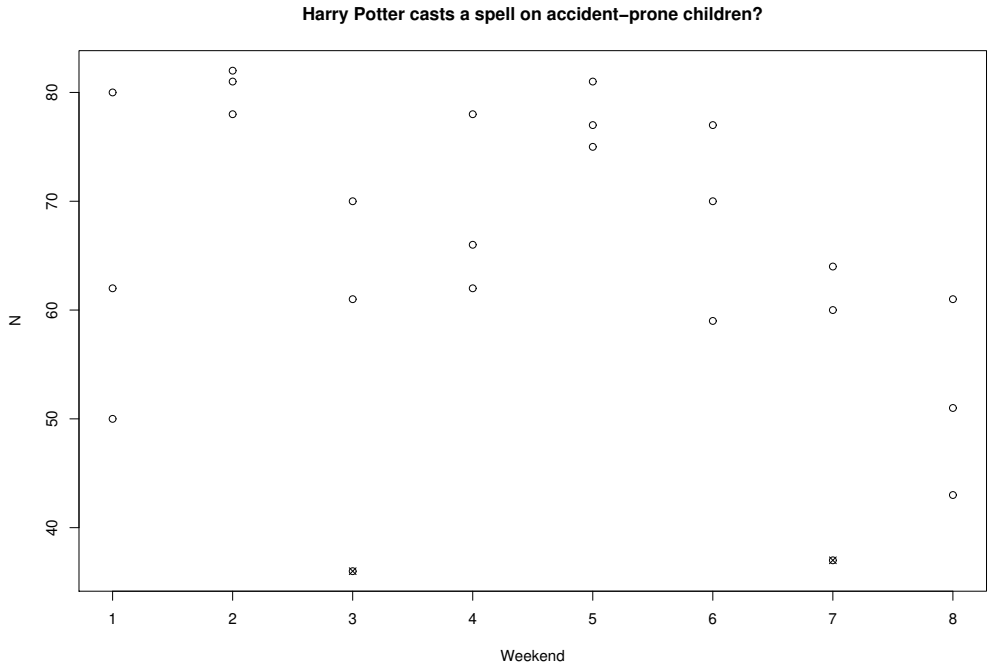

Figure 24: Harry Potter and the John Radcliffe hospital

```
# this has deviance 26.7 on 14 df, with large residuals for the HP weekends
i <- 1:24 # so we see what happens if we omit those two special points
next.glm <- glm(N~  weekend + year, poisson, subset=(i!=3)&(i!= 23))
# this has deviance 11.7 on 12 df, & you can see that
last.glm <- glm(N~  weekend, poisson, subset=(i!=3)&(i!= 23))
# should fit well: indeed,it has deviance 15.7 on 14 df.
```

iii) 'Death rates of characters in soap operas on British television: is a government health warning required?' BMJ Dec 20, 1997, by Crayford, Hooper (a former Cambridge Diploma student) and Evans, gave Table 3, of which an extract is printed below. These authors studied mortality in 4 well-known UK soap operas, Coronation Street, Eastenders, Brookside and Emmerdale (for which my brother was once Producer) from 1985 (the start of Eastenders, the newest of the 4 operas) to mid-1997. The Table shows
the name of the soap opera
the total number of deaths
the total number of deaths from 'external causes', eg murder, car crash, etc
Epmf, the expected proportional mortality fraction from 'external causes' in an age-matched population (ie age-matched for the particular soap opera)

soap	totaldeaths	extdeaths	Epmf
CorSt	14	6	.17
EastE	17	11	.22
Brooks	26	20	.28
Emmerd	28	17	.24

The authors comment that 'characters in soap operas lead very dangerous lives', and 'their lives are more dangerous even than those of Formula One racing drivers or bomb disposal experts'.
Consider the following analysis in R. What is it telling you? Figure 25 shows you

