R Commander an introduction

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Preface

This material is intended as an introductory guide to data analysis with R Commander. It was written as part of an applied statistics course, given at the Wellcome Trust Sanger Institute, Hinxton, UK. The principle aim is to provide a step-by-step guide on the use of R Commander to carry out exploratory data analysis and the subsequent application of statistical analysis to answer questions widely asked in the life sciences.

These notes (version 2) were written with R commander version 2.0-2 under a Window's operating system. This document is available for download from the Comprehensive R Archive Network (http://cran.r-project.org/) and is provided free-of-charge with no warrantee for its use. It is not to be modified from this form without explicit authorization from the author.

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R Commander

Course Content

1. Starting R commander and importing data
    - 1.1 What is R Commander?
    - 1.2 References and additional reading material
    - 1.3 Installing R Commander
    - 1.4 Starting R Commander
    - 1.5 Data entry
        - 1.5.1 Manual entry
        - 1.5.2 Import from text file
        - 1.5.3 Import from Excel
2. Using R Commander to obtain descriptives
    - 2.1 Checking categorical variables
    - 2.2 Checking continuous variables
3. Modifying the dataset
    - 3.1 Compute a new variable
    - 3.2 Converting numeric variables to categorical variables
    - 3.3 Sub-dividing data
4. Using R Commander to explore data
    - 4.1 Graphically
        - 4.1.1 Histograms
        - 4.1.2 Normal Q-Q plots
        - 4.1.3 Scatterplots
        - 4.1.4 Boxplots
    - 4.2 Shapiro-Wilk test for normality
    - 4.3 Kruskal-Wallis Test
5. Using R commander to apply statistical tests
    - 5.1 Comparing the mean
        - 5.1.1 Student’s *t*-Test
        - 5.1.2 Paired Student’s *t*-Test
        - 5.1.3 Single Sample *t*-Test
        - 5.1.4 One-way ANOVA
        - 5.1.5 Two-way ANOVA
    - 5.2 Comparing the variance
        - 5.2.1 Bartlett’s test
        - 5.2.2 Levene’s test
        - 5.2.3 Two variance F-test
    - 5.3 Non-parametric Tests
        - 5.3.1 Two-sample Wilcoxon Test

1. Starting R commander and importing data

1.1 What is R Commander?

It is free statistical software. R commander was developed as an easy to use graphical user interface (GUI) for R (freeware statistical programming language) and was developed by Prof. John Fox to allow the teaching of statistics courses and removing the hindrance of software complexity from the process of learning statistics. This means it has drop down menus that can drive the statistical analysis of data. It is considered the most viable R-alternative to commercial statistical packages like SPSS (Wikipedia). The package is highly useful to R novices, since for each analysis run it displays the underlying R code.

Home page: http://socserv.mcmaster.ca/jfox/Misc/Rcmdr/

It also has an additional 29 plug-ins which provide support for specific analyses, graphics, books and teaching. See http://www.rcommander.com/ which has a table of available plug ins and links for further information.

1.2 References and additional reading material

- "The R Commander: A Basic-Statistics Graphical User Interface to R" John Fox Journal of Statistical Software 2005, Volume 14, Issue 9.

- http://www.wlu.ca/documents/42689/Introduction_to_R_and_R_Commander.pdf

- http://socserv.mcmaster.ca/jfox/Misc/Rcmdr/Getting-Started-with-the-Rcmdr.pdf

- http://courses.statistics.com/software/RCommander/RC00.htm

1.3 Installing R commander

You need to first install R and then R commander.

The following link provides good instructions for installation of R:

http://jekyll.math.byuh.edu/other/howto/R/R.shtml

The following link provides good instructions for installation of R commander:

http://jekyll.math.byuh.edu/other/howto/R/Rcmdr.shtml

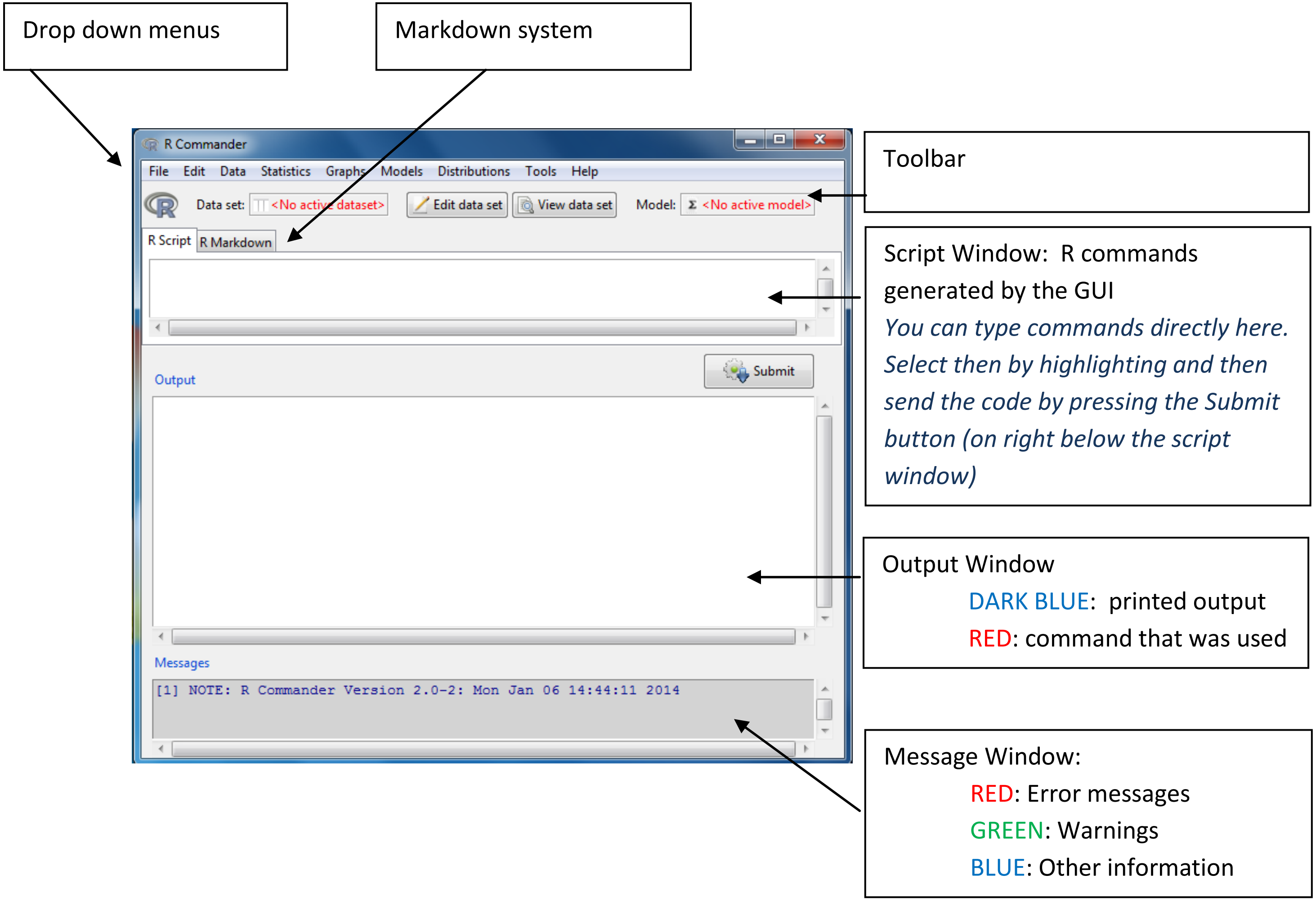
1.4 Starting the R Commander

i. Open R program

e.g. double click on R icon or start/all programs/R

ii. To open the R commander program type at the prompt library("Rcmdr") and press return.

The R commander window shown below will open.



Drop down menus

Markdown system

Toolbar

Script Window: R commands generated by the GUI

You can type commands directly here. Select then by highlighting and then send the code by pressing the Submit button (on right below the script window)

Output Window

DARK BLUE: printed output

RED: command that was used

Message Window:

RED: Error messages

GREEN: Warnings

BLUE: Other information

```
[1] NOTE: R Commander Version 2.0-2: Mon Jan 06 14:44:11 2014
```

Note: Graphs will appear in a separate Graphics Device Window. Only the most recent graph will appear. You can use page up and page down keys to recall previous graphs.

Drop down Menu item	
File	Menu items for loading and saving script files; for saving output and the R workspace; and for exiting.
Edit	Menu items (Cut, Copy, Paste, etc.) for editing the contents of the script and output windows. Right clicking in the script or output window also brings up an edit “context” menu
Data	Submenus containing menu items for reading and manipulating data.
Statistics	Submenus containing menu items for a variety of basic statistical analyses.
Graphs	Menu items for creating simple statistical graphs.
Models	Menu items and submenus for obtaining numerical summaries, confidence intervals, hypothesis tests, diagnostics, and graphs for a statistical model, and for adding diagnostic quantities, such as residuals, to the data set. Distributions Probabilities, quantiles, and graphs of standard statistical distributions (to be used, for example, as a substitute for statistical tables).
Distributions	Probabilities, quantiles, sampling and graphs of standard statistical distributions
Tools	Menu items for loading R packages unrelated to the Rcmdr package (e.g., to access data saved in another package), and for setting some options.
Help	Menu items to obtain information about the R Commander (including an introductory manual derived from this paper). As well, each R Commander dialog box has a Help button.

Toolbar buttons	
Data set	Shows the name of the active dataset Button: allows you choose among dataset currently in memory which to be active
Edit data set	Allows you to open the active dataset
View data set	Allows you to view the active dataset
Model	Shows the name of the active statistical model e.g. linear model Button: allows you to choose among current models in memory

Menu items are inactive (ie, greyed out) if not applicable to the current context.

1. 5 Data input

1.5.1 Manual entry

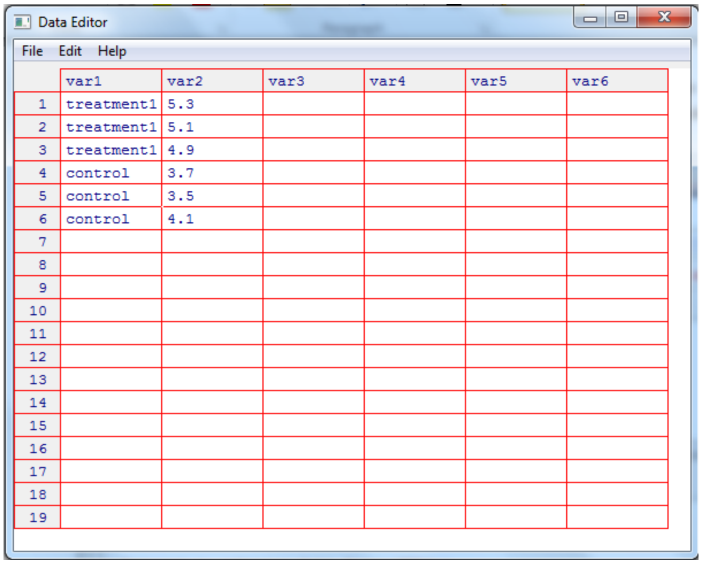
i. Start a new data set through Data -> New data set

ii. Enter a new name for the dataset -> OK

⚠ **Note**: the name cannot have spaces in it

⚠ **Note**: R is case-sensitive hence mydata ≠MyData

iii. A data editor window where you can type in your data using a typical spreadsheet format. Each row corresponds to an independent object e.g. a subject on which a measurement was made.



	var1	var2	var3	var4	var5	var6
1	treatment1	5.3				
2	treatment1	5.1				
3	treatment1	4.9				
4	control	3.7				
5	control	3.5				
6	control	4.1				
7						
8						
9						
10						
11						
12						
13						
14						
15						
16						
17						
18						
19						

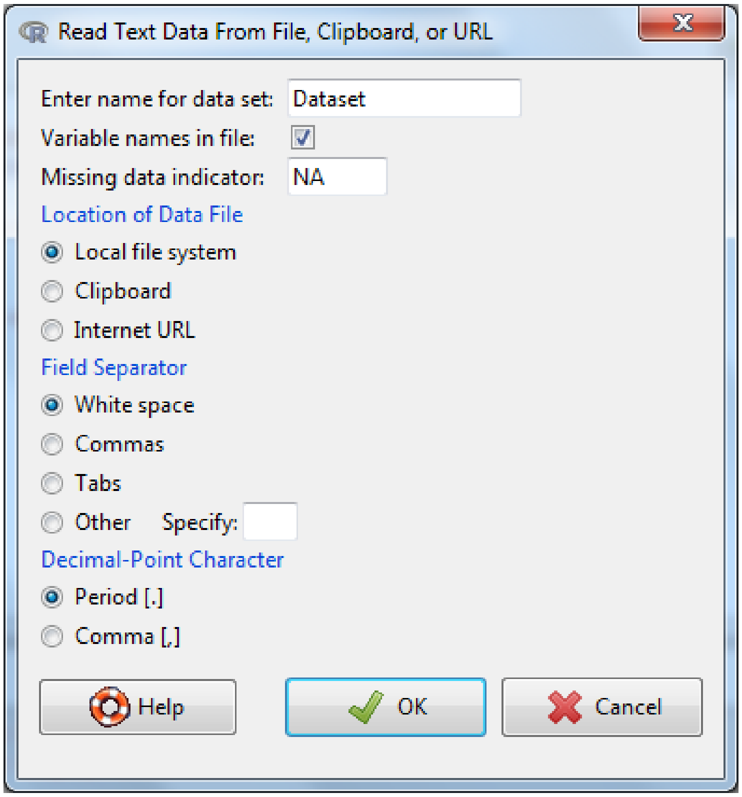
iv. Define the variables (column) by clicking on the column label and then in the resulting dialog box enter the name and type. Where type can be numeric (quantitative) or character (qualitative). Click on the x in the right hand corner to close this dialog box.

v. This data frame is then the active dataset for R commander.

1.5.2 Import from text file

⚠ **Note**: the data file will need to be organized as a classic data frame. Each column represents a single variable e.g. glucose level. Each row represents an individual. The header information needs to be contained in a single row.

i. Data -> Import data -> from text file



Read Text Data From File, Clipboard, or URL

Enter name for data set: Dataset

Variable names in file: ☑

Missing data indicator: NA

Location of Data File

● Local file system

○ Clipboard

○ Internet URL

Field Separator

● White space

○ Commas

○ Tabs

○ Other Specify:

Decimal-Point Character

● Period [.]

○ Comma [,]

ii. Chose a name for the new dataset (note you cannot have spaces)

iii. Specify the characteristics of the data files (e.g. commas for csv files) -> OK

iv. Browse and select the file/Open

Once data is imported you should double-check the file was read-in correctly:

v. Message window: are there any errors?

vi. Do the number of rows and columns look as expected?

vii. View the data via View data set button

1.5.3 Import from Excel

Data files can be read in from Excel, however they often have issues. It is recommended that instead the file is converted to a text file and then import as detailed in 1.5.2.

How?

1. Within Excel: Office -> Save As and select the comma-delimited (.csv) file format.

2 Using R Commander to obtain descriptives

Role of descriptives?

1. Checking for errors

   Looking for values that fall outside the possible values for a variable

   Looking for excess number of missing values

2. As descriptives

   To describe the sample in your report

   To address specific research questions

2.1 Checking categorical variables

i. Statistics -> Summaries -> Frequency Distributions -> Select the variables->OK

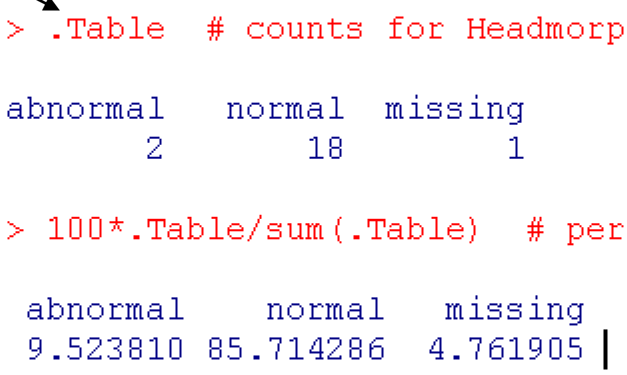
ii. Output: For each variable you selected it will tell you the frequency for each level.

The red text following prompt:

R code used to generate output

Red text following #:

Explanation of what the code is doing



```
> .Table  # counts for Headmorphology

abnormal   normal  missing
       2       18        1

> 100*.Table/sum(.Table)  # percentages for Headmorphology

 abnormal    normal   missing
 9.523810 85.714286  4.761905
```

The output of analysis is shown in blue

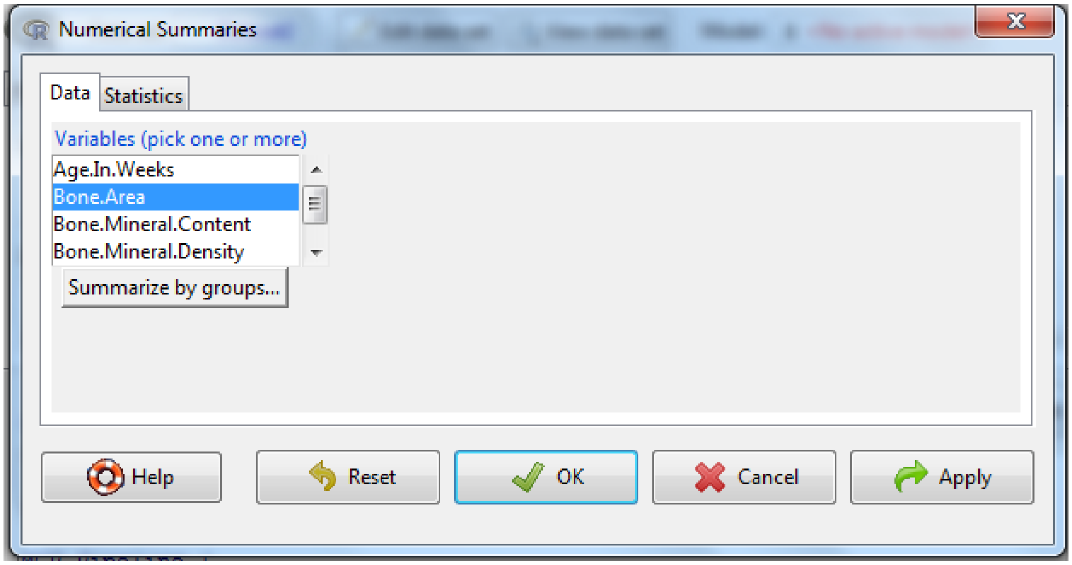
v. Check for unexpected levels e.g. norm rather than normal.

vi. Check the number of missing values does it seem appropriate?

2.2 Checking continuous variables

i. Statistics -> Summaries -> Numerical summaries

ii. Select the variables of interest

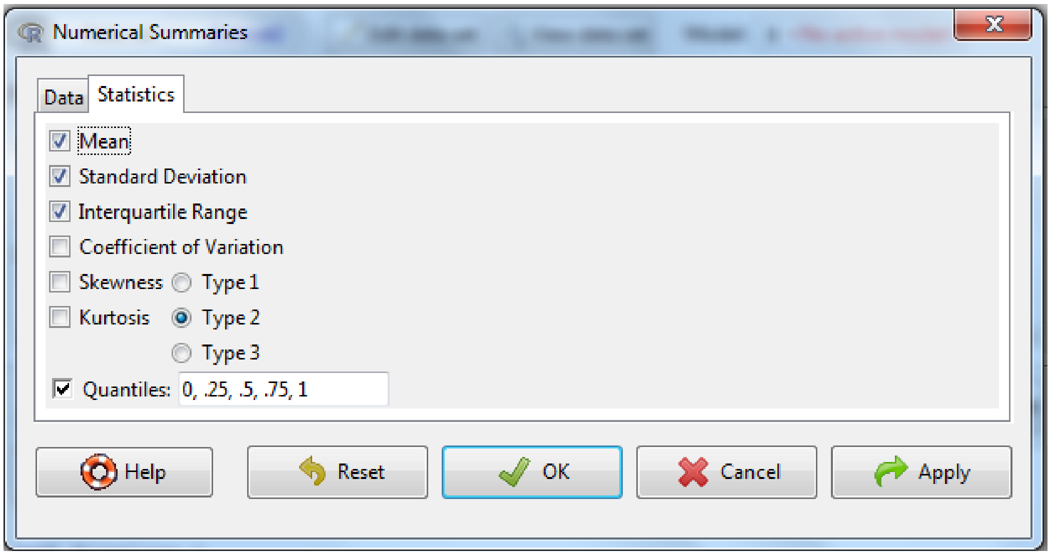


Variables (pick one or more)

Age.In.Weeks
Bone.Area
Bone.Mineral.Content
Bone.Mineral.Density

iii. If you have multiple groups (e.g. control versus treatment) click on summarize by groups and select the appropriate variable -> OK

iv. Select the statistics tab to amend the output as required.



