

RAMAN manual

Documentation for RAMAN version 1.73

Copyright (C) 1999 by Ross A. Alford, School of Tropical Biology,
James Cook University, Townsville, Queensland 4811 Australia.
email ross.alford@jcu.edu.au

Legal information:

All commercial rights reserved. This documentation and the program RAMAN.EXE may not be sold or included in any compilation that is sold for profit without the written permission of the author. They may be included in archives of software accessible for download or in compilations that are sold for prices sufficient only to cover the costs of production.

Although the software has been exhaustively tested, the author cannot be held responsible for any errors that may exist, nor for any consequences ensuing from such errors. Use of the software or of results derived from it are entirely at the risk of the user.

Contents

Introduction.....	2
Installing The Program	3
Setting Up The Data.....	3
Running The Program	6
Setting The Options.....	8
Interpreting The Output	11
Using And Interpreting Output Written To Disk Files	13
References	15

Introduction

RAMAN (RANdomization MANova) is a program written to make tests of one-way hypotheses on multivariate data using randomization as simple to perform as possible.

RAMAN will accept data sets of up to 2000 observations (cases or lines), with up to 1024 different variables in each observation, and up to 100 different treatments.

It uses rerandomization of the data to produce Monte Carlo tests of the hypothesis that all treatments in a one-way design have similar response vectors. It will also automatically perform all pairwise comparisons of treatments, and give tests of the null hypothesis for each pair both adjusted and unadjusted for multiple comparisons.

The program makes it possible to test hypotheses that could not be tested using standard parametric techniques because insufficient degrees of freedom would be available, or because the data may not fit the assumption of multivariate normality of errors.

The statistics that can be calculated and tested include the standard MANOVA test as given by Wilks' Λ , the hypothesis (see Manly 1991 or 1997) that the sum of $\log(F)$ taken over the univariate ANOVAs for each response variable is relatively large, and the hypotheses that the sum of the squared or unsquared Euclidean distances between observations and their group centroids is relatively small (Manly 1991 or 1997, Cade and Richards 2001, Mielke and Berry 2001). The sum of Euclidean distances statistic is particularly easy to deal with, as it has a simple and easily understood geometric interpretation (Cade and Richards 2001)..

The basic algorithms used in the program were derived from FORTRAN source code included in the first edition of B. F. J. Manly's excellent book, *Randomization and Monte Carlo Methods in Biology*, published by Chapman and Hall, London. For further reading I would recommend that book, or the second edition, now titled *Randomization, Bootstrap, and Monte Carlo Methods in Biology*, also published by Chapman and Hall, London.

I also recommend reading the manual for BLOSSOM (Cade and Richards 2001), an excellent software package distributed free by the US Geological Survey, and available from <http://www.mesc.usgs.gov/products/software/blossom.shtml>, and the book *Permutation methods: A distance function approach*, written by P. W. Mielke and K. J. Berry, and published in 2001 by Springer-Verlag, NY.

Regardless of what statistic or statistics are calculated, RAMAN performs hypothesis tests by 1) calculating the value of the statistic(s) from the data in their original form, 2) repeatedly randomly reassigning all of the observations in the data sets to treatments (with the constraint that each treatment is assigned the same number of observations it had in the original arrangement of the data), recalculating the statistic(s) of interest., 3) comparing the observed values to the values from the randomly-reassigned observations, and 4) keeping track of how many random reassignments produce values as extreme or more extreme than the observed values. If the observed values result from genuine effects of the treatments on the variables measured, one would expect that statistics would be less extreme in most cases when observations are randomized among treatments. The principles behind this are discussed in detail by Manly (1991, 1997) and by the other references listed at the end of this document.

The concept of computing 99% binomial confidence intervals for P-values calculated from randomization tests was derived from the existence of this feature in the program StatXact (version 4), published by Cytel Software (<http://www.cytel.com/>).

Installing The Program

Download the file RAMAN.EXE, and copy it into a directory that is on the DOS PATH. The C:\Windows and C:\Windows\command directories are good places to put it. If it is in one of these directories, it can be run from any other directory on your computer. Alternatively, you can put it into a directory not on the path, but you will then need to be in that directory to run the program. You may want to put this manual in and the sample data file testdata.csv somewhere, perhaps in a new subdirectory reserved for working with RAMAN and its output files.

Setting Up The Data

It is simplest to set up your data using a spreadsheet, such as Microsoft™ Excel™.

Cell A1 (top left) should contain text that describes the data--what experiment it was, what date it was collected on, or anything else useful. This can be up to 255 characters long.

The second row of the spreadsheet should contain a name for the treatments in the first column (the word 'treat' will do if you are not feeling more creative, but this cell must have something in it). In the second column through the last column, it should contain the names of the response variables that make up each response vector. These names must be 8 characters or less long, and should be made up of letters and numbers only; they should not contain blanks or punctuation, with the exception of the underline character, which can be substituted for blanks.