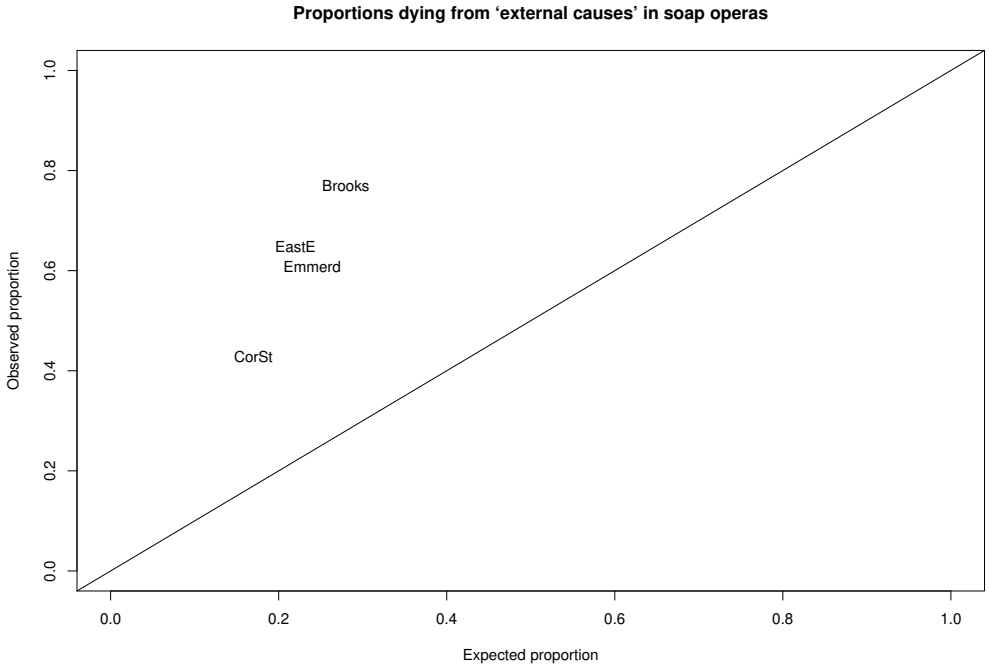

Figure 25: Warning: acting in a soap opera could damage your health

the plot of the observed proportion of 'external causes' deaths, against Epmf, the expected proportion.

```
soap.data <- read.table("soap.data", header=T)
attach(soap.data)
p<- extdeaths/totaldeaths
plot(Epmf,p,type="n",xlim=c(0,1),ylim=c(0,1),xlab="Expected proportion",
+ ylab="Observed proportion")
text(Epmf, p, labels=soap)
abline(0,1)
title("Proportions dying from 'external causes' in soap operas")
first.glm <- glm(extdeaths/totaldeaths ~ 1, binomial, weights=totaldeaths)
summary(first.glm)
cbind(extdeaths/totaldeaths, Epmf)
x <-  log(Epmf/(1-Epmf))
next.glm<- glm(extdeaths/totaldeaths ~ x, binomial, weights=totaldeaths)
```

You will see that the coefficient of x in the second glm is $2.173 (se = 1.079)$.
If you check the original article on http://bmj/bmjjournals.com, you can see a photograph from *Brookside*, captioned 'Gladys meets her controversial end with the help of her family'.

19. Results from the Corus chess tournament: An application of the Bradley-Terry model

The Times, February 1, 2006, gave the results of 'The top group at the Corus tournament at Wijk aan Zee in Holland'. The Times presented the results as the off-diagonal elements of a 14×14 matrix, with $1, 1/2, 0$ corresponding to a Win, Draw or Loss, respectively. In fact the key part of the data consists of just the $14 \times 13/2$ elements of the matrix which are above the diagonal, but here I choose to read in these as 91 rows of data, indicating which players, P1, ..., P14 beat, drew or lost against which other player. Thus, for example, the first row of the data matrix given below shows that when P1 played P2, the result was a Draw; the third row of the data matrix shows that when P1 played P4, the result was a Win for P1.