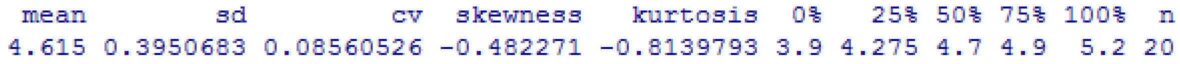
☑ Mean
☑ Standard Deviation
☑ Interquartile Range
☐ Coefficient of Variation
☐ Skewness ○ Type 1
☐ Kurtosis ● Type 2
○ Type 3
☑ Quantiles: 0, .25, .5, .75, 1

Note 1: type refers to the algorithm used in the calculation of kurtosis and skewness. Default of 2 is the current norm. Further information can be found at: http://cran.r-project.org/web/packages/e1071/e1071.pdf

Note 2: Definition of Kurtosis, Skewness and Coefficient of Variation is explained in the output table in the next section

Note 3: The **quantiles** are values which divide the distribution such that there are a given proportion of observations below the quantile. For example, the median is the central value of the distribution, such that half the points are less than or equal to it and half are greater than or equal to it. If you enter 0.2 you asking what is the value of the variable which of all the measures has 20% of the data smaller than it and 80% larger than this value.

Output:



```
  mean        sd         cv  skewness   kurtosis  0%   25% 50% 75% 100%  n
 4.615 0.3950683 0.08560526 -0.482271 -0.8139793 3.9 4.275 4.7 4.9  5.2 20
```

Understanding the output:

output	What is it?
mean	Measure of central tendency
sd	Standard deviation - a measure of variability in the data
cv Coefficient of variance	The coefficient of variation (CV) is a normalized measure of variance. It is calculated as the ratio of the standard deviation to the mean. It can be compared across variables as the variability is now on a standardised scale.
Skewness	Skewness is a measure of symmetry. The output can be positive or negative. A negative value indicates negative skew indicates meaning that the *tail* on the left side of the distribution is *longer* than the right side and the bulk of the values lie to the right of the mean. A positive value indicates positive skew indicates that the *tail* on the right side is *longer* than the left side and the bulk of the values lie to the left of the mean. A zero value indicates that the values are relatively evenly distributed on both sides of the mean
kurtosis	Kurtosis is a measure of whether the data are peaked or flat relative to a normal distribution. A standard normal distribution has a kurtosis of zero. A positive kurtosis indicates a "peaked" distribution and negative kurtosis indicates a "flat" distribution.
n	Number of readings
NA	Number of missing values
0%	Minimum value
25%	The value below which 25 percent of the observations may be found.
50%	The value below which 50 percent of the observations may be found.
75%	The value below which 75 percent of the observations may be found.
100%	Maximum value

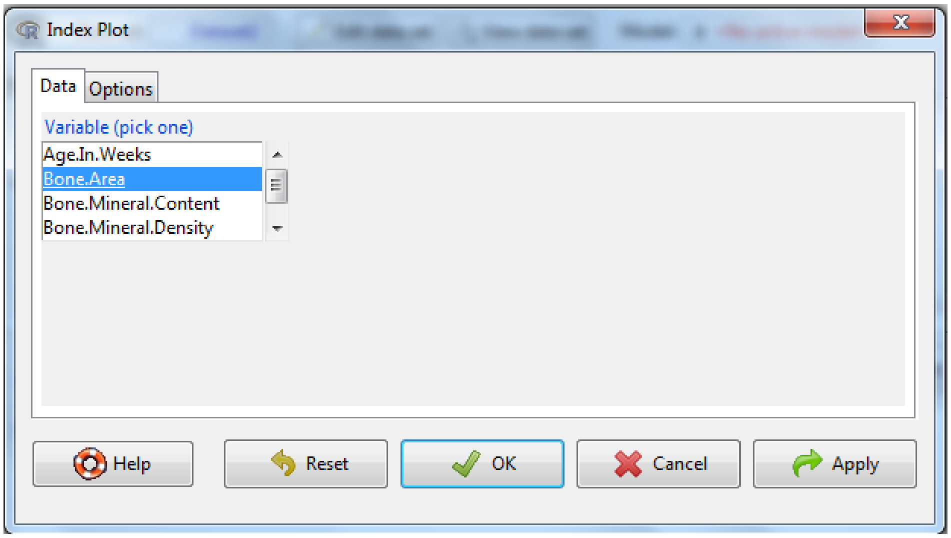
v. Check your minimum and maximum values – do they make sense?

vi. Check the number of missing values – if there are a lot of missing values you need to ask why?

vii. Do the mean score(s) make sense? Is it what you expect from previous experience?

viii. Identifying the outlier

Graphs -> Index Plot



Index Plot

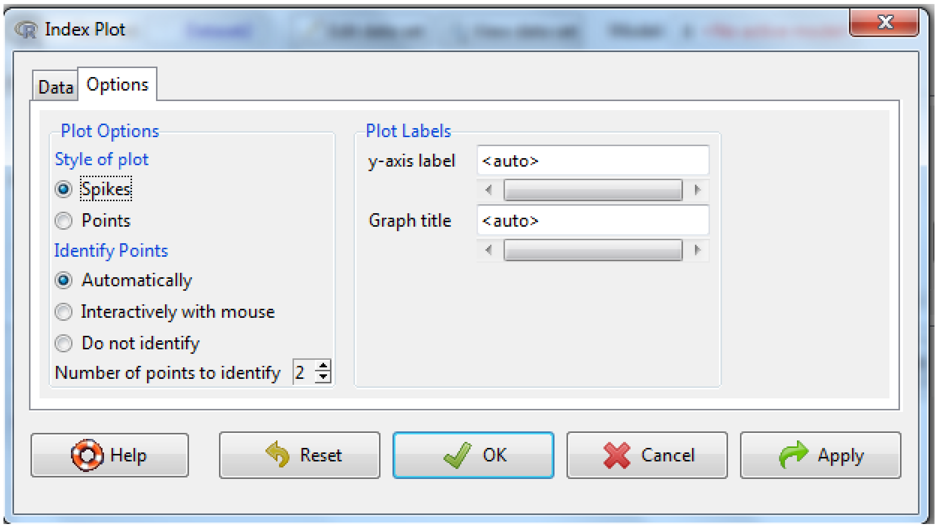
Data | Options

Variable (pick one)

- Age.In.Weeks
- Bone.Area
- Bone.Mineral.Content
- Bone.Mineral.Density

ix. Select the variable of concern

x. Select the options tab to bespoke the output



Index Plot

Data | Options

Plot Options

Style of plot

● Spikes

○ Points

Identify Points

● Automatically

○ Interactively with mouse

○ Do not identify

Number of points to identify 2

Plot Labels

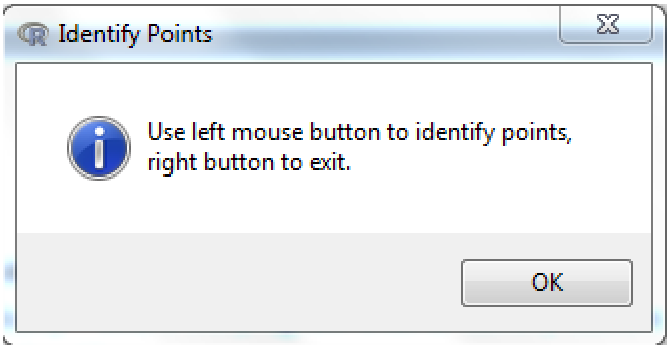
y-axis label <auto>

Graph title <auto>

xi. Outliers can be identified either by selecting

i. Automatically – where the program tries to identify outliers

ii. Interactively with mouse, this will lead to the following message on how you select which points/spikes to identify.



Use left mouse button to identify points, right button to exit.

xii. The graph can be amended by

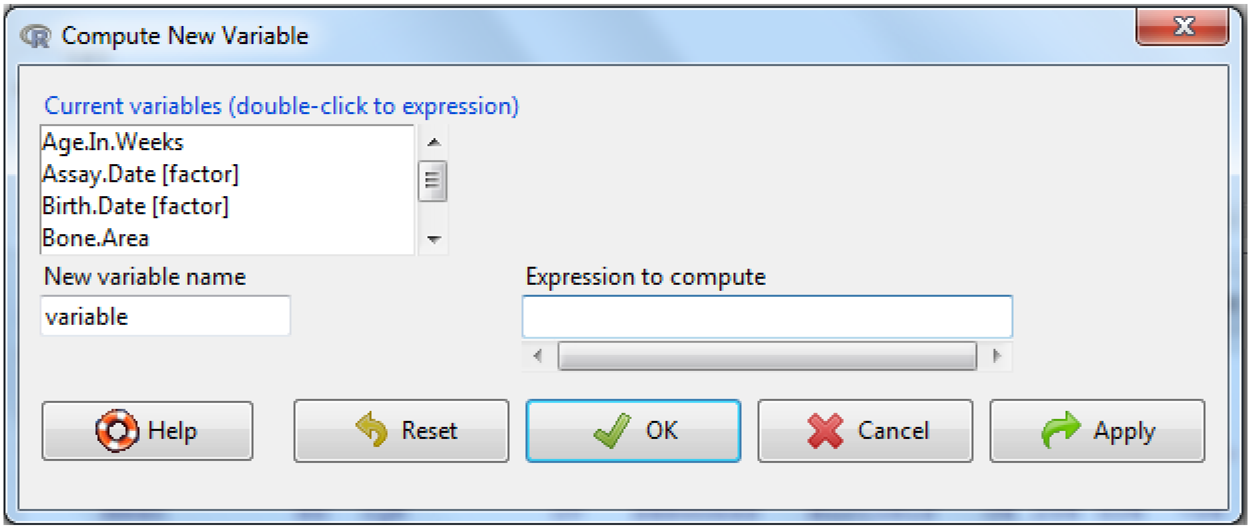
- i. Adding title
- ii. Amending the axis label
- iii. Whether it is spikes or individual points.

xiii. Click to OK to visualize the graph

3. Modifying the dataset

3.1 Compute a new variable

i. Data -> Manage variables in active data set -> Compute new variable



Age.In.Weeks
Assay.Date [factor]
Birth.Date [factor]
Bone.Area

New variable name: variable

Expression to compute:

ii. Enter new variable name

iii. An expression (equation) is written to reflect the calculation required. The table below indicates the operators available and examples of how it could be used. Note: Double clicking on a variable in the current variables box will send the variable to the expression.

Operators	Function	Example 1	Example 2
x + y	Addition	Variable 1 + Variable 2	Variable 1 + 25
x – y	Subtraction	Variable 1 – Variable 2	35 - Variable 1
x * y	Multiple	Variable 1*Variable 2	100*Variable 1
x / y	Division	Variable 1/Variable 2	Variable 1 / 63
x ^ y	X to the power of Y	Variable 1 ^ Variable2	Variable1^10
log10(x)	Log10 transformation	Log10(Variable 1)	
log(x, base)	Log transformation to a specified base	Log(Variable 1, 2)	

3.2 Converting numeric variables to categorical variables

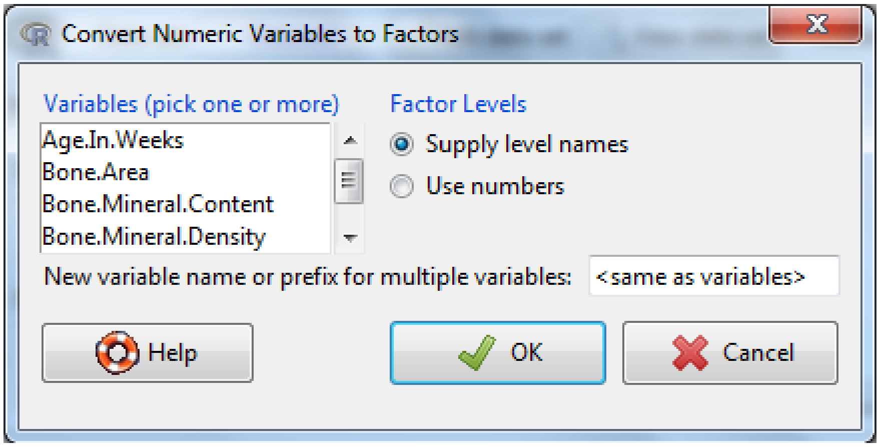
Categorical variables are measures on a nominal scale i.e. where you use labels. For example, rocks can be generally categorized as igneous, sedimentary and metamorphic. The values that can be taken are called levels. Categorical variables have no numerical meaning but are often coded for easy of data entry and processing in spreadsheets. For example gender is often coded where male =1 and female = 2. Data can thus be entered as characters (e.g. 'normal') or numeric (e.g. 0, 1, 2). It is important to ensure the program distinguishes between categorical variables entered numerically and those variables whose values have a direct numerical meaning.

Assessing whether a variable is entered as categorical:

i. Edit Data Set -> click on each row header and it will tell you it is numeric/categorical

Converting numeric variables to factors:

i. Data -> Manage variables in active data set -> Convert numeric variables to factors…



Convert Numeric Variables to Factors

Variables (pick one or more)

Age.In.Weeks
Bone.Area
Bone.Mineral.Content
Bone.Mineral.Density

Factor Levels

● Supply level names

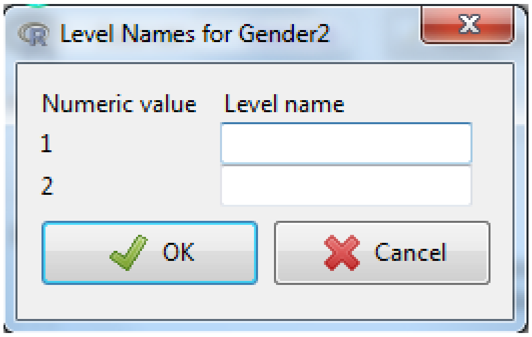
○ Use numbers

New variable name or prefix for multiple variables: <same as variables>

ii. Select the variables

iii. You can generate a new variable by entering a name in box “new variable name….” or over-write the original name.

iv. The levels of the factor can be defined either by selecting Use numbers where the current numbers become the levels or select Supply level names. If you select Supply level names then another dialog box will appear to enter the name for each numeric value.



Level Names for Gender2

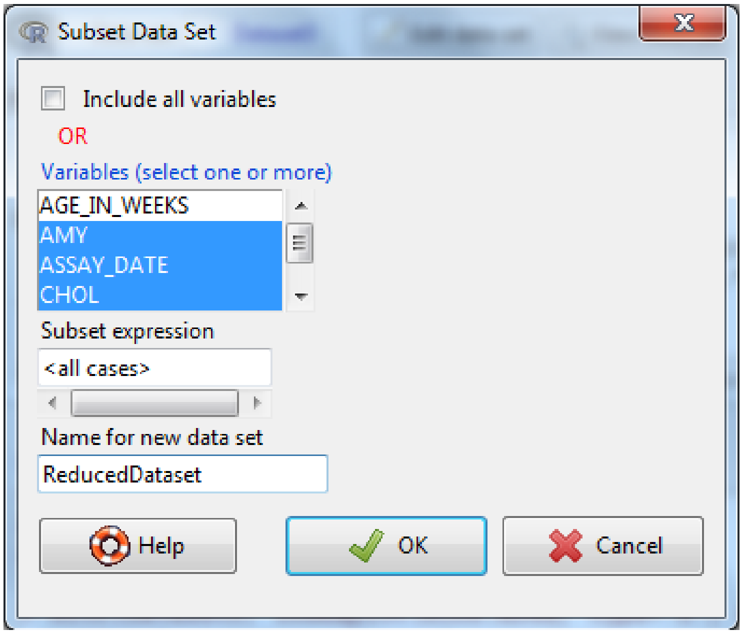
Numeric value	Level name
1	
2	

v. OK

3.3 Sub-dividing data

3.3.1 by columns (variables)

i. data -> active data set -> subset active data set..



Subset Data Set

□ Include all variables

OR

Variables (select one or more)

AGE_IN_WEEKS
AMY
ASSAY_DATE
CHOL

Subset expression

<all cases>

Name for new data set

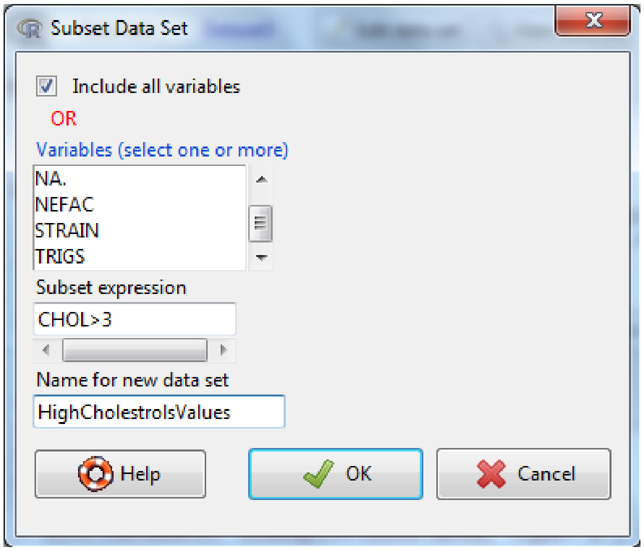
ReducedDataset

ii. Untick the Include all variables and Hold the CTRL key to select the variables you wish to keep

iii. Give the new dataset a name -> OK

3.3.2 by rows (and variables if you wish)

i. Data -> active dataset -> subset active dataset



☑ Include all variables

OR

Variables (select one or more)

NA.
NEFAC
STRAIN
TRIGS

Subset expression: CHOL>3

Name for new data set: HighCholestrolsValues

ii. Select the variables you wish to include in the new dataset

iii. Write a ‘subset expression’ which is a rule to drive the selection of rows

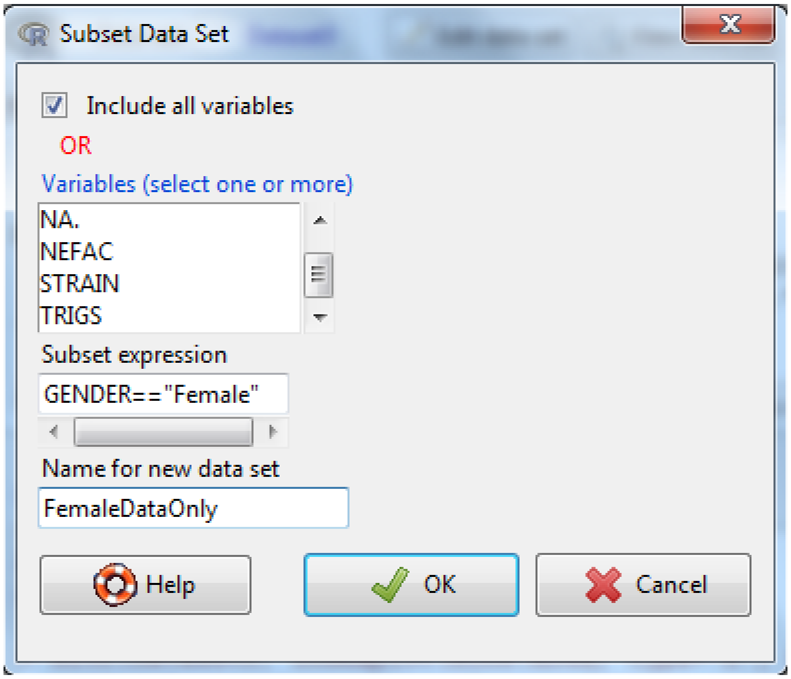
Symbol/code	Name	Use
==	equality	used to indicate the variable should equal
!=	Inequality	used to indicate the variable should not equal
&	And	used to combine multiple expressions
|	Or	used to combine multiple expressions
is.na(varname)		Include the missing values of a variable
!is.na(varname)		Exclude the missing values of a variable
>	Greater than	
<	Less than	
>=		More than or equal to
<=		Less than or equal to

Note 1: If you use a name in an expression you need to surround the name with double quotes e.g. “name”.

