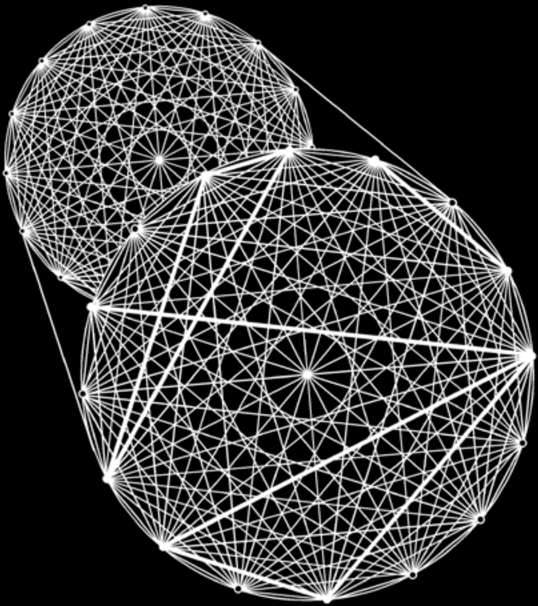
PC-ORD™ 7



PC-ORD™

Multivariate Analysis of Ecological Data

Version 7
User's Booklet

mjm
SOFTWARE

Suggested citation:

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Cover: The essence of multivariate analysis is the extraction of a small number of important relationships from a very large number of possible relationships.

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What is PC-ORD For?

PC-ORD is a Windows program for multivariate analysis of ecological data entered in spreadsheets. The terminology in the software is tailored for ecologists. We emphasize nonparametric tools, graphical representation, and randomization tests for analysis of community data. In addition to utilities for transforming data and managing files, PC-ORD offers many data exploration, ordination, and classification techniques not available in major statistical packages including: CCA, DCA, MRPP, perMANOVA, two-way clustering, TWINSPAN, Beals smoothing, diversity indices, species lists, Mantel test, many ordination overlay methods (quantitative, symbol-coding, color-coding, grid, joint plot, biplot, successional vector, hilltop), various rotation methods, 3D ordination graphics, indicator species analysis, Bray-Curtis ordination, city-block distance measures, species-area curves, tree data summaries, publication-quality dendrograms, and autopilot NMS.

Very large data sets can be analyzed. Most operations accept a matrix of up to 32,000 rows or 32,000 columns and up to 536,848,900 matrix elements, provided that your computer has adequate memory (see System Requirements, p. 4).

Virtually any multivariate data set consisting of a set of entities, each with a number of attributes, is adaptable to PC-ORD. In community ecology, the **main matrix** usually contains species abundance data in a set of samples. These data can easily be imported from Excel or other software. In addition to this main matrix, a **second matrix**, often containing environmental data, can be entered for analysis of its relationship to the first matrix. The inclusion of this second matrix greatly enriches the system's analytical capabilities. You can also use a **traits matrix** to study how species traits and functions relate to community patterns and environment. All three matrices are displayed in PC-ORD in file viewing windows.

In studies of species traits or functional groups, one of the matrices contains traits or relative use of a set of resources by various species, subspecies, or individuals. A matrix of sites × functional groups or sites × traits can be produced by multiplying a community matrix by the functional group or trait matrix.

Where is the Manual?

The full manual is built into PC-ORD, so we have not produced a paper manual. Our context-sensitive Help system can be accessed at any time by pressing F1 or clicking a Help button.

How Do I Get Started?

After you install the software, click on *Help* | *Contents* in the main menu. Then navigate to *Getting Started* in the help system. The most important topics to read at first are:

Data Preparation,
Spreadsheet Format, and
Typical Flow of Analysis

Managing Files and Projects

You should keep your data and results in a folder that is separate from the folder that contains PC-ORD. If you have more than one PC-ORD project, you can keep the files from each project in a separate folder or put them in a single folder. PC-ORD helps you resume work where you left off with *File* | *New Project*, *File* | *Open Project* and *File* | *Save Project* menu items. Details of how PC-ORD manages folders and projects are given under the *Open Project* topic in the PC-ORD Help system. See the topic *File Management Definitions* for explanations of folder types, projects, and how PC-ORD tracks file histories.

A “**Project**” in PC-ORD is a set of files associated with each other, along with the options and settings used prior to the time the project is saved. When you open a project, files are opened, the contents of the PC-ORD windows are restored, and your options and settings are restored from the last time you saved them. This information is stored in a file with the extension *.7prj.

File | *New* | *Project* starts a new named PC-ORD project. It allows you to import or open a set of files to start the project, clears the file histories, and closes any open windows in PC-ORD.

System Requirements

Hardware Required

- 80486 or higher CPU (including Pentium 4, Athlon, Celeron, etc.)
- 8 MB RAM (more RAM enables analysis of larger data sets)
- 20 MB of available hard disk space

Operating System: Windows 98, NT, ME, 2000, XP, Vista, Windows 8, and Windows 10. PC-ORD runs on 64-bit machines but in 32-bit mode.

Spreadsheet Software Recommended: A spreadsheet program capable of writing files in *.csv, *.xls, *.xlsx, or format is recommended (e.g., Excel). Many statistical software packages also export *.csv, *.xls, and *.xlsx files.

Network Environments

Recommended setup:

1. PC-ORD Executable files are installed in a network folder and can shared by multiple users.
2. Users keep data files and temporary files on their own hard disks (preferred choice) or in their own folder on a network drive (slower choice) or removable drive. Generic instructions for a typical network setup are given below. These presume that PC-ORD has already been installed on your network by your network administrator.

Put a PC-ORD icon on your desktop:

1. Ask your network administrator for the location of the folder containing the PC-ORD executable files.
2. Navigate in the file system to that folder.
3. Look for the file ***CreateDesktopShortcut***.exe.
4. Double click on *CreateDesktopShortcut*. This mini-program will create an icon on your desktop that points to PC-ORD on the server and to a local folder for storing your temporary files. From then on, you should use that PC-ORD icon to start PC-ORD.
5. Select *Local* under *Start In* if you plan to do your analyses mainly on one machine. Select *Network or removable drive* if you want to take your PC-ORD session with you between machines. Then *Browse* to a removable drive or network drive to which you have write privileges. Note that conflicts will result if multiple users are using the same folder at the same time.

6. Click OK. If you do not have write privileges to the selected folder, you will receive an error message, “You do not have write privileges to Start In Folder” or “File access denied.” In that case, choose a different drive or folder.

