

# BIOMstat

**for Windows**

**Statistical software for biologists**

Version 4.0

User guide

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**Exeter Software**

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## Introduction

BIOMstat performs many of the standard statistical computations needed in biological research. It includes modules for descriptive statistics, analysis of discrete and meristic data, analysis of variance and of covariance, regression and correlation analyses, and non-parametric analyses. BIOMstat is also designed to be easy to use and appropriate for use in the classroom. Analyses are selected from a hierarchical system of buttons within folders along the left side of the main window and the parameters for a particular analysis are specified by filling-in information and checking options in the form displayed to its right. The results of the computations appear in output windows whose contents can be examined, printed, copied and pasted to other Windows programs, or saved to a file. Icons are available on a toolbar for plots appropriate for the particular analysis just completed.

Version 4 of BIOMstat was developed to accompany the 4th edition of the text *Biometry* (Sokal, R. R. and F. J. Rohlf, 2012. *Biometry*. W. H. Freeman and Co.: New York). An option can be selected so that the results of the computations are cross-referenced to specific pages in *Biometry* (relevant discussions in the text and Boxes showing the computational steps). However, the methods are general and this software can be used in conjunction with other text books.

Most of the statistical computations in this program are based on well-tested algorithms developed in the original FORTRAN versions of the program (BIOM, by FJR) first published as an appendix to the first edition of *Biometry* back in 1969. However, version 3 has major changes over the earlier versions. The previous suite of separate FORTRAN programs have been translated to Pascal and combined into a single program. A MS Windows-based user interface has been added which makes the program much easier to use than previous versions. In addition, new statistical methods have been added, taking into account some of the new methods added to the 4th edition of *Biometry*. Version 3.3 added many types of plots appropriate for the analyses included in this program. There are, for example, histogram plots so one can see the general distribution of ones data, scatter plots to show relations between pairs of variables, and special plots appropriate for particular analyses. The help file has examples of all the types of plots. Version 4.0 added further refinements and it takes advantage of additional features that Windows 7 makes possible.

This version was written using Delphi 2007 by F. James Rohlf. Early code and design were made by Dennis E. Slice. Dean Adams helped by testing the program and doing his best to find ways in which the program could be made to crash.

Once BIOMstat has been installed, users are encouraged to make use of the extensive help file as it describes all of the statistical methods included in BIOMstat. The purpose of this UserGuide is just to provide instructions on installation and getting started.

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# Installation

## System requirements

1. A PC-compatible computer with MS Windows Vista, 7 or 8 installed. It works well on 64 bit versions of Windows.
2. A hard drive with at least 10 MB of available disk space.

## Installing BIOMstat

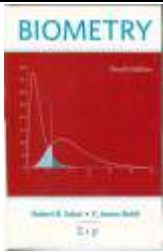
The following is a set of step by step instructions for installing the software. Minimal familiarity with using MS Windows is assumed.

1. Start Windows.
2. Insert the BIOMstat Install CD as appropriate or else place the downloaded setup program in a convenient folder. Double-click on the setup.exe file unless it starts automatically from the CD.
3. The Install program will request the unlocking code provided with the software. Click on the **Next** button to continue the installation process or the **Back** button to return to a previous screen.
4. The Install program will ask for the drive and directory where you would like to install BIOMstat. You may accept the suggestion or enter a new location. A new directory will be created if the directory does not exist already. Note: you can reuse the same directory as earlier versions. Click **Next** to the continue installation.
5. When the setup program finishes you should have a new folder on the Start menu called BIOM (unless you specified a different name) with icons for the BIOMstat and BIOMedit programs, their help files, and an Uninstall program (see below). The following files will be placed on your hard disk: `biomstat.exe`, `biomstat.ovr`, `biomstat.chm`, `biomedit.exe`, `readme.txt`, and `biomstat.pdf`. Sample data files will be placed in the `BIOM\DATA` directory.

When you run the BIOMstat program the first time you will be prompted to enter your name, institution, and the serial/registration number.

## Uninstall procedure

Should you have to remove this software from your computer you only need to double-click on the Uninstall icon in the BIOM folder on the startup menu. This will delete the files and the directory for BIOMstat. You do not need to delete BIOMstat in order to install a new version.



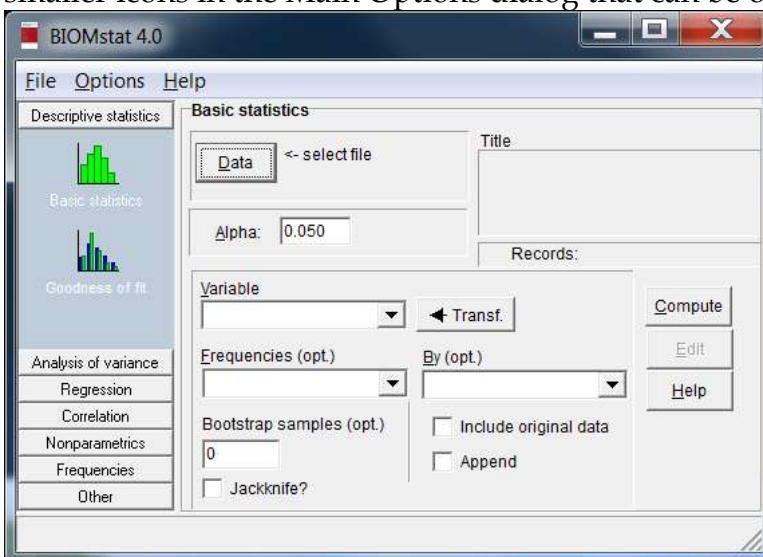
# How to use BIOMstat

After installation, there should be a BIOMstat icon in the BIOM folder. Double-click on that icon to start the program. Before you can make use of the program to analyze your own data you will have to prepare data files in a format compatible with BIOMstat. Files can be either ASCII files or Excel files. With the database version of BIOMstat, dBase, Paradox, FoxPro, Access, and other standard database files can also be used. See the chapter on data file formats and the help file for more information.