Note 2: the variable name is case-sensitive (i.e. it has to match exactly the name used as a column header).

Example: GENDER == “Female”

Example 2: GENDER == “Female” & AGE <= 25



☑ Include all variables

Subset expression: GENDER=="Female"

Name for new data set: FemaleDataOnly

iv. Give the dataset a new name -> OK.

4. Using R Commander to explore data

4.1 Graphically

The R commander is able to generate a variety of basic statistical graphs. The graphic output in R commander is limited by the choice offered in the menu. There are too many options to be incorporated sensible. Whilst in R, using the command line, the options are endless. Section 7 of this course, gives examples of how the graphical output can be amended by altering the R code. For further adjustments, I would recommend speaking to an R user, or using books, and web resources to learn more.

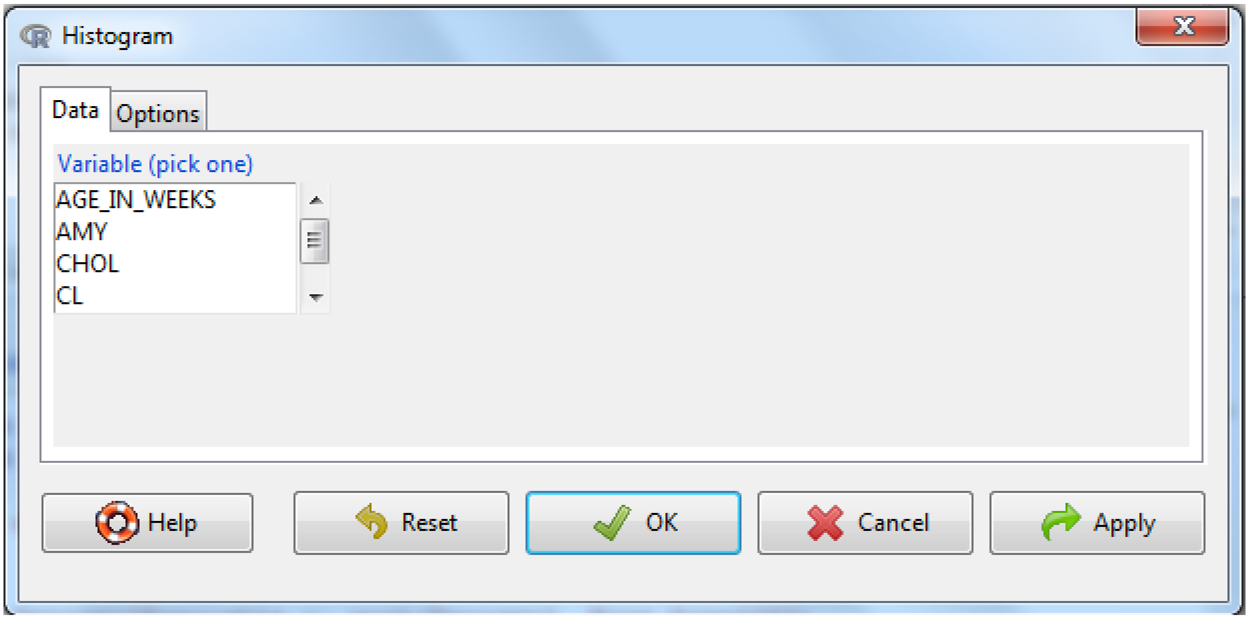
Some references for producing graphs in R

R Graphics (Computer Science and Data Analysis) by Paul Murrell
http://www.harding.edu/fmccown/R/
http://www.statmethods.net/graphs/index.html
http://freshmeat.net/articles/creating-charts-and-graphs-with-gnu-r
http://www.ats.ucla.edu/stat/R/library/lecture_graphing_r.htm

4.1.1 Histograms

In statistics, a histogram is a graphical display of tabulated frequencies, shown as bars. It shows what proportion of cases fall into each of several categories.

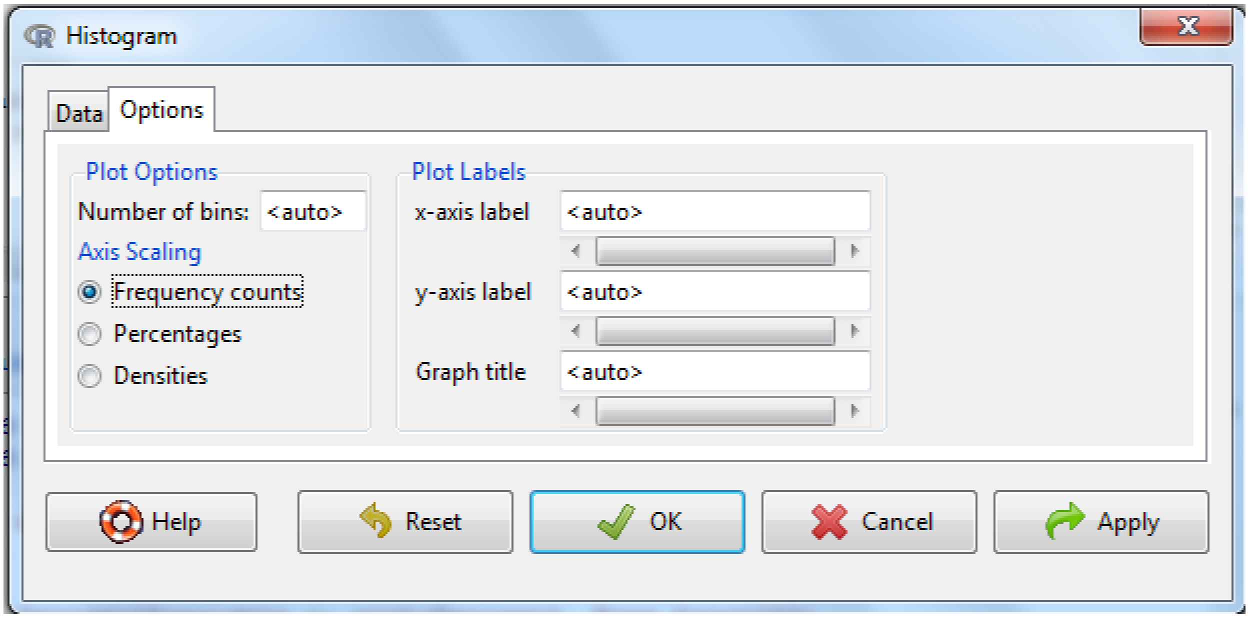
i. Graphs -> Histogram…



ii. Select the variable of interest

iii. Then select the options tab to bespoke the final graph

a. Labels, x-axis, y-axis and title, can be customized here.
b. The scale can be as counts, percentage or densities as required.
c. Finally the number of bins can be determined automatically or defined by entering a number.



Number of bins: <auto>

● Frequency counts
○ Percentages
○ Densities

x-axis label <auto>

y-axis label <auto>

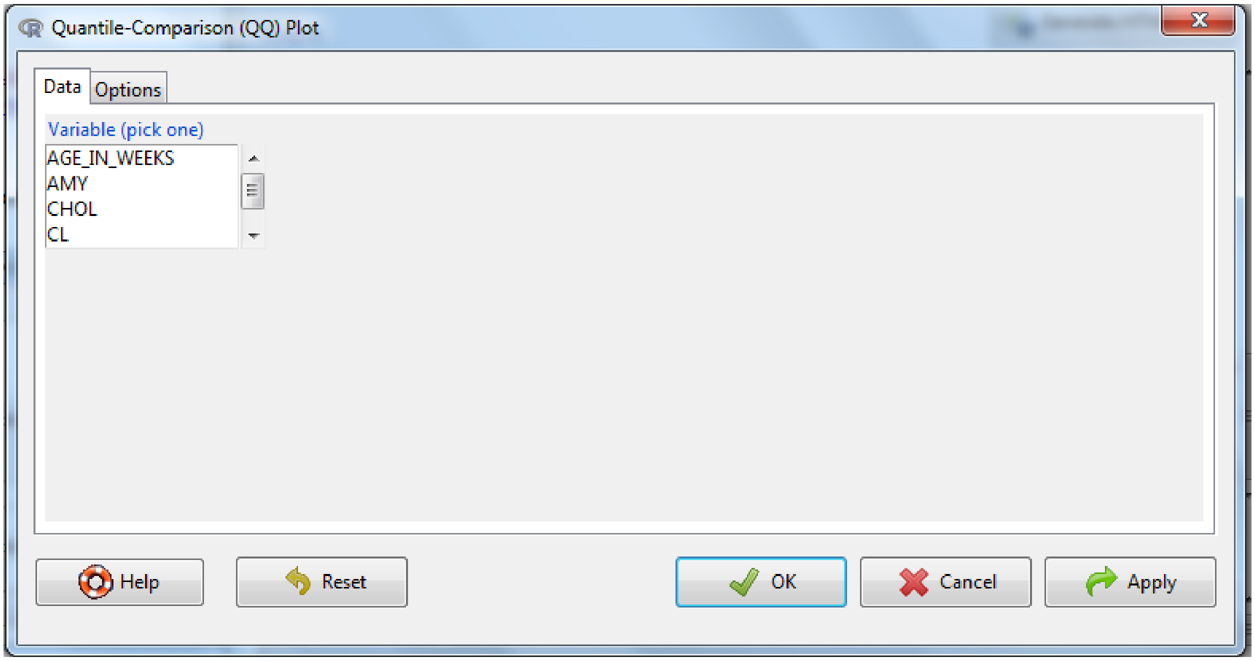
Graph title <auto>

4.1.2 Norm Q-Q plots

In statistics, a Q-Q plot ("Q" stands for *quantile*) is a probability plot, which is a graphical method for comparing two probability distributions by plotting their quantiles against each other. If the two distributions being compared are similar, the points in the Q-Q plot will approximately lie on the line *y* = *x*. A norm Q-Q plot compares the sample distribution against a normal distribution.

Additional information:
http://www.cms.murdoch.edu.au/areas/maths/statsnotes/samplestats/qqplot.html
http://webhelp.esri.com/arcgisdesktop/9.2/index.cfm?TopicName=Normal_QQ_plot_and_general_QQ_plot

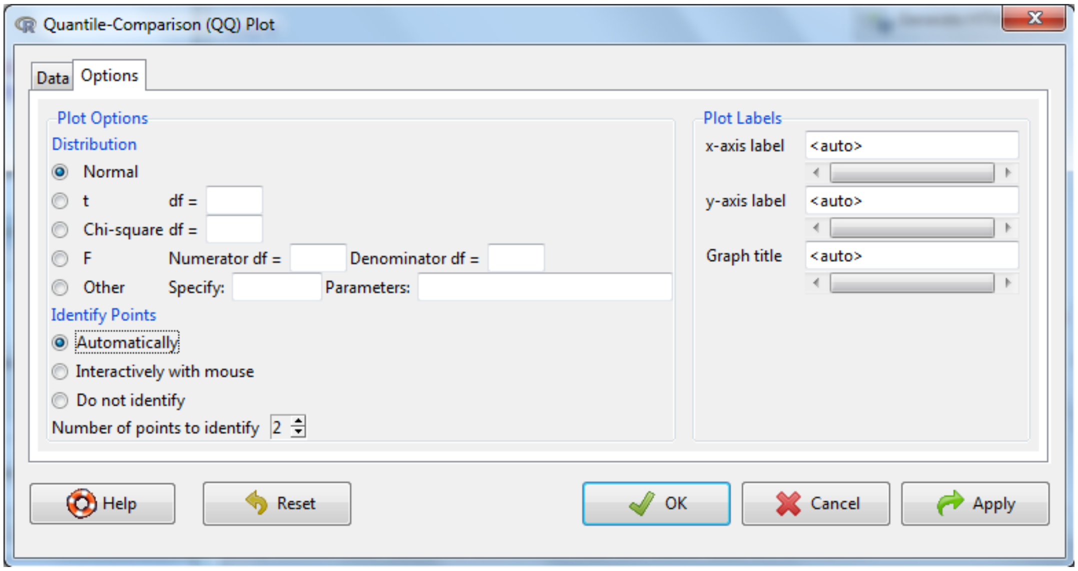
i. Graphs -> Quantile-comparison plot…



ii. Select variable of interest

iii. Then select the options tab to bespoke the final graph

a. Labels, x-axis, y-axis and title, can be customized here.
b. The distribution type and associated characteristics defined. Select normal for a normal Q-Q plot.
c. There is an option to identify outliers. You can either have outliers automatically labelled with the index number or interactively where you select the data point to label with a mouse click.



Plot Options

Distribution

● Normal

○ t df =

○ Chi-square df =

○ F Numerator df = Denominator df =

○ Other Specify: Parameters:

Identify Points

● Automatically

○ Interactively with mouse

○ Do not identify

Number of points to identify 2

Plot Labels

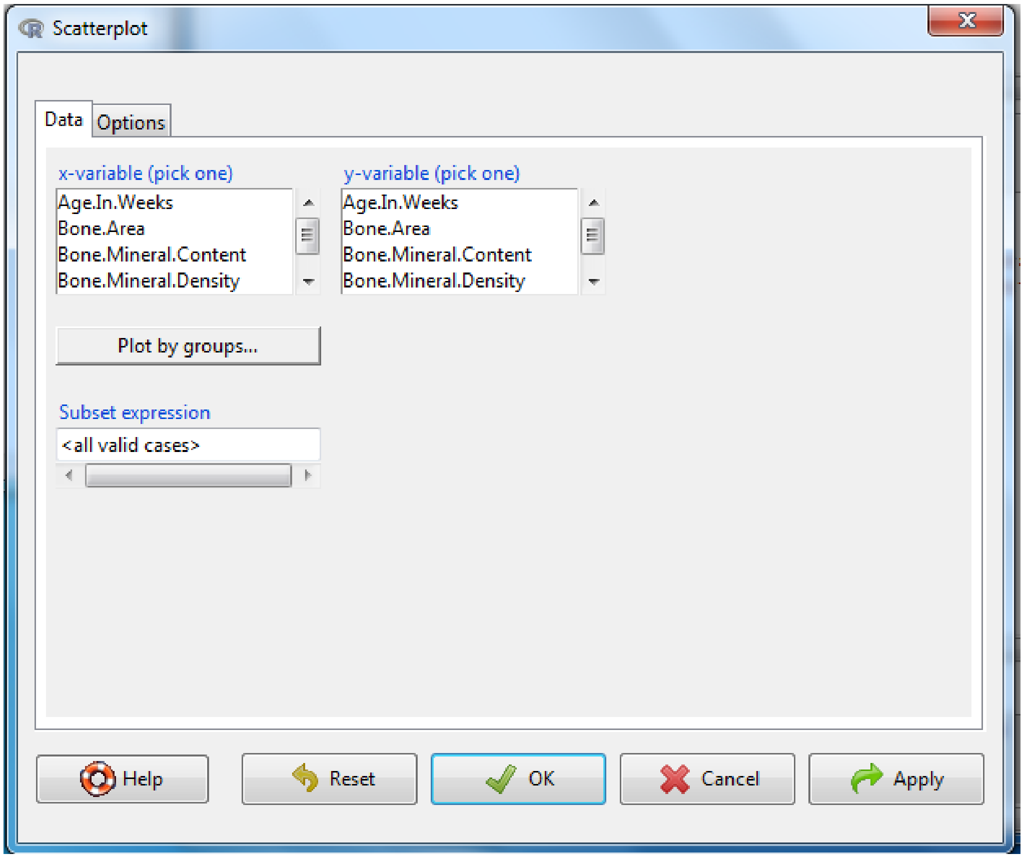
x-axis label <auto>

y-axis label <auto>

Graph title <auto>

4.1.3 **Scatterplots**

i. Graphs -> Scatterplot…



x-variable (pick one)

Age.In.Weeks
Bone.Area
Bone.Mineral.Content
Bone.Mineral.Density

y-variable (pick one)

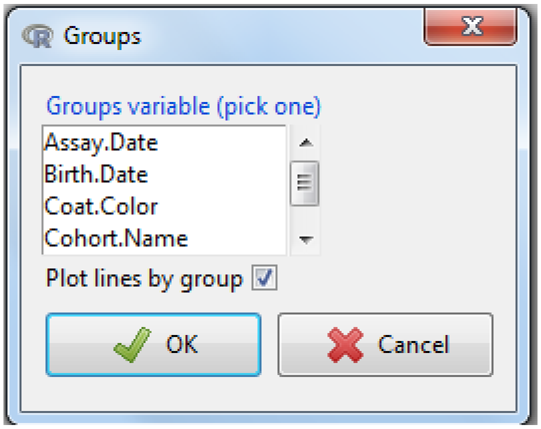
Age.In.Weeks
Bone.Area
Bone.Mineral.Content
Bone.Mineral.Density

Subset expression

<all valid cases>

ii. Select the variables for x-axis and y-axis

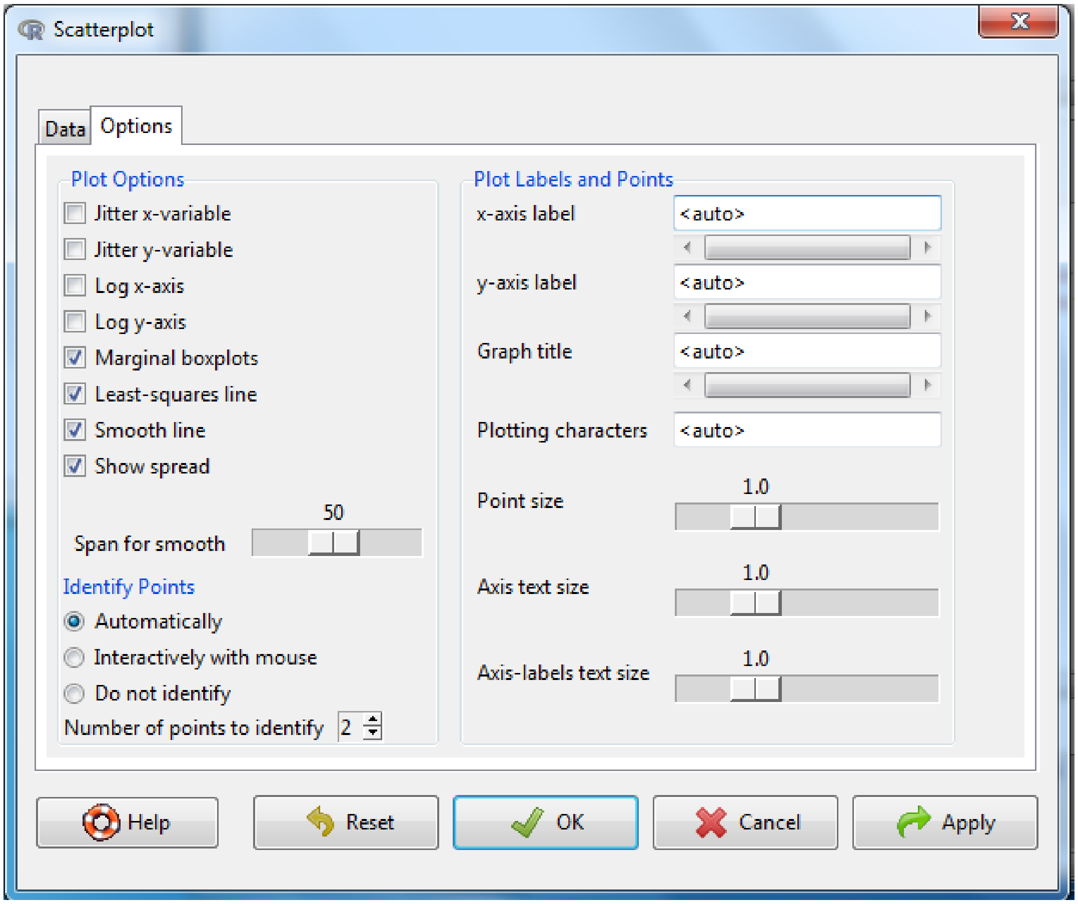
iii. You have the option to plot by groups which will lead to the following dialog box, where you can select the grouping variable and whether you want the fitted lines to be for the whole data or by group.



Plot lines by group ☑

iv. Then select the options tab to customise the final graph.