Important points

1. If you try to run PC-ORD directly from the executable folder on the network, errors will immediately result, unless you have write-privileges to that folder, which will seldom be the case.

2. Each user needs a unique folder in which to store their data and results. This is the “User data folder.” The user data folder can be either on a local drive or on a network drive. However, the user’s folder must be unique to that user or workstation and the user must have write access to that folder. We strongly recommend using a local drive rather than a network drive for the user data folder. This will speed the rate of screen refreshing when manipulating windows containing your data.

3. The “*Start in*” folder MUST be changed to that unique user’s folder. To set this after installation, right-click the PC-ORD icon, select “*Properties,*” and type the name of the user’s folder into the “*Start in*” box.

For class use

1. Same as above, but each user should copy the data files provided for the class into their own folders.

2. In computer classrooms, users may want to define their *Start in* folder as a removable USB drive. This allows users to preserve their own settings from one session to the next, regardless of which machine they are using. Note, however, that users can also accomplish this by using their own logical drive on the network, if such is available. This is slower than using a local hard drive.

Limitations

Each analysis in PC-ORD has its own memory demands, and thus its own memory limitations. The largest matrix that will run depends on the particular analysis, the number of rows, and the number of columns. A given analysis will not run if ANY ONE of the following limitations is not met:

1. rows x columns < 536,848,900
2. rows < 32,000 (23,170 if a square distance matrix is calculated)
3. columns < 32,000 (23,170 for PCA)
4. less than 2GB of available memory in your machine (this is the total memory in your machine less that being used by other processes)

All analyses that require one or more square distance matrices (Cluster Analysis, MRPP, NMS, PerMANOVA, etc.) are particularly greedy for memory.

You can evaluate your memory needs with the Memory Requirements utility provided under the File menu.

You can increase your available memory by closing software that you are not using.

Technical Help

We use email to answer technical questions about the MjM Software from registered users.

If you experience unexpected behavior, often someone else will have detected the same problem and it will already be fixed. So before you contact us…

- Please download the latest fixes from our website <www.pcord.com>, and determine whether the problem still exists in the latest version.
- Check the **Frequently Asked Questions** (FAQ) section on our website.
- Check the **Google users group** (http://groups.google.com/group/pc-ord)
- Please include the full version number (check the title bar of the PC-ORD menu or the headers on your output files. Specify not just “version 7” but “version 7.05” or whatever exact version you are using.

Updates and Fixes

Fixes will be posted on the MjM website as needed. PC-ORD maintenance fixes are free and can be downloaded from www.pcord.com. Click on *Help* | *Check For Software Updates*. The numbers for the current version and your version will be displayed. If the current version on the website is more recent than your version noted in PC-ORD title bar, click “yes” to download the update. The latest version will be downloaded, installed, and PC-ORD reopened.

Contact Us

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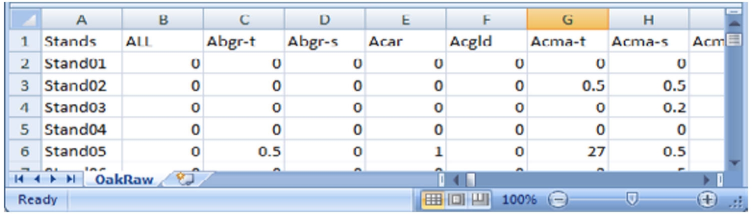
Using PC-ORD: a Brief Overview

You can quickly learn the basics of PC-ORD by following four steps:

1. Prepare your data.
2. Open PC-ORD and import your data files.
3. Run an analysis.
4. Explore your results graphically.

1. Prepare Your Data



	A	B	C	D	E	F	G	H	
1	Stands	ALL	Abgr-t	Abgr-s	Acar	Acgld	Acma-t	Acma-s	Acm
2	Stand01	0	0	0	0	0	0	0	
3	Stand02	0	0	0	0	0	0.5	0.5	
4	Stand03	0	0	0	0	0	0	0.2	
5	Stand04	0	0	0	0	0	0	0	
6	Stand05	0	0.5	0	1	0	27	0.5	

A. Put your data into spreadsheets (e.g. Excel) with the sample units as rows and variables as columns. Assign a short name to each row and column.

B. Your variables will be partitioned into two or three files, one with response variables (**main matrix**; e.g., species presence, abundance, or other measure of performance), another with potential controlling factors or design variables (**second matrix**; e.g., environmental variables), and optionally a **traits matrix** with species traits. You partition your data by creating separate *.xlsx files, creating separate worksheets within a single spreadsheet file, or partitioning a single spreadsheet as you import to PC-ORD (see below).

2. Start a Project and Import Your Data

A. Start PC-ORD by clicking on the PC-ORD icon.

B. *File* | *New Project* In the future, when you open an existing project (*.7prj), PC-ORD restores the five main windows (main, second, and trait matrices, graph file, result file) to the way they were at the time you last saved the project. Your options and settings for the analyses and graphing are also saved.

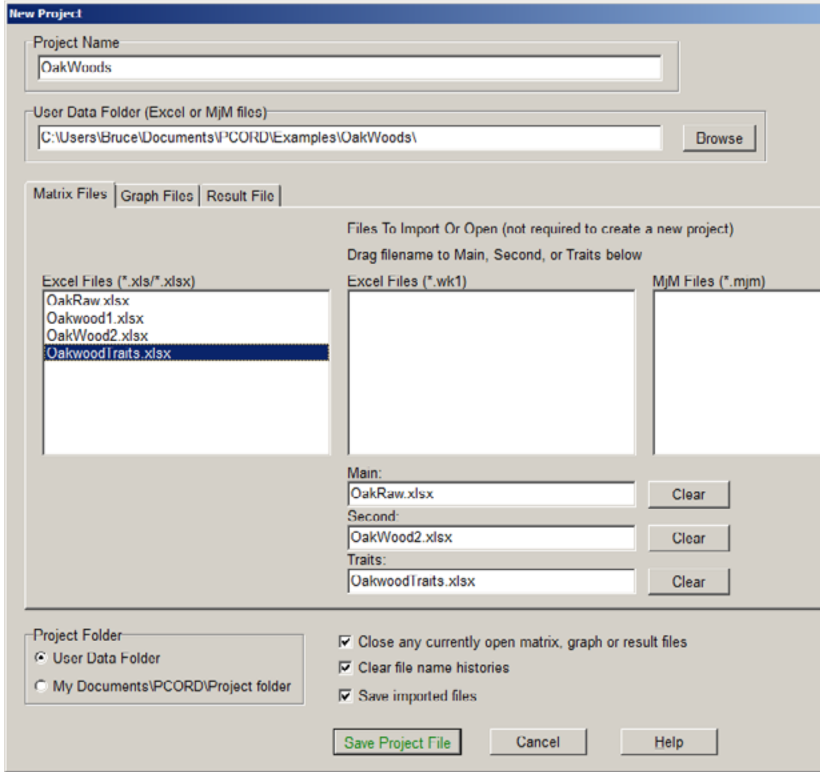
C. Fill in the *New Project* dialog (see next page) with **Project Name** (a short memorable name, such as "OakWoods")

- Select the **User Data Folder** that contains your spreadsheet(s).
- Drag the Excel file name for the species data from the left column into the "**Main**" box of the New Project dialog to create the main matrix. (You can also do this for *.csv files).
- Drag the file name for the environmental data into the "**Second**"
- Drag the file name for the species trait data (if available) into the "**Traits**" box.