The third through last rows of the worksheet should contain the data. The first column of each observation is the treatment code; this can be any alphanumeric value of up to 8 characters in length. It can contain underlines and a few other punctuation characters (including parentheses,

(' and ')), but cannot contain embedded blanks, and cannot be more than 8 characters long. Obviously, all observations in each treatment must share the same code, which must differ from the code for all other treatments.

Observations do not need to be sorted by treatment. The second through the last columns of each observation should contain data values, which must be numeric. These may include decimal points but should include nothing else except digits. Observations with missing values should be eliminated from the data set before attempting analysis; they cannot be included and will cause the program to fail with an error message when it attempts to load the data.

Once the worksheet is organised as above, it should be saved, using a filename of 8 characters or less, with the 3 character extension '.CSV'. It should be saved as a comma-delimited list, not in the native format of the spreadsheet program being used. If you are using Excel™, one of the options in the 'Save As' dialog box will be to save the data as a comma-delimited file.

An example of how the data should look in a spreadsheet is:

	A	B	C	D	E	F	G	H	I
1	Larval mass at metamorphosis; percent survival to metamorphosis; and length of larval period								
2	Density	Avemass	Pctsurv	AveLP					
3	High	284.67	23.78	36.21					
4	Low	384.41	27.79	22.85					
5	Medium	343.3	35.73	31.69					
6	High	279.45	22.46	35.22					
7	Low	453.14	30.7	27.49					
8	Medium	340.66	32.75	35.33					
9	High	292.84	22.58	42.41					
10	Low	381.67	31.04	27.41					
11	Medium	368.35	29.53	35.2					
12	High	293.7	21.17	33.35					
13	Low	383.97	31.14	25.56					
14	Medium	366.91	29.69	23.46					
15	High	272.41	25.93	36.24					
16	Low	419.82	37.75	26.22					
17	Medium	351.69	30	29.1					
18	High	296.38	30.14	29.61					
19	Low	385.52	35.04	26.59					
20	Medium	341.04	34.52	27.14					
21	High	311.54	25.61	29.27					
22	Low	362.61	37.06	25.78					
23	Medium	357.91	40.83	27.33					
24	High	277.18	20.65	31.37					
25	Low	386.48	31.75	25.75					
26	Medium	325.35	31.7	31.57					
27									
28									

When this is saved in a comma-delimited data file, it should look like this (if loaded into a program such as notepad):

```
Larval mass at metamorphosis; percent survival to metamorphosis; and length of larval period,,  
Density,Avemass,Pctsurv,AveLP  
High,284.67,23.78,36.21  
Low,384.41,27.79,22.85  
Medium,343.3,35.73,31.69  
High,279.45,22.46,35.22  
Low,453.14,30.7,27.49  
Medium,340.66,32.75,35.33  
High,292.84,22.58,42.41  
Low,381.67,31.04,27.41  
Medium,368.35,29.53,35.2  
High,293.7,21.17,33.35  
Low,383.97,31.14,25.56  
Medium,366.91,29.69,23.46  
High,272.41,25.93,36.24  
Low,419.82,37.75,26.22  
Medium,351.69,30,29.1  
High,296.38,30.14,29.61  
Low,385.52,35.04,26.59  
Medium,341.04,34.52,27.14  
High,311.54,25.61,29.27  
Low,362.61,37.06,25.78  
Medium,357.91,40.83,27.33  
High,277.18,20.65,31.37  
Low,386.48,31.75,25.75  
Medium,325.35,31.7,31.57
```

Note that as long as each treatment has a unique code, the observations don't need to be in any particular order; in this data file, they are organized by the blocks in which the experiment was done, but the blocks are ignored in analyses. The data would produce exactly the same results if all the Low treatment observations were first, followed by the Medium, followed by the High, or in any other order.

A data file organized as above should have the extension .csv; if it does not, RAMAN may try to interpret it using a different format and may not run properly.

You must close the file in your spreadsheet program before trying to load it into RAMAN. If the program terminates with a "IO-Error 5" when you try to execute an analysis, you probably have not closed the file in the spreadsheet, and RAMAN cannot get access to it to read it. Close it in your spreadsheet program and try again.