- Labels, x-axis, y-axis and title, can be customized here both in content and plotting characteristics.
- There is an option to identify outliers. You can either have outliers automatically labelled with the index number or interactively where you select the data point to label with a mouse click.
- If you wish the x or y axis can be logged.
- Marginal boxplots: If this selected, then along each axis is shown a boxplot of the variable for that axis.
- Jitter: this is useful when there are many data points to see if they are overlaying, as a function is used to randomly perturb the points but this does not influence line fitting.
- Least-square line can be selected to fit a best fit linear regression line.
- Smooth line – will fit a loess line which is a locally weighted line and is used to assess whether the assumption of linearity is appropriate. There is an option to amend the number of data points used in the smooth process.
- Show spread – this will give a dotted line surrounding the data and fitted curves and shows the standard deviation of the data.



Plot Options

- ☐ Jitter x-variable
- ☐ Jitter y-variable
- ☐ Log x-axis
- ☐ Log y-axis
- ☑ Marginal boxplots
- ☑ Least-squares line
- ☑ Smooth line
- ☑ Show spread

Span for smooth 50

Identify Points

- ● Automatically
- ○ Interactively with mouse
- ○ Do not identify

Number of points to identify 2

Plot Labels and Points

x-axis label <auto>

y-axis label <auto>

Graph title <auto>

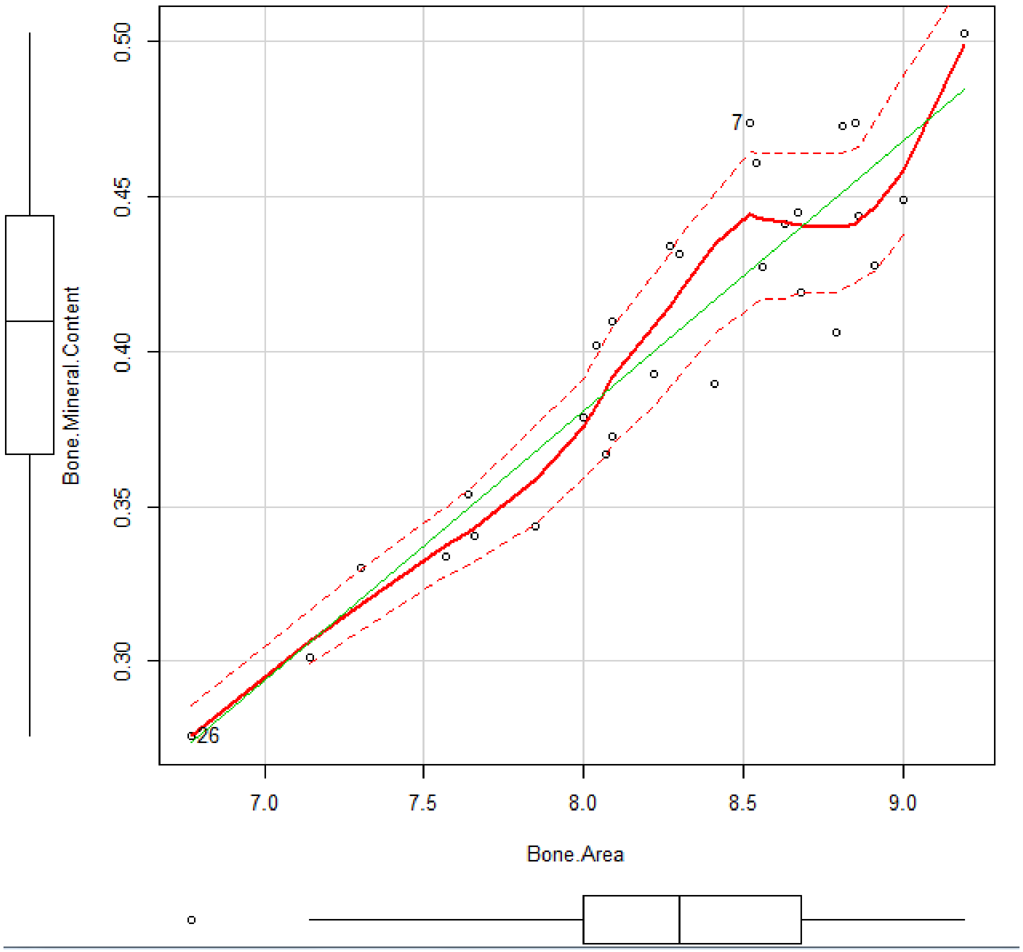
Plotting characters <auto>

Point size 1.0

Axis text size 1.0

Axis-labels text size 1.0

Interpreting the output:



⚠ The green line: is the best fit linear regression

The red line: is loess line. A loess line is a locally weighted line and is used to assess whether the assumption of linearity is appropriate. Visually you are looking to see whether the loess line suggestions a significant deviation from the linear.

The dotted lines indicate the spread of the data.

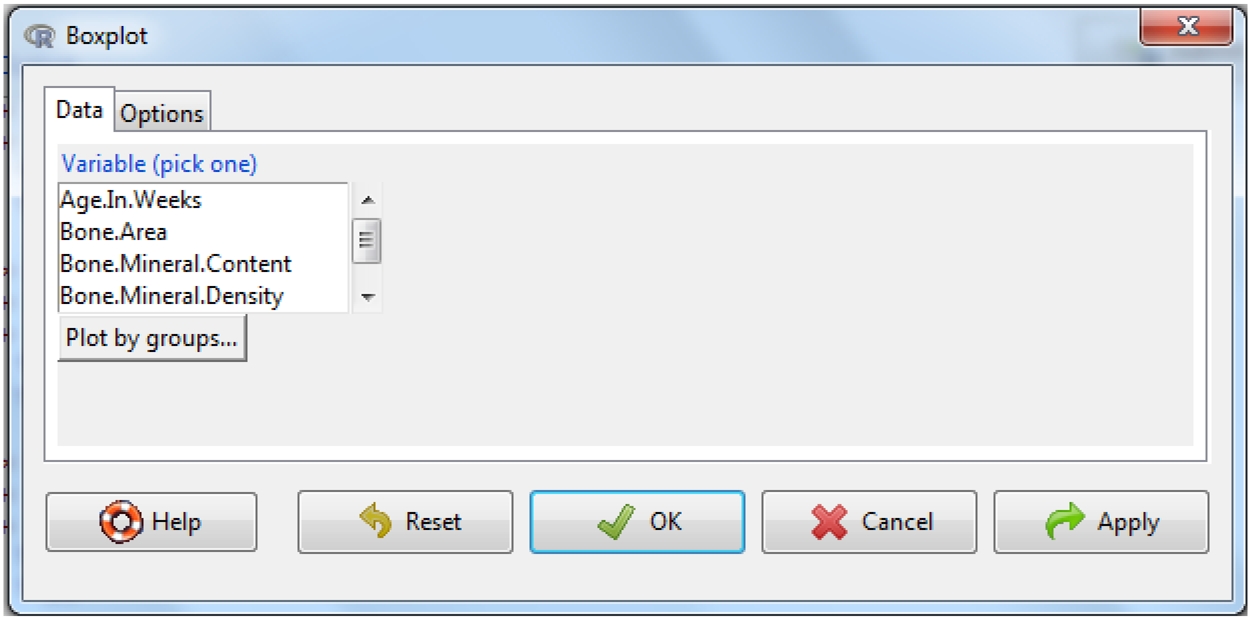
The box plots give an indication to the spread of each variable independently.

4.1.4 Box plots

A boxplot, or box and whisker diagram, provides a simple graphical summary of a set of data. It is a convenient way of graphically visualising data through their five-number summaries: the smallest observation (minimum), lower quartile (Q1), median (Q2), upper quartile (Q3), and largest observation (maximum). A quartile is any of the three values which divide the sorted dataset into four equal parts, so that each part represents one fourth of the sampled population. Outliers, points which are more than 1.5 the interquartile range (Q3-Q1) away from the interquartile boundaries are marked individually.

a. Graphs -> Boxplot…

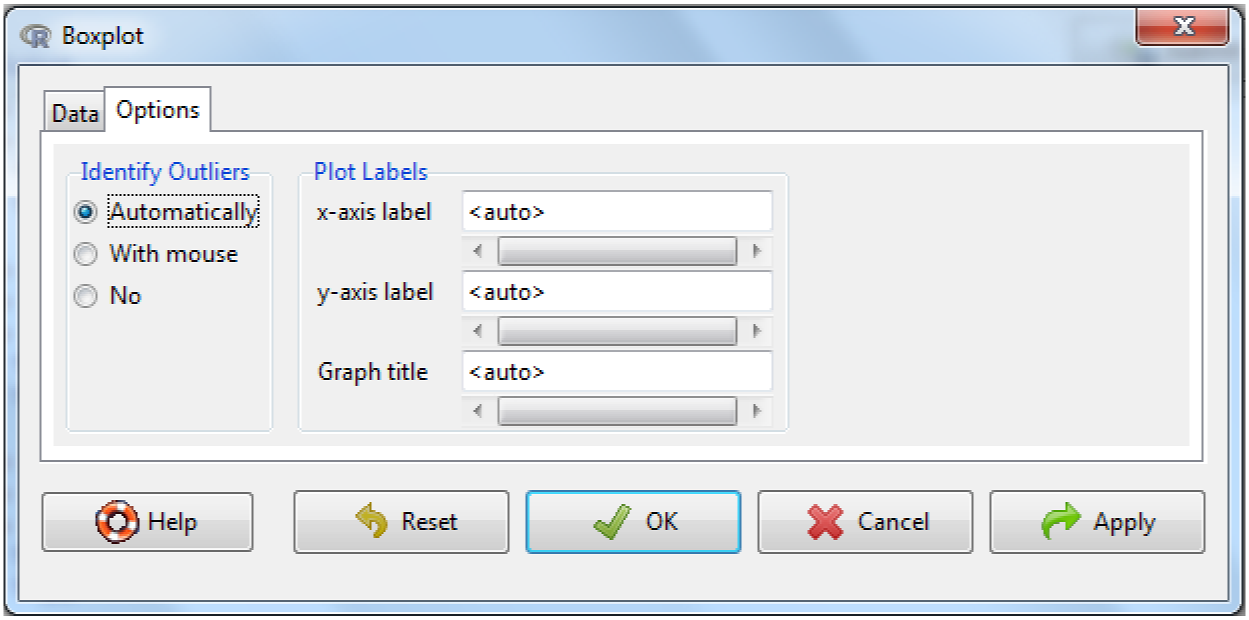
b. Select the variable of interest



c. Plot by groups: allows you to have multiple boxplots in the same graph split by a categorical variable.

d. Then select the options tab to customize the final graph.

- Labels, x-axis, y-axis and title, can be customized here both in content and plotting characteristics.
- There is an option to identify outliers. You can either have outliers automatically labelled with the index number or interactively where you select the data point to label with a mouse click.



Identify Outliers
● Automatically
○ With mouse
○ No

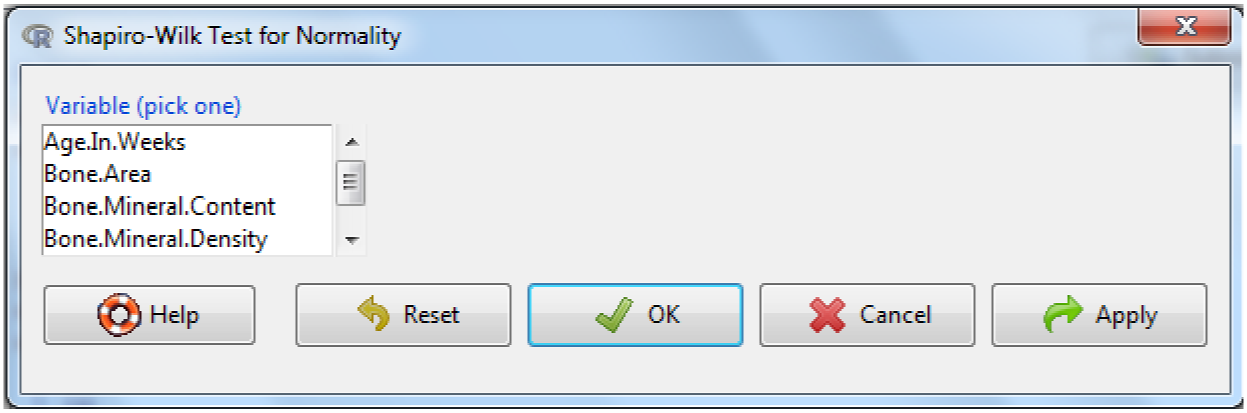
Plot Labels
x-axis label <auto>
y-axis label <auto>
Graph title <auto>

e. OK

4.2 Shapiro-Wilk test for normality

This is a hypothesis tests with the null hypothesis that the data comes from a normal distribution. Hence if the *p*-value is below the significance threshold (typically 0.05), then the null hypothesis is rejected and the alternative hypothesis is accepted. Here the alternative hypothesis is that the data does not come from a normal distribution.

a. Statistics -> Summaries -> Shapiro-Wilk test of normality



Variable (pick one)
Age.In.Weeks
Bone.Area
Bone.Mineral.Content
Bone.Mineral.Density

b. Select the parameter of interest

c. OK

d. Interpretation: If the *p*-value is below the significance threshold, then there the null hypothesis is rejected allowing the acceptance of the alternative hypothesis that the data does not come from a normal distribution.

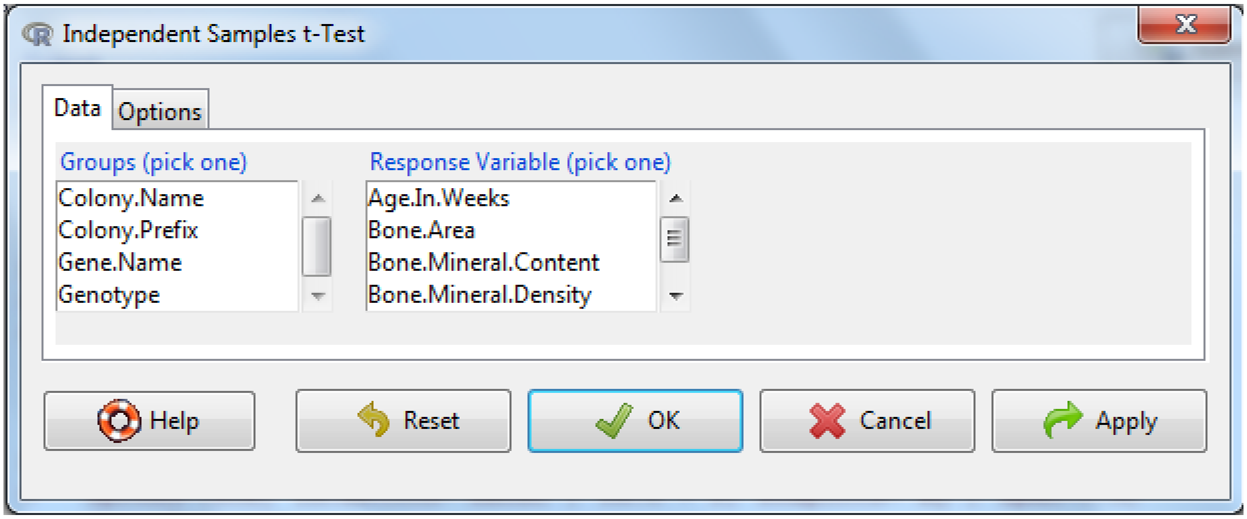
5. Using R commander to apply statistical tests

5.1 Comparing means

5.1.1 Student's *t*-Test

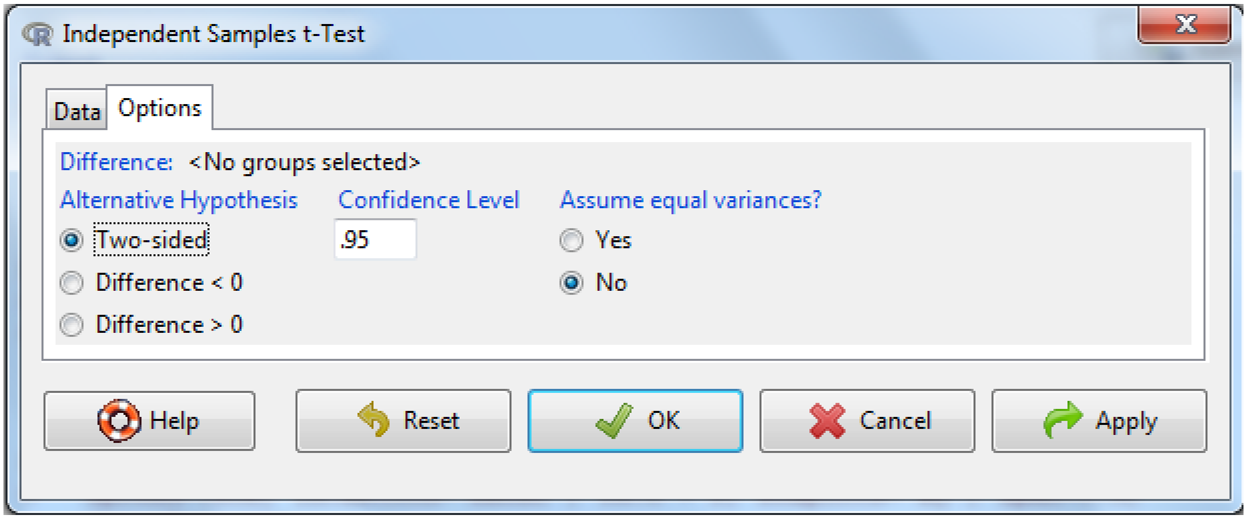
The two-sample Student's *t*-Test is used to determine if two population means are equal.

a. Statistics -> Means -> Independent Samples *t*-Test



b. Select the grouping variable e.g. genotype and the response variable e.g. Bone.Area

c. Under the options tab, there are three things to consider



Difference: <No groups selected>

Alternative Hypothesis
● Two-sided
○ Difference < 0
○ Difference > 0

Confidence Level
.95

Assume equal variances?
○ Yes
● No

- The alternative hypothesis - Typically you select a two-sided hypothesis; this means the change in mean can be either an increase or a decrease.
- The confidence level: the threshold at which you reject the null hypothesis and accept the alternate hypothesis. Typically this is 0.05, which is a 5% risk that the difference is a sampling effect rather than a true population difference.
- Assume equal variances: yes or no. As variance is a measure of the spread of the data, if the spread of the data is different between the two groups then for the statistical test to work reliable you need to select No. This can be assessed visually by looking at boxplots of the data (section 4.1.4) and statistically (section 5.2). If you do not assume equal variance this test is equivalent to the Welch *t*-Test and is considered more robust. Small departures from equal variance significantly affect the robustness of results.

d. OK.

e. Interpretation? If the *p*-value is below the significance threshold, then there is a significant difference in the mean scores for each of the two groups.

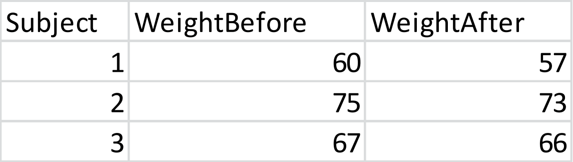
5.1.2 Paired student's *t*-Test

In a paired experiment, there is a one-to-one correspondence between the values in the two samples (e.g. before and after treatment, paired subjects e.g. twins). A paired approach is considered more sensitive as it is looking for a treatment difference excluding initial biological differences. As such the null hypothesis for this statistical test is that the average difference (second measurement minus first) is zero.