The next section gives a tutorial on how to use BIOMstat to carry out a single-classification analysis of variance using the sample data `singl.dta` (note: this Courier font will be used in this documentation for names of files, for data contained within them, and for information the user has to enter). Sample data files are placed in the TESTDATA subdirectory during installation and are also available as part of the help system. The Ariel font will be used to refer to information displayed on the screen by the program (such as names of fields where the user has to enter information).

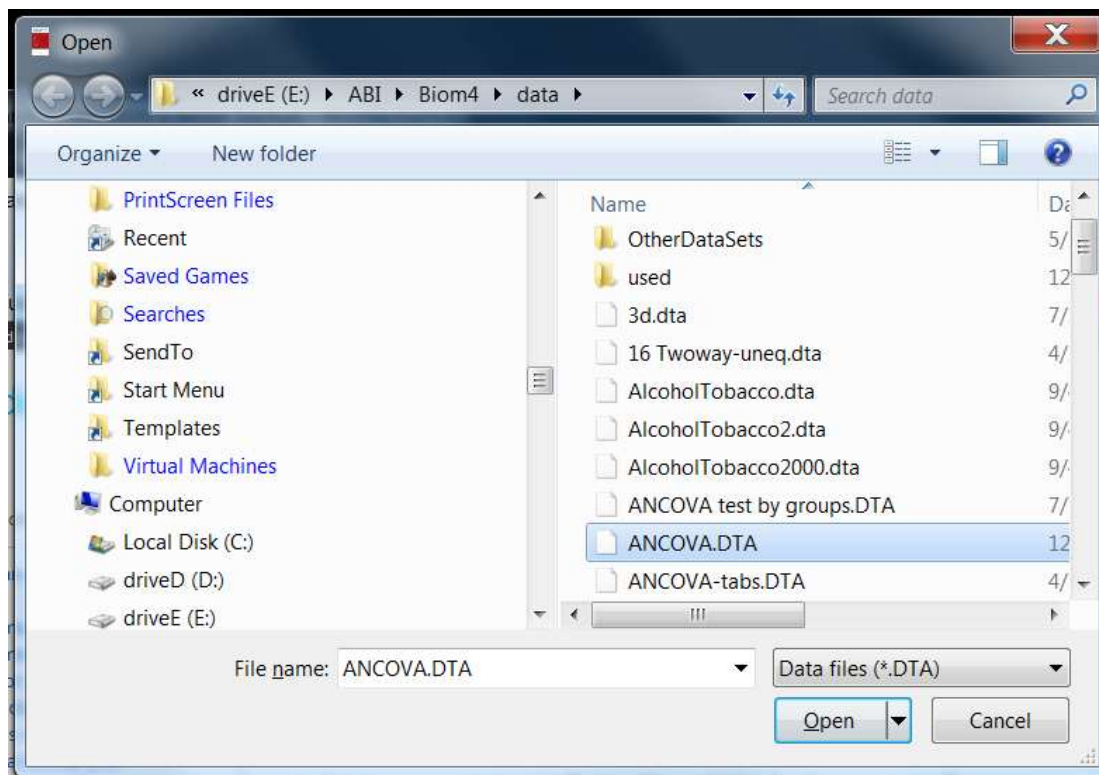
## A sample session

The initial screen consists of a vertical series of buttons grouped in folders along the left side of the window (see below). The first step is to find the folder corresponding to the desired type of method. For example, the “Basic statistics” button is located within the “Descriptive statistics” folder. In the example shown below large icons are shown. They can be changed to smaller icons in the Main Options dialog that can be opened from the Options menu.



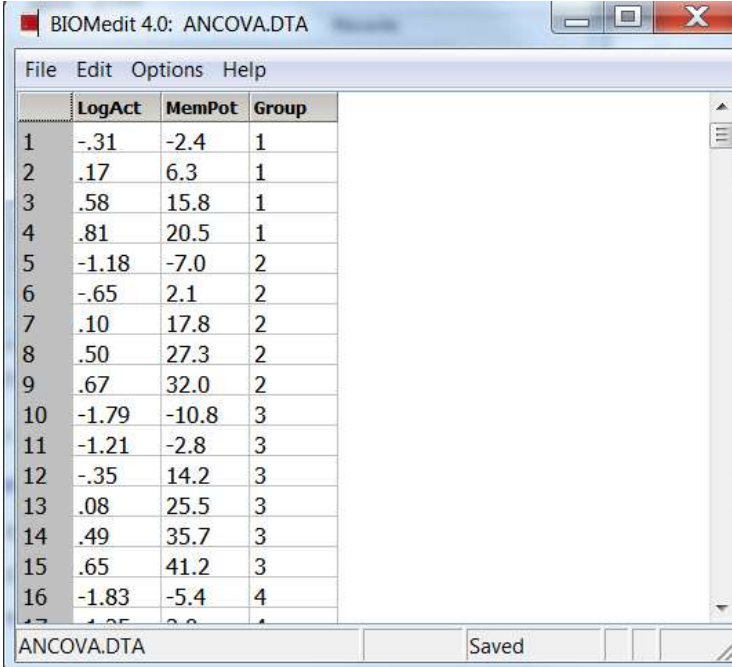
The screenshot shown above shows what it will look like after clicking on the “Basic statistics” icon. It shows on the right the particular options needed for this module.

If you have a data file ready for processing you should click on the “Data” button to load your data file by selecting it from the list in the file-open dialog box. An example of the file-open dialog box is shown below.