Scoring $1, 1/2, 0$ for a Win, Draw or Loss respectively, the total scores for the 14 players were P1 (Anand)= 9, P2 (Topalev)= 9, P3 (Adams, the British player)= 7.5, P4 (Ivanchuk)=7.5, P5 (Gelfand)= 7, P6 (Karjakin)= 7, P7 (Tiviakov)= 6.5, P8 (Leko) = 6.5, P9 (Aronian)= 6.5,

P10 (VanWely) = 6, P11 (Bacrot)= 5.5, P12 (Mamedyarov)= 4.5, P13 (Kamsky)=4.5, P14 (Sokolov)=4.

The dataset is given below: can you think of a more economical way to read it in, getting R to do the work of setting up the patterned 'design' variables P1, ..., P14?

```
W Dr L P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12 P13 P14
0 1 0 1  -1  0  0  0  0  0  0  0   0   0   0   0
0 1 0 1   0 -1  0  0  0  0  0  0   0   0   0   0
1 0 0 1   0  0 -1  0  0  0  0  0   0   0   0   0
1 0 0 1   0  0  0 -1  0  0  0  0   0   0   0   0
1 0 0 1   0  0  0  0 -1  0  0  0   0   0   0   0
0 1 0 1   0  0  0  0  0 -1  0  0   0   0   0   0
1 0 0 1   0  0  0  0  0  0 -1  0   0   0   0   0
0 1 0 1   0  0  0  0  0  0  0 -1   0   0   0   0
1 0 0 1   0  0  0  0  0  0  0  0  -1   0   0   0
1 0 0 1   0  0  0  0  0  0  0  0   0  -1   0   0
0 1 0 1   0  0  0  0  0  0  0  0   0   0  -1   0
0 0 1 1   0  0  0  0  0  0  0  0   0   0   0  -1
0 1 0 1   0  0  0  0  0  0  0  0   0   0   0   0
0 0 1 0   1 -1  0  0  0  0  0  0   0   0   0   0
0 1 0 0   1  0 -1  0  0  0  0  0   0   0   0   0
0 1 0 0   1  0  0 -1  0  0  0  0   0   0   0   0
1 0 0 0   1  0  0  0 -1  0  0  0   0   0   0   0
0 1 0 0   1  0  0  0  0 -1  0  0   0   0   0   0
0 1 0 0   1  0  0  0  0  0 -1  0   0   0   0   0
1 0 0 0   1  0  0  0  0  0  0 -1   0   0   0   0
1 0 0 0   1  0  0  0  0  0  0  0  -1   0   0   0
1 0 0 0   1  0  0  0  0  0  0  0   0  -1   0   0
0 1 0 0   1  0  0  0  0  0  0  0   0   0  -1   0
1 0 0 0   1  0  0  0  0  0  0  0   0   0   0  -1
1 0 0 0   1  0  0  0  0  0  0  0   0   0   0  -1
```

```
1 0 0 0   0  1 -1  0  0  0  0  0  0   0   0   0   0
0 0 1 0   0  1  0 -1  0  0  0  0  0   0   0   0   0
0 1 0 0   0  1  0  0 -1  0  0  0  0   0   0   0   0
0 1 0 0   0  1  0  0  0 -1  0  0  0   0   0   0   0
0 1 0 0   0  1  0  0  0  0 -1  0  0   0   0   0   0
0 1 0 0   0  1  0  0  0  0  0 -1  0   0   0   0   0
0 1 0 0   0  1  0  0  0  0  0  0 -1   0   0   0   0
0 1 0 0   0  1  0  0  0  0  0  0  0  -1   0   0   0
0 1 0 0   0  1  0  0  0  0  0  0  0   0  -1   0   0
1 0 0 0   0  1  0  0  0  0  0  0  0   0   0  -1   0
0 1 0 0   0  1  0  0  0  0  0  0  0   0   0   0  -1
0 1 0 0   0  0  1 -1  0  0  0  0  0   0   0   0   0
1 0 0 0   0  0  1  0 -1  0  0  0  0   0   0   0   0
0 1 0 0   0  0  1  0  0 -1  0  0  0   0   0   0   0
0 1 0 0   0  0  1  0  0  0 -1  0  0   0   0   0   0