⚠ Note: **Data File Format**

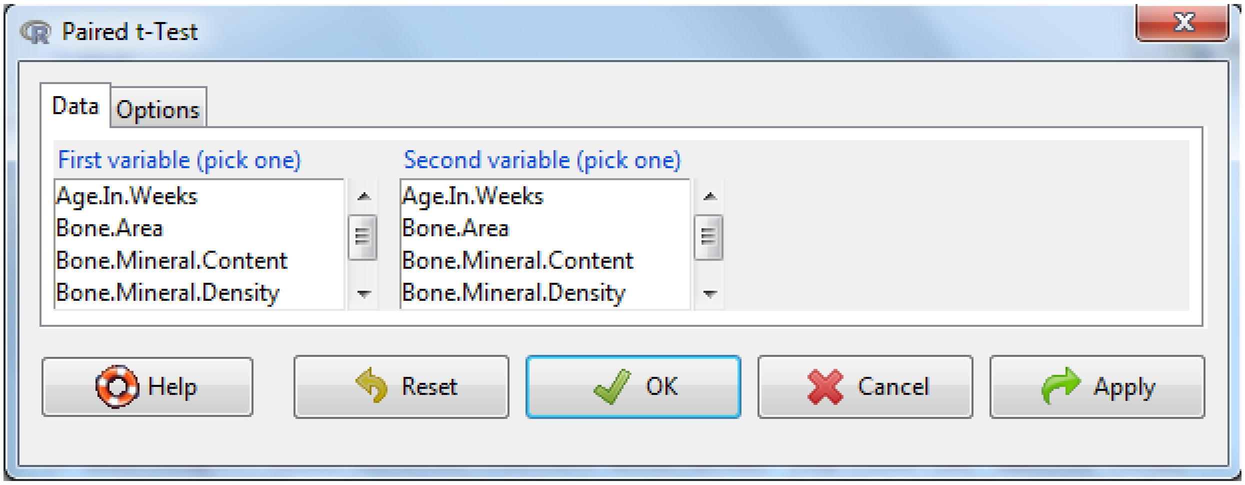
Need two columns; one that contains the first number in each data set pair (e.g., "before" data) and another column that contains the second number in each data set pair. Pairs of numbers must be in the same row.

Example layout:



Subject	WeightBefore	WeightAfter
1	60	57
2	75	73
3	67	66

a. Statistics -> Means -> Paired *t*-Test



First variable (pick one)

Age.In.Weeks
Bone.Area
Bone.Mineral.Content
Bone.Mineral.Density

Second variable (pick one)

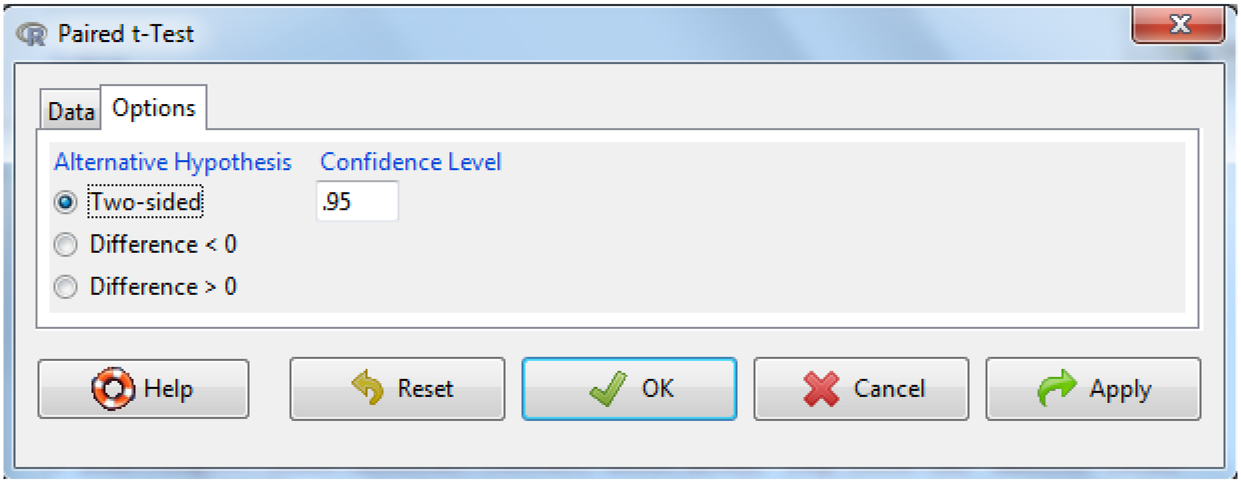
Age.In.Weeks
Bone.Area
Bone.Mineral.Content
Bone.Mineral.Density

b. Select the first variable

c. Select the second variable

d. Under the options tab, there are two things to consider

- The alternative hypothesis can be two sided where the change in mean difference can be either an increase or a decrease or defined as an increase or a decrease.
- The confidence level: the threshold at which you reject the null hypothesis and accept the alternate hypothesis. Typically this is 0.05, which is a 5% risk that the difference is a sampling effect rather than a true population difference.



Alternative Hypothesis

● Two-sided
○ Difference < 0
○ Difference > 0

Confidence Level

.95

e. OK.

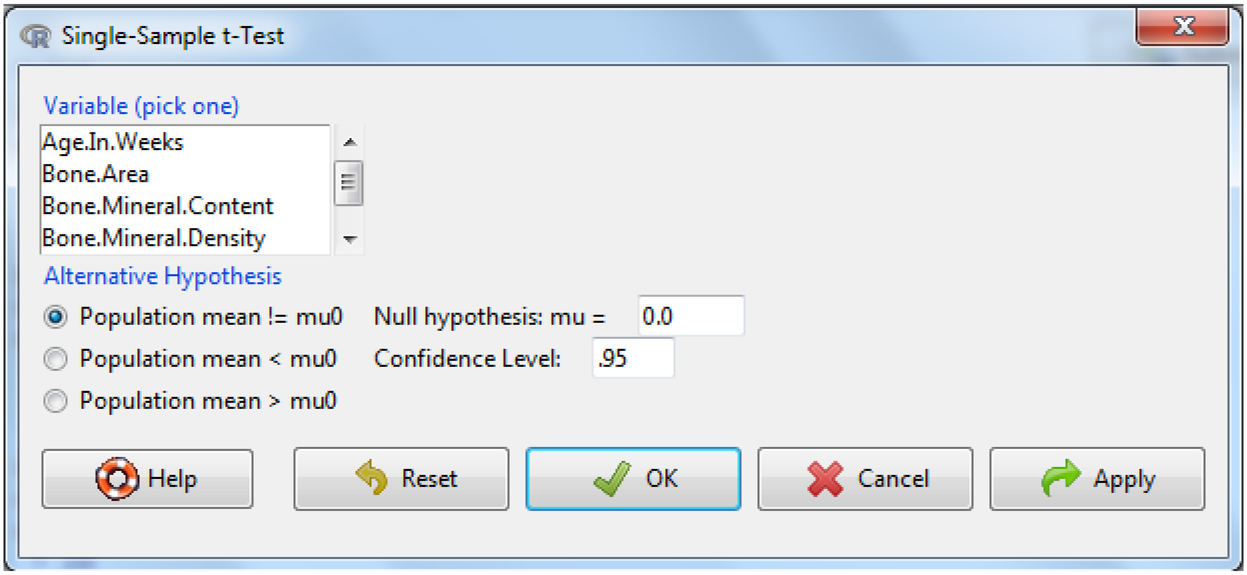
f. Interpretation?

- If the *p*-value is below the significance threshold, then the mean difference is not equal to 0
- The mean of the difference indicates the average difference (variable 1-variable 2)
- The 95% confidence interval is the confidence interval around the mean difference.

5.1.3 Single sample *t*-Test

The single sample *t*-Test tests a null hypothesis that the population mean is equal to a specified value. If this value is zero (or not entered) then the confidence interval for the sample mean is given.

a. Statistics -> Means -> Single-sample *t*-Test



● Population mean != mu0
○ Population mean < mu0
○ Population mean > mu0

Null hypothesis: mu = 0.0

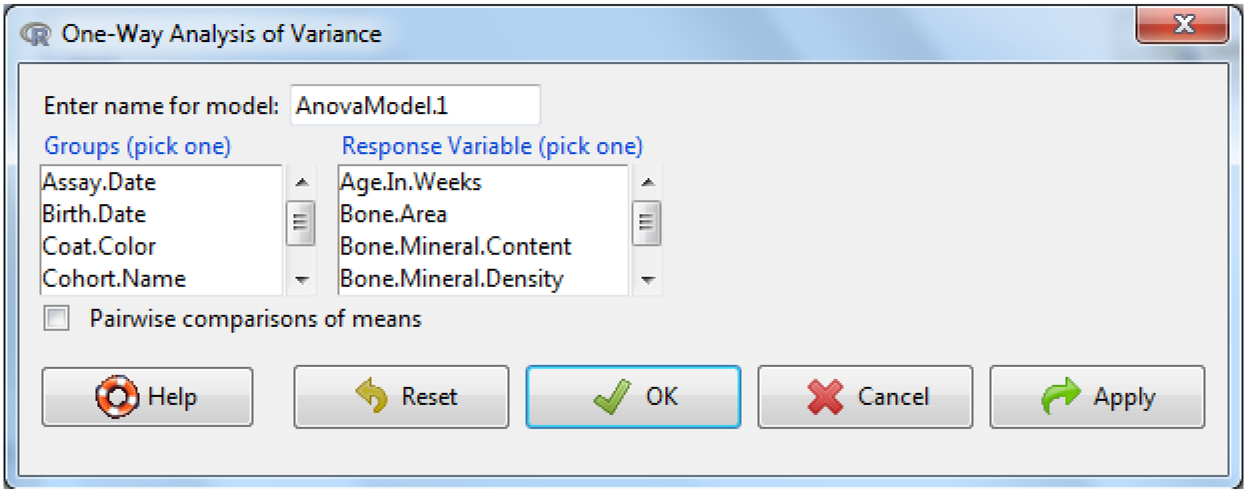
Confidence Level: .95

b. Select the variable of interest
c. Enter the proposed mean (Null hypothesis: mu=)
d. Typically the confidence level of 0.95 is used.
e. Three alternative hypothesis are possible:
    a. The mean does not equal the specified value (Population mean != mu0)
    b. The mean is less than the specified value
    c. The mean is more than the specified value
f. OK.
g. Interpretation? If the *p*-value is below the significance threshold, then the means is not equal to the specified value.

5.1.4 One-Way ANOVA

This test is used when you wish to compare the mean scores of more than two groups. Analysis of variance is so called because it compares the variance (variability in scores) between the different groups (believed to be due to the grouping variable) with the variability within each of the groups (believed to be due to chance). The ratio of the variance is converted to a p-value which assesses the chance that this difference in variance arises from sampling affects. A significant *p*-value indicates that we can reject the null hypothesis which states that the populations means are equal. It does not however tell us which of the groups are different. If a significant score is obtained in the one-way ANOVA then post-hoc testing is used to tell where the difference arose. The software uses Tukey post-hoc comparison procedure which is essential like a Student's *t*-Test however the test takes into account the risk of accumulating false positives as multiple tests are being conducted.

a. Statistics -> Means -> One-Way ANOVA



One-Way Analysis of Variance

Enter name for model: AnovaModel.1

Groups (pick one)

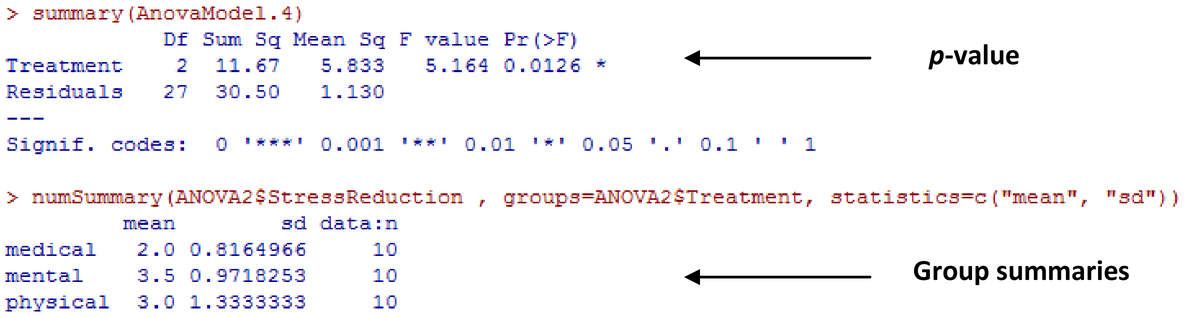
Assay.Date
Birth.Date
Coat.Color
Cohort.Name

Response Variable (pick one)

Age.In.Weeks
Bone.Area
Bone.Mineral.Content
Bone.Mineral.Density

□ Pairwise comparisons of means

b. Enter a name for the model
c. Select a response variable as the variable of interest
d. Select the grouping variable
e. OK
f. Interpretation?



```
> summary(AnovaModel.4)
            Df Sum Sq Mean Sq F value Pr(>F)
Treatment    2  11.67   5.833   5.164 0.0126 *
Residuals   27  30.50   1.130
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> numSummary(ANOVA2$StressReduction , groups=ANOVA2$Treatment, statistics=c("mean", "sd"))
         mean        sd data:n
medical   2.0 0.8164966     10
mental    3.5 0.9718253     10
physical  3.0 1.3333333     10
```

***p*-value**

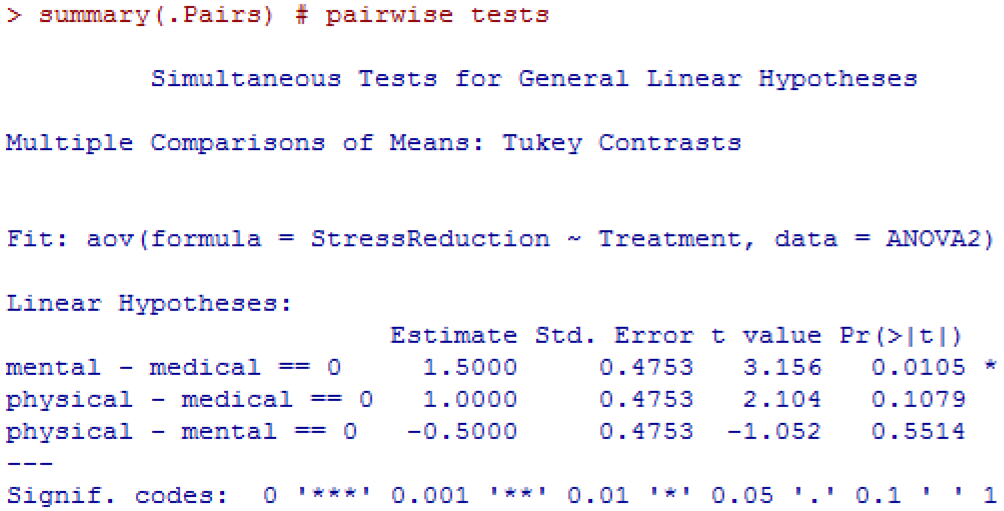
Group summaries

If the *p*-value is below the significance threshold, then the somewhere there is a statistically significant difference in the means of two or more groups.

g. If the *p*-value is significant, repeat the analysis with the pairwise comparisons of means button ticked. This repeats the analysis with the groups being compared to each other group using Tukey contrasts

h. Interpretation?

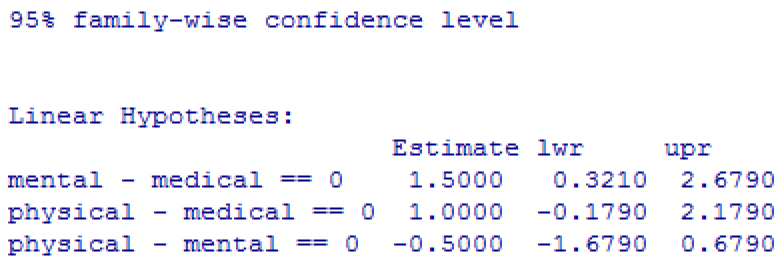
- For each possible pair wise comparison, the software calculates the mean difference for each comparison and tests it with the null hypothesis that the difference should be zero and returns a p-value on this statistical test.



```
> summary(.Pairs) # pairwise tests

         Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: aov(formula = StressReduction ~ Treatment, data = ANOVA2)

Linear Hypotheses:
                        Estimate Std. Error t value Pr(>|t|)
mental - medical == 0     1.5000     0.4753   3.156   0.0105 *
physical - medical == 0   1.0000     0.4753   2.104   0.1079
physical - mental == 0   -0.5000     0.4753  -1.052   0.5514
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

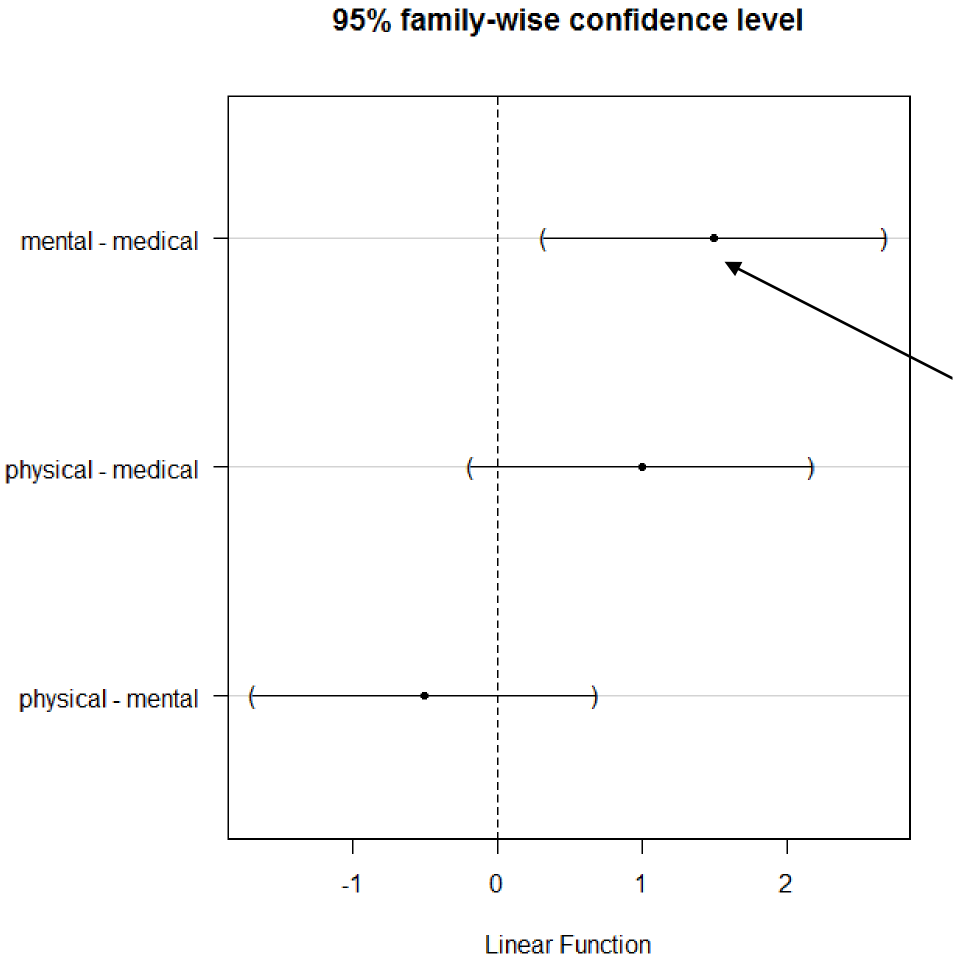
Calculated p-values for each comparison

- It also calculates the 95% confidence interval on the observed mean differences for each pair-wise comparison