D. Click on "*Save Project File*"

E. Choose *Excel Simple Spreadsheet* in the *Import File Type* dialog. This means that each column in your spreadsheet has a variable name at the top of it.

F. If you have more than one worksheet in the file you will be asked to select which one to open for each matrix being imported.



Project Name: OakWoods

User Data Folder (Excel or MjM files): C:\Users\Bruce\Documents\PCORD\Examples\OakWoods\

Files To Import Or Open (not required to create a new project)

Drag filename to Main, Second, or Traits below

Excel Files (*.xls/*.xlsx):
- OakRaw.xlsx
- Oakwood1.xlsx
- OakWood2.xlsx
- OakwoodTraits.xlsx

Excel Files (*.wk1)

MjM Files (*.mjm)

Main: OakRaw.xlsx

Second: OakWood2.xlsx

Traits: OakwoodTraits.xlsx

Project Folder

● User Data Folder

○ My Documents\PCORD\Project folder

☑ Close any currently open matrix, graph or result files

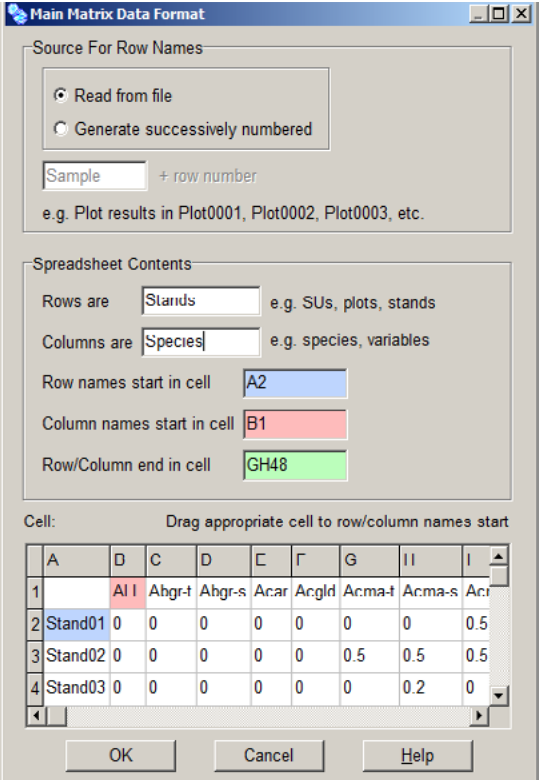
☑ Clear file name histories

☑ Save imported files

G. The *Data Format* dialog is displayed, allowing you to specify the content of the matrix:

- what are the rows?
- what are the columns?
- where they are named?

You must provide column (variable) names in your spreadsheet. But if you have no row names, you can generate them automatically with a check box.



Main Matrix Data Format

Source For Row Names

● Read from file
○ Generate successively numbered

Sample + row number

e.g. Plot results in Plot0001, Plot0002, Plot0003, etc.

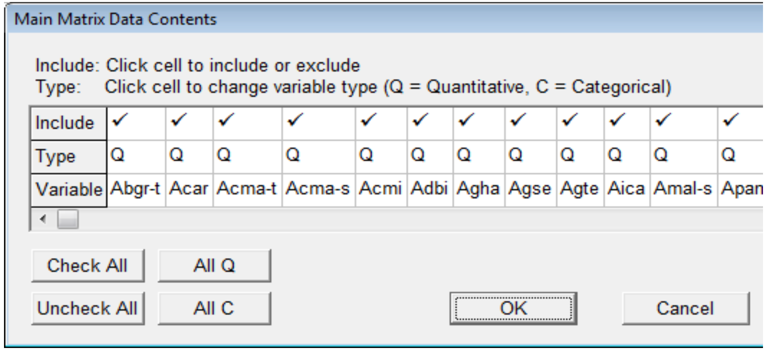
Spreadsheet Contents

Rows are: Stands (e.g. SUs, plots, stands)
Columns are: Species (e.g. species, variables)
Row names start in cell: A2
Column names start in cell: B1
Row/Column end in cell: GH48

Cell: Drag appropriate cell to row/column names start

	A	B	C	D	E	F	G	H	I
1		All	Abgr-t	Abgr-s	Acar	Acgld	Acma-t	Acma-s	Acr
2	Stand01	0	0	0	0	0	0	0	0.5
3	Stand02	0	0	0	0	0	0.5	0.5	0.5
4	Stand03	0	0	0	0	0	0	0.2	0

H. Then use the following dialog to indicate which variables to extract and the variable type for each. In this case we selected all species for the main matrix. We declared each variable to be type "Q" (quantitative). In general, presence-absence data in the main matrix should be treated as "Q" variables. Click *OK* and the matrix will be imported.



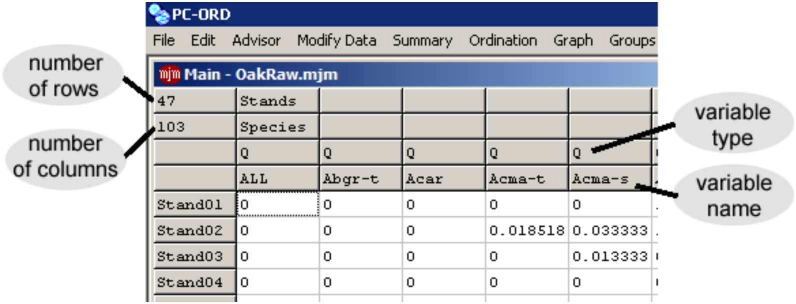
Main Matrix Data Contents

Include: Click cell to include or exclude
Type: Click cell to change variable type (Q = Quantitative, C = Categorical)

Include	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Type	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q
Variable	Abgr-t	Acar	Acma-t	Acma-s	Acmi	Adbi	Agha	Agse	Agte	Aica	Amal-s	Apan

I. The matrix will be written to a temporary file, temp.mjm for the main matrix, temp2.mjm for the second matrix, or temp3.mjm for the traits matrix. After your approval, the temporary file becomes the main matrix, complete with with header rows (see next page). Now save it under a new name of your choice, for example, "OakWood1.mjm."