1 0 0 0   0  0  1  0  0  0  0 -1  0   0   0   0   0
0 1 0 0   0  0  1  0  0  0  0  0 -1   0   0   0   0
0 1 0 0   0  0  1  0  0  0  0  0  0  -1   0   0   0
0 1 0 0   0  0  1  0  0  0  0  0  0   0  -1   0   0
1 0 0 0   0  0  1  0  0  0  0  0  0   0   0  -1   0
1 0 0 0   0  0  1  0  0  0  0  0  0   0   0   0  -1
0 1 0 0   0  0  0  1 -1  0  0  0  0   0   0   0   0
0 1 0 0   0  0  0  1  0 -1  0  0  0   0   0   0   0
0 1 0 0   0  0  0  1  0  0 -1  0  0   0   0   0   0
0 1 0 0   0  0  0  1  0  0  0 -1  0   0   0   0   0
0 1 0 0   0  0  0  1  0  0  0  0 -1   0   0   0   0
1 0 0 0   0  0  0  1  0  0  0  0  0  -1   0   0   0
0 1 0 0   0  0  0  1  0  0  0  0  0   0  -1   0   0
0 0 1 0   0  0  0  1  0  0  0  0  0   0   0  -1   0
1 0 0 0   0  0  0  1  0  0  0  0  0   0   0   0  -1
0 1 0 0   0  0  0  0  1 -1  0  0  0   0   0   0   0
0 1 0 0   0  0  0  0  1  0 -1  0  0   0   0   0   0
0 1 0 0   0  0  0  0  1  0  0 -1  0   0   0   0   0
0 1 0 0   0  0  0  0  1  0  0  0 -1   0   0   0   0
1 0 0 0   0  0  0  0  1  0  0  0  0  -1   0   0   0
1 0 0 0   0  0  0  0  1  0  0  0  0   0  -1   0   0
1 0 0 0   0  0  0  0  1  0  0  0  0   0   0  -1   0
1 0 0 0   0  0  0  0  1  0  0  0  0   0   0   0  -1
0 1 0 0   0  0  0  0  0  1 -1  0  0   0   0   0   0
0 1 0 0   0  0  0  0  0  1  0 -1  0   0   0   0   0
0 1 0 0   0  0  0  0  0  1  0  0 -1   0   0   0   0
0 0 1 0   0  0  0  0  0  1  0  0  0  -1   0   0   0
0 1 0 0   0  0  0  0  0  1  0  0  0   0  -1   0   0
1 0 0 0   0  0  0  0  0  1  0  0  0   0   0  -1   0
0 1 0 0   0  0  0  0  0  1  0  0  0   0   0   0  -1
0 1 0 0   0  0  0  0  0  0  1 -1  0   0   0   0   0
0 0 1 0   0  0  0  0  0  0  1  0 -1   0   0   0   0
```

```
0 1 0 0   0  0  0  0  0  0  1  0  0 -1   0   0   0
1 0 0 0   0  0  0  0  0  0  1  0  0  0  -1   0   0
1 0 0 0   0  0  0  0  0  0  1  0  0  0   0  -1   0
0 1 0 0   0  0  0  0  0  0  1  0  0  0   0   0  -1
0 0 1 0   0  0  0  0  0  0  0  1 -1  0   0   0   0
0 1 0 0   0  0  0  0  0  0  0  1  0 -1   0   0   0
1 0 0 0   0  0  0  0  0  0  0  1  0  0  -1   0   0
1 0 0 0   0  0  0  0  0  0  0  1  0  0   0  -1   0
1 0 0 0   0  0  0  0  0  0  0  1  0  0   0   0  -1
0 1 0 0   0  0  0  0  0  0  0  0  1 -1   0   0   0
0 1 0 0   0  0  0  0  0  0  0  0  1  0  -1   0   0
0 0 1 0   0  0  0  0  0  0  0  0  1  0   0  -1   0
0 1 0 0   0  0  0  0  0  0  0  0  1  0   0   0  -1
0 1 0 0   0  0  0  0  0  0  0  0  0  1  -1   0   0
1 0 0 0   0  0  0  0  0  0  0  0  0  1   0  -1   0
0 1 0 0   0  0  0  0  0  0  0  0  0  1   0   0  -1
0 0 1 0   0  0  0  0  0  0  0  0  0  0   1  -1   0
0 1 0 0   0  0  0  0  0  0  0  0  0  0   1   0  -1
0 1 0 0   0  0  0  0  0  0  0  0  0  0   0   1  -1
```