```
95% family-wise confidence level


Linear Hypotheses:
                          Estimate lwr     upr
mental - medical == 0      1.5000   0.3210  2.6790
physical - medical == 0    1.0000  -0.1790  2.1790
physical - mental == 0    -0.5000  -1.6790  0.6790
```

- Graphically it visualizes these calculated values. You are looking for comparisons where the mean difference confidence interval does not span zero indicating a statistically significant difference between these groups.



This group comparison has an estimated difference of 1.5 and the confidence interval on this estimate does not span zero. Thus this is the source of the significant difference.

5.1.5 Two way ANOVA

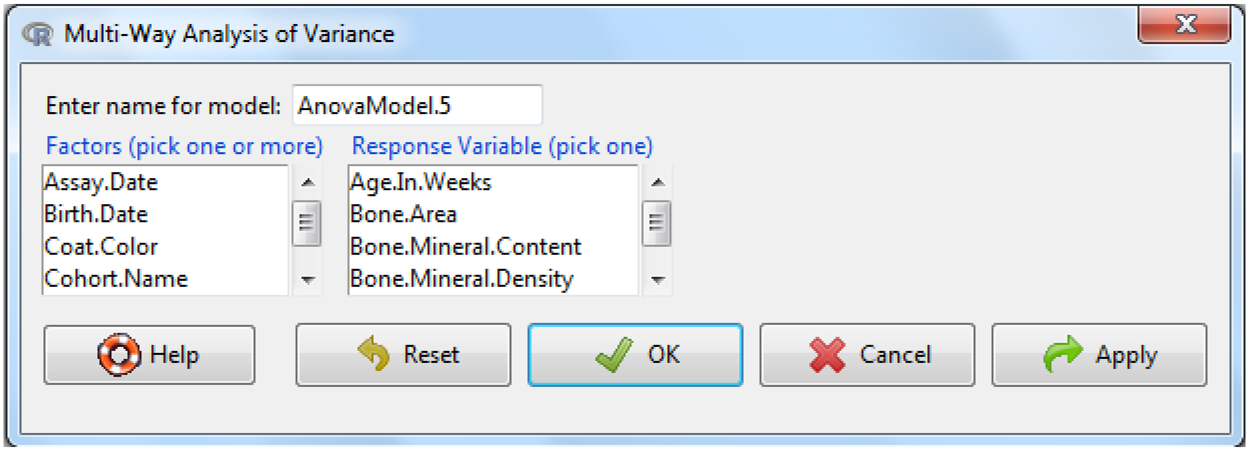
This test is used when you wish to investigate the effect of two independent variables on a dependent variable simultaneously. This involves multiple null hypotheses being tested and hence multiple p-values are calculated.

The null hypotheses:

1. There is no difference in the means of factor A
2. There is no difference in means of factor B
3. There is no interaction between factors A and B

The alternative hypothesis for 1 and 2 is: the means are not equal. The alternative hypothesis for case 3 is: there is an interaction between A and B. An interaction means the independent variables (factors) have a complex influence on the dependent variable. Therefore the main effects alone will not tell the full story and hence the cell means must be examined for each sub-group.

a. Statistics -> Means -> Multi-Way ANOVA



Enter name for model: AnovaModel.5

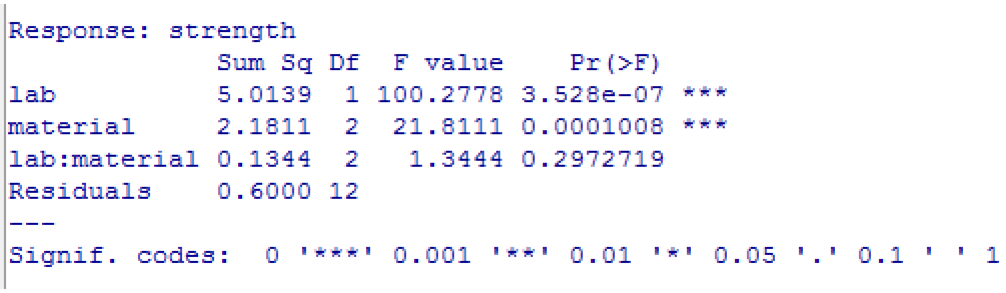
b. Enter a name for the model

c. Select the factors (two for a two-way anova)

d. Select the response variable

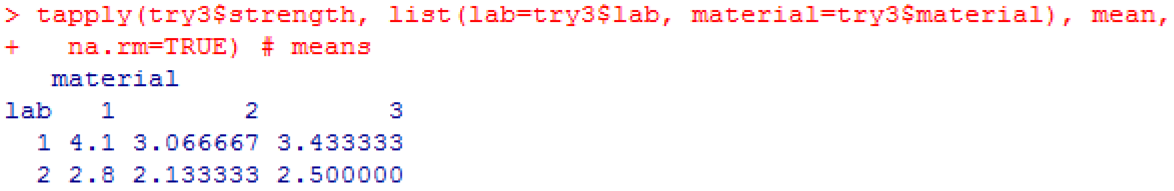
e. OK

f. Interpretation?

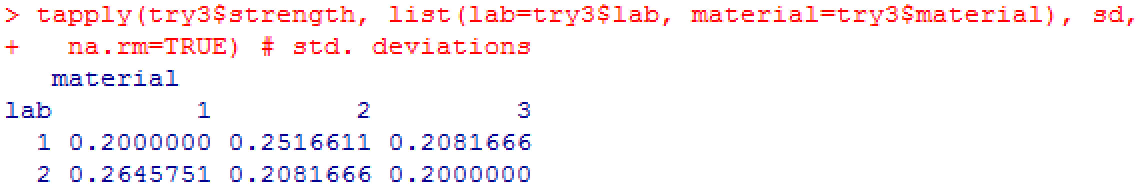


```
Response: strength
              Sum Sq Df  F value    Pr(>F)    
lab           5.0139  1 100.2778 3.528e-07 ***
material      2.1811  2  21.8111 0.0001008 ***
lab:material  0.1344  2   1.3444 0.2972719    
Residuals     0.6000 12                       
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The ANOVA test output lists the significance of the main effects tested (example above: lab and material). These have significant main effects if the p-value is less than 0.05 and this is shown with stars. The significance of the interaction (example: lab*material) is also tested and in the example above is not significant.

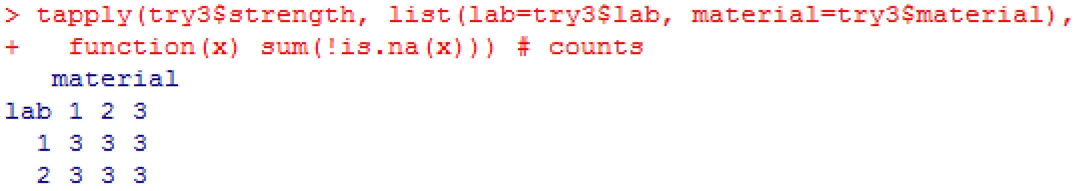


```
> tapply(try3$strength, list(lab=try3$lab, material=try3$material), mean,
+   na.rm=TRUE) # means
   material
lab   1        2        3
  1 4.1 3.066667 3.433333
  2 2.8 2.133333 2.500000
```



```
> tapply(try3$strength, list(lab=try3$lab, material=try3$material), sd,
+   na.rm=TRUE) # std. deviations
   material
lab         1         2         3
  1 0.2000000 0.2516611 0.2081666
  2 0.2645751 0.2081666 0.2000000
```

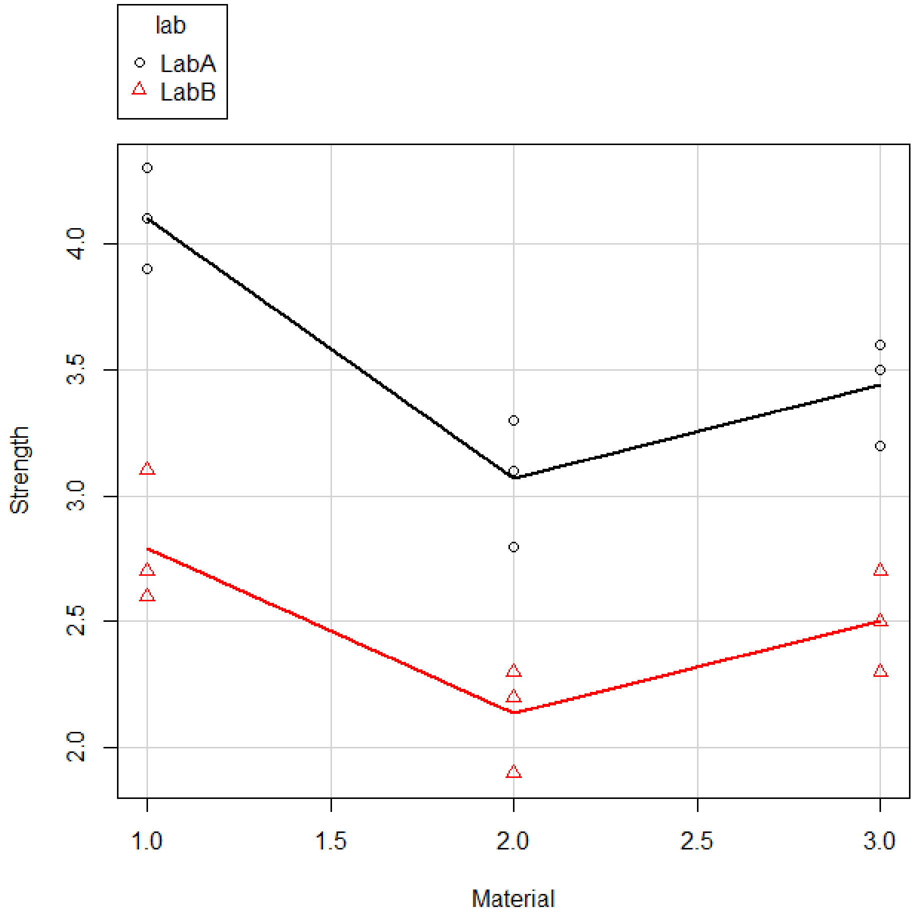
Below the ANOVA output is the mean and standard deviation measures for each group.



```
> tapply(try3$strength, list(lab=try3$lab, material=try3$material),
+   function(x) sum(!is.na(x))) # counts
   material
lab 1 2 3
  1 3 3 3
  2 3 3 3
```

Finally it tells you how many measures were used in each group via the count function.

It is important to visualize the data as well as complete statistical analysis, which confirm the statistical output makes sense. The following graph was generated via scatterplot functionality (section 4.1.3). Visually you can see that the strength depends on material and lab but there is no interaction between lab and material as the lines are parallel.



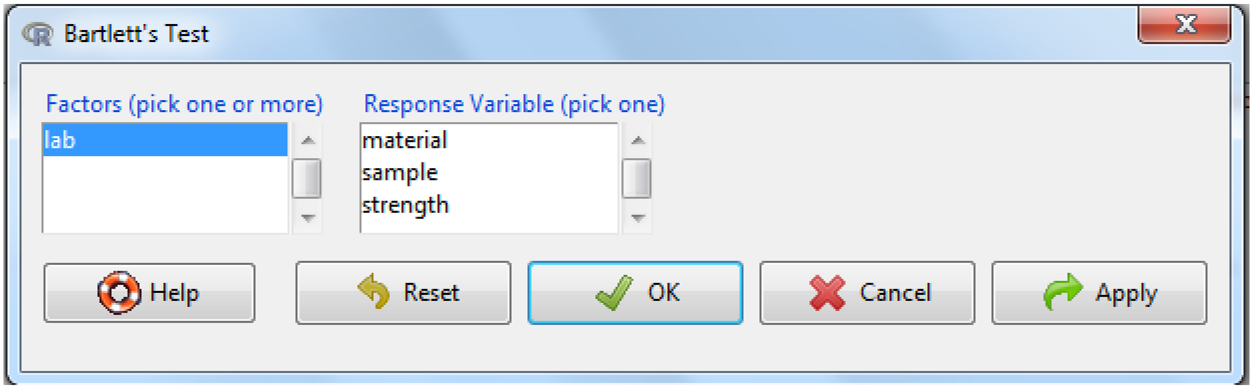
5.2 Comparing the variance

These tests, test if different samples have equal variance (homogeneity of variance). The null hypothesis is that the variance is equal across all groups. When the calculated *p*-value falls below a significance threshold (typically 0.05) then the null hypothesis is rejected and the alternative hypothesis is accepted that the variance is not equal across groups.

5.2.1 Bartlett's test

Bartlett's test is sensitive to departures from normality. That is, if your samples come from non-normal distributions, then Bartlett's test may simply be testing for non-normality rather than for a difference in variance. The Levene's test (5.2.2) is an alternative to the Bartlett's test that is less sensitive to departures from normality.

a. Statistics -> variances -> Bartlett's test

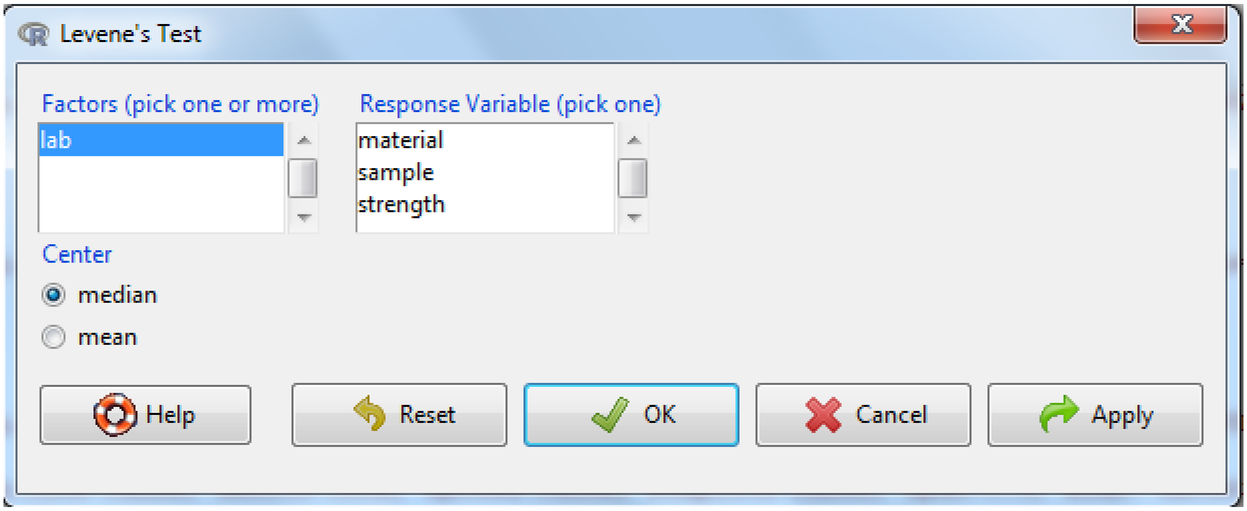


b. Select the Factors (grouping variable)
c. Select the response variable
d. OK
e. Interpretation: If the *p*-value is below the significance threshold, then the variance is not equal across the different groups.

5.2.2 Levene's test

The Levene's test is less sensitive than the Bartlett test (5.2.1) to departures from normality. If you have strong evidence that your data do in fact come from a normal, or nearly normal, distribution, then Bartlett's test has better performance.

a. Statistics -> variance -> Levene's test



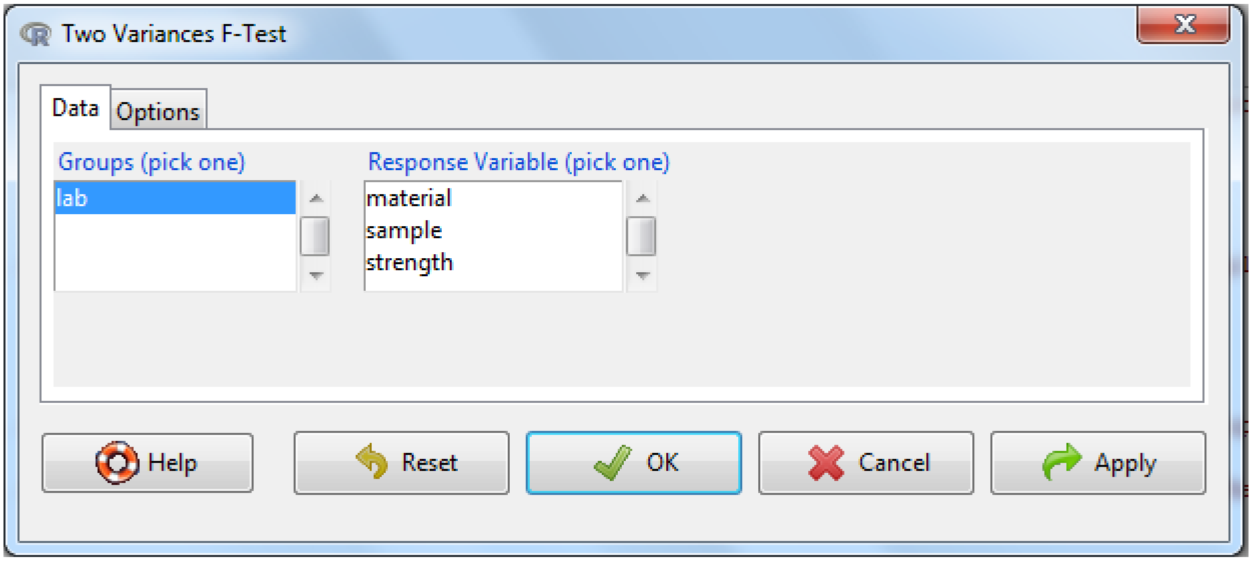
b. Select the Factors (grouping variable)
c. Select the response variable
d. Centre refers to how the central tendency is estimated for each group. Mean gives the original Levene's test; the default, median, provides a more robust test. The median is the default as in the statistical literature this is the current preferred method of calculation.
e. OK

f. Interpretation: If the *p*-value is below the significance threshold, then the variance in the groups is not equal.

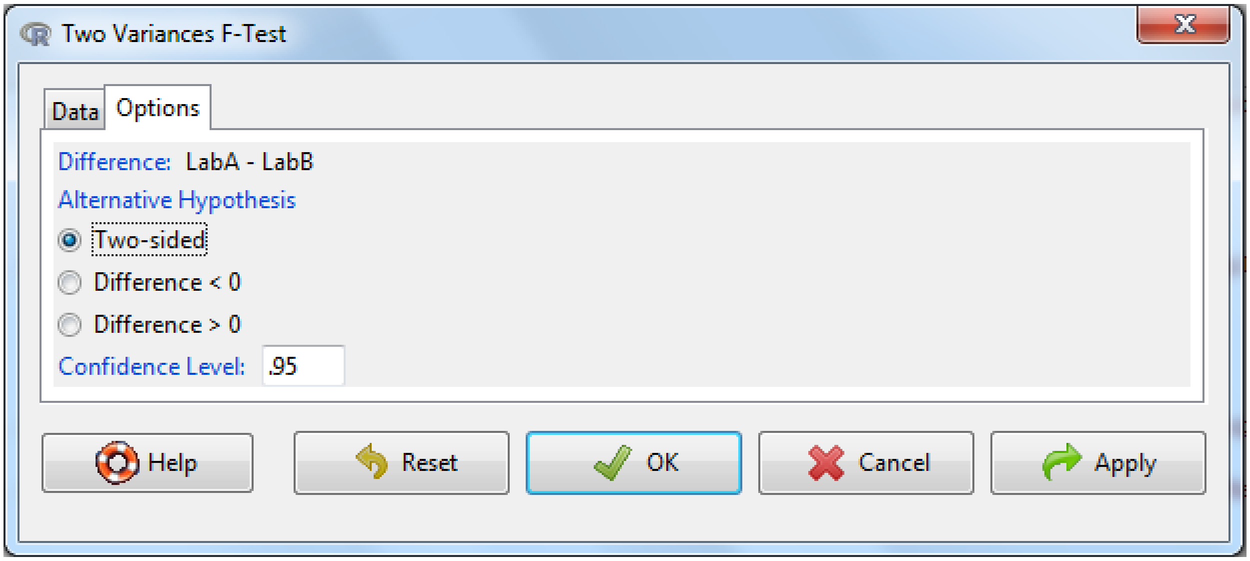
5.2.3 Two variances F-test

An F-Test, is used to test if the standard deviations of two populations are equal. This test can be a two-tailed test or a one-tailed test. The two-tailed version tests against the alternative that the standard deviations are not equal. The one-tailed version only tests in one direction that is the standard deviation from the first population is either greater than or less than (but not both) the second population standard deviation. The choice is determined by the problem. For example, if we are testing a new process, we may only be interested in knowing if the new process is less variable than the old process.

a. Statistics -> variances -> Two variances F-test



b. Select the grouping variable
c. Select the response variable
d. Under the options tab there are two things to consider
    - The alternative hypothesis can be two sided where the difference in standard deviation can be either an increase or a decrease or it can be one sided where it could either be an increase or a decrease.
    - The confidence level: the threshold at which you reject the null hypothesis and accept the alternate hypothesis. Typically this is 0.05, which is a 5% risk that the difference is a sampling effect rather than a true population difference.



Two Variances F-Test

Difference: LabA - LabB

Alternative Hypothesis

● Two-sided

○ Difference < 0

○ Difference > 0

Confidence Level: .95

e. OK

f. Interpretation: When the *p*-value falls below the significance threshold the null hypothesis is rejected and the alternative hypothesis is accepted.

