FATHOM
for
Matlab

A Matlab Toolbox for Multivariate Ecological & Oceanographic Data Analysis

by

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`Introduction` *FATHOM Toolbox for Matlab*

Description

FATHOM: Matlab Toolbox for Ecological & Oceanographic Data Analysis

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References

Jones, D. L. 2002. Users manual for FATHOM: a MATLAB toolbox for Multivariate Ecological & Oceanographic Data Analysis. Available from:

`http://www.rsmas.miami.edu/personal/djones/`

Details

The FATHOM Toolbox is a collection of Matlab functions and scripts I've written for my everyday use. I'm releasing them to the public in order to encourage the sharing of code and prevent duplication of effort. If you find this toolbox useful, drop me a line. I'd also appreciate bug reports and suggestions for improvements.

While I've made every attempt to write functions that provide accurate and precise results, the functions in this toolbox are provided as is, with no guarantees and are only intended for non-commercial use. These routines have been developed and tested under Matlab 6.1 (Release 12.1) under Windows 2000.

Please note that this users manual is currently under construction and is presently incomplete.

Note

There is currently only one issue related to installation that you need to be aware of:

f_nmds: NonMetric Multidimensional Scaling

This function calls Mark Steyver's NMDS routine. For it to work you must install his toolbox from:

`http://www-psych.stanford.edu/ msteyver/programs_data/mdszip.zip`

I've been able to obtain better results with this program by editing Steyver's `mds.m` file and changing

```
randn( ’state’,seed );
```

to

```
rand( 'state',seed );
```

This allows you to draw from *Uniformly distributed random numbers* for initial configurations rather than *Normally distributed random numbers*.

`f_anosim` *Analysis of Similarity*

Description

One-way Analysis of Similarity

Usage

```
[r,p] = f_anosim(xDis,grps,rank,iter,pw,plt)
```

Arguments

`xDis`	symmetric distance matrix
`grps`	row vector designating group membership for objects in xDis
`rank`	optionally rank distances in xDis (default = 1)
`iter`	# iterations for permutation test (default = 1000)
`pw`	do pairwise tests (default = 1)
`plt`	make diagnostic plot (default = 0)

Details

This function performs a multivariate ANOSIM by computing an unstandardized Mantel Statistic between an (optionally ranked) distance matrix and a model matrix; the model matrix is derived from a row vector designating group membership. Results are equivalent to Clarke's method. The permutation test permutes the rows/columns of the distance matrix `xDis`. Pairwise tests between each group are also optionally run. Permutation tests are based on the complete permutation distribution when it is $<$ 5000, otherwise it is randomly sampled the number of times specified by `iter`.

ANOSIM assmumes that under the null hypothesis distances within groups are smaller than those between groups, thus significant differences can arise between groups having different dispersions but identical centroids. Diagnostic boxplots are provided as a way to check this and prevent Type I error.

Care must be taken when coding grouping factors (i.e., `grps` and `xDis` must be sorted ascending prior to running the function); see example below.

This program has been tested against Clarke's *Primer 5 for Windows* and gives the same results.

Value

The function returns the following values:

`r`	strength of relationship (ranges from -1 to 1)
`p`	permutation-based probability of no difference between groups

Author(s)

Dave Jones

References

Clarke, K. R. 1993. Non-parametric multivariate analyses of changes in community structure. Aust. J. Ecol. 18: 117-143.

Clarke, K. R. 2002. Personal Communication.

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam. (pp.552; 561-562)

See Also

`f_anosim2`, `f_npManova`, `f_mantel`, and `f_modelMatrix`

Examples

Load the file, `anosim.mat`, in the `data` folder. This data is from Gray et al. (1990) and ships with Clarke's *Primer* program. There is 1 response variable: `species`, representing abundances of 174 species (rows) from 39 collection sites (columns), and 1 factor, `grps`, a row vector specifying group membership (i.e. categories representing distance from the center of an oilfield).

```
>> load anosim.mat
>> species2 = f_transform(species,1); % square-root transform species abundances:
>> dis = f_braycurtis(species2); % Bray-Curtis symmetric distance matrix
>> [r,p] = f_anosim(dis,grps)

==================================================
         1-way ANOSIM RESULTS:
--------------------------------------------------
Groupings:
 1  1  1  1  1  1  2  2  2  2  2  2  2  2  2  2  3  3  3  3  3  3  3  3  3  3  3  3  4  4  4

Global Test:
  R = 0.5413  p = 0.0010 (1000 of 408316439225392430000 possible perms)

Pair-Wise Tests:
```

```
  1  2: R = 0.5539  p = 0.0020 (1000 of 8008 possible perms)
  1  3: R = 0.8200  p = 0.0010 (1000 of 18564 possible perms)
  1  4: R = 0.9277  p = 0.0010 (1000 of 12376 possible perms)
  2  3: R = 0.1596  p = 0.0890 (1000 of 646646 possible perms)
  2  4: R = 0.7635  p = 0.0010 (1000 of 352716 possible perms)
  3  4: R = 0.5584  p = 0.0010 (1000 of 1352078 possible perms)

==================================================
r =     0.54128
p =     0.001
```

Gray, J. S., K. R. Clarke, R. M. Warwick, & G. Hobbs. 1990. Detection of initial effects of pollution on marine benthos: an example from the Ekofisk and Eldfisk oilfields, North Sea. Mar. Ecol. Prog. Ser. 66:285–299.

`f_anosim2`	*Two-way Analysis of Similarity*

Description

Two-way crossed ANOSIM with no replication

Usage

```
[r,p] = f_anosim2(dis,fac1,fac2,{rank},iter)
```

Arguments

`dis`	symmetric distance matrix
`fac1`	vector of integers (or chars) specifying levels of factor 1 for rows/cols of distance matrix
`fac2`	vector of integers (or chars) specifying levels of factor 2 for rows/cols of distance matrix
`rank`	optionally rank distances in xDis (default = 1)
`iter`	# iterations for permutatin test (default = 1000)

Details

This program handles missing data in a 2-way layout design that would occur when one (or more) of the treatment levels is missing from a block. The one-tailed permutation-based significance test permutes the treatment levels *separately* within each block.