You can either type in the name of the file or use the controls shown above to click on a filename (perhaps after having changed to another directory). In the “Files of type” window you can also select “Excel files”.

Alternatively, you can select “Edit” from the File menu to load the data editor that allows you to modify an existing file or to create a new one. Shown below is an edit session displaying the first part of the `ancova.dta` file.



The screenshot shows a window titled "BIOMedit 4.0: ANCOVA.DTA". The window contains a menu bar with "File", "Edit", "Options", and "Help". Below the menu bar is a table with the following data:

	LogAct	MemPot	Group
1	-.31	-2.4	1
2	.17	6.3	1
3	.58	15.8	1
4	.81	20.5	1
5	-1.18	-7.0	2
6	-.65	2.1	2
7	.10	17.8	2
8	.50	27.3	2
9	.67	32.0	2
10	-1.79	-10.8	3
11	-1.21	-2.8	3
12	-.35	14.2	3
13	.08	25.5	3
14	.49	35.7	3
15	.65	41.2	3
16	-1.83	-5.4	4

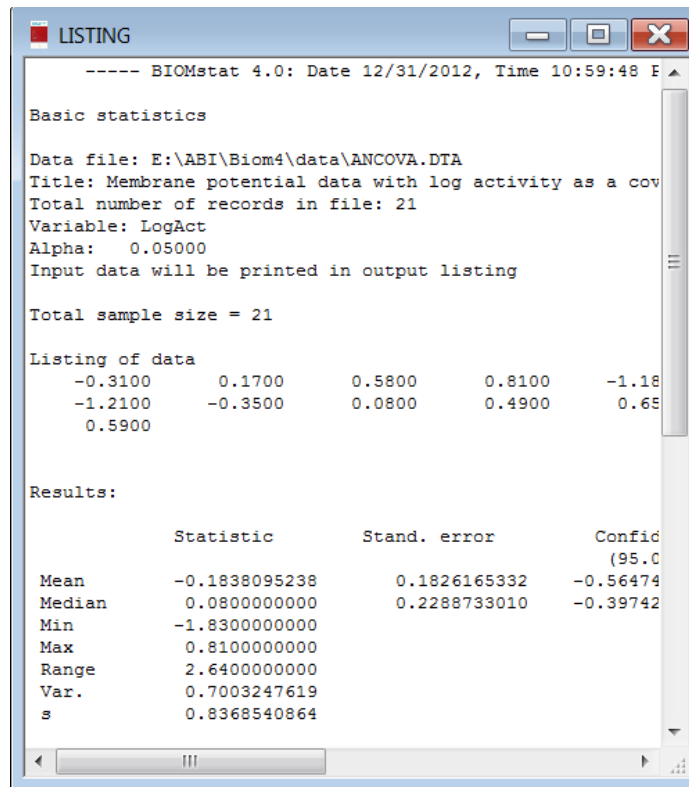
At the bottom of the window, there is a status bar with the text "ANCOVA.DTA" and a "Saved" indicator.

When the data file is complete, you can select the variable in your dataset that correspond to the dependent variable (**LogAct** in the `ancoma.dta` file) and the variable that groups the data into samples (**Group** in this example). A completed dialog is show below. Note that the title and the number of data records in the dataset are displayed. Note that the file must first be saved to disk before it can be loaded (or reloaded) into a BIOMstat module.

The "Include original data" checkbox is present in the dialog box for every analysis. If it is checked then the original input data will be included in the output listing (useful to make sure the program has interpreted your data properly but may not be necessary if you are making many analyses with the same dataset). If the "Append" box is checked then the output of the next run will be appended to any previous output of this program. This can be useful if you are studying the effects of different options and you would like a single print-out of all the runs. The "By" field, present on most dialog boxes, is used to specify an input variable that divides the data into blocks that are to be analyzed separately. The output listings are not kept permanently so you should use the "File|Save as" item on the listing window's menu to save any you wish to keep (they will be saved as plain ASCII text files).

You can then select (e.g., click with the left mouse button) the "Compute" button to actually perform the computation. A new window will pop-up and display the listing file containing the results. An example is shown below in which part of the listing file is visible in the window.





```

LISTING
----- BIOMstat 4.0: Date 12/31/2012, Time 10:59:48 F
Basic statistics
Data file: E:\ABI\Biom4\data\ANCOVA.DTA
Title: Membrane potential data with log activity as a cov
Total number of records in file: 21
Variable: LogAct
Alpha: 0.05000
Input data will be printed in output listing


Total sample size = 21

Listing of data
-0.3100    0.1700    0.5800    0.8100   -1.18
-1.2100   -0.3500    0.0800    0.4900    0.65
 0.5900

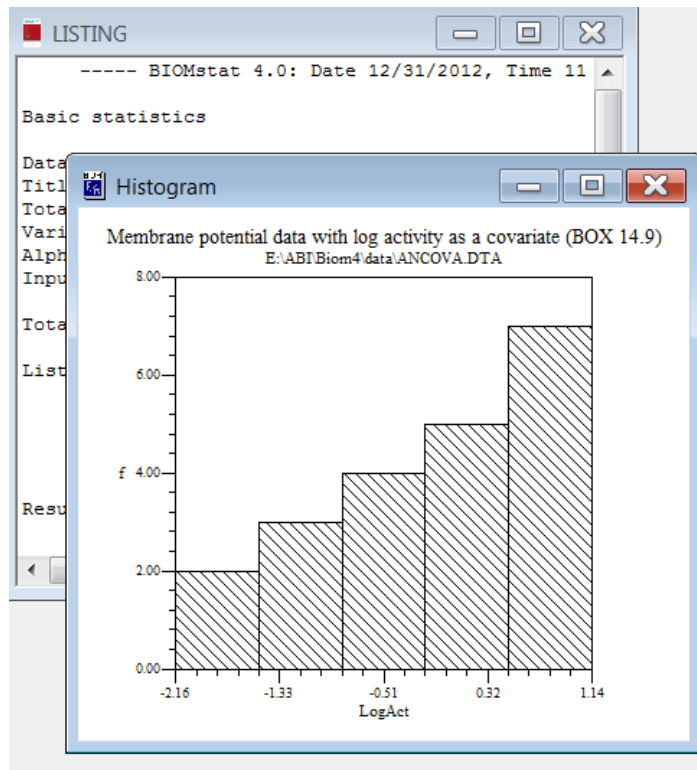
Results:

          Statistic      Stand. error      Confid
                               (95.0
Mean      -0.1838095238      0.1826165332     -0.56474
Median    0.0800000000      0.2288733010     -0.39742
Min       -1.8300000000
Max        0.8100000000
Range     2.6400000000
Var.      0.7003247619
s         0.8368540864