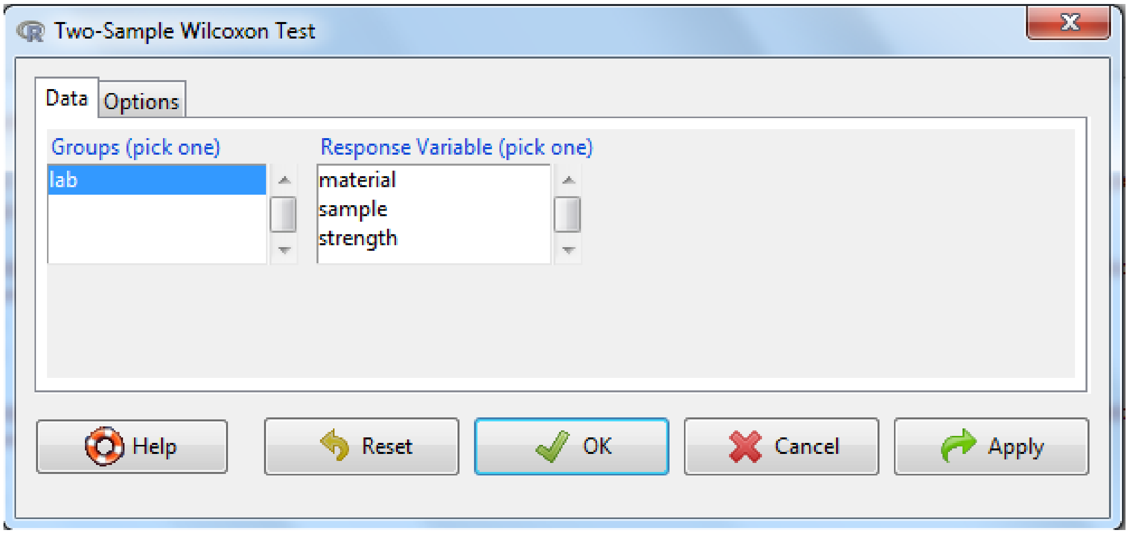
5.3 Non parametric tests

These are statistical tests which are distribution free methods as they do not rely on assumptions that the data are drawn from a given probability distribution.

5.3.1 Two-sample Wilcoxon Test

Non-parametric equivalent to the Student's *t*-Test. Can also be called two-sample Mann-Whitney U test. This test assesses whether the values in two samples differ in size.

a. Statistics -> Non-parametric tests -> Two sample Wilcoxon test



Two-Sample Wilcoxon Test

Groups (pick one): lab

Response Variable (pick one): material, sample, strength

b. Select the grouping variable

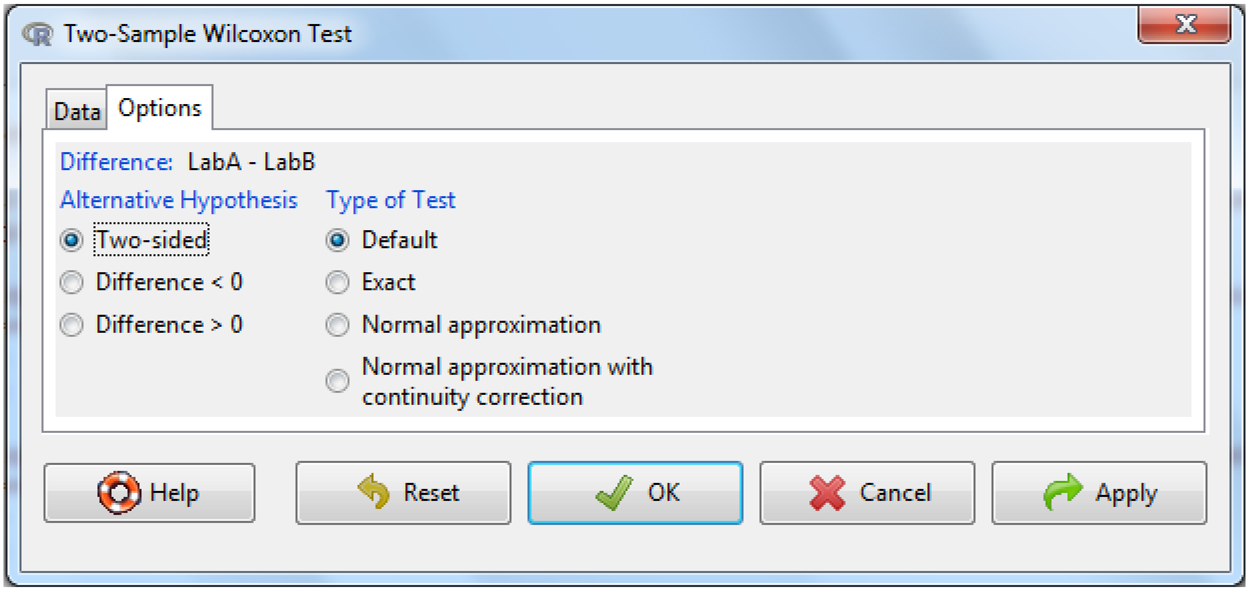
c. Select the response variable (variable of interest)

d. Under the options tab there are two things to consider

    a. The alternative hypothesis can be two sided where the difference can be either an increase or a decrease or it can be one sided where it could either be an increase or a decrease.

    b. Type of test.

        - To speed up calculations, assumptions can be made about distributions of parameters needed to be estimated in the test e.g. normal approximation or normal approximation with continuity correction. It is fine for this to occur when the number of samples is large. An exact test is one that is defined without parametric assumptions and evaluated without using approximate algorithms. The function will revert naturally to an exact test if n is low (<50) and there are no ties (equivalent values) when default is selected and hence is the recommended setting.
        - Further information on types of tests can be found at http://www.amstat.org/publications/jse/v18n2/bellera.pdf.



Two-Sample Wilcoxon Test

Difference: LabA - LabB

Alternative Hypothesis
● Two-sided
○ Difference < 0
○ Difference > 0

Type of Test
● Default
○ Exact
○ Normal approximation
○ Normal approximation with continuity correction

e. OK

f. Interpretation: When the *p*-value falls below the significance threshold the null hypothesis is rejected and the alternative hypothesis is accepted.

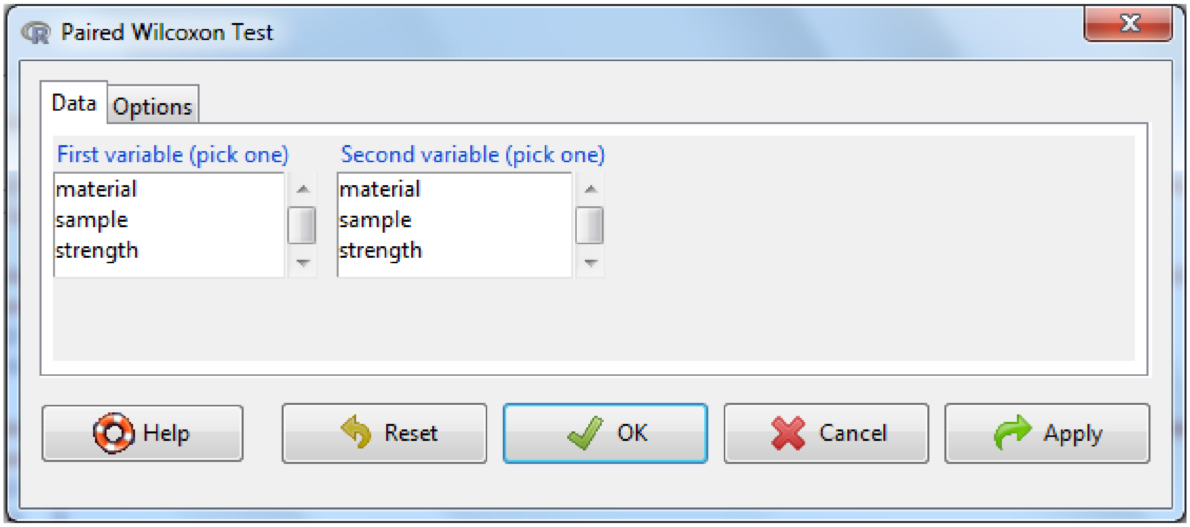
5.3.2 Paired-sample Wilcoxon Test

The Wilcoxon test for paired samples is the non-parametric equivalent of the paired samples *t*-test.

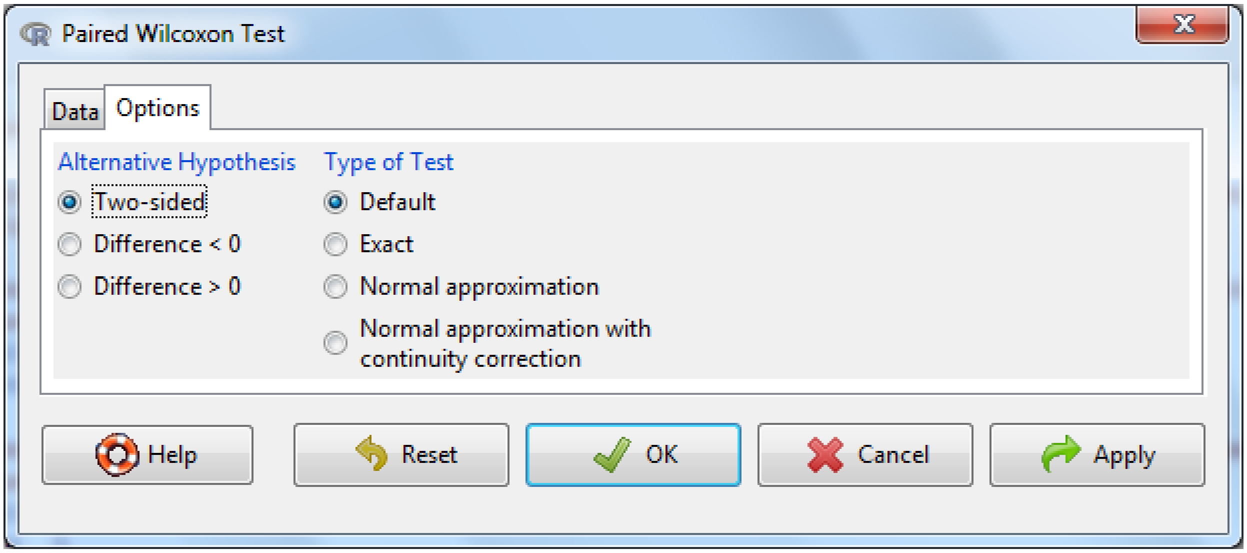
⚠ Note: **Data Format**

Need two columns; one that contains the first number in each data set pair (e.g., "before" data) and another column that contains the second number in each data set pair. Pairs of numbers must be in the same row.

a. Statistics -> Non-parametric tests -> Paired- sample Wilcoxon test



b. Select the first variable
c. Select the second variable
d. Under the options tab there are two things to consider
    a. The alternative hypothesis can be two sided where the difference in standard deviation can be either an increase or a decrease or it can be one sided where it could either be an increase or a decrease.
    b. Type of test.To speed up calculations, assumptions can be made about distributions of parameters needed to be estimated in the test e.g. normal approximation or normal approximation with continuity correction. It is fine for this to occur when the number of samples is large. An exact test is one that is defined without parametric assumptions and evaluated without using approximate algorithms. The function will revert naturally to an exact test if n is low (<50) and there are no ties (equivalent values) when default is selected and hence is the recommended setting.


Paired Wilcoxon Test

Alternative Hypothesis
● Two-sided
○ Difference < 0
○ Difference > 0

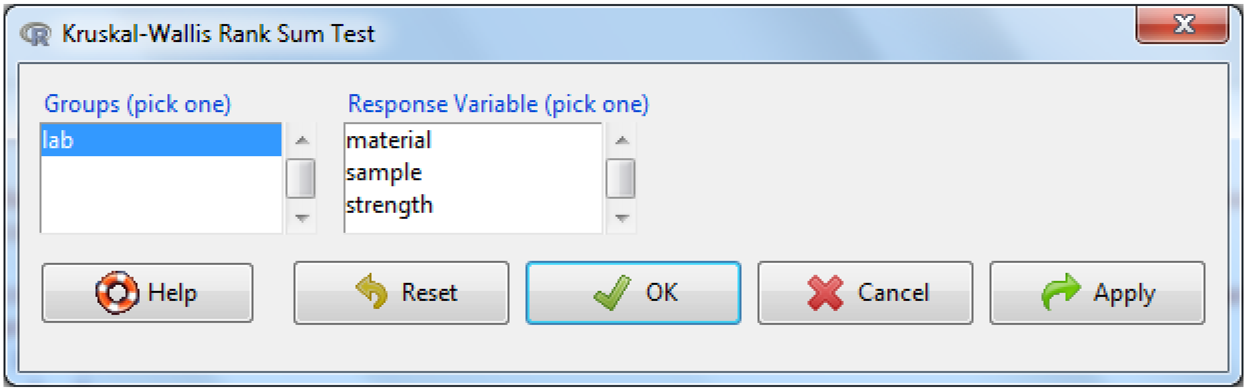
Type of Test
● Default
○ Exact
○ Normal approximation
○ Normal approximation with continuity correction

e. OK
f. Interpretation: When the *p*-value falls below the significance threshold the null hypothesis is rejected and the alternative hypothesis is accepted.

5.3.3 Kruskal-Wallis Test

This test is a non-parametric method for testing equality of population medians among groups. It is identical to an ANOVA (5.1.4) with the data replaced by their ranks. It is an extension of the Two-sample Wilcoxon test to 3 or more groups.

a. Statistics -> Non-parametric tests -> Kruskal-Wallis test


Kruskal-Wallis Rank Sum Test

Groups (pick one)
lab

Response Variable (pick one)
material
sample
strength

b. Select the grouping variable
c. Select the response variable (variable of interest)
d. OK
e. Interpretation: When the *p*-value falls below the significance threshold, the alternative hypothesis is accepted that the population medians among groups tested are not equal.

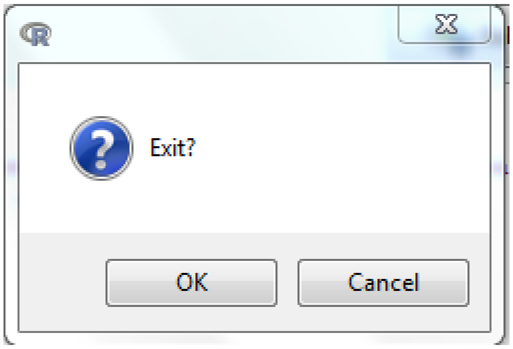
f. This test does not tell you where the differences are, just that two or more groups differ in their median. Post-hoc testing is then required between each pair-wise group of interest using the two-sample Wilcoxon Test (5.3.1).

6. Odds and Ends

6.1 Exiting and saving script

a. File -> Exit -> From R Commander and R -> OK

b. You will then be asked to confirm that you wish to Exit

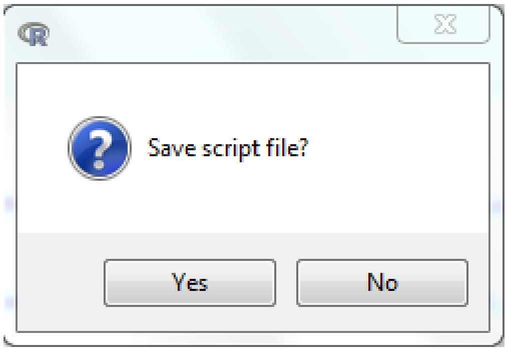


Exit?

c. You will then be asked whether you want to save the script file.

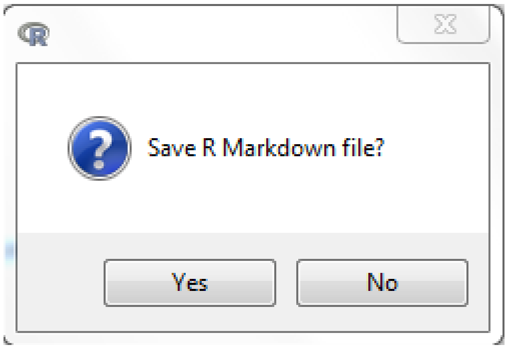
There are two advantages to saving the script

- Provides a record of the analysis completed.
- During the next session the user can ‘get back to where you left off’ by opening a saved script and submitting the code.



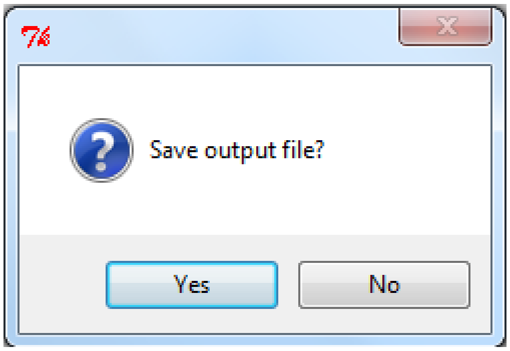
Save script file?

d. Then you will be asked whether you want to save R Markdown file. The markdown file is discussed in more detail in section 6.2.3.



Save R Markdown file?

e. Finally you will be asked whether you want to save the output file. This saves the R workspace and all the objects (e.g. datasets, or models you created). This can be useful as you would not need to reload everything to continue studies however note that unless you remember all the objects you have generated you can get confused by objects (datasets/parameters) being carried over and used mistakenly. It is generally considered better to save scripts (coding).



Save output file?

6.2 Saving and printing Output

6.2.1 Copying text

Highlight the text with the mouse -> ctrl-c and paste ctrl-v as you would for any window application.

6.2.2 Copying graphs

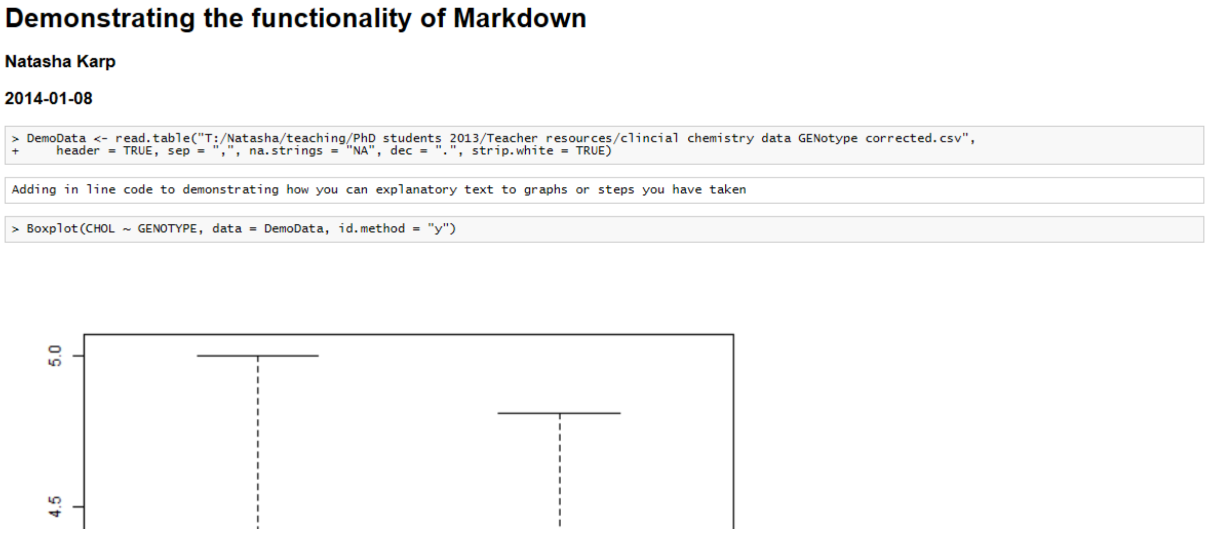
Right-click on the graph, select 'Copy as meta-file' and past directly into Word or PowerPoint.

Alternatively can also save the graph as an independent file:
Graphs -> Save graph to file -> as bitmap/EPS/PDF .....

6.2.3 MarkDown System

To address the need for reproducibility where analysis is transparent and reported, there is a system which can generate a report showing code and output. This is achieved through the MarkDown System which is a tab located on the Rscript window.