Parts of the header for a PC-ORD matrix.

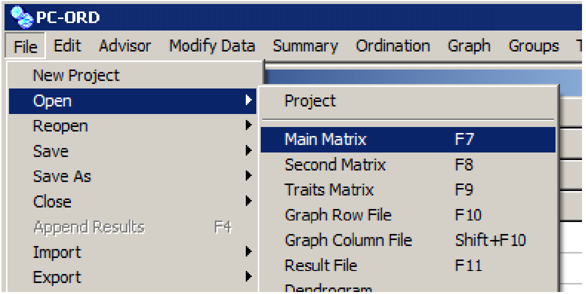


47	Stands				
103	Species				
	Q	Q	Q	Q	Q
	ALL	Abgr-t	Acar	Acma-t	Acma-s
Stand01	0	0	0	0	0
Stand02	0	0	0	0.018518	0.033333
Stand03	0	0	0	0	0.013333
Stand04	0	0	0	0	0

The steps given above result in a matrix in PC-ORD format with header rows, as explained in the illustration above. The purpose of the header rows is to make the files self-documenting, to allow more informative dialogs, and to make your graphics and output files easier to understand.

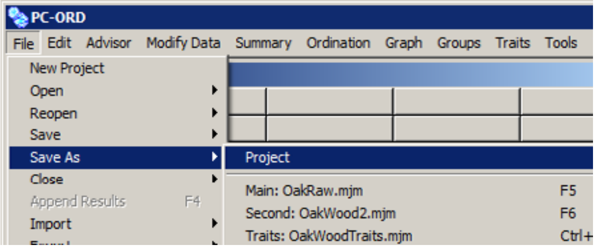
If you selected more than one matrix in the *New Project* dialog, then the process above will be repeated for each matrix, beginning with step 2F.

Once your project is established, you can open other data matrices within the same project by using *File* | *Open* (for *.mjm files) or *File* | *Import* (for other formats).



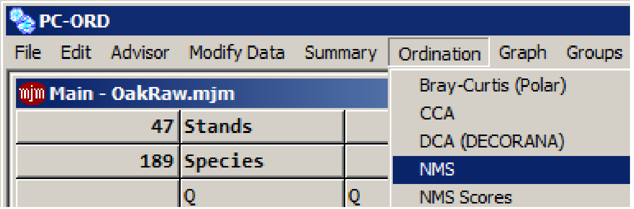
Remember that after importing you should save each matrix as a separate spreadsheet in *.mjm format. This will save you steps, every time you use that file.

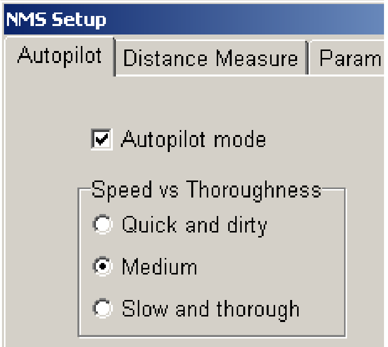
At any time you can update the files associated with your project with *File* | *Save* | *Project* (or *File* | *Save As* | *Project*).



3. Run an Analysis

Select an analytical method from the main menu. For this example, we will use nonmetric multidimensional scaling (NMS or NMDS), one of the most powerful ordination methods, especially adept at extracting nonlinear gradients in species composition.





☑ Autopilot mode

Speed vs Thoroughness

○ Quick and dirty

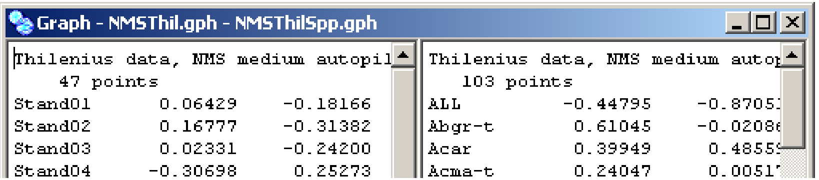
● Medium

○ Slow and thorough

This example uses the Oak Woods data set provided with the software and available for download at www.pcord.com. Choose autopilot mode with medium thoroughness ("speed vs. thoroughness" sets the compromise between fast results and a thorough search for the solution of best fit). On the "Distance Measure" tab, choose Sørensen (Bray-Curtis), a good distance measure for community data. When running NMS in autopilot mode, all of the other options except the "tie handling" option (see *Help* system) are grayed out and set automatically.

NMS iteratively searches for the best solution, then reports the results. A new result file will appear, along with windows containing coordinates for the stands (GRAPHROW.GPH) and the species (GRAPHCOL.GPH). Save each of these three files with a new name. Select *File* | *Save as* | *Result.txt*, then enter a new name, for example *NMSThil.txt*. (Named after Thilenius, the source of the data). Use a similar procedure to save the row and column coordinates, for example as *NMSThil.gph* and *NMSThilSpp.gph*. **Time-saving tip**: Use *File* | *Save* | *All* to save all of those files with a common base name.

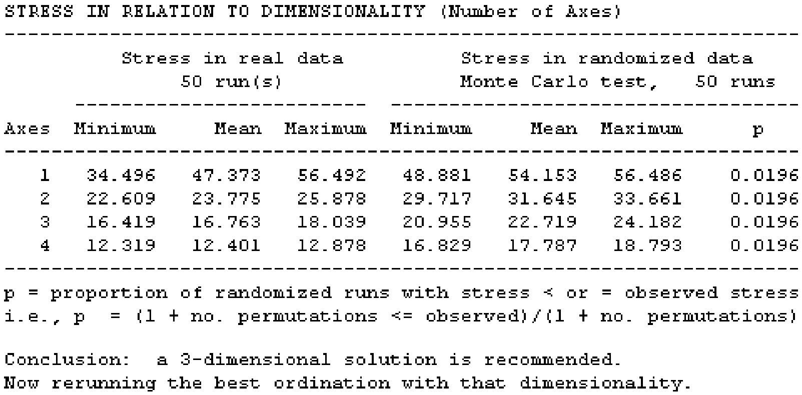
In the example below, the two graph files have been saved with those names, the first one containing the coordinates (ordination scores) for the 47 stands, the second one containing the coordinates for the 103 species.



```
Thilenius data, NMS medium autopil
    47 points
Stand01          0.06429     -0.18166
Stand02          0.16777     -0.31382
Stand03          0.02331     -0.24200
Stand04         -0.30698      0.25273
```

```
Thilenius data, NMS medium autop
   103 points
ALL            -0.44795     -0.8705
Abgr-t          0.61045     -0.0208
Acar            0.39949      0.4855
Acma-t          0.24047      0.0051
```