```

Scroll the window up and down to study the results, save it to a file, print it, or copy part of it and paste it into some other Windows program -- such as a wordprocessor. To close the output window, you can either double-click on the upper left corner of the window, press the **Alt-F4** keys or you can also click on the  in the upper right corner of the window). Selecting "File|Close" on the menu minimizes the listing window rather than closing it.

Finally, one can click on the graphics icons on the toolbar just below the menu line. Clicking the histogram icon results in the following plot.

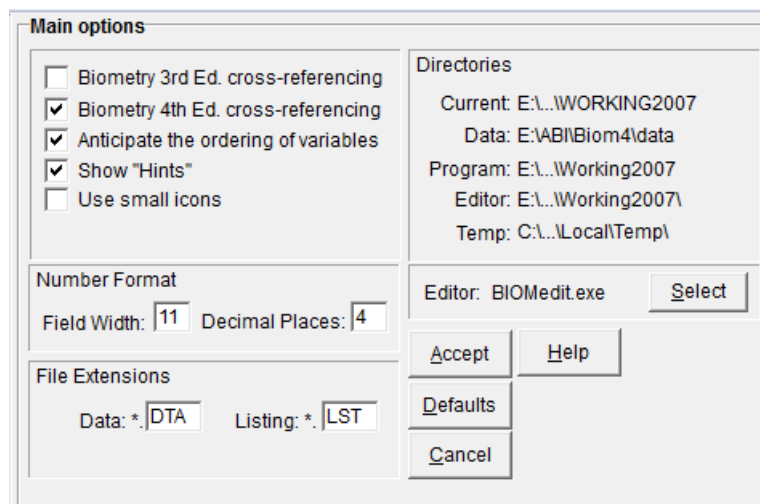


The Plot Options window for this plot can be opened from the Options menu of the output window or by right clicking on the plot. This window allows you to change the class marks, class interval, scales for the abscissa, and the properties (color, line thickness, and pattern) of the histogram bars. Examples of the various graphics options dialog boxes are shown in the Graphics section below (page 11).

## Main Options

If you select "Options|Main Options" on the menu of the main window, a dialog (see below) will be displayed that lets you to set a number of options such as:

- Whether the output listing cite references to the 3<sup>rd</sup> or 4<sup>th</sup> editions of Biometry.
- Whether small or large icons will be used in the main window.
- Whether the dialog boxes should try to guess which variables go in which fields? They assume that grouping variables (if present) correspond to the initial variables and the dependent variable is listed last.
- Whether "fly-by" help hints are to be shown when the mouse cursor passes over a control in one of the dialog boxes.
- What 3 character extension is used for data and listing files.
- The default field width and decimal places for listing data. The use of this field can force more precision in the output listings.
- The editor can be changed from the default Windows notepad editor. The "Select" button to change this to an editor of your choice. If you select a wordprocessor then make sure you save data files as plain ASCII text files.



## Graphics

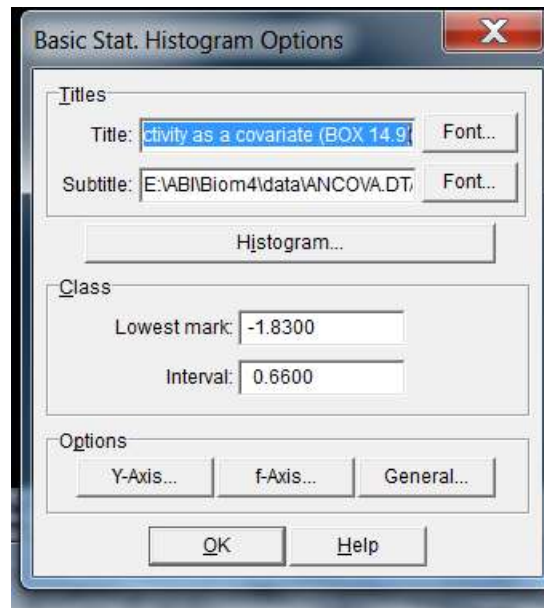
Most of the computational modules provide plots that help one visualize the results of an analysis or to detect departures from its assumptions. The set of available plots is indicated by the icons on the toolbar in the Results Window that contains the Listing Window. The right-most icons are always (except for the Mantel module) for a simple 2D  $x,y$  scatterplot if the current data file contains at least two variables and a 3D  $x,y,z$  scatterplot if the current data file contains at least three variables. You can use these modules to plot any variable against any other. This is sometimes useful for detecting problems in the data. Place the mouse cursor over an icon to receive a "hint" about the type of plot it produces. Click on the desired icon to produce a plot. You can also select a plot from the View menu item.