This program has been tested against Clarke's *Primer 5 for Windows* and gives the same results.

Please be patient when running this program with large datasets and/or high values for `iter`.

Value

The function returns the following values:

`r`	strength of treatment effect (averaged across all blocks)
`p`	permutation-based significance test

Note

`fac1` and `fac2` must be equal to row/col size of `dis`.

Author(s)

Dave Jones

References

Clarke, K. R. & R. M. Warwick. 1994. Similarity-based testing for community pattern: the two-way layout with no replication. Mar. Bio. 118: 167-176.

See Also

`f_anosim`, `f_npManova`, `f_mantel`, and `f_modelMatrix`

Examples

For an example of a *Two-Way ANOSIM with no replication* load the file, `anosim2.mat`, in the `data` folder. This data is from Warwick (1971) and ships with Clarke's *PRIMER* program. There is 1 response variable, `dis`, representing a Bray-Curtis symmetric distance matrix from 4th root transformed species abundances, and 2 factors: `site` and `time`.

```
>> load anosim2.mat
>> tic;[r,p] = f_anosim2(dis,site,time,1,1000);toc
(Please wait...running 1000 permutations for each of 2 factors.)


============================================================
Results of 2-way crossed ANOSIM (no replication):
------------------------------------------------------------

Strength of 'TIME' effect (averaged across all 'SITE' blocks):
  R = 0.0555 p = 0.2190 (1000 iterations)
  # permuted statistics greater than or equal to R = 218

Strength of 'SITE' effect (averaged across all 'TIME' blocks):
  R = 0.3574 p = 0.0010 (1000 iterations)
  # permuted statistics greater than or equal to R = 0

============================================================

elapsed_time = 121.74
```

Warwick, R. M. 1971. Nematode associations in the Exe estuary. J. Mar. Biol. Ass. U.K. 51:439–454

`f_bartlett` *Bartlett's Test*

Description

Bartlett's Test for Homogeneity of Variances

Usage

```
[pval, chisq, df] = f_bartlett(x)
```

Arguments

`x`	column vector of input data
`grps`	column vector specifying group membership

Details

Under the null hypothesis of equal variances, the test statistic `chisq` approximately follows a chi-square distribution with `df` degrees of freedom; `pval` is the p-value (1 minus the CDF of this distribution at `chisq`) of the test.

This program has been tested against the SAS code `bartlett.sas` and gives similar results.

Value

The function returns the following values:

`pval`	probability that the null hypothesis is true
`chisq`	test statistic
`df`	degrees of freedom

Author(s)

Original Octave code `bartlett_test.m` by KH ⟨Kurt.Hornik@ci.tuwien.ac.at⟩. Ported to Matlab by Dave Jones.

Examples

Load the file, `bartlett.mat`, in the `data` folder.

```
>> load bartlett.mat
>> [pval,chisq,df] = f_bartlett(x,grps)
pval =
     0.034381
chisq =
       8.6464
df =
     3
```

f_bioenv *Biotic - Environmental Correlation*

Description

Correlation of primary (biotic) symmetric distance matrix with all possible subsets of secondary (environmental) matrix.

Usage

```
[res,resLabels] = f_bioenv(dis,matrix,labels,metric,trim,out)
```

Arguments

`dis`	symmetric distance matrix
`matrix`	2°matrix (rows = variables, cols = samples)
`labels`	cell array of variable labels of 2°matrix; e.g., `labels = {'temp' 'sal' 'depth' 'O2'}`
`metric`	distance metric to use for 2°matrix; 0 = Euclidean (default); 1 = Bray-Curtis
`trim`	return only this many of the top Rho's per subset size class; 0 = return all (default)
`out`	send results to screen (= 1, default) or cell array with filename; e.g., `out = {'results.txt'}`

Value

The function returns the following values:

`res`	cell array, 1st column = Rho, 2nd:end are variable indices
`resLabels`	cell array of variable names

Note

This function requires `combnk.m` from the *Matlab Statistics Toolbox.* The code could be modified to utilize the freely available `choosenk.m` instead.

For `out`, an existing file with the same name as specified will be **deleted**. Tabulated results are also sent to the screen or file, depending on the value of `out`.

The # of rows of `dis` must equal the # columns of `matrix`.

Author(s)

Dave Jones

References

Clarke,K. R. & M. Ainsworth. 1993. A method of linking multivariate community structure to environmental variables. Mar. Ecol. Prog. Ser. 92:205-219.

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam. xv + 853 pp.

See Also

`f_braycurtis`, `f_euclid`

Examples

Load the file, `spiders.mat`, in the `data` folder. This is data from van der Aart & Smeenk-Enserink (1975) and is Hunting spider abundances for 12 species (`spiders`) taken from 28 sites (`site_labels`) and associated environmental data (`env`).

```
>> load spiders.mat
>> spiders2 = f_transform(spiders',3)'; % log-transform abundances
>> dis = f_brayCurtis(spiders2'); % Bray-Curtis dissimilarity matrix
>> [res,resLabels] = f_bioenv(dis,env',env_labels,0,5,1);

There are 63 possible subsets of 6 variables
  Processing    6 subsets of   1 variables
  Processing   15 subsets of   2 variables
  Processing   20 subsets of   3 variables
  Processing   15 subsets of   4 variables
  Processing    6 subsets of   5 variables
  Processing    1 subsets of   6 variables

 ==========================================
 Rho    Variables
 ==========================================

 1
 0.7037 water
 0.5486 light
 0.5197 sand
 0.4962 cover
 0.4097 twigs
 0.2611 herbs
```

```
2
0.7591 twigs water
0.7578 light water
0.7115 light sand
0.7073 cover water
0.7018 sand water

3
0.8110 sand twigs water
0.7870 light sand water
0.7561 cover light sand
0.7505 cover sand water
0.7496 cover twigs water

4
0.8159 cover sand twigs water
0.7995 cover light sand water
0.7982 light sand twigs water
0.7845 cover herbs sand water
0.7751 herbs light sand water

5
0.8065 cover light sand twigs water
0.8061 cover herbs light sand water
0.8047 cover herbs sand twigs water
0.7723 herbs light sand twigs water
0.7270 cover herbs light twigs water

6
0.7996 cover herbs light sand twigs water
```

van der Aart, P. J. M. & N. Smeenk-Enserink. 1975. Correlations between distributions of hunting spiders (Lycosidae, Ctenidae) and environmental characteristics in a dune area. Netherlands Journal of Zoology 25: 1-45.