Inspect the result file. See Chapter 16 in McCune & Grace (2002) on NMS for background on how to interpret the results. Because random starting configurations are used, your results will differ somewhat from those given here if you are trying the example Oak Woods data set. A key portion of the results file is the table of stress in relation to dimensionality (number of axes; see next page). The stress table also includes a report on the randomization test:



```
STRESS IN RELATION TO DIMENSIONALITY (Number of Axes)
--------------------------------------------------------------------
          Stress in real data           Stress in randomized data
               50 run(s)                Monte Carlo test,   50 runs
      -------------------------  -----------------------------------
Axes  Minimum      Mean  Maximum Minimum      Mean  Maximum       p
--------------------------------------------------------------------
   1   34.496    47.373   56.492  48.881    54.153   56.486    0.0196
   2   22.609    23.775   25.878  29.717    31.645   33.661    0.0196
   3   16.419    16.763   18.039  20.955    22.719   24.182    0.0196
   4   12.319    12.401   12.878  16.829    17.787   18.793    0.0196
--------------------------------------------------------------------
p = proportion of randomized runs with stress < or = observed stress
i.e., p  = (1 + no. permutations <= observed)/(1 + no. permutations)

Conclusion:  a 3-dimensional solution is recommended.
Now rerunning the best ordination with that dimensionality.
```

From the randomization test results on the right half of the table, note that the *p*-values indicate that solutions of any dimensionality from 1 through 4 are stronger than expected by chance. Autopilot chose a 3D solution because it reduced the minimum final stress in the real data by over 5 units, versus a 2D solution, while still giving a small *p*-value. The minimum stress for the best 3D solution was 16.4.

4. Explore Your Results Graphically

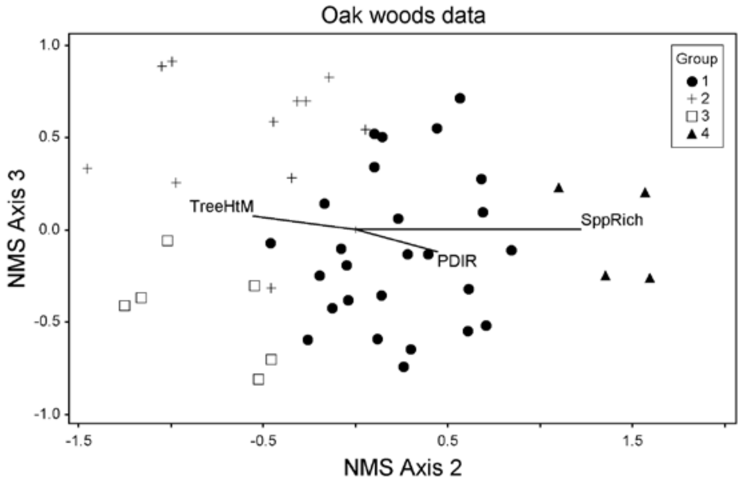
You can explore your ordination results with:

- 2D and 3D ordination graphs
- Joint plots (*Graph* | *Joint Plot*) with variables from the second matrix
- Determine how much of the variation in the distance matrix is represented in the ordination diagram (*Graph* | *Statistics* | *Percent of Variance in Distance Matrix*),
- Graphically examine the relationships between the ordination and individual variables in the second matrix (*Graph* | *Overlay From Second Matrix*),
- Calculate linear and rank correlation coefficients between axis scores and variables in the second matrix (*Statistics* | *Correlations With Second Matrix*),
- Rotate the diagram so that major vectors in the joint plot are aligned with the axes (select *Graph* | *Joint* plot, then *Rotate* | *By Angle Continuous*. Select 5° for the increment and click *Next* repeatedly to gradually rotate the ordination. See Chapter 15 in McCune and Grace (2002).
- Use “successional vectors” to connect before-and-after or other sequential measurements.

Selected examples of these are shown below.

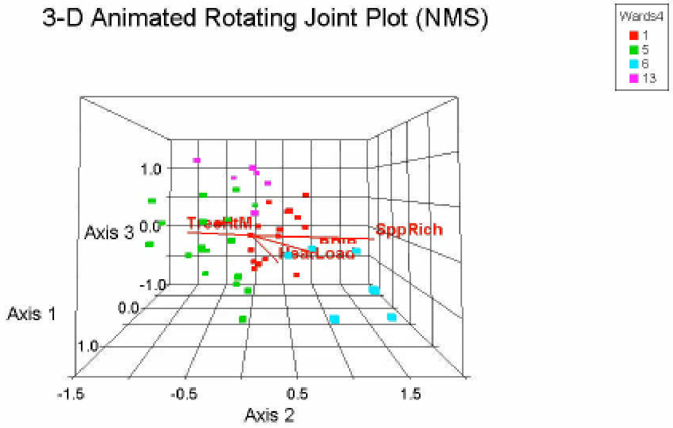
Joint plot

A joint plot superimposes on the ordination a set of radiating lines. These show relationships between variables in the second matrix and the ordination scores. In this case we also set the symbols to code for the categorical variable "Group," based on a separate cluster analysis of stands in species space. "TreeHtM" (tree height) and "SppRich" (species richness) are strongly and oppositely related to the second axis. Group 4 is relatively rich in species. "PDIR" (potential direct incident radiation) is rather weakly related to axis 2. The ordination has been rotated to align the strongest correlations with the horizontal axis.