The size and aspect ratio of a plot can be changed by dragging a corner of the plot or maximize its window for better viewing. You can also minimize the Listing Window to get it out of the way.

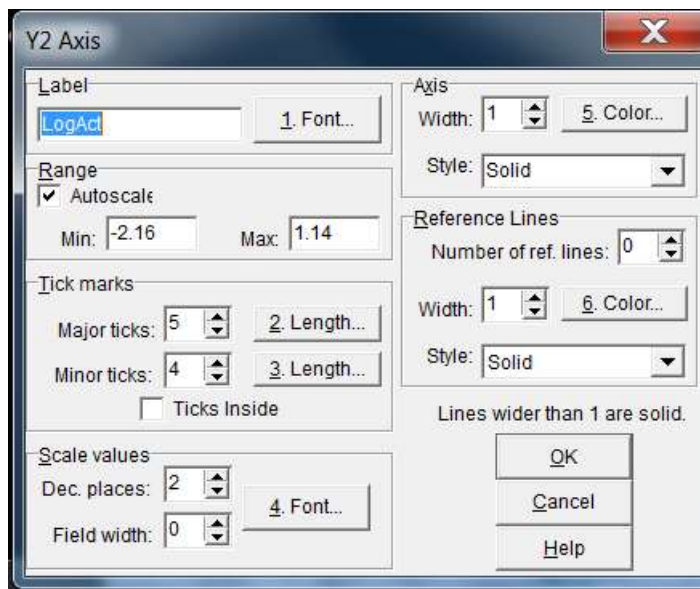
The File menu options allow you to preview or print a plot and setup your printer.

Select the "Options|Plot Options" menu item to display a dialog that allows you to set options specific to the current plot and also to set general plot options. The options specific to each plot allow you to customize the color and other attributes for the titles, subtitles, and any symbols, lines, and bars used in a plot. The axes buttons allow you to adjust the scale and appearance of each axis. Depending on the module, there may be check boxes that allow you to include or suppress the plotting of certain items. The General button brings up the general plotting options (see below). Press the "OK" button to accept the changes and close this window.

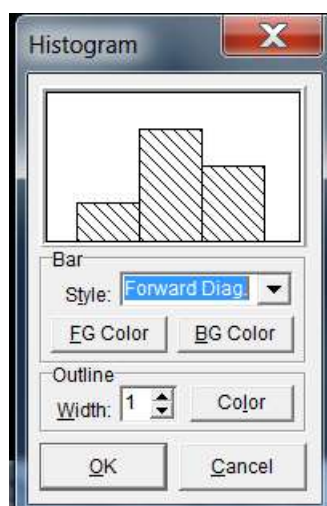
An example plot-options dialog is shown below for the BASTAT module. It allows one to change the attributes for the histogram and the axes.



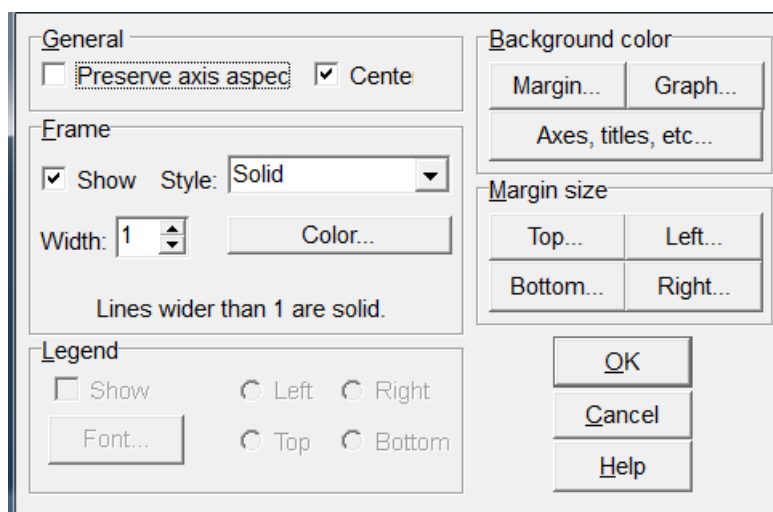
Pressing the Y-axis button results in the following dialog box that allows you to change many aspects of the Y-axis in the current plot.



For various plots, you can also change fonts, colors, plotting symbols, and histogram bars. Each have their own options window. For example, the dialog box for changing the attributes of the bars in the Single classification anova histograms is shown below.



Clicking on the General button on a plot options dialog brings up a dialog box where you can control the general layout of the plot. You can change the color and other attributes of the plot background, the frame around the plot, the margin outside a plot, and the location of the legend (if appropriate). An example is shown below.



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# Data file formats

To use your own data with the program you first have to prepare data files. Data are in the form of a table or matrix with columns corresponding to variables and rows to the observations. They may be stored as ASCII text files with special keywords (as described below), as Excel files (see below), or as database files (*e. g.*, dBase, Paradox, or Access table files). The variables consist of both the measurements being analyzed and also numerical codes indicating the grouping of observations into samples.

## ASCII files

There are four kinds of input records. Each of them starts with a keyword and ends with a semicolon.

<code>title</code>	Title or comment about the data file. It is used to label the output listing. This record is optional.
<code>vars</code>	List of the names of the variables (columns) in the data table. This record is required and must come before the data since it defines the number of columns that the program should process. Qualitative variables (those using alphanumeric codes) are indicated by the presence of the "\$" character in the variable name. This character can be changed in the options dialog window. No spaces are allowed within a variable name (but you can use the underscore "_" character).
<code>data</code>	The actual data follow this keyword. The number of columns must match the number of variable names provided in the vars record. The number of rows corresponds to the total number of observations. The entries for each row must be separated by at least one blank, comma, or tab character. Note: the Mantel module is unique in that it uses the "symmatrix" keyword instead. It requires the data in the form of a lower ½ matrix including the diagonal. There is no predefined limit to the number of records in any one dataset.
<code>end</code>	This indicates the last line of the file to be processed. Information following this record will be ignored.