Suggestion for analysis.
Let $W_{ij} = 1$ if Player i beats Player j, let $W_{ij} = 0$ otherwise.
Let $Dr_{ij} = 1$ if Player i draws with Player j, let $Dr_{ij} = 0$ otherwise.
Define $Y_{ij} = 2 * W_{ij} + Dr_{ij}$: thus $0 \leq Y_{ij} \leq 2$.
Assume Y_{ij} are independent binomial, with $Y_{ij} \sim Bi(2, p_{ij})$. (This will be an over-simplification, but as we will see, it actually works quite well.) We fit the model $log(p_{ij}/(1 - p_{ij})) = \alpha_i - \alpha_j$, for $1 \leq i < j \leq 14$, with the parameter $\alpha_{14} = 0$ for identifiability. (Thus each of the first 13 players is being compared with Player 14.)

```
Y = 2*W + Dr ; tot = rep(2, times=91)
first.glm = glm(Y/tot ~ P1 + P2 + P3 + P4 + P5 + P6 + P7 + P8 +
+ P9 + P10 + P11 + P12 + P13 + P14 - 1, family = binomial, weights=tot)
summary(first.glm)
.....................
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.5465  -0.4442  -0.1074   1.1513   1.6651

Coefficients: (1 not defined because of singularities)
    Estimate Std. Error z value Pr(>|z|)
P1    1.5676     0.5967   2.627   0.0086 **
P2    1.5676     0.5967   2.627   0.0086 **
P3    1.0861     0.5757   1.886   0.0592 .
P4    1.0861     0.5757   1.886   0.0592 .
P5    0.9342     0.5723   1.632   0.1026
P6    0.9342     0.5723   1.632   0.1026
P7    0.7838     0.5704   1.374   0.1694
P8    0.7838     0.5704   1.374   0.1694
```

```
P9    0.7838     0.5704   1.374   0.1694
P10   0.6334     0.5699   1.111   0.2664
P11   0.4815     0.5709   0.843   0.3990
P12   0.1668     0.5781   0.288   0.7730
P13   0.1668     0.5781   0.288   0.7730
P14       NA         NA      NA       NA
---
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 110.904  on 91  degrees of freedom
Residual deviance:  92.739  on 78  degrees of freedom
AIC: 189.44
Number of Fisher Scoring iterations: 4
```

Exercise: show that $cor(\hat{\alpha}_1, \hat{\alpha}_2) = 0.52$.
Note that the dataset shows that P1 actually lost to P13: this corresponds to a deviance residual which is large and negative (-2.5465). According to our model, this is an unexpected result.
You could consider a more sophisticated model, which does not assume probabilities $p^2, 2pq, q^2$ for the outcomes W, Dr, L of any given match. For example, try

```
polr()
```

from the MASS library. This is then a 'proportional odds' model, for the 'response variable' Y. It gets harder then to interpret the results!
Although in this case, we see that $\hat{\alpha}_1, \hat{\alpha}_2, \ldots, \hat{\alpha}_{14} = 0$ are almost exactly a linear function of the original 'scores' $9, 9, 7.5, \ldots, 4$, for a different dataset this may not be the case. Consider the (somewhat crazy, but not impossible) data set given below, for a 'tournament' between 4 players, with $Y = 2W + Dr$, as before.

```
      Y P1 P2 P3 P4
[1,] 2  1 -1  0  0
[2,] 0  1  0 -1  0
[3,] 1  1  0  0 -1
[4,] 0  0  1 -1  0
[5,] 0  0  1  0 -1
[6,] 0  0  0  1 -1
```

Hence although P1 beats P2, he loses to P3, draws with P4, and P2 loses to both P3 and P4, and P3 loses to P4.