`f_biplotEnv2` *Biplot for 2-d Ordination*

Description

Create a distance biplot consisting of a 2-d ordination with environmental correlation vectors.

Usage

```
[biplot,Rsq] = f_biplotEnv2(crds,env,special,iter,scale,offset,sLabels)
```

Arguments

`crds`	matrix of ordination coordinates (rows = sites; cols = dimensions)
`env`	matrix of (transformed) environmental variables (rows = sites, cols = variables)
`special`	type of correlation; 0 = Pearson's, 1 = Spearman's (default)
`iter`	# of iterations for permutation test (default = 0)
`scale`	scaling factor for `env` vectors (default = 1)
`offset`	offset of labels in plot (default = 0)
`sLabels`	cell array of vector labels; if empty they are autocreated e.g., `sLabels = {'sal' 'tmp' 'elev'}`

Value

The function returns the following values:

`biplot`	2 column matrix sepcifying x-y coordinates of endpoints for scaled `env` vectors to overlay on ordination
`Rsq`	column matrix of correlation with each axis (a permutation test is performed when `iter`>0)

Author(s)

Dave Jones

References

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam. xv + 853 pp. (page 586)

Legendre, P. 2001. (personal communication).

See Also

`f_biplotEnv3`, `f_biplotSpecies`, `f_vectorfit`

`f_biplotEnv3` *Biplot for 3-d Ordination*

Description

Create a distance biplot consisting of a 3-d ordination with environmental correlation vectors.

Usage

```
[biplot,Rsq] = f_biplotEnv3(crds,env,special,iter,scale,offset,sLabels,plotflag,minP)
```

Arguments

`crds`	matrix of ordination coordinates (rows = sites; cols = dimensions)
`env`	matrix of (transformed) environmental variables (rows = sites, cols = variables)
`special`	type of correlation; 0 = Pearson's, 1 = Spearman's (default)
`iter`	# of iterations for permutation test (default = 0)
`scale`	scaling factor for `env` vectors (default = 1)
`offset`	offset of labels in plot (default = 0)
`sLabels`	cell array of vector labels; if empty they are autocreated e.g., `sLabels = {'sal' 'tmp' 'elev'}`
`minP`	if p-value of correlation > minP, then correlation is NOT used (default = 0.05)

Value

The function returns the following values:

`biplot`	3 column matrix sepcifying xyz coordinates of endpoints for scaled `env` vectors to overlay on ordination
`Rsq`	column matrix of correlation with each axis (permutation-based significance provided when `iter`>0)

Author(s)

Dave Jones

References

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam. xv + 853 pp. (page 586)

Legendre, P. 2001. (personal communication).

See Also

`f_biplotEnv2`, `f_biplotSpecies`, `f_vectorfit`

`f_biplotSpecies` *Species Biplot*

Description

Create species vectors for ordination distance biplot.

Usage

```
[biplot,rsq] = f_biplotSpecies(crds,species,special,iter,scale,offset,sLabels);
```

Arguments

`crds`	matrix of ordination coordinates (rows = sites; cols = eigenvectors or dimensions)
`species`	matrix of (transformed) species abundances (rows = sites, cols = variables)
`special`	type of correlation; 0 = Pearson's (default), 1 = Spearman's
`iter`	# of iterations for permutation test (default = 0)
`scale`	scaling factor for `species` vectors (default = 1)
`offset`	offset of labels in plot (default = 0)
`sLabels`	cell array of species labels (if empty autocreate) e.g., `sLabels = {'sp1' 'sp2' 'sp3'}`

Value

The function returns the following values:

`biplot`	2 column matrix sepcifying x-y coordinates of endpoints for scaled `species` vectors to overlay on ordination
`Rsq`	column matrix of correlation with each axis (permutation-based significance provided when `iter`>0)

Author(s)

Dave Jones

References

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam. xv + 853 pp.

Legendre, P. & E. Gallagher. Ecologically meaningful transformations for ordination biplots of species data. Oecology 129: 271–280.

See Also

`f_biplotEnv2`, `f_biplotEnv3`, `f_vectorfit`

`f_braycurtis` *Bray–Curtis Dissimilarity*

Description

This functions calculates a Bray-Curtis symmetric dissimilarity matrix from an input data matrix specifying species abundances per sample site.

Usage

```
dist = f_braycurtis(X);
```

Arguments

`X`	species x site data matrix

Details

Value

The function returns the following values:

`dist`	symmetric dissimilarity matrix

Note

The input data matrix should be codes as species (rows) versus sites (columns). An nxn symmetric dissimilarity matrix will be returned where n is the number of sites.

Author(s)

```
=====================================================================
       Copyright (c) 1997 B. Planque - Sir Alister Hardy Foundation
       for Ocean Science <bp@wpo.nerc.ac.uk>
       Permission is granted to modify and re-distribute this code
       in any manner as long as this notice is preserved.
       All standard disclaimers apply.
=====================================================================
```

Slightly modified by Dave Jones after `distance.m` in the *EDAT Toolbox* to only calculate a Bray–Curtis distance matrix between columns.

See Also

`f_euclid`

`f_brokenstick` *Broken-Stick model*

Description

This function is used to determine the # of significant ordination dimensions via the *Broken-Stick* model.