Running The Program

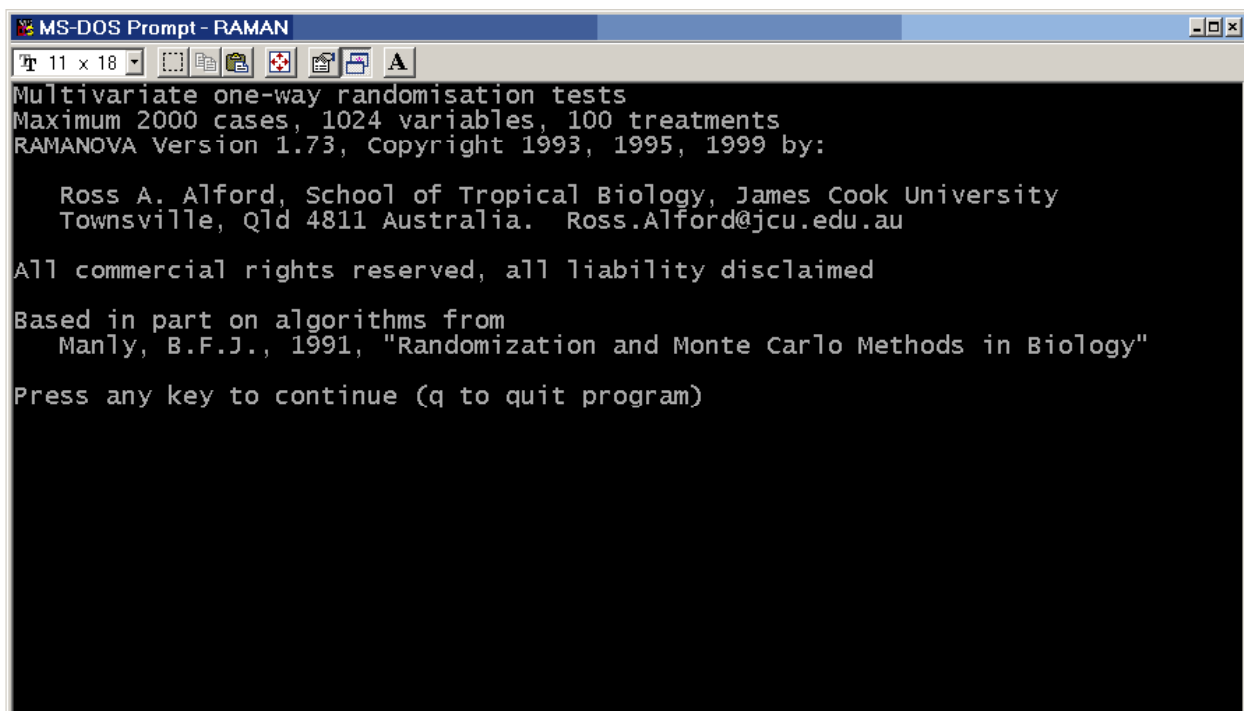
Open a DOS window, change directories until you are in the directory containing the data file. You will then see a command prompt like:

```
C:\data\>
```

Enter the name of the executable file on the command line, and press the Enter key:

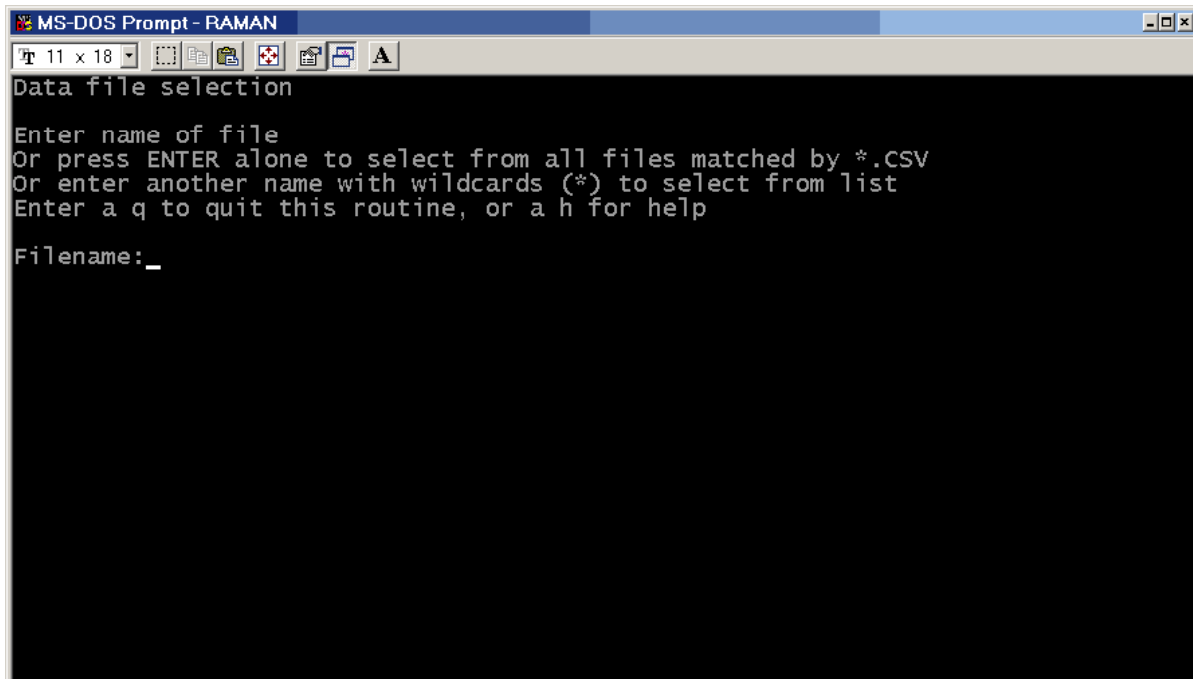
```
C:\data\raman173
```

The program will run, and you will see a screen like this:



```
MS-DOS Prompt - RAMAN
Multivariate one-way randomisation tests
Maximum 2000 cases, 1024 variables, 100 treatments
RAMANOVA Version 1.73, Copyright 1993, 1995, 1999 by:
    Ross A. Alford, School of Tropical Biology, James Cook University
    Townsville, Qld 4811 Australia.  Ross.Alford@jcu.edu.au
All commercial rights reserved, all liability disclaimed
Based in part on algorithms from
    Manly, B.F.J., 1991, "Randomization and Monte Carlo Methods in Biology"
Press any key to continue (q to quit program)
```

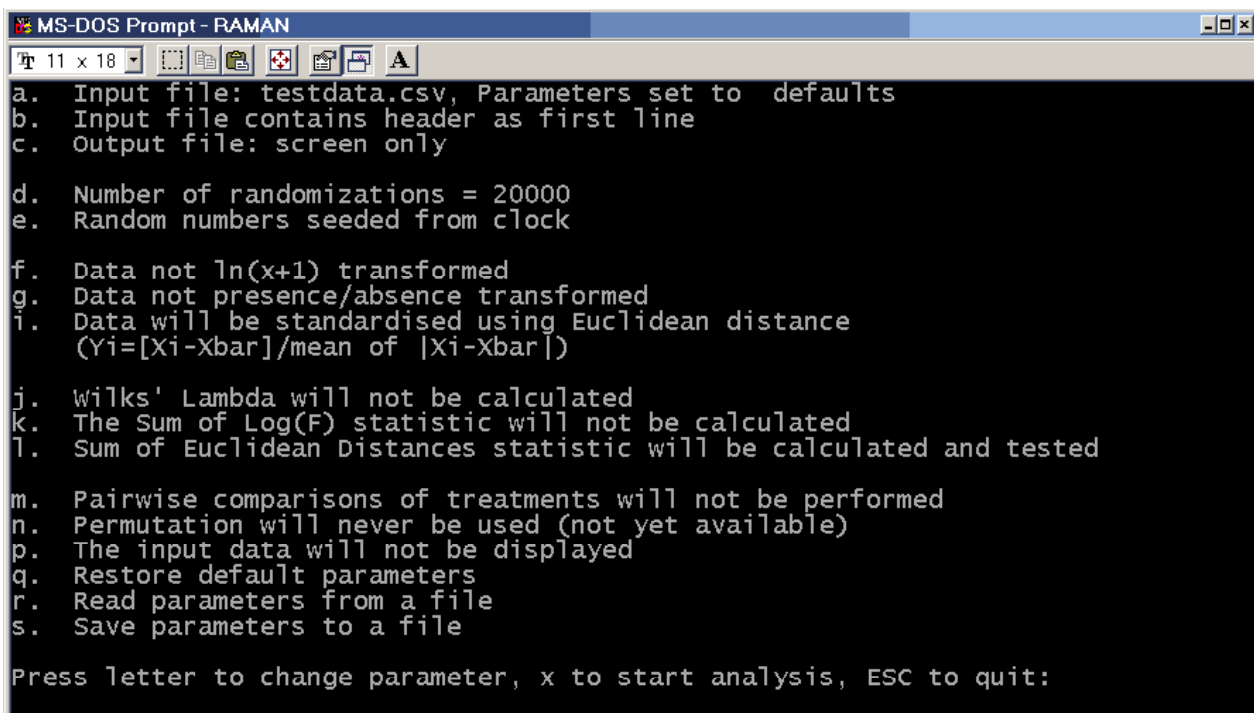
After you press a key, you will see:



```
MS-DOS Prompt - RAMAN
Data file selection
Enter name of file
Or press ENTER alone to select from all files matched by *.CSV
Or enter another name with wildcards (*) to select from list
Enter a q to quit this routine, or a h for help
Filename: _
```

At this point, you can type in the name of the data file and press the Enter key, or just press enter and you will see a list of all the files that have the .csv extension in the current directory. Once you get this list, you can use the arrow keys on the keyboard to move until the desired filename is highlighted, then press enter to select that file for analysis.