June 21, 2006
Of course I could not resist trying out the same technique for the results of the World Cup, Group B. Here are the data, in similar format to the chess tournament data.
Key to column headings W=win, Dr = Draw, L= Lose, P1=England, P2= Sweden, P3= Trinidad and Tobago, P4= Paraguay.

```
  W Dr L P1 P2 P3 P4
1 0  1 0  1 -1  0  0
2 1  0 0  1  0 -1  0
3 1  0 0  1  0  0 -1
4 0  1 0  0  1 -1  0
5 1  0 0  0  1  0 -1
6 0  0 1  0  0  1 -1

> Y = 2*W + Dr ; tot = rep(2, times=6)
> first.glm = glm(Y/tot ~ P1 + P2 + P3 - 1,family =binomial,weights=tot)
> summary(first.glm)
Call:
glm(formula = Y/tot ~ P1 + P2 + P3 - 1, family=binomial,weights=tot)
Coefficients:
   Estimate Std. Error z value Pr(>|z|)
P1   2.0426     1.4166   1.442    0.149
P2   1.3169     1.2675   1.039    0.299
P3  -0.7257     1.2522  -0.580    0.562
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 11.090  on 6  degrees of freedom
Residual deviance:  5.318  on 3  degrees of freedom
AIC: 14.091
Number of Fisher Scoring iterations: 5
```

and now, to take account of the overdispersion.

```
>summary(first.glm, dispersion=5.318/3)
Call:
glm(formula = Y/tot ~ P1 + P2 + P3 - 1, family = binomial, weights = tot)
Coefficients:
   Estimate Std. Error z value Pr(>|z|)
P1   2.0426     1.8861   1.083    0.279
P2   1.3169     1.6875   0.780    0.435
P3  -0.7257     1.6672  -0.435    0.663
(Dispersion parameter for binomial family taken to be 1.772667)
    Null deviance: 11.090  on 6  degrees of freedom
Residual deviance:  5.318  on 3  degrees of freedom
AIC: 14.091
Number of Fisher Scoring iterations: 5
```

On this scale, the final 'scores' for the 4 teams are
$2.0426, 1.3169, -0.7257, 0$ which (you check) are very closely correlated with the final Points for the 4 teams of $7, 5, 1, 3$ respectively.
I was quite surprised how well the above worked, considering that we have only 6 independent observations from which to estimate 3 parameters, and of course the model is very simple.
Football pundits among you can construct more sophisticated models, eg making use of the actual match scores $(2-2, 2-0, 1-0, 0-0, 1-0, 0-2)$.
Footnote: If the last row of the dataset had been

```
 6 1  0 0  0  0  1 -1
```

ie if in fact Trinidad and Tobago had beaten Paraguay, you can check that the 3 parameter estimates have HUGE se's: presumably the log-likehood function is in some way degenerate, and is no longer a nice convex function.

New for 2008: the Group A results (taken from The Independent, June 16, 2008)

```
# P1= Switzerland, P2 = Portugal, P3 = Turkey, P4 = CzechR
 goal totgoal P1  P2  P3  P4
  2      2    1  -1  0   0
  1      3    1   0  -1  0
  0      1    1   0   0  -1
  2      2    0   1  -1  0
  3      4    0   1   0  -1
  3      5    0   0   1  -1
```

Here I have rather boldly (since I'm pretty ignorant about football) changed the format. Thus the first row of the data indicates that in the match between Switzerland and Portugal, there were a total of 2 goals, of which 2 were scored by Switzerland. You might like to try

```
first.glm <-glm(goal/totgoal~P1+P2+P3-1,binomial,weights=totgoal)
```

You will find that this doesn't work very well, perhaps because the first row of the data was a rather surprising result. The model would fit much better if the first row had been

```
 0     2    1  -1  0   0
```