Usage

```
f_brokenstick(nvars)
```

Arguments

`nvars`	# of variables (e.g., sample sites)

Value

The function returns the following values:

`varExplained`	% variance explained

Author(s)

Original Matlab code, `brokestk.m`, by R. E. Strauss, modified by Dave Jones.

References

Frontier, S. 1976. Etude de la decroissance des valeurs propres dans une analyze en composantes principales: comparison avec le modele de baton brise. J. Exp. Mar. Biol. Ecol. 25:67–75.

Jackson, D. A. 1993. Stopping rules in principal components analysis: a comparison of heuristial and statistical approaches. Ecology 74:2204–2214.

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam. xv + 853 pp. (p. 410)

See Also

`f_pca`

`f_cap`	*Canonical Analysis of PCoA*

Description

The function performs a Canonical Analysis of Principal Coordinates using any distance (dissimilarity) matrix.

Usage

```
[crds,trc,ccor,H,p1,p2,centroids] = f_cva(yDis,x,rank,iter,plt,verb)
```

Arguments

`yDis`	square symmetric distance matrix derived from response variables
`x`	(1) vector of integers specifying group membership for objects in `yDis`, (2) ANOVA design matrix specifid by dummy coding, or (3) matrix of explanatory variables (rows = observations, cols = variables)
`rank`	optionally rank distances in `yDis` (default = 0)
`iter`	# iterations for permutation test (default = 0)
`plt`	optionally plot results (default = 1)
`verb`	optionally send results to display (default = 1)

Value

The function returns the following values:

`crds`	coordinates of canonical axes (= Qstar)
`trc`	trace statistic
`ccor`	canonical eigenvalues (1st value is greatest root statistic)
`p1`	randomized probability of trace statistic
`p2`	randomized probability of greatest root statistic
`centroids`	centroids of groups defined in `x`

Note

This program performs nonparametric *Multiple Discriminant Analysis* on **any** symmetric distance matrix when the input for `x` is (1) a vector specifying group membership. It performs generalized *Canonical Variates Analysis* when `x` is (2) an ANOVA design matrix or (3) a matrix of explanatory variables.

Use `f_designMatrix` to create an ANOVA design matrix for input as `x`; the matrix should be full rank (not singular) and do **not** include an intercept term (a column of all 1's).

The program asks the user to specify how many axes of Q to retain for the analysis (m). Examine the `EIGENVALUES` and `% VARIATION EXPLAINED` output in the command window and try to include as much information in Q as possible with as few axes as possible.

This program has been tested against the numerical example in Legendre & Legendre (1998:p.626) and provides similar output. The `% variation explained` for each canonical axis, calculated by `f_cap`, are almost identical to that computed by `manova1.m` in the *Matlab Statistical Toolbox* (version 3) for the `Iris` data.

This program requires `ortha.m` by Andrew Knyazev <knyazev@na-net.ornl.gov> & Rico Argentati, which is included the present toolbox and available from:

`http://www-math.cudenver.edu/ aknyazev/software/MATLAB/`

Author(s)

Dave Jones

References

Anderson, M. J. 2002. CAP: a FORTRAN program for canonical analysis of principal coordinates. Dept. of Statistics University of Auckland. Available from:

`http://www.stat.auckland.ac.nz/PEOPLE/marti/`

Anderson, M. J. & T. J. Willis. 2002. Canonical analysis of principal coordinates: and ecologically meaningful approach for constrained ordination. Ecology (In Press).

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam. pp.616–631.

See Also

`f_npManova`, `f_anosim`, `f_anosim2`, `f_mantel`, `f_designMatrix`

`f_mregress` *Multiple Linear Regression*

Description

This program performs Multiple Linear Regression using Least Squares Estimation via Matlab's QR factorization.

Usage

```
[F,t,R2,yfit,b,resid] = f_mregress(x,y,iter,perm,verb);
```

Arguments

`x`	matrix of independent variables (column-wise)
`y`	column vector of dependent variable
`iter`	# of iterations for permutation test (default = 0)
`perm`	permute residuals instead of raw data (default = 1)
`verb`	verbose output of results to display (default = 1)

Details

This function solves the equation such that:

`y = b(0) + b(1)*(X(:,1)) + b(2)*(X(:,2))...+ b(k)*(X(:,k))`,

where k = # of predictor variables.

Value

The function returns the following values (`F` and `t` are structures):

`F.stat`	F-statistic
`F.para_p`	parametric p-value for 1-tailed test of F
`F.perm_p`	permutation p-value for 1-tailed test of F
`t.stat`	t-statistic for partial regression coefficients
`t.para_p`	parametric p-value for 1-tailed test of t
`t.perm_p`	permutation p-value for 1-tailed test of t
`R2`	coefficient of multiple determination (R^2, goodness-of-fit)
`yfit`	fitted values of y
`b`	regression coefficients (1st value is the y-intercept)
`resid`	residuals

Note

The regression coefficients are computed using Least Squares Estimation (via the \ operator), which is preferred over methods that require taking the inverse of a matrix. R2, the coefficient of multiple determination, is a measure of goodness-of-fit and gives the proportion of variance of Y explained by X.

Parametric (and optional permutation) tests of significance for the F- and t-statistics are performed. The permutation test is conducted when `iter` > 0 and allows for permutation of either the raw data or the residuals of the full regression model. Permutation of the raw data involves random permutation of the rows (= observations) of Y relative to the rows of X. The permutation test is preferred over the parametric test when the data are non-normal. Permutation of the residuals (vs. the raw data) is preferred when data have extreme values (i.e., outliers).

This function has been tested against Legendre & Casgrain's `regressn.exe` program and gives similar output.

Calculation of parametric p-values for `F` and `t` require `fpdf` and `tcdf` from the *Matlab Statistics Toolbox*; these could be replaced by `df` and `dt` from the free *Stixbox Toolbox*.