You will now see the main RAMAN parameter selection screen, where you set up the analysis that is to be performed. It looks like this:



```
MS-DOS Prompt - RAMAN
a. Input file: testdata.csv, Parameters set to defaults
b. Input file contains header as first line
c. Output file: screen only
d. Number of randomizations = 20000
e. Random numbers seeded from clock
f. Data not ln(x+1) transformed
g. Data not presence/absence transformed
i. Data will be standardised using Euclidean distance
  (Yi=[Xi-Xbar]/mean of |Xi-Xbar|)
j. Wilks' Lambda will not be calculated
k. The Sum of Log(F) statistic will not be calculated
l. Sum of Euclidean Distances statistic will be calculated and tested
m. Pairwise comparisons of treatments will not be performed
n. Permutation will never be used (not yet available)
p. The input data will not be displayed
q. Restore default parameters
r. Read parameters from a file
s. Save parameters to a file
Press letter to change parameter, x to start analysis, ESC to quit:
```

Setting The Options

Pressing a key corresponding to any of the letters at the left of the screen will allow you to change the item shown to the right of the letter. Details of what will happen are:

- a. Pressing A will take you back to the input data file selection menu, allowing you to choose a different data file for analysis.
- b. Pressing B allows you to change the expected format of the input file. This option is included for backwards compatibility with other programs, such as Brian Manly's software. It should normally not be changed, or if it is accidentally selected, option 2, input file contains header as first line, should be selected.
- c. Pressing C allows you to select where output from the program will be directed. Output is always sent to the screen; pressing the c key allows you to choose to send it to a file as well. The file will be in standard ASCII text format, and if loaded into a program like Word™, it should be displayed and printed using a fixed pitch font such as Courier New. The default is to send output to the screen only; you will probably want to send it to a file as well unless you are running preliminary analyses.
- d. Pressing D allows you to select how many random reorderings of the data will be carried out to create randomization distributions of the test statistic or statistics. The default is 20,000 reorderings, which is usually enough to lead to a reasonably narrow 99% confidence interval for test statistics. When a P value is very close to a critical value, you may want to increase this number; for slow computers and large data sets you may want to decrease it, although less than 5000 is probably not a good idea.
- e. Pressing E allows you to change how the random number generator used to reorder observations among treatments while generating randomization distributions is initialized. Normally, the random number is initialized from the system clock, which means that it starts at an arbitrary point. The number that is used is reported in output, for possible re-use should this be necessary. When you press E, you will be prompted for a number, which should either 0, meaning that the generator will be initialized from the clock, or an integer between 1 and 32767. Entering an integer in that range will mean that the random number generator is initialized with that number, and will mean that the same sequence of random numbers will be generated each time the program is run with that seed value.
- f. Pressing F toggles between two possible settings. The default is that the data are not transformed using the $\ln(n+1)$ transformation before being analyzed. The alternative is that they are. The $\ln(n+1)$ transformation is often applied to data that are counts, because (among other things) it often uncouples the mean and the variance of count data.
- g. Pressing G toggles between two possible settings. The default is that the data are not transformed to 1 for present (any data value other than 0) or 0 for absent prior to further analysis. The alternative is that they are. This transformation can be

useful for ecological data, where it may be worthwhile to compare the outcomes of examining differences among treatments when the data are counts of individuals present for each species in each observation with the outcomes when the data are simply 1 for that species being present and 0 for it being absent. Setting the presence-absence transformation on will turn off standardization (option h), and it cannot be turned on until the presence-absence transformation is turned off.

- i. Pressing I allows you to choose how data are standardized within variables (columns) before being analyzed. Most standard multivariate statistics use data that are standardized to mean zero, variance 1 before being analyzed. This removes effects of differing measurement scales among variables. The transformation used is:

$$Y_i = \frac{X_i - \bar{X}}{S_x}$$

Where Y_i is a transformed observation, X_i is an original observation, \bar{X} is the mean of that variable taken over all treatments, and S_x is the standard deviation of the variable taken over all treatments. The default for RAMAN is to use a different standardization, more suitable for use with the sum of Euclidean distances statistic, in which each value of each variable is standardized so that the mean of all observations of that variable is zero and the mean distance of all observations is one unit:

$$Y_i = \frac{X_i - \bar{X}}{\text{mean of } |X_i - \bar{X}|}$$

This preserves linear relationships among data better than the usual standardization. It is also possible to choose not to standardize data at all, which may lead to unpredictable consequences since variables measured on different scales (for example cm and mm) will be weighted differently in determining distances among points in multivariate space, but may be useful if all variables are intrinsically on a common scale and differences caused by different ranges need to be preserved.

- j. Pressing J turns the calculation and testing of the Wilks' Λ (lambda) statistic on or off. The default is off. If Λ is to be calculated, the data should be standardized to unit variance, and there must be sufficient univariate degrees of freedom to allow inversion of the H'H matrix. If there are not, an error message is displayed that suggests turning this option off and rerunning the program.
- k. Pressing K turns the calculation of the sum of log(F) statistic on or off. This statistic is simply the sum of ln(F) of the univariate ANOVAS calculated for each variable (column) of the data set. A large sum of log(F) suggests that that the means of treatments differ significantly. See Manly (1991, 1997). The default for this statistic is off.