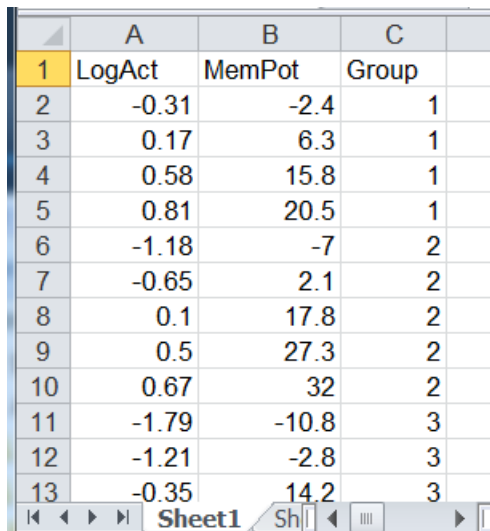
## Excel files

The format for an Excel data file is quite simple – each variable corresponds to a column in the spreadsheet with the first value in each column taken as the name of the variable. However, the variable labels must not contain any blanks. As with the BIOMstat data files, qualitative variables are indicated by the presence of a "\$" character within the variable name. There can be only one dataset in a spreadsheet.

Optionally, the variables can be preceded by title and comment lines. The title cell (there can be only one) must start with 'title:'. For example, cell A1 could contain the following string:

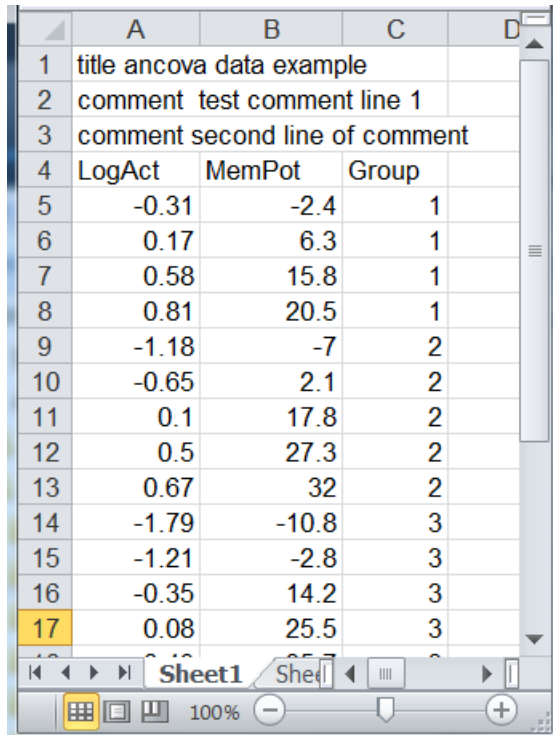
'title: data from nutrition experiment'. One or more comment cells can be provided. Each must contain 'comment:'. For example, cells A2 and A3 could contain the following: 'comment: variable 1 was measured in mm' and 'comment: variable 2 is in degrees Celsius'.

**Note:** BIOMstat can only read Excel files (values changed in BIOMedit but they *cannot* be saved back to an Excel file). The changed file can be saved as an ASCII data file. An example of a data file in Excel is shown below (there are no title or comment cells in this example).



	A	B	C
1	LogAct	MemPot	Group
2	-0.31	-2.4	1
3	0.17	6.3	1
4	0.58	15.8	1
5	0.81	20.5	1
6	-1.18	-7	2
7	-0.65	2.1	2
8	0.1	17.8	2
9	0.5	27.3	2
10	0.67	32	2
11	-1.79	-10.8	3
12	-1.21	-2.8	3
13	-0.35	14.2	3

An example with both a title cell (A1) and two comment cells (A2 and A3) is shown below.



	A	B	C	D
1	title ancova data example			
2	comment test comment line 1			
3	comment second line of comment			
4	LogAct	MemPot	Group	
5	-0.31	-2.4	1	
6	0.17	6.3	1	
7	0.58	15.8	1	
8	0.81	20.5	1	
9	-1.18	-7	2	
10	-0.65	2.1	2	
11	0.1	17.8	2	
12	0.5	27.3	2	
13	0.67	32	2	
14	-1.79	-10.8	3	
15	-1.21	-2.8	3	
16	-0.35	14.2	3	
17	0.08	25.5	3	

## Examples of ASCII data files

Data file with a single variable (such as might be used with the Basic Statistics module). The data elements cannot be entered with several on the same line since each line corresponds to an observation.

```

title Aphid stem mother femur length data (BOX 2.1);
vars FemLen;
data
3.3
3.5
3.6
3.6
3.6
3.6
3.8
3.8
3.8
3.8
3.9
3.9
3.9
4.1
4.1
4.2
4.3
4.3
4.3
4.3
4.4
4.4
4.5
4.7
4.4
;
end;
```

- Data file for a 2x2 contingency table (such as used with the RxC or Fisher modules). The first two variables indicate the rows and columns and the third variable gives the cell frequencies.

```

title Ant invasion data (Box 17.7);
vars Species Invaded? f;
data
1 1 2
1 2 13
2 1 10
2 2 3
;
end;
```

- Example of a SYMMATRIX data file as used by the Mantel module. The matrix is a 10x10 lower ½ matrix (including diagonal).



```
title Genetic distances (Box 18.10);
vars 3G 8L-11P 8F 8ABC 11YZ 11D 11X 3RS 8O 15L;
SYMMATRIX
0
.02040 0
.04143 .03944 0
.01213 .02549 .05285 0
.01246 .01362 .04473 .01682 0
.02868 .03908 .04109 .02195 .04362 0
.03393 .03347 .03313 .04774 .04928 .04567 0
.03023 .02816 .08473 .02804 .02605 .05730 .05661 0
.03784 .03229 .03276 .02445 .02767 .02986 .04330 .04805 0
.05698 .06308 .07491 .03722 .03377 .06550 .10242 .05331 .03661 0
;
end;
```

There are many examples of ASCII data files in the help file. There are also sample listings and plots (with annotations) from every computational module.