Author(s)

Dave Jones with help from `news://comp.soft-sys.matlab`

References

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam. xv + 853 pp. (pp. 517, 606-612)

Legendre, P. 2002. Program for multiple linear regression (ordinary or through the origin) with permutation test - User's notes. Depart. of Biological Sciences, University of Montreal. 11 pages. Available from: `http://www.fas.umontreal.ca/biol/legendre/`

Neter, J., W. Wasserman, & M. H. Kutner. 1989. Applied linear regression models. 2nd Edition. Richard D. Irwin, Inc. Homewood, IL.

Sokal, R. R. & F. J. Rohlf. 1995. Biometry - The principles and practice of statistics in bioligical research. 3rd ed. W. H. Freeman, New York. xix + 887 pp.

Examples

The example dataset, `mregress.mat`, can be found in the *data* folder and is an excerpt from Table 16.1 of Sokal & Rohlf (1995).

```
>> load mregress.mat
>> tic;
>> [F,t,yfit,coefs,resid] = f_mregress(x,y,10000);
>> toc;
```

```
Permuting the data 9999 times...
=====================================================================
 Multiple Linear Regression via QR Factorization:
---------------------------------------------------------------------
R2            F-stat        parametric-p  permutation-p
---------------------------------------------------------------------
0.51611       20.26553      0.00000       0.00010
---------------------------------------------------------------------

---------------------------------------------------------------------
Variable      b             t-stat        parametric-p  permutation-p
---------------------------------------------------------------------
    intercept 77.23671      3.59122       0.00045       0.00060
            1 -1.04805      -2.80777      0.00384       0.00220
            2 0.02430       5.07607       0.00000       0.00050
---------------------------------------------------------------------

# permutations of residuals =  9999
All significance tests are One-Tailed
=====================================================================
elapsed_time =
       57.092
```

`f_nmds` *Non-metric Multidimensional Scaling*

Description

This function is used to run Mark Steyvers' Non-metric Multidimensional Scaling program.

Usage

```
config = f_nmds(dist,ndims,initial,plotflag,maxiter,conv,rotate);
```

Arguments

`dist`	symmetric dissimilarity matrix
`ndims`	number of dimensions of solution (default = 2)
`initial`	initial config: 1 = Torgeson-Young scaling (default); 0 = random
`plotflag`	plot results (default =1)
`maxiter`	max # iterations (default = 50)
`conv`	convergence criterion (default = 0.001)
`rotate`	rotate final configuration to Principal Coordinates (default = 1)

Value

The function returns the following values (`config` is a structure):

`config.mds`	configuration of solution in (`ndims`) dimensions
`config.stress`	final stress of solution
`config.dim`	# dimensions of solution
`config.rsq`	Mantel statistic comparing fitted distances with original dissimilarities

Note

This program requires the *Matlab Optimization Toolbox* and Mark Steyvers' Nonmetric Scaling Toolbox, available from:

`http://www-psych.stanford.edu/~msteyver/programs\us data/mdszip.zip`

I've been able to obtain best results with this program by editing Steyver's `mds.m` file and changing `randn( 'state',seed )` to `rand( 'state',seed )`. This allows you to draw from *uniformly* distributed random numbers for initial configurations rather than *normally* distributed random numbers.

Author(s)

Modified after Mark Steyvers' original Matlab code, `domds.m`, by Dave Jones. Added support for variable random seed, rotate to PCA, Mantel statistic, and formatting of output.

See Also

`f_pcoa`, `f_pca`

`f_npManova` *Nonparametric MANOVA*

Description

This program performs a nonparametric, permutation-based MANOVA on any symmetric distance (or dissimilarity) matrix.

Usage

```
result = f_npManova(yDis,x,type,rank,iter,pw,verb)
```

Arguments

`yDis`	square symmetric distance matrix derived from response variable(s)
`x`	matrix of integers specifying group membership for objects in yDis (column-wise) or a matrix of explanatory variables
`type`	x specifies group membership or factor levels (default = 0); x is a matrix of explanatory variables (=1)
`rank`	optionally rank distances in yDis (default = 0)
`iter`	# iterations for permutation test (default = 0)
`verb`	optionally send results to display (default = 0)

Details

The permutation test in this program currently only supports permutation of the raw data.

Value

This function returns the following values (`result` is a structure):

`result.so`	source of variation
`result.df`	degrees of freedom
`result.SS`	sum of squares
`result.MS`	mean square
`result.F`	F-statistics
`result.p`	permutation-based significance probabilities

Note

Special care must be taken when coding levels of nested factors, i.e. treatment levels of a nested factor must not be **repeated** across different levels of the main factor. For example use: `main factor = [1 1 1 2 2 2 3 3 3]'` `nested factor = [1 2 3 4 5 6 7 8 9]'`

instead of: `nested factor = [1 2 3 1 2 3 1 2 3]'`

More examples can be found in Appendix A.

This program takes a regression approach to ANOVA using the General Linear Model (GLM) and constructs F-ratios using the **unrestricted** form of the model. The F-ratios used for each type of test are provided in Appendix B of the User's Manual. Some of these differ somewhat from those used in textbook examples, especially for balanced, mixed-model designs, but are the same as those used in most computer programs that use GLM (e.g., SAS and MINITAB).

To perform a classical (M)ANOVA use a symmetric Euclidean distance matrix as input for the response variable. The real power of this function, however, comes from its ability to use, say, a Bray-Curtis distance matrix derived from species abundances from a community ecology study.

After determining a significant factor effect, you may wish to use f_npManovaPW to perform *a posteriori* multiple comparison tests.

Author(s)

Dave Jones

References

Anderson, M. J. 2002. DISTML v.2: a FORTRAN computer program to calculate a distance-based multivariate analysis for a linear model. Dept. of Statistics University of Auckland. Available from:

`http://www.stat.auckland.ac.nz/PEOPLE/marti/`

Anderson, M. J. 2000. NPMANOVA: a FORTRAN computer program for non-parametric multivariate analysis of variance (for any two-factor ANOVA design) using permutation tests. Dept. of Statistics, University of Auckland. Available from:

`http://www.stat.auckland.ac.nz/PEOPLE/marti/`

Anderson, M. J. 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecology 26: 32-46.