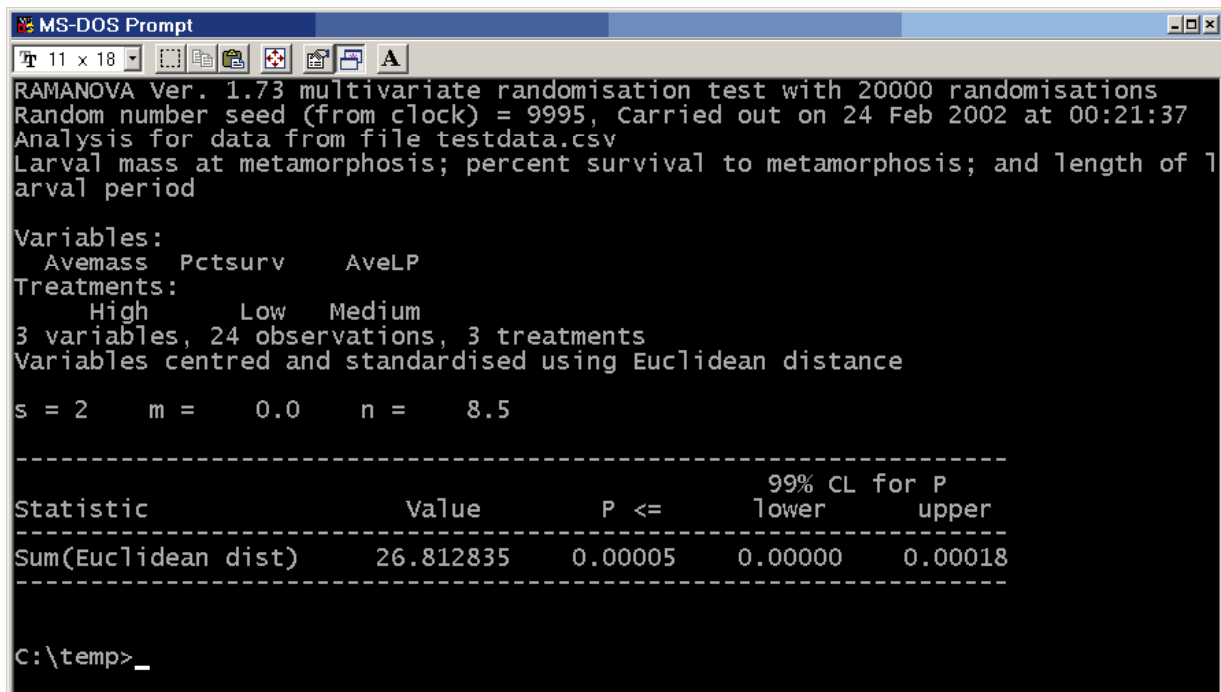
- i. Pressing L presents three options. The default is to calculate and test the sum of Euclidean distances statistic. The sum of Euclidean distances is simply the sum across all treatments of the total distance in multivariate space between each data point (observation) and the centroid (treatment average) for that treatment. If the data points for treatments are clustered at different locations in multivariate space, this will be relatively small; if they are dispersed throughout multivariate space, this will be large. The sum of the squared Euclidean distances is similar, but instead of the absolute value of the distance of each point from its group centroid, this statistic sums the square of the distance. It can be more strongly affected by outlying points, and may be a poorer test statistic than the sum of the Euclidean distances (see Mielke and Berry 2001 and Cade and Richards 2001). A third option is to not calculate either Euclidean distance statistic.
- m. Pressing M switches between two options. The default is to calculate an overall test for no differences among treatments, and stop. The second is to proceed to compare all possible pairs of treatments. This option can be very useful when there are several treatments, as otherwise post-hoc or preplanned pairwise comparisons would have to be done by editing the data set. When this option is selected, both the standard P-value, calculated by comparing the observed value of the test statistic(s) to their randomization distribution(s), and P-values adjusted for multiple comparisons using Sidak's adjustment (which is slightly more powerful than Bonferroni's adjustment), are presented. If output is being sent to the screen only, the program will pause after the initial analysis and each pairwise comparison to allow reading the results; but if output is being sent to a file, the initial results and pairwise comparisons may flash past quickly and examining the output file will be necessary.
- o. Pressing O will cause the program either to pause each time the screen is full of information, or to run as fast as possible with no pauses. This option will only appear if output is being sent to a file using option c. When output is not being sent to a file, this option does not appear since the program must pause or you might miss the output of analyses.
- p. Pressing P will cause the program to display each line of input data as it is read. This option can be useful to check that data are being read in correctly.
- q. Pressing Q will reset all of the program's parameters to their default values.
- r. Pressing R will cause the program to read parameter values from a file. This can be very useful if you are experimenting with the program or with how transformations affect the outcomes of analyses. You will be presented with three options: 1) don't read parameters after all, 2) choose the name of an input file, which acts similarly to the data file input screen, allowing you to enter a filename or choose from a list of possibilities, 3) read from a parameter file with the same base filename as the data file being analyzed,, but the extension .prm.
- s. Pressing S will present you with three options: 1) write the current program parameters to a file file with the same base filename as the data file being analyzed,, but the extension .prm, 2) choose another file name, which acts like the usual file name choice screen, or 3) don't save the current parameters after all.