# Descriptions of methods

## Introduction

Furnished below is a description of the common to most of the modules as well as a description of the BASTAT module as an example. See the help file (either online or the PDF file) included with the BIOMstat program. Each section lists the purpose of the statistical method, its assumptions, how to setup the dialog box, and a description of the output listing. These sections are not intended to replace a good statistics text (such as *Biometry*) which would give much more detail about each method and how the results should be interpreted.

There are two standard check-boxes on all of the dialog boxes statistical analyses (i.e., except for the estimation of  $n$  and the statistical calculator).

- If “Include original data” is checked then a listing of the input data will be included in the output listing window. This is useful to make sure that BIOMstat has correctly interpreted your data file.
- If “Append” is checked then the output listing will be appended to the end of any previous listing for the current computational module.

There are also four standard buttons on the dialog boxes for each statistical analysis.

- **Data**, loads a data file into the program.
- **Compute**, the entries in the dialog box are checked and the corresponding module executed.
- **Edit**, the built-in edit program is executed using the currently selected data file. You may choose which edit program is called if an error is encountered in reading the file (by default the Windows Notepad program is used) in the Options dialog box (page 10).
- **Help**, the help file is loaded and set to display help for the current dialog box. You can also just push the **[F1]** key. Note: the help is extensive. It includes examples of data sets for every statistical method.

## Transformations

The following data transformations are available for use in most of the computational modules:

$ Y $	absolute value of $Y$
$\sqrt{Y}$	square root of $Y$
$\sqrt{(Y+.5)}$	square root of $(Y+1/2)$
$Y^2$	square of $Y$
$\ln Y$	natural log of $Y$
$\log Y$	log to base 10 of $Y$

$\log(Y+1)$	log to base 10 of $(Y+1)$
$\sin^{-1}(\sqrt{Y})$	arc sine of square root of $Y$ (assumed to be a proportion)
$\sin^{-1}(\sqrt{\%})$	arc sine of square root of $Y/100$ ( $Y$ assumed to be a percentage)
$1/Y$	reciprocal of $Y$
$Y^p$	$Y$ to the power $p$ , $p$ furnished in the power field of the transformation dialog box.
$(Y^p - 1)/p$	The Box-Cox transformation. The optimum value of $p$ is estimated and then the power transformation used. Only the Basic Statistics (page 21) and the Homogeneity of Variances modules allow the use of the Box-Cox transformation.

---

# Basic statistics

## Purpose

Computes descriptive statistics for continuous variables. The mean, minimum, maximum, range, standard deviation, variance, median, skewness ( $g_1$ ), kurtosis ( $g_2$ ), and their confidence limits are given. A Kolmogorov-Smirnov test is also provided for a goodness of fit of the data to a normal distribution using the estimated mean and variance. The Box-Cox transformation can be used to find the power transformation that results in the best fit to the Normal distribution. This exponent can then be used for the power transformation in this and other modules of BIOMstat. Bootstrap estimates of the mean, variance, and coefficient of variation can also be computed along with their parametric and nonparametric estimates **of their confidence intervals**.

## Assumptions

These methods are based on the assumption that the variables are continuous, independent, and normally distributed (or can be transformed to approximate normality).

## How to use

First use the Data button to specify a data file. The module accepts either raw data in the form of a single column of values or a frequency distribution with the Variable field indicating the class marks and the Frequencies field indicating the frequencies for each class. Set the Alpha field to the probability level to be used in setting  $(1-\alpha)100\%$  confidence limits.

### Dialog box fields:

Data	Select a previously prepared data file.
Alpha	Probability level to be used in setting $(1-\alpha)100\%$ confidence limits.
Variable	Select the dependent variable for the analysis and (optionally) a transformation.
Frequencies	Optionally, select the variable that indicates the frequencies for each class if the input data are in the form of a frequency distribution. Otherwise, this field must be left blank.
Bootstrap samples	If a value greater than 0 is entered then bootstrap estimates and confidence limits of the mean, variance, and coefficient of variation will be computed.

Jackknife? If checked, then jackknife estimates of the mean, variance, and coefficient of variation are computed.

By Optionally, select a variable that will be used to split the dataset into a series of separate analyses.

Standard check boxes: Include original data, Append.

Standard buttons: Compute, Edit, Help.

## Output listing

The output consists of a table of the various statistics computed -- mean, median, variance, standard deviation, coefficient of variation  $V$ , measures of skewness  $g_1$ , and kurtosis  $g_2$ . These are followed by their standard errors and confidence intervals where applicable. Tests for skewness and kurtosis are followed by the D'Agostino-Pearson test, see D'Agostino et al. (1990) for the computational methods. The results of the  $\delta$ -corrected Komolgorov-Smirnov test for goodness of fit to the normal distribution using the estimated mean and variance is given at the end. Both  $D_{\max}$  and the delta-corrected statistics,  $g_0$  and  $g_1$  are given. The Shapiro-Wilk statistic  $W$  is given along with its probability.