McArdle, B. H. & M. J. Anderson. 2001. Fitting multivariate models to community data: a comment on distance-based redundancy analysis. Ecology 290-297.

Sokal, R. R. & F. J. Rohlf. 1995. Biometry — The principles and practice of statistics in biological research. 3rd ed. W. H. Freeman, New York. xix + 887 pp.

Underwood, A. J. 1981. Techniques of analysis of variance in experimental marine biology and ecology. Oceanogr. Mar. Biol. Ann. Rev. 19: 513-605.

Zar, J. H. 1999. Biostatistical analysis. 4th ed. Prentice Hall, Upper Saddle River, NJ.

See Also

`f_npManovaPW`,`f_cap`, `f_anosim`, `f_anosim2`, Appendix A, Appendix B

Examples

For an example of a *One-Way Model I Anova with replication (balanced design)* load the file, `sr_09p5.mat`, in the `data` folder. This is data from Box 9.5 of Sokal & Rohlf (1995) and has 1 response variable, `age`, and 1 fixed factor: `clone`.

```
>> load sr_09p5.mat
>> dis = f_euclid(age’);
>> result = f_npManova(dis,[clone],0,0,1000,1);

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    ’Source’      ’df’    ’SS’           ’MS’           ’F’           ’p’
    ’factor 1’    [ 1]    [0.0064286]    [0.0064286]    [0.014063]    [0.872]
    ’residual’    [12]    [   5.4857]    [  0.45714]    [     NaN]    [  NaN]
    ’total’       [13]    [   5.4921]    [      NaN]    [     NaN]    [  NaN]

      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

See Appendix A for more examples.

`f_procrustes` *Procrustes Analysis*

Description

Generalized orthogonal Procrustes rotation of matrix Y to X, maximizing similarity and minimizing sum-of-squared distances.

Usage

```
[Xscl,Yrot,m2,resid,prob] = f_procrustes(X,Y,stnd,iter,plotflag)
```

Arguments

`X`	reference matrix (rows = observations, cols = variables)
`Y`	target matrix to rotate
`stnd`	standardize variables (default = 0)
`iter`	# iterations for permutation test (default = 0)
`plotflag`	plot fitted results (default = 0)

Details

This function performs an orthogonal least-squares Procrustes analysis on 2 rectangular data matrices (X & Y) by minimizing the sum-of-squared distances between corresponding elements of the 2 matrices. This is done by translating, scaling, mirroring, and rotating Y to fit X. The symmetric orthogonal Procrustes statistic (m^2) is a measure of goodness-of-fit of Y to X after rotation and provides the residual sum-of-squares, which varies from 0 to 1. Smaller values of m^2 indicate better fit.

Value

The function returns the following values (`resid` is a structure):

`Xscl`	centered & scaled form of X
`Yrot`	centered, scaled, & rotated form of Y
`m2`	symmetric Procrustes statistic, ranges from 0–1 (smaller values indicate better fit)
`resid`	structure of residuals ($*$.dim, $*$.obs, $*$.sse)
`prob`	permutation-based significance of `m2`

Note

If the # of variables (columns) in X $<$ Y, it is padded with 0's and allows one to, say, rotate an ordination to an environmental variable.

When `stnd` = 1 each variable is standardized to mean 0 and variance 1 so they will contribute equal weight to the fitting process. This, however, may distort the final configurations.

An optional permutation-based significance test of m^2 is performed when `iter` > 0 to assess the statistical concordance between X & Y.

`resid.dim` provides the length of each observation along each dimension after rotation. This allows interpretation of the direction of increase when Y codes for, say, an environmental gradient.

`resid.obs` provides the total length of each observation, which is a measure of goodness-of-fit for each observation; (smaller values = better fit).

`resid.sse` (like `m2`) is a measure of total concordance between X and Y (smaller values = better fit);

Author(s)

Dave Jones

References

Cox, M. A. A. & T. F. Cox. Local minima in nonmetric multidimensional scaling. Submitted to Statistics & Computing. Available from `http://www.ncl.ac.uk/mds/`

Legendre, P. & L. Legendre. 1998. Numerical ecology. 2nd English ed. Elsevier Science BV, Amsterdam.

Oksanen, J. 2002. Users manual for Vegan: R functions for vegetation ecologists. Available from:

`http://cc.oulu.fi/~jarioksa/softhelp/vegan.html`

Peres-Neto, P. R. 2000. Documentation for program PROTEST.EXE. Dept. of Zoology, University of Toronto. Available from: `http://www.zoo.utoronto.ca/jackson/software/`.

Peres-Neto, P. R. & D. A. Jackson. 2001. How well do multivariate data sets match? The advantages of a Procrustean superimposition approach over the Mantel test. Oecologia 129: 169–178.

Rohlf, F. J. & D. Slice. 1990. Extensions of the Procrustes method for the optimal superimposition of landmarks. Syst. Zool. 39(1): 40–59.

See Also

`f_mantel`, `f_bioenv`

Examples

The example dataset, `cox_cox.mat`, can be found in the *data* folder and includes Cox & Cox's (submitted) Nonmetric Multidimensional Scaling solution (`sol`) to a distance matrix (`dis`) and one obtained using *f_nmds* (`nmds`).

```
>> load cox_cox.mat
>> [Xscl,Yrot,m2,resid,prob] = f_procrustes(sol,nmds,0,1000,1);m2,resid.sse,prob

Permuting the data 999 times...
m2 =
      0.69182
ans =
      0.54873
prob =
         0.01
```

`f_shadeBox` *Shade subsets of a time series plot*

Description

This function is used to shade subsets of a time series plot in order to highlight specific time periods. It should be called after creating a time series plot and should use the same scaling factor.

Usage

`f_shadebox(region)`

Arguments

`region`	2-d matrix defining regions along the Y-axis to shade (column 1 = start, column 2 = stop)
`scale`	scaling factor used in time series plot (defaut = 1)

Details

`region` specifies a variable currently loaded in the Matlab workspace.

`'region'` specifies a space-delimited ASCII file in the Matlab path.

Value

The function modifies the current figure.

Author(s)

Dave Jones

Examples

Load the file, `shadeBox.mat`, in the `data` folder.