The following image demonstrates the type of output you can obtain



Demonstrating the functionality of Markdown

Natasha Karp

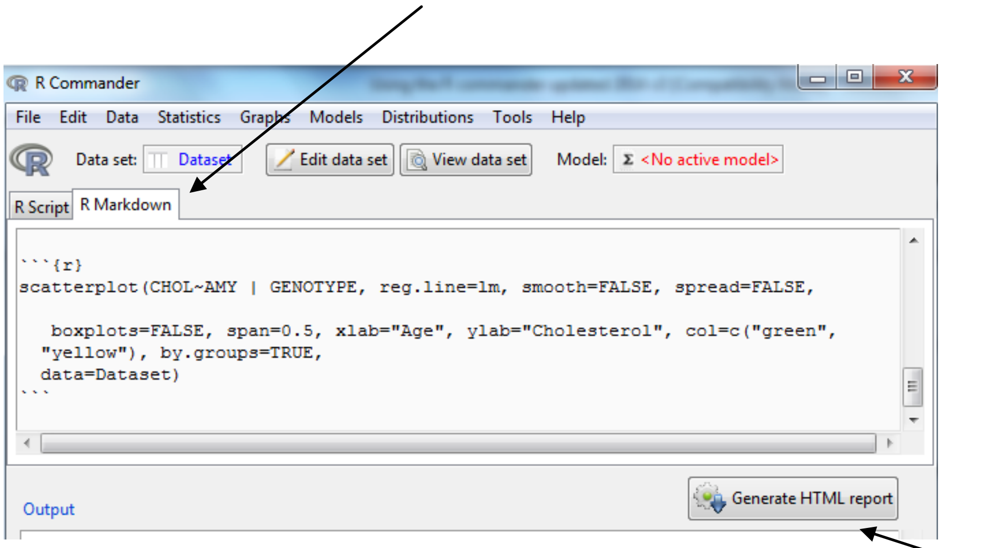
2014-01-08

```
> DemoData <- read.table("T:/Natasha/teaching/PhD students 2013/Teacher resources/clincial chemistry data GENotype corrected.csv",
+     header = TRUE, sep = ",", na.strings = "NA", dec = ".", strip.white = TRUE)
```

```
Adding in line code to demonstrating how you can explanatory text to graphs or steps you have taken
```

```
> Boxplot(CHOL ~ GENOTYPE, data = DemoData, id.method = "y")
```

- To achieve this select the R Markdown tab and you can see that automatically R scripts are copied into a template of output.

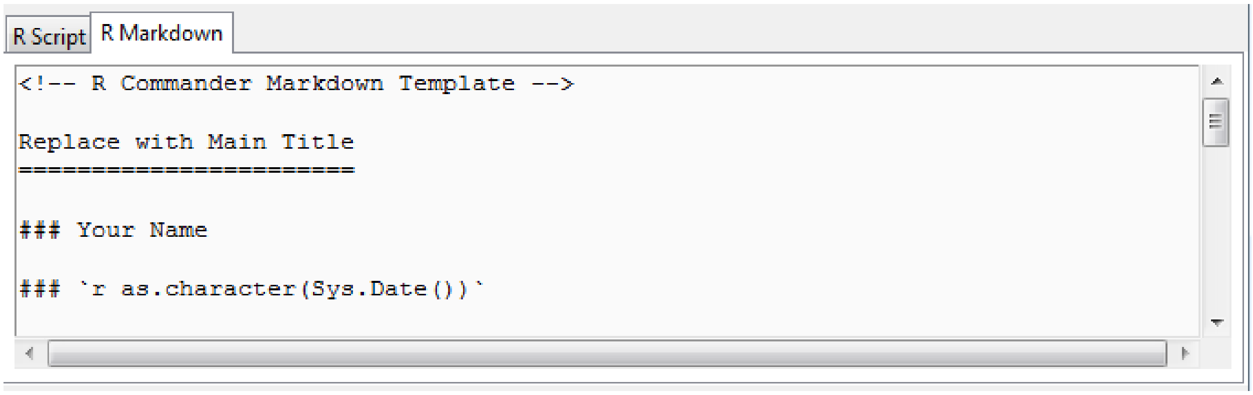


R Markdown tab

Activate button

~~~
```{r}
scatterplot(CHOL~AMY | GENOTYPE, reg.line=lm, smooth=FALSE, spread=FALSE,

   boxplots=FALSE, span=0.5, xlab="Age", ylab="Cholesterol", col=c("green",
  "yellow"), by.groups=TRUE,
  data=Dataset)
```
~~~

- There are some prompts e.g. “Replace with Main Title”



```
<!-- R Commander Markdown Template -->

Replace with Main Title
=======================

### Your Name

### `r as.character(Sys.Date())`
```

- You can add explanatory text can be added by typing in the window and surrounding it by back ticks. In the example above I added

```
Adding in line code to demonstrating how you can explanatory text to graphs or steps you have taken
```

- The HTML report (easily editable into a word processor, like Microsoft Word or OpenOffice) is generated with a click.
- Further information can be obtained at: http://www.rstudio.com/ide/docs/authoring/using_markdown

6.3 Entering commands directly into the script window

Commands generated by the R Commander appear in the script window, and you can type and edit commands in this window. To send this script you have to highlight the relevant text and press the “Submit” button.

⚠ Notes:

1. All lines of a multi-line command must be submitted simultaneously for execution. Commands that extend over more than one line should have the second and subsequent lines indented by one or more spaces or tabs.

7. Amending the graphical output

One of the main reasons data analysts turn to **R** is for its strong graphic capabilities. However, with R commander, the options on graphs are limited and they don't look too pretty and aren't ideal for reports or presentations. Here I go through some examples of what you can do and then it should give you grounding for proceeding further if you require. The overall strategy is to call the code for the basic graph and then amend the code manually by altering the graphics parameters or by calling a second function to do a particular job (e.g. adding a label).

For future advice and support on R and graphs I recommend:

1. R Graphics by Paul Murrell
2. Data Analysis and Graphics Using R: An Example-based Approach by John Maindonald and John Braun.

Amending code - things to notes

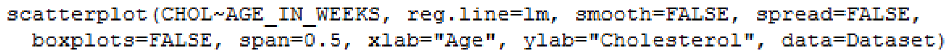
1. If you add another parameter (instruction) to a function it needs to form part of the list so it is placed within the bracket of information passed to that function and a comma is placed between each instruction.
2. If you are using words to describe the colour you want or to add a label then it needs to be surrounded by quote marks (i.e. "") marks so the software knows that it is looking at string (i.e. text) information.
3. Script is particularly to form so capitals etc. matter.

7.1 Adding a line

a. Use the drop down menus to request a scatter graph. The code used can be seen in the Rscript window.

The function name comes first and then in brackets are the arguments that are passed to the function to direct how it works.

Function name →



```
scatterplot(CHOL~AGE_IN_WEEKS, reg.line=lm, smooth=FALSE, spread=FALSE,
  boxplots=FALSE, span=0.5, xlab="Age", ylab="Cholesterol", data=Dataset)
```

b. To add a line, a second function (abline) is needed. The parameters within the brackets are used to pass the information to the function. These are used to control the line placement within the graph. If you do not specify the parameter then the parameter will be set to the default settings (in this case NULL).

Abline structure: abline(a = NULL, b = NULL, h = NULL, v = NULL, , ...)

parameter	Description	Default
a	intercept	NULL
b	Slope	NULL
h	the y-value(s) for horizontal line(s).	NULL
v	the x-value(s) for vertical line(s).	NULL
...	graphical parameters such as `col`, `lty` and `lwd` and the line characteristics `lend`, `ljoin` and `lmitre`.	

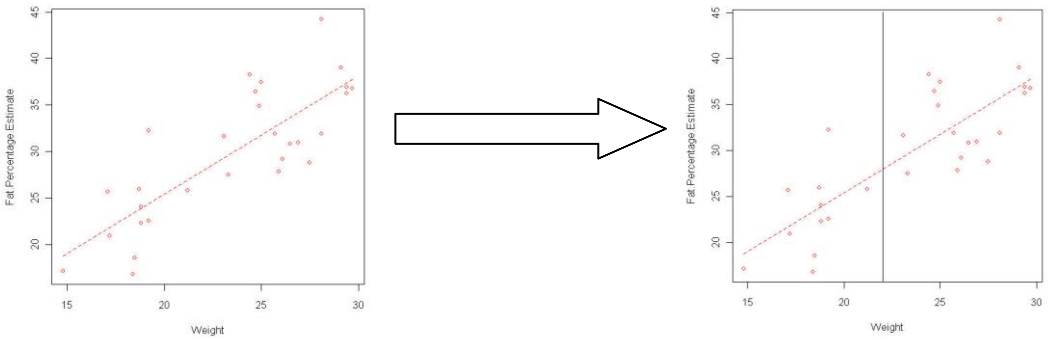
c. Adding a vertical line at point x

   i. Type code abline(v=x) into the script window

   ii. Highlight the code and submit.

Example:

```
scatterplot(Fat.Percentage.Estimate~Weight, reg.line=lm, smooth=FALSE,
 labels=FALSE, boxplots=FALSE, span=0.5, data=DEXA)
abline(v=22.5)
```



d. Adding a horizontal line at point x

   i. Type code abline(h=x) into the script window

   ii. Highlight the code and submit.

e. Adding a line of a known equation

- Type code abline(a=x, b=y) into the script window

- Highlight the code and submit.

f. Adding an equivalence line

   i. Type code abline(b=1) into the script window

   ii. Highlight the code and submit.

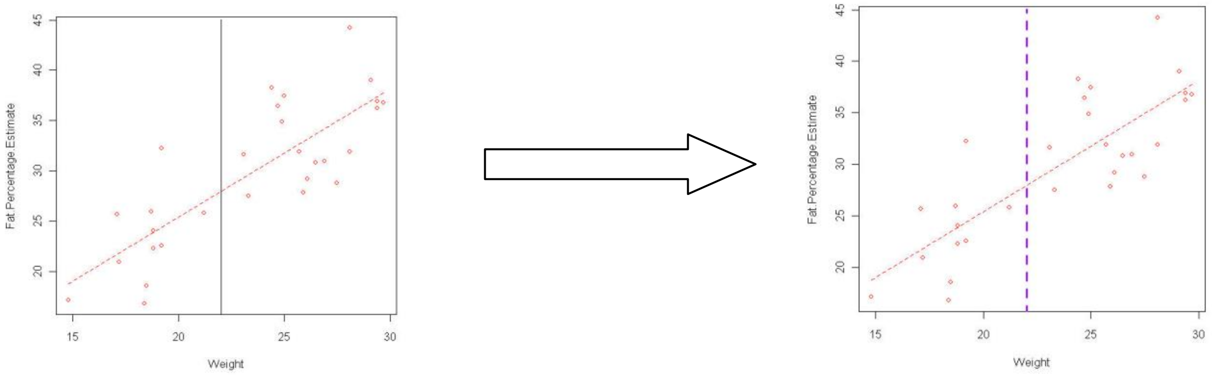
7.2 Amending the line parameters

A number of parameters can be added to the abline function to amend the output

col	The easiest way to specify a colour is to use the name eg “red”. R understands 657 different colour names. Type colours() to see a full list of known names.
lty	The line type. Line types can either be specified as an integer (0=blank, 1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings `"blank"`, `"solid"`, `"dashed"`, `"dotted"`, `"dotdash"`, `"longdash"`, or `"twodash"`, where `"blank"` uses ‘invisible lines’ (i.e., does not draw them).
lwd	The line width, a *positive* number, defaulting to `1`.

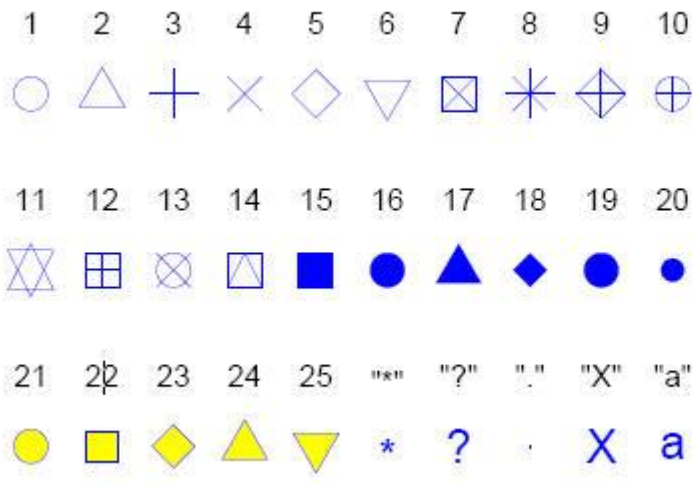
Example:

```
scatterplot(Fat.Percentage.Estimate~Weight, reg.line=lm, smooth=FALSE,
  labels=FALSE, boxplots=FALSE, span=0.5, data=DEXA)
abline(v=22.5, col="purple", lty="dashed", lwd=3)
```



7.3 Amending the plot symbol

R provides a fixed set of 26 data symbols for plotting and the symbol is controlled by the **pch** setting. Pch 21 to 25 allow a fill colour separate from the border colour, with the **bg** setting controlling the fill colour in these cases.



Example:

scatterplot(Fat.Percentage.Estimate~Weight, reg.line=lm, span=0.5, data=DEXA)

scatterplot(Fat.Percentage.Estimate~Weight, reg.line=lm, pch= 2, col= “red”, span=0.5, data=DEXA)

7.4 Adding a text label

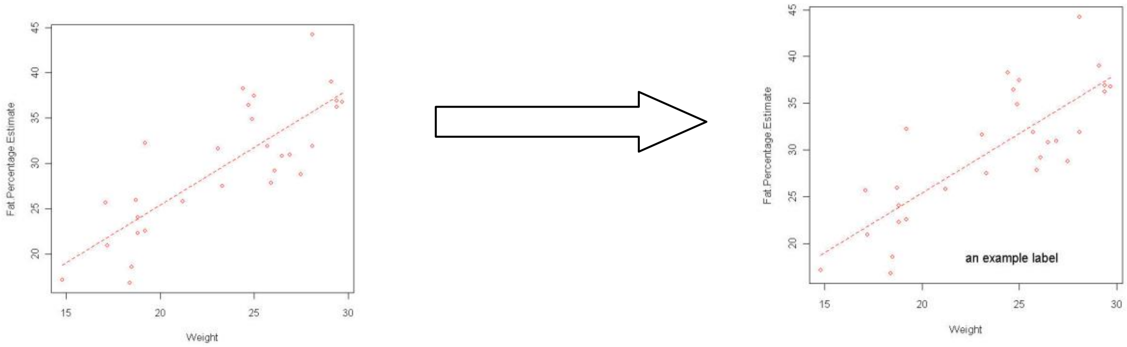
Here a second function (text) is used to add the text. The parameters within the brackets are used to pass the information to the function to drive what text and where the text is placed. If you do not specify the parameter then the parameter will be set to the default settings.

Text function: text (x, y, label, col)

Parameter	Description	Default
X, y	Coordinates where the text “labels” should be written	
label	This specifies the text to be written	
col	Colour of the text.	Black

Example 1

```
scatterplot(Fat.Percentage.Estimate~Weight, reg.line=lm, smooth=FALSE,
  labels=FALSE, boxplots=FALSE, span=0.5, data=DEXA)
text(x=25, y=20, label ="an example label")
```



7.5 Amending the plot colours

7.5.1 For a box plot

a. Use the drop down menus to request a boxplot graph.

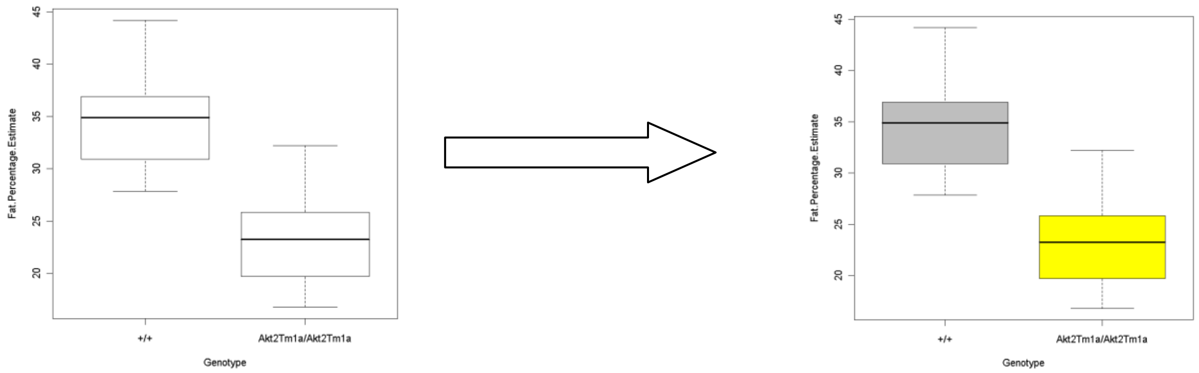
b. Amend the script by adding a col parameter.

   i. To add a single colour to all boxplots add col="COLOUR OF YOUR CHOICE" to the code.

   ii. To alter each boxplot individually you need to add a list of colours with length matching the number of boxplots to the code.
   Eg. col=c("red", "black", "green")

   iii. Highlight the amended code and submit.

   iv. Example: boxplot(Fat.Percentage.Estimate~Genotype, lab="Fat.Percentage.Estimate", xlab="Genotype", col=c("grey", "yellow"), data=DEXA)



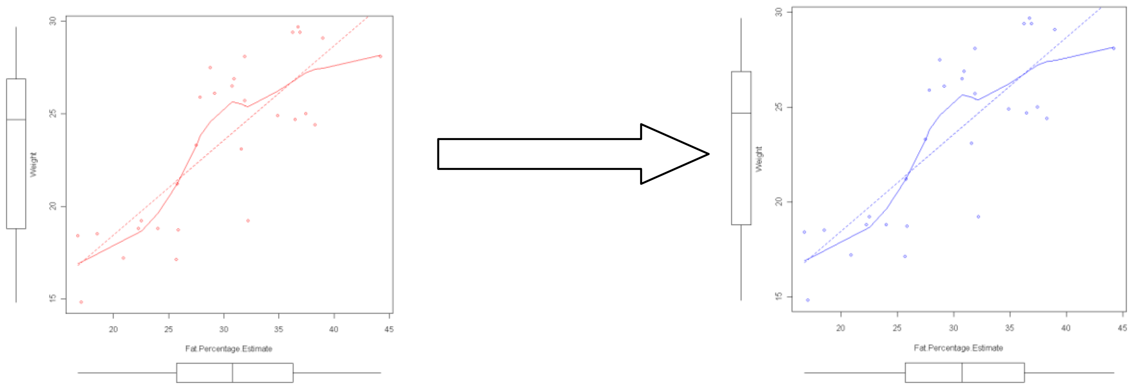
7.5.2 For a scatter plot

a. Using the drop down menus to request a scatter graph.

b. You can change the colour of the scatter graphs by using the col parameter.

   a. For a graph with one group you enter col="blue" into the list.

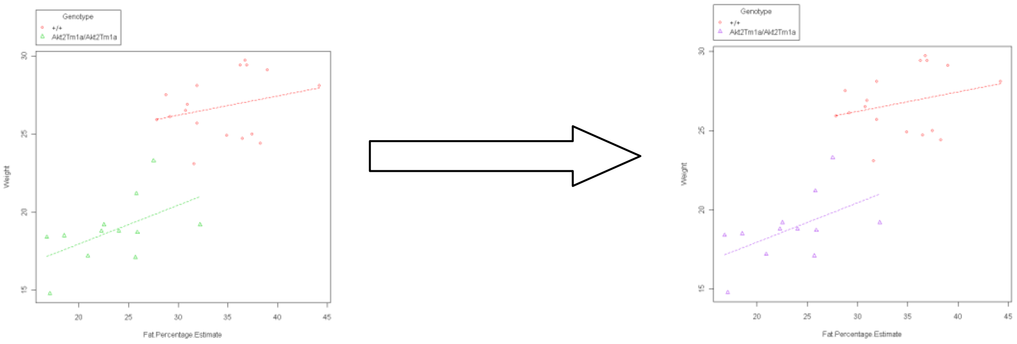
      Example: scatterplot(Weight~Fat.Percentage.Estimate, reg.line=lm, smooth=TRUE, labels=FALSE, boxplots='xy', span=0.5, col="blue", data=DEXA)



   b. For a graph with multiple groups:

      You add the colours as a list (E.g. col=c("red", "purple")).

      Example: scatterplot(Weight~Fat.Percentage.Estimate | Genotype, reg.line=lm, smooth=FALSE, labels=FALSE, boxplots=FALSE, span=0.5, by.groups=TRUE, data=DEXA, col=c("red", "purple"))


Genotype
+/+
Akt2Tm1a/Akt2Tm1a
Weight
15
20
25
30
20
25
30
35
40
45
Fat Percentage Estimate
Genotype
+/+
Akt2Tm1a/Akt2Tm1a
Weight
15
20
25
30
20
25
30
35
40
45
Fat Percentage Estimate