Speaking of the World Cup, The Independent, June 28, 2006, gives the following dataset for which you might try Poisson regression:
'Hall of shame: Red cards at World Cups'

```
Year Venue Number
1930 Uruguay 1
1934 Italy   1
1938 France  4
1950 Brazil  0
1954 Switzerland 3
1958 Sweden  3
1962 Chile   6
1966 England 5
1970 Mexico  0
1974 W.Germany 5
1978 Argentina 3
1982 Spain   5
1986 Mexico  8
```

```
1990 Italy  16
1994 USA    15
1998 France 22
2002 Korea/Japan 17
2006 Germany* 25
* does not include the figures for the WHOLE set of matches
```

20. New for 2007: what is the median lifetime of a President of the Royal Statistical Society?
This gives you a very small-scale introduction to the important topic of Survival Data Analysis.
'Long live the president' is the title of the Editor's comment in the June 2007 Newsletter of the Royal Statistical Society. Here is the dataset giving the lifetime, in years, of all 34 Presidents of the Royal Statistical Society. This is a nice little example of 'censored' data: the 'status' variable listed below takes the value 1 for an observed death (eg the first person listed was known to die at age 94 years) but status is 0 if the actual lifetime is unknown. For example the last person listed is only known to have lifetime 55 years or more (in other words, happily this person is still alive). In this case the observation is said to be 'censored' (strictly speaking, it was a right-censored observation). Actuaries work out ways of constructing 'survival curves' from such data, and here we will use the appropriate R-library to do the work for us. The 'proper' mathematical explanation is not given here. Suffice it to say that we are working out the survival curve, say $\hat{S}(t)$, which is the estimator of

$$S(t) = Pr(T > t)$$

where T is the lifetime. Our estimator $\hat{S}(t)$ is known as the Kaplan-Meier estimate. Remarkably, it is a 'distribution-free' or 'non-parametric' estimator. The formula for the estimate of the variance of $\hat{S}(t)$ was derived by M.Greenwood in 1926. Using this formula enables us to plot confidence bands for the unknown $S(t)$.
Here is the dataset on the lifetimes of the 34 RSS Presidents: happily many of them are still alive.

years	status
94	1
94	1
93	1
92	1
92	1
91	1
90	0
90	0
87	1
85	0
85	1
84	1
84	0
83	0
83	0
83	0
83	1
79	0
79	1
77	1
77	1

```
 77     1
 76     1
 76     0
 74     0
 73     0
 71     0
 68     0
 64     0
 62     0
 61     0
 57     0
 57     0
 55     0
```

```
 > library(survival)  # to let the expert do the work for us!
 > Surv(years, status) # this creates a 'survival object
 #  + indicates a censored observation (ie that person is still alive)
[1] 94  94  93  92  92  91  90+ 90+ 87  85+ 85  84  84+
[14] 83+ 83+ 83+ 83  79+ 79
[20] 77  77  77  76  76+ 74+ 73+ 71+ 68+ 64+ 62+ 61+ 57+ 57+ 55+

> fit<- survfit(Surv(years, status)~1) #this does the Kaplan-Meier estimation
> fit
Call: survfit(formula = Surv(years, status) ~ 1)

      n  events  median 0.95LCL 0.95UCL
     34      15      91      85     Inf
```