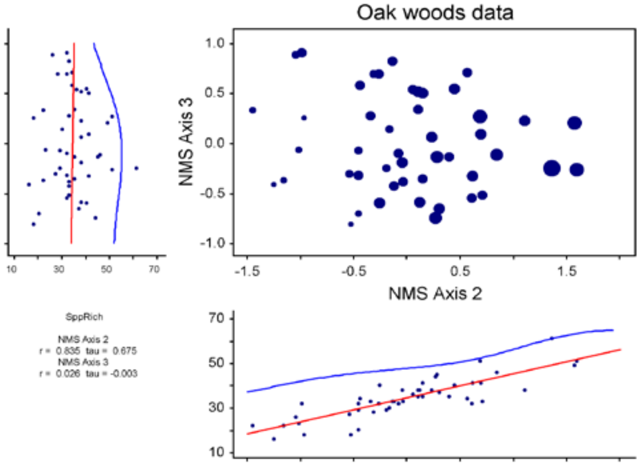
3D Joint Plot

Joint plots for ordinations with three axes can also be produced in 3D (*Graph | Ordination | 3D*). The graph below used the same ordination scores as in the previous example, though not rotated. Much more informative than this static view is the capability to rotate this 3D picture continuously, allowing you to see the three dimensional structure more clearly. You can save the rotating figure as an animated GIF, for use in presentations and web sites (*File | Save Animated GIF As*).



Overlay From Second Matrix

Individual variables in both the main and second matrix can be overlaid on ordinations. Categorical overlays are shown by different colors or symbols (not shown). Quantitative overlays are shown by making the size of the symbol proportional to the overlay variable. “Side scatterplots” are also shown. These simple, bivariate scatterplots show a variable in relation to score on a particular axis. The red line is the best linear fit. The blue line is an envelope built with a smoothing function.



Other Graph Types

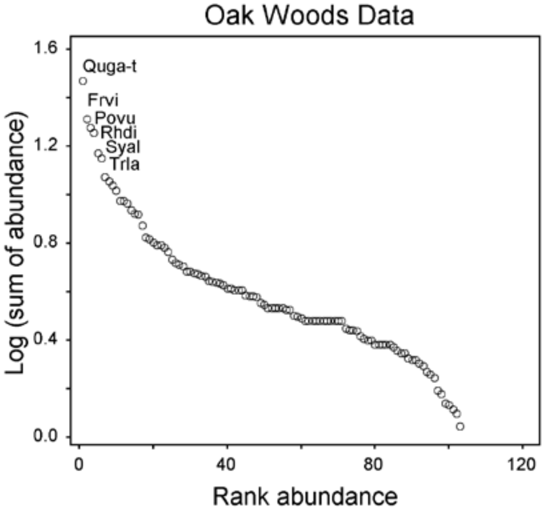
The next few pages illustrate additional tools in PC-ORD for graphically exploring your data.

Dominance Curves

Dominance curves, also known as dominance-diversity curves, are used to study the distribution of abundance among species in a data set. These curves are interesting descriptors of communities in their own right, but have also been used to inform ecological theory.

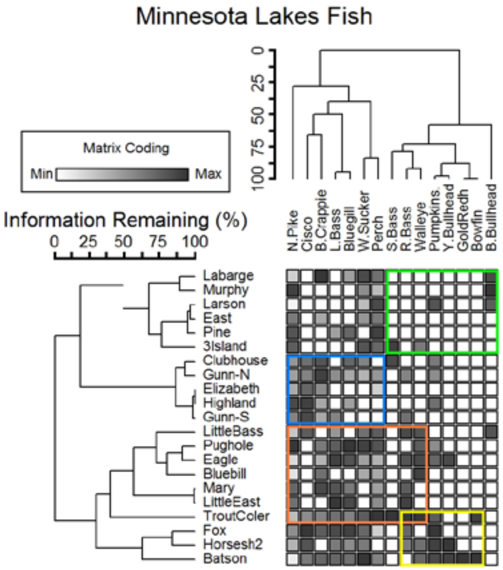
Each point is a species plotted as the log of total abundance against the rank order of abundance.

Another use of dominance curves is to observe the effect of data transformations and relativizations on the relative abundance of species, an important consideration for distance-based analyses. See examples on p. 72 in McCune and Grace (2002), *Analysis of Ecological Communities*.



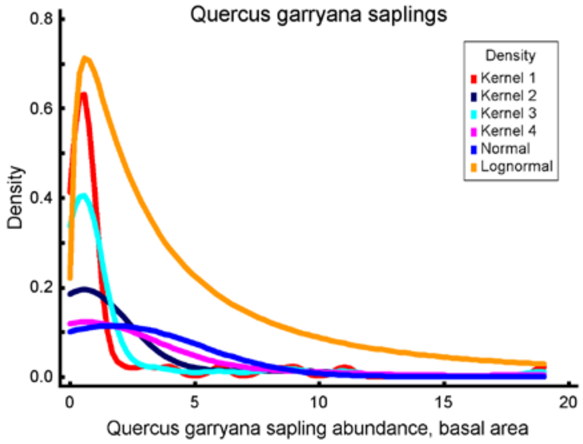
Two-way Cluster Analysis

You can perform cluster analysis of rows and columns of a single matrix (*Groups* | *Two-way Cluster Analysis*). The matrix of shaded squares represents the sample unit × species matrix, while the dendrograms show the clustering. The intensity of the shading is proportional to the abundance of the species. The axes show information remaining for sample unit (left) and species (top) clustering.



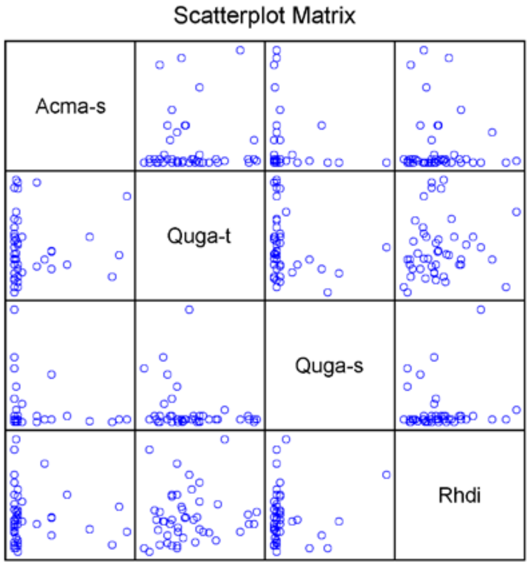
Distributions

You can represent frequency distributions of continuous or discrete variables with smooth density estimates. This is not density in the sense of numbers per unit area or volume, but rather the density of our observations along a continuous scale. We offer a selection of methods for representing your observed data, along with some classic distributions for comparison to your data; for example, normal, lognormal, poisson, binomial, and negative binomial. We use the "method of moments," calculating the parameter estimates (moments) from the observed data, then inserting them as parameters into the theoretical distributions.