Finally, pressing X will execute the program, running the analysis as currently specified, or pressing the Esc key will stop the program.

As the program runs, a bar will show the percentage of each set of randomizations that has been completed. After this reaches 100%, a table of output will appear.

Interpreting The Output

If you run the program using its default parameters on the sample data set, you will get an output screen like that below (although it is possible that the P value may be slightly different, because it is likely that the random number seed will be somewhat different):



```
MS-DOS Prompt
RAMANOVA Ver. 1.73 multivariate randomisation test with 20000 randomisations
Random number seed (from clock) = 9995, Carried out on 24 Feb 2002 at 00:21:37
Analysis for data from file testdata.csv
Larval mass at metamorphosis; percent survival to metamorphosis; and length of 1
arval period

Variables:
  Avemass  Pctsurv  AveLP
Treatments:
  High      Low      Medium
3 variables, 24 observations, 3 treatments
Variables centred and standardised using Euclidean distance

s = 2      m = 0.0      n = 8.5

-----
Statistic          Value          P <=          99% CL for P
                  lower          upper
-----
Sum(Euclidean dist) 26.812835    0.00005      0.00000      0.00018
-----

C:\temp>_
```

The first line identifies the program and version, and reports how many random reorderings of observations among treatments were used to generate the randomization distribution(s) against which the test statistic(s) were compared.

The second line reports what number was used to seed the random number generator, and the date and time on which the analysis was performed.

The third line identifies the file from which the data were read, and the fourth (and possibly later) lines repeat the heading that was present on the first line of the data file.

The next section specifies the names of the measured variables and the treatments, and summarizes the numbers of variables, observations and treatments.

Next, the program reports what technique was used, if any, to center and standardize the data by columns (variables) before analysis.

The next line reports the degrees of freedom these data would have for a standard MANOVA.

Finally, the table presents the calculated test statistic or statistics and the results of comparing it with the randomization distribution. In this case, we did not change any options, so the program defaulted to standardizing the data using Euclidean distance and calculating only the sum of Euclidean distances statistic. The P value in this example shows that the calculated total Euclidean distance between observations and their group centroids was the smallest of the total of 20,000 distances calculated (the one based on the original data and 19,999 based on random reassignments of the observations among treatments). The 99% CL (confidence limits) for the P value are based on the binomial distribution, and mean that, if we repeated this analysis a large number of times, we would expect that 99% of the time the P value would fall between these limits. If the upper 99% confidence limit is less than our selected threshold for rejection of the null hypothesis (usually $\alpha = 0.05$) that the treatments do not differ, we can reject that null hypothesis with considerable confidence; it is very unlikely that a different run of the program would lead us to a different conclusion. Since, in this case, the upper 99% confidence limit of 0.00018 is much less than 0.05, we would reject H_0 , and conclude that the treatments affected the locations of the points in the multivariate space defined by the variables measured.

If we ran the program again, but wanted to do more conventional multivariate tests, we could once again select the testdata file, and while the parameters screen is displayed, press i followed by 1, so that the data are standardized to unit variance, then press j so that Wilks' Λ will be calculated and tested, k so that the sum of log(F) statistic will be calculated and tested, and l followed by 2, so that the sum of the squared Euclidean distances will be calculated and tested. If we then press x, the output will look like:

```

MS-DOS Prompt
11 x 18
Random number seed (from clock) = 8888, Carried out on 24 Feb 2002 at 00:23:20
Analysis for data from file testdata.csv
Larval mass at metamorphosis; percent survival to metamorphosis; and length of larval period

Variables:
  Avemass  Pctsurv   AveLP
Treatments:
  High     Low     Medium
3 variables, 24 observations, 3 treatments
Variables centred and standardised to unit variance

s = 2    m =    0.0    n =    8.5

-----
Statistic                Value          P <=          99% CL for P
                        lower          upper
-----
Wilks' lambda            0.090430      0.00005       0.00000       0.00018
Sum of log(F)            9.287080      0.00005       0.00000       0.00018
Sum[(Euclid dist)^2]    24.588053     0.00005       0.00000       0.00018
-----

C:\temp>

```

The top lines are the same, except that the time and date have changed and a different random number seed is being used. The variables are now being centered and standardized to unit variance, and the values and P values for the three selected test statistics appear in the table. In this case, all three give results similar to one another and to the analysis based on Euclidean distance; it is clear that the treatments really do affect the responses.

Using And Interpreting Output Written To Disk Files

Although testing any single hypothesis will never cause more output to appear than will fit on the screen, you are likely to want to make permanent records of the outcomes of analysis, and possibly to print them out. To do this, use option c of RAMAN.