```
>> load shadeBox.mat
>> plot(time,speed,'b-');
>> f_shadeBox(region);
```

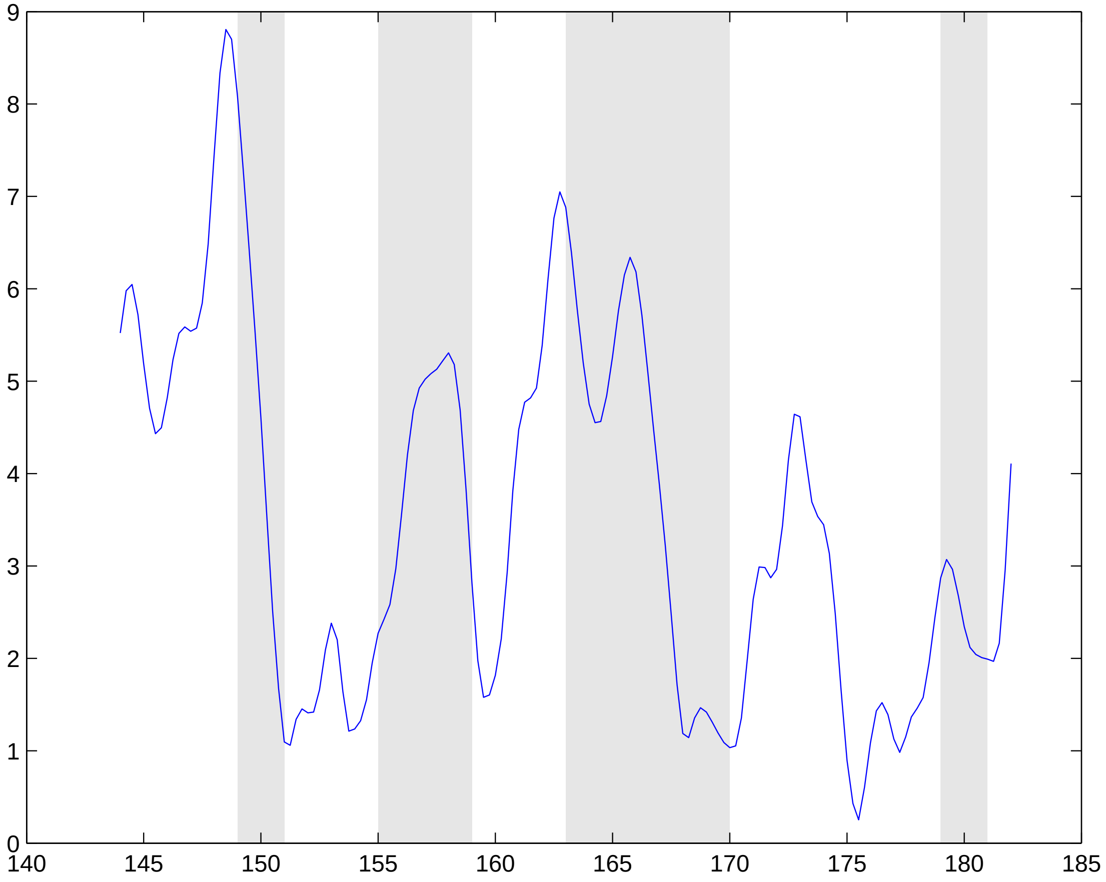

Figure 1: Example of f_shadeBox

`f_vecAngle` *Counter-clockwise angle between 2 points*

Description

This function is used to determine the counter-clockwise angle (in degrees) between points A and B.

Usage

```
theta = f_vecAngle(a,b);
```

Arguments

`a`	2-d row vector for point a (= [xa ya])
`b`	2-d row vector for point a (= [xb yb])

Value

The function returns the following values:

`theta`	angle between `a` & `b` in degrees

Note

The points are considered to be Cartesian coordinates of the heads of vectors starting at the origin.

Note that the counter-clockwise angle from (A -> B) is not necessarily equal to that from (B -> A).

This function is vectorized, so A and B may each be 2-d matrices specifying multiple pairs of points.

Author(s)

Dave Jones

References

Feldman, M. 1997. The Win95 Game Programmer's Encyclopedia. Available from:

`http://www.geocities.com/SiliconValley/2151/win95gpe.html`

See Also

`f_vecMagDir`, `f_vecTrans`, `f_vecUV`

Examples

```
>> a = [0 10; -10 -10];
>> b = [-10 -10; 0 10];
>> theta = f_vecAngle(a,b)
theta =
   135
   225
```

`f_vecDiagram` *Progressive Vector Diagrams*

Description

This function is used to create Progressive Vector Diagrams from time series data of wind or moored current meter velocity vectors. This type of diagram is used to produce a Lagrangian display of Eulerian measurements.

Usage

`f_vecDiagram(u,v,units)`

Arguments

`u,v`	unrotated vector components
`units`	m/s (=1) or cm/s (=2) (default = 0)

Value

The function creates a new figure

Note

`units` is an optional parameter that allows calculation of the spatial units in the plot. A velocity vector specifying 1 m/s covers 3.6 km/hr (there is 3600 sec in an hour).

Author(s)

Dave Jones

See Also

`f_vecPlot`

Examples

Load the file `vecPlot.mat` from the `data` folder.