So we see that for the 34 Presidents, there were 15 known deaths, and the estimate of the median lifetime is 91 years.
Now we get detailed information on our survivor function. Note that this is computed in terms of the ordered observed death times. The first of these is 76 years, at which 24 individuals were known to be 'at risk', and exactly 1 died, leaving us with $23/24 = 0.958$ as the estimate of $S(76)$, and (using an obvious notation) $\sqrt{p(1-p)/n}$ as the corresponding se.
At the next observed death time, 77 years, we have 22 people at risk, and 3 deaths, leaving $S(77)$ as $(23/24) \times (19/22) = 0.828$.
(Can you see why we are computing the product of 2 probabilities?)
The corresponding estimated survivor function, and its confidence bands, are given in Figure 26.

```
> summary(fit)
Call: survfit(formula = Surv(years, status) ~ 1)

 time n.risk n.event survival std.err lower 95% CI upper 95% CI
   76     24       1    0.958  0.0408        0.882        1.000
   77     22       3    0.828  0.0785        0.687        0.997
```

```
   79     19       1    0.784  0.0856        0.633        0.971
   83     17       1    0.738  0.0921        0.578        0.943
   84     13       1    0.681  0.1010        0.509        0.911
   85     11       1    0.619  0.1092        0.438        0.875
   87      9       1    0.550  0.1167        0.363        0.834
   91      6       1    0.459  0.1284        0.265        0.794
   92      5       2    0.275  0.1266        0.112        0.678
   93      3       1    0.183  0.1129        0.055        0.613
   94      2       2    0.000      NA           NA           NA
> plot(fit,xlim=c(50,100),xlab="years",ylab="survival probability")
> abline(.5, 0) # to find the median
```

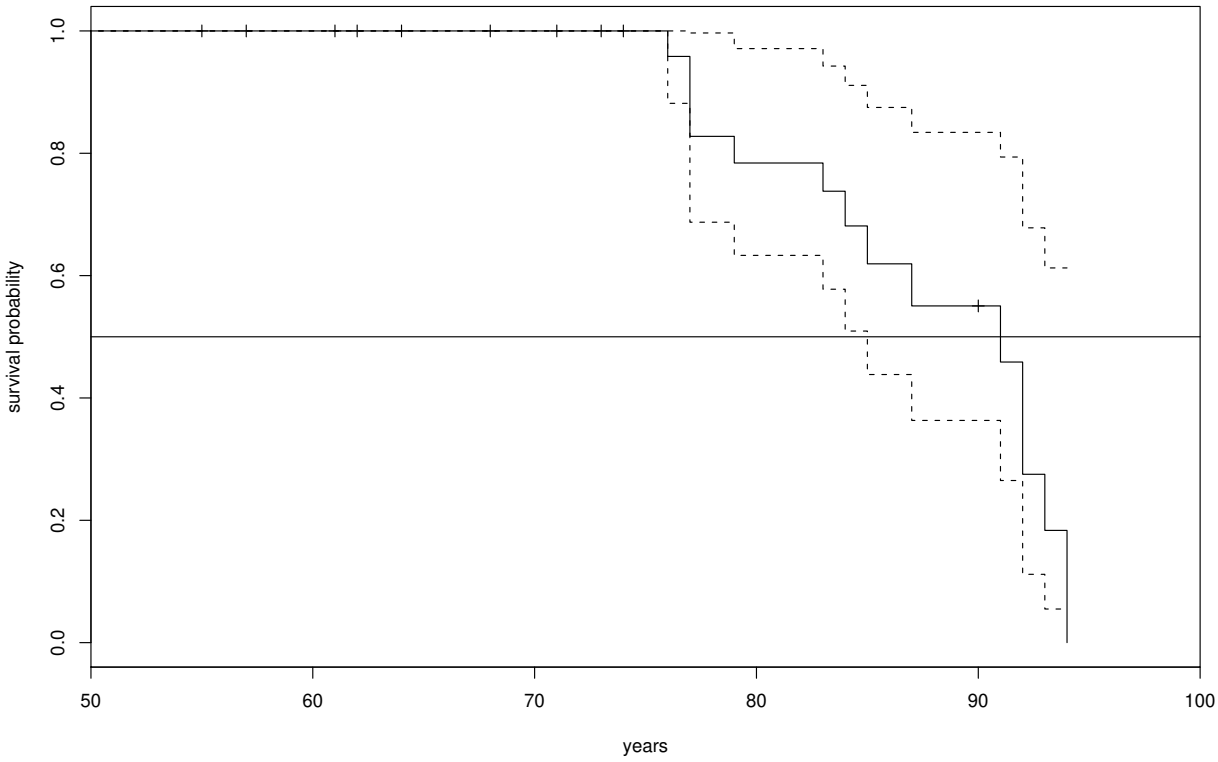

Figure 26: Survival curve for RSS presidents

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