Scatterplot Matrix

A scatterplot matrix is one of the simplest but most effective ways to assess whether or not your variables are linearly related and to evaluate the need for data transformation. *Graph* | *Scatterplot Matrix* produces a matrix of simple scatterplots in a simplified format. Use a picklist to choose from variables in both the main and second matrices. This example shows all pairwise scatterplots among the variables Acma-s, Quga-t, Quga-s, and Rhdi.

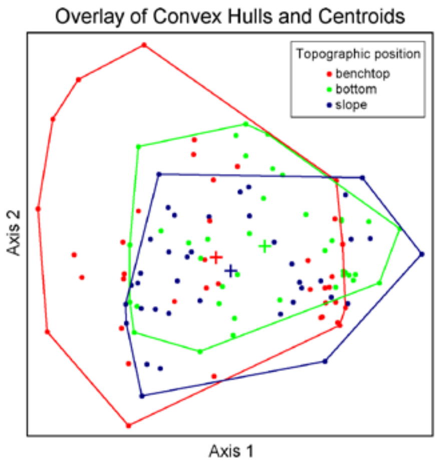


Convex Hulls and Group Centroid Overlays

PC-ORD 7 provides two additional overlays for ordinations (in addition to color-coding, symbol coding, joint plots, biplots, grids, and vectors): convex hulls and group centroids. Both apply to groups of sample units (rows), and are illustrated below.

A convex hull uses a polygon to enclose all of the points in a group. The shapes are “convex” because the interior angles of the polygon are always ≤ 180°. The purpose of this overlay is to show the outline of a group in an ordination or a scatterplot, helping the viewer to discern if and how groups are separated or overlap.

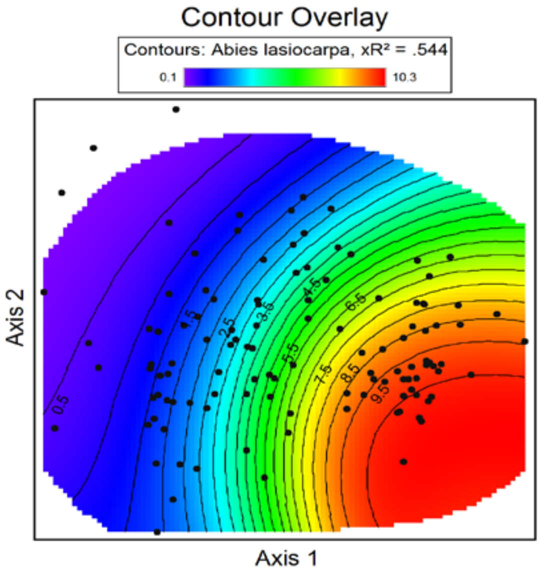
The centroid of a cloud of points on an ordination is the average position of those points in the ordination space (shown as a large “+” in the figure). If your data are subdivided into groups you can display the centroid of each of those groups in the ordination space.



Contour Overlay

A contour overlay on an ordination is essentially a 3D response surface. The contours and shading describe the overlay variable in relation to two ordination axes. Contouring can be displayed with several methods: contour lines, a gradation of color, or a grayscale. Or you can use a combination of both contour lines and shading (or color), as shown.

Think of the data points in the ordination as benchmarks on the landscape. The 2D ordination is the map. The benchmarks are the known points. The contours interpolate between the benchmarks. To calculate fit we get the estimated values on the smooth surface for the benchmarks. We then sum the squared differences between the observed values and the estimated values, as a basis for calculating the degree of fit, as measured by R^2.

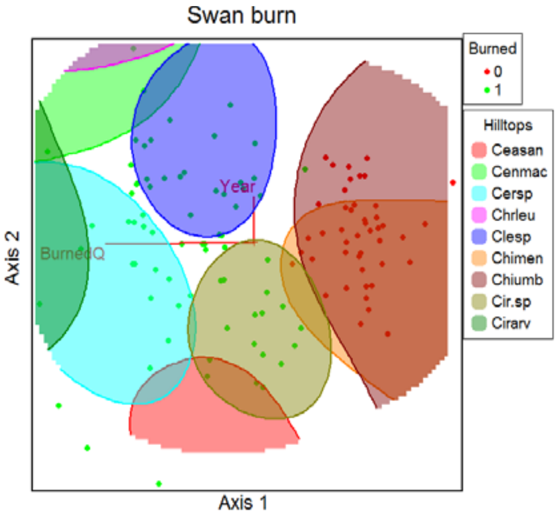


Hilltop Plot

A hilltop plot shows more than one nonlinear response surface at a time as an overlay on a single ordination. This enables simultaneous display of non-linear community–trait–environment associations.

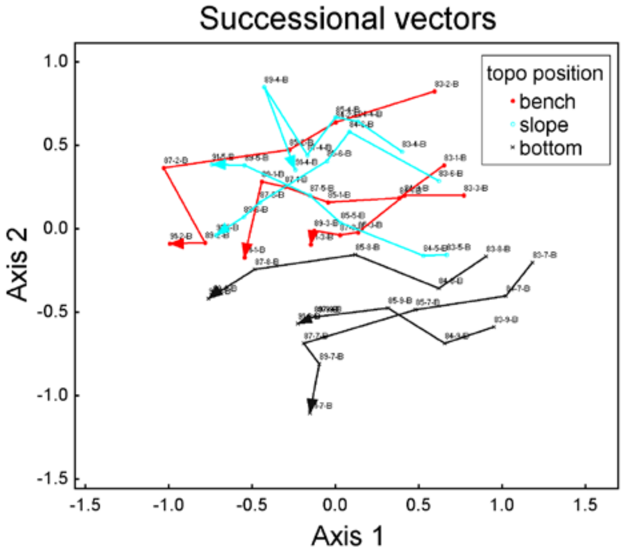
For each selected overlay variable, we trace a particular contour that is specified as a percentage of that variable's range. Each contained area is a "hilltop", and multiple partially transparent hilltops are superimposed on one ordination. The resulting diagram shows the maxima of many nonlinear overlay variables.

The main difference between hilltops and contour plots is that contour plots can only show one variable at a time, while hilltops can show multiple variables on the same ordination. This comes at a loss of information in that most of the contour plot is discarded when converting to a hilltop.