For example, to analyze the data in testdata.csv, determine which of the three possible pairwise combinations of treatments differ significantly according to the sum of Euclidean distances statistic, and write the output into a file, run RAMAN and select testdata.dat for analysis. Then press c at the options screen, followed by 3 so the output will be written to a file called testdata.txt, which can easily be loaded into a word processor for examination and printing. Also press m so that pairwise comparisons of treatments will be performed. Finally, press x to execute the analyses. If you are using a fast PC, the tests and output will flash by very quickly; too quickly to follow on the screen. Run Word or your favorite word processing program, and load the file testdata.txt. You may have to specify that it be put into a non-proportionally spaced font, such as Courier New, so that the spacing of the tabular output is not disrupted by proportional spacing of letters. After loading into your word processor, the output should look like that shown in Box 1 on the following page.

The first section of the output reports the results of the overall test of significance, in a format similar to that shown on the screen, but including which version of the program produced the results. The remainder of the output presents the results of each pairwise comparison, including the value(s) of the test statistic(s) for that pair of treatments with the rest of the data ignored, the P value calculated by from re-randomizing that subset of the data the indicated number of times and comparing the observed value of the statistic with the randomization distribution, the lower and upper 99% binomial confidence limits for the P value, and finally the P value adjusted using Sidak's adjustment for multiple comparisons. If only certain pairwise comparisons are considered, as a result of preplanning which pairs of treatments to compare, or if you wish to preserve the comparisonwise error rate at $\alpha=0.05$, either the P value from the randomization distribution, or the upper 99% confidence limit of that value, are the ones to use in deciding whether a pair of treatments differ significantly. If the pairwise comparisons are not preplanned and you wish to preserve the experimentwise type I error rate at $\alpha=0.05$, the Sidak-adjusted P values should be used. See Hochberg and Tamhane (1989) for a very useful discussion of the philosophy and practice of multiple comparisons.

I would consider that the initial overall analysis preserves the experimentwise error rate at $\alpha=0.05$, and would examine the upper binomial 99% confidence limits for each pairwise comparison, keeping a comparisonwise error rate of $\alpha=0.05$ and maximizing the power to

detect differences between the treatments. In this example, all pairs of treatments differ significantly, even if the Sidak-adjusted P values are used.

Box 1. Output written to .txt file by RAMAN testing for significant treatment effects using Euclidean distances for all treatments and each pair of treatments in the sample data file testdata.csv.

```

RAMANOVA Ver. 1.73 multivariate randomisation test with 20000 randomisations
Random number seed (from clock) = 11377, Carried out on 24 Feb 2002 at 14:22:48
Analysis for data from file testdata.csv
Larval mass at metamorphosis; percent survival to metamorphosis; and length of larval period

Variables:
  Avemass  Pctsurv   AveLP
Treatments:
  High     Low     Medium
3 variables, 24 observations, 3 treatments
Variables centered and standardised using Euclidean distance

s = 2      m =    0.0      n =    8.5

-----
Statistic                Value          P <=      99% CL for P
                        lower          upper
-----
Sum(Euclidean dist)     26.812835   0.00005   0.00000   0.00018
-----

RAMANOVA Ver. 1.73 multivariate randomisation test with 20000 randomisations
Comparison of treatment High and treatment Low

3 variables, 16 observations, 2 treatments
Variables centered and standardised using Euclidean distance

s = 1      m =    0.5      n =    5.0

-----
Statistic                Value          P <=      99% CL for P
                        lower          upper      Sidak P
-----
Sum(Euclidean dist)     14.788282   0.00015   0.00000   0.00037   0.00045
-----

RAMANOVA Ver. 1.73 multivariate randomisation test with 20000 randomisations
Comparison of treatment High and treatment Medium

3 variables, 16 observations, 2 treatments
Variables centered and standardised using Euclidean distance

s = 1      m =    0.5      n =    5.0

-----
Statistic                Value          P <=      99% CL for P
                        lower          upper      Sidak P
-----
Sum(Euclidean dist)     19.895571   0.00030   0.00000   0.00062   0.00090
-----

RAMANOVA Ver. 1.73 multivariate randomisation test with 20000 randomisations
Comparison of treatment Low and treatment Medium

3 variables, 16 observations, 2 treatments
Variables centered and standardised using Euclidean distance

s = 1      m =    0.5      n =    5.0

-----
Statistic                Value          P <=      99% CL for P
                        lower          upper      Sidak P
-----
Sum(Euclidean dist)     26.186194   0.00090   0.00035   0.00145   0.00270
-----

```

References

Cade BS & Richards JD. 2001. *User Manual for BLOSSOM Statistical Software*. Midcontinent Ecological Science Center, U.S. Geological Survey, Fort Collins, Colorado USA. available from <http://www.mesc.usgs.gov/products/software/blossom.shtml>

Manly BFJ. 1991. *Randomization and Monte Carlo methods in biology*. London, Chapman and Hall.

Manly BFJ. 1997. *Randomization, bootstrap and Monte Carlo methods in biology*. London, Chapman and Hall.

Mielke PW & Berry KJ. 2001. *Permutation methods: A distance function approach*. Springer-Verlag, NY. 352pp.