If the resampling number is greater than 0, bootstrap estimates and their standard errors will be given for the mean, variance, and the coefficient of variation. Confidence limits are also computed both as an estimate plus or minus  $t$  times their standard error and also nonparametrically as the upper and lower  $\alpha/2$  values among the bootstrap estimates.

If the jackknife box is checked then jackknife estimates of the mean, variance, and coefficient of variation will be computed.

Histogram and normal quantile plots can be viewed.

## Output listing example

The following example is based on the aphid data from Box 2.1 in Biometry.

```
Data file: Box 2_1.DTA
Title: Aphid stem mother femur length data (BOX 2.1)
Total number of records in file: 25
Variable: FemLen
Alpha: 0.05000
```

Total sample size = 25

The following is a list of various statistics and their standard errors (where available).

Results:

	Statistic	Stand. error	Confidence limits (95.00%)	
Mean	4.0040000000	0.0731391368	3.8291323683	4.1788676317
Median	3.9000000000	0.0916652802	3.6808383972	4.1191616028
Min	3.3000000000			
Max	4.7000000000			
Range	1.4000000000			
Var.	0.1337333333			
s	0.3656956841			
V (%)	9.1332588424	1.3292234325	5.9552318139	12.3112858709
$g_1$	-0.0180738236	0.4636835008	-0.9270766016	0.8909289545
$g_2$	-0.9450804483	0.9017205463	-2.7128088237	0.8226479270

The following gives the results of applying the Kolmogorov-Smirnov test for goodness of fit to the normal distribution.

Kolmogorov-Smirnov statistic

Test fit to normal distribution using estimated parameters.

Dmax = 0.15086

Dallal & Wilkinson (1986) approximation to Lilliefors test:  $P > 0.1$

Khamis delta-corrected statistics:

$D_0 = 0.13702$ ,  $D_1 = 0.16586$

$g_0 = 0.13702$ ,  $g_1 = 0.12420$ ,  $0.05 < P \leq 0.1$

Shapiro-Wilk test for normality:

Shapiro-Wilk  $W = 0.95790$ ,  $P = 0.3742$

Result of bootstrap sampling:

Bootstrap statistics:

Statistic	Mean	Std	L1	L2
Mean	3.9755368000	0.0674634932	3.8432787752	4.1077948248
Var	0.1128235200	0.0215540140	0.0705682026	0.1550788374
V	0.0841437074	0.0084320402	0.0676132118	0.1006742030

Nonparametric conf. limits):

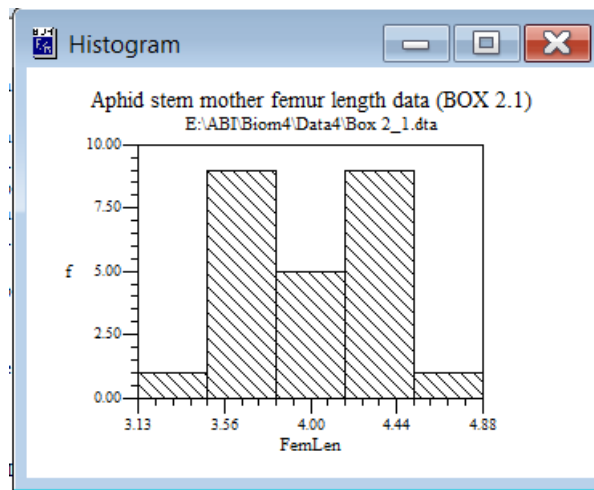
Coeff	L1	L2
Mean	3.8640	4.0840
Var	0.0792	0.1502
V	0.0703	0.0981

Results of Jackknife:

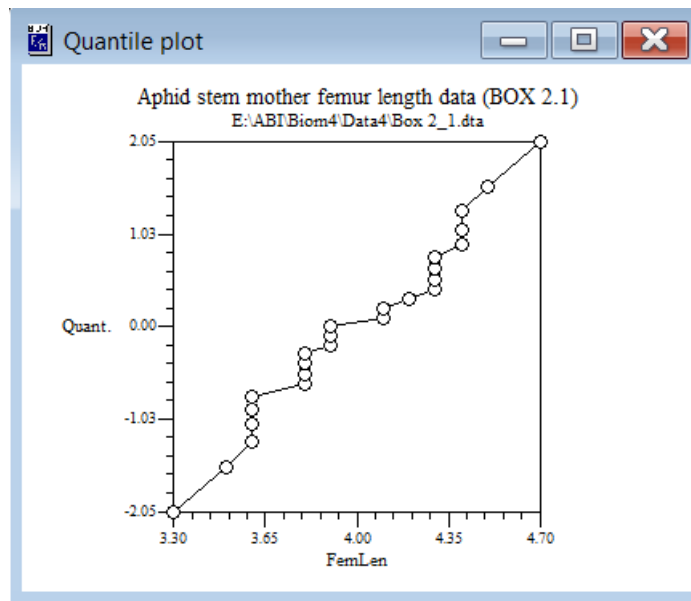
Jackknife statistics and their standard errors:

Statistic	Mean	SE	L1	L2
Mean	4.0040000000	0.0731391368	3.8530482401	4.1549517599
Var	0.1337333333	0.0285258914	0.0748587870	0.1926078797
V	0.0918392506	0.0100809796	0.0710331314	0.1126453699

Example of a histogram plot. The class marks, tics, and the scaling of the axes have been adjusted from the defaults.



Example of a normal quantile plot for the aphid data. The general trend is that of a straight line which is consistent with sampling from a normal distribution.



### Basic statistics - technical details

The bootstrap estimates of the mean and coefficient of variation are based on a random sampling (with replacement) of observations from the entire sample.

The jackknife estimates are based on the variation in the estimates with each observation left out in turn.

## Other software from Applied Biostatistics Inc.

### NTSYS-pc

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