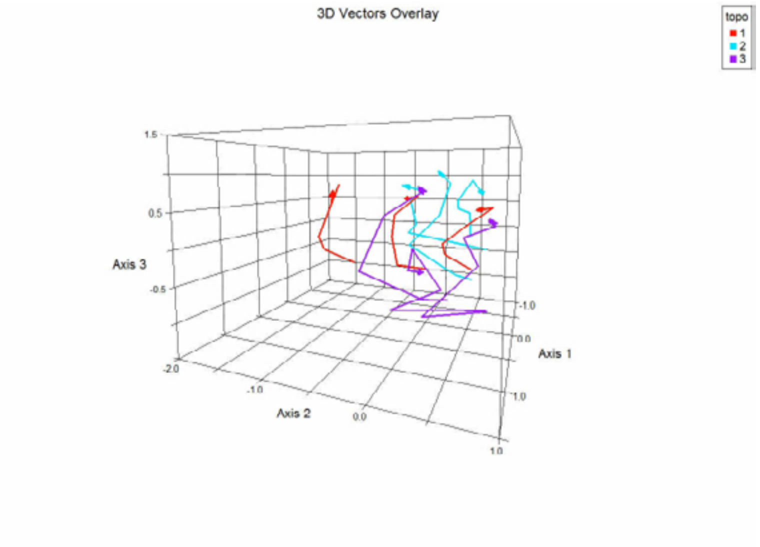
Successional Vectors

Vectors can be used whenever a number of sample units have been followed through time. They show the trajectory of communities in species space. They can also be used to indicate a directional change due to any other factor such as the shift between treatment and control in paired-sample designs. But the most common use for this option is for successional vectors or other temporal vectors. For example, say you recorded species abundance in a set of plots, revisiting those plots every year. By connecting the data points in temporal sequence, you can see the "trajectory" of each sample unit in relation to the others. Vectors can also be used for data with spatial rather than temporal series. In this case the vectors represent spatial differences rather than temporal changes.



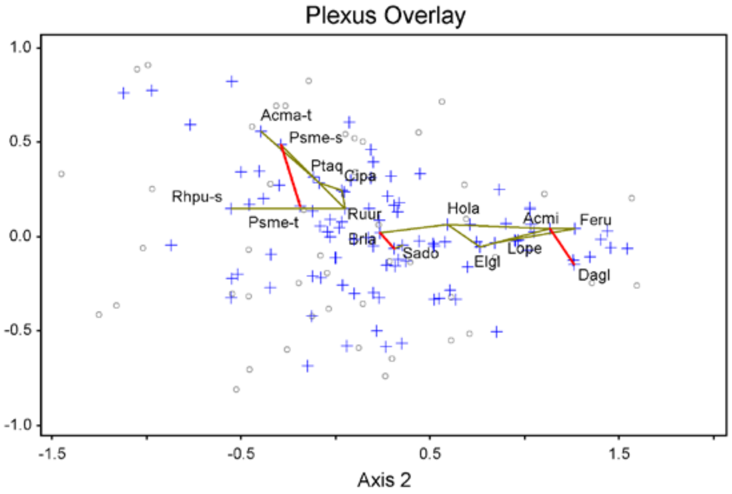
Overlays in Rotating 3D

Many of the ordination overlays are available in both 2D and 3D representations. The following example shows a rotating *.gif of temporal vectors, similar to the previous page but in 3D. Note that when viewed from some angles, the three topographic positions (color coded) are clearly separate. (If this figure is not rotating, then your viewer does not support this rotating GIF. You should, however, be able to embed rotating gifs in PowerPoint presentations and pdfs.)



Plexus Diagrams

A species plexus overlay shows a network of positive associations among species where the positions of the points are controlled by ordination results. A plexus can be overlaid on any ordination that includes scores for the species (columns). Lines connect species ("+") with strong positive associations, while negative associations or non-associations are ignored. In the diagram below, strong positive associations are shown by red lines, while weaker positive associations are shown by olive lines. You set the criteria for "strong" and "weak". In this example sample units are shown by circles.



A Decision Tree for Beginners

PC-ORD includes a decision tree (*Advisor* | *Wizard*) to help you decide how to analyze your data. You can also use the wizard as a self-teaching tool. We attempt to deal only with relatively common data analysis problems that you are likely to encounter with ecological community data. In practice, many data sets have peculiarities or complexities that do not fit well into this decision tree. Strive for understanding and experience beyond what is captured in the decision tree. Think creatively about the best approach to your particular question and data. Remember to think beyond the range of tools included in the decision tree, for example, "is this question best answered with a univariate method?" or "Is this problem best suited to a habitat model, where we have a single species response variable in relationship to multiple predictors?" Most simple univariate problems can be adequately addressed with the major statistical software packages. For habitat modeling, consider HyperNiche (see www.hyperniche.com), particularly if you like the interface in PC-ORD and our emphasis on tools that deal well with nonlinear responses along ecological gradients and interactions among ecological factors.

The decision tree consists of a set of nodes, all connected to a starting point, the root node. Your answers to questions about the purpose of the analysis or the nature of the data link a node to other nodes.

Nodes are of two kinds, **Question-Answer** nodes, and **Conclusion-Action** nodes. Question-Answer nodes navigate you through the tree. Conclusion-Action nodes are endpoints on the tree. Conclusion-Action nodes state the conclusion, followed by one or more actions: an option to run an analysis, a suggestion for an analysis (which may or may not be part of PC-ORD), or some other recommendation.

Batch Commands for Advanced Users

You can **automate a series of commands** to perform repetitive tasks or to apply **resampling techniques** in your analyses. For example, you may wish to process a series of data sets in an identical way, changing only the input files. Or, you might want to use **bootstrap resampling to calculate a confidence interval** for a statistic of particular interest. This requires taking a random sample of a data set, performing an analysis, then repeating those steps many times.

A **batch command** is an action item selected from the PC-ORD menu system, along with the options chosen in any subsequent dialog boxes. A **batch set** is a sequence of batch commands. A **loop** is a programming structure that repeats itself a set number of times or until some criterion is met. Loops may be nested within other loops. An **iteration** is one cycle of a loop. To **glean** statistics from a result file is to scan through it, pulling out key statistics and tabulating them. This is useful for repeated runs of a specific analysis with a loop, for example calculating confidence intervals based on bootstrap resampling of a data set.

The steps to create and execute a batch of commands are as follows:

1. Plan the sequence of operations and any loop structure.
2. Record each component action.
3. Save each command with a descriptive name.
4. After all component commands have been recorded, create a set of commands with *File | New Batch Set* and drag commands into the set.
5. Add the loop structure(s) if desired.
6. When the batch is complete, save it as a named file (*Save As Batch Se*t), then click *Run*.