```
>> load vecPlot.mat
>> f_vecDiagram(u,v,1);
```

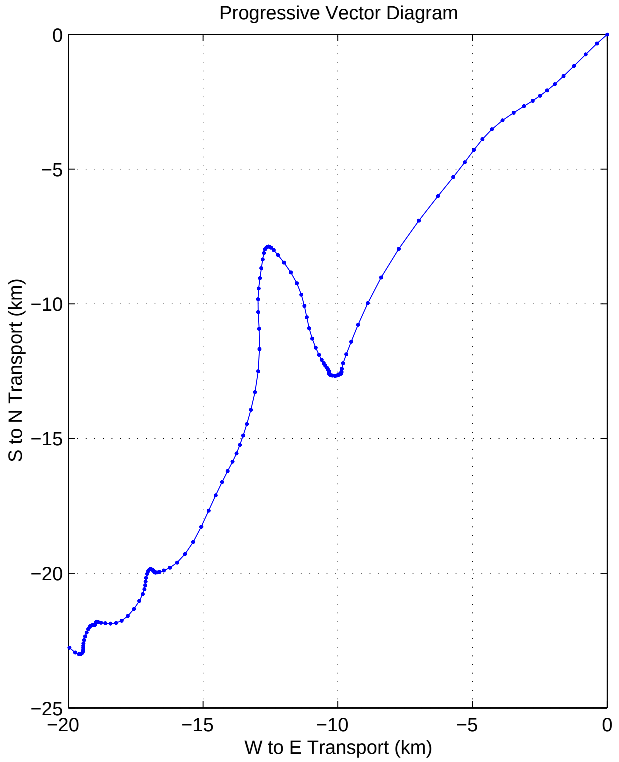

Figure 2: Example of f_vecPlot

`f_vecMagDir` *Magnitude & Direction from U,V vector components*

Description

This function is used to obtain Polar coordinates (magnitude & direction) of a vector given its Cartesian coordinates (U & V vector components). The direction is the counter-clockwise angle of rotation.

Usage

```
[mag,dir] = f_vecMagDir(u,v);
```

Arguments

`u,v`	column vectors of Cartesian coordinates of heads of vector components

Details

The programs uses the Matlab function `ATAN2` which relies on the sign of both input arguments to determine the quadrant of the result.

Value

The function returns the following values:

`mag`	length of vector
`dir`	angle of rotation (in degrees between 0–360)

Author(s)

Dave Jones

See Also

`f_vecAngle`, `f_vecTrans`, `f_vecUV`,

Examples

```
>> u = [0 -10]';
>> v = [10 -10]';
>> [mag,dir] = f_vecMagDir(u,v)
mag =
           10
       14.142
dir =
    90
   225
```

`f_vecPlot`	*Plot time series of velocity vectors*

Description

This function is used to plot time series of wind or current meter velocity vectors using Matlab's `quiver` function.

Usage

`f_vecPlot(jdate,u,v,scale,units,jRange);`

Arguments

`jdate`	column vector of Julian dates
`u,v`	corresponding vector components
`scale`	scale factor (default = 1)
`units`	Y-axis label; e.g., `units = 'm/s'` (default = none)
`jRange`	limits of dates to plot; e.g., `jRange = [min max]` (default = auto)

Value

The function produces a new figure;

Note

This function is necessary in order to obtain vectors that have the proper length and angle of rotation. An optional scaling factor can be applied allowing the user control over the amount of overlap among vectors and/or the scaling of vectors relative to the overall time series. The X-axis is scaled accordingly. The Y-axis allows easy, visual interpretation of vector length.

U,V components of velocity vectors can be extracted from data specifying only Speed and Direction using f_vecUV.

Author(s)

Dave Jones

See Also

`f_julian`, `f_vecUV`, `f_shadeBox`

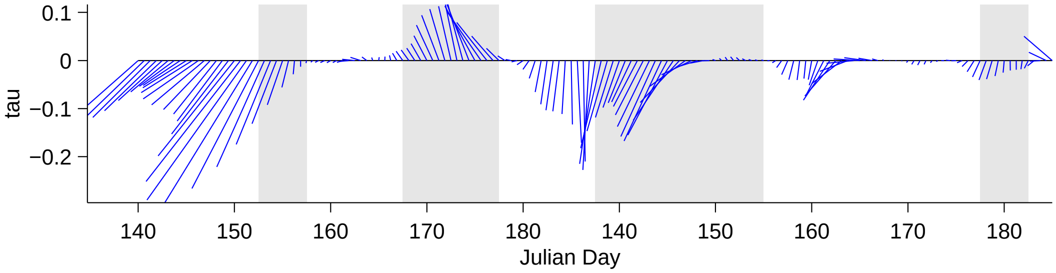

Figure 3: Example of f_vecPlot

Examples

Load the file `vecPlot.mat` from the `data` folder.

```
>> load vecPlot.mat
>> f_vecPlot(date,u,v,20,'tau',[140 182]);
>> axis tight;
>> f_shadeBox(subsets,20);
```

`f_vecTrans` *Transform 2-d vector coordinates*

Description

This function is used to rotate, translate, and/or scale 2dimensional Cartesian coordinates. If the input coordinates specify the heads of (velocity) vectors, they may additionally be converted to unit length.

Usage

```
[tx,ty] = f_vecTrans(x,y,rot,transl,scale,unit);
```

Arguments

`x,y`	column vectors specifying coordinate pairs
`rot`	angle of rotation in degrees (default = 0)
`transl`	translation `[dx dy]` (default = [0 0])
`scale`	scaling factor `[sx sy]` (default = [1 1])
`unit`	convert vectors to unit length (default = 0)

Details

This function uses the following matrices for transforming coordinates:

Rotation matrix: (θ is in radians):

$$\begin{pmatrix} \cos(\theta) & -\sin(\theta) & 0 \\ \sin(\theta) & \cos(\theta) & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

Translation matrix:

$$\begin{pmatrix} 1 & 0 & tx \\ 0 & 1 & ty \\ 0 & 0 & 1 \end{pmatrix}$$

Scaling matrix:

$$\begin{pmatrix} sx & 0 & 0 \\ 0 & sy & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

Value

The function returns the following values:

`tx,ty`	transformed coordinates

Note

X and Y coordinates can be translated or scaled asymmetrically if 2 values are specified for these parameters. If only 1 value is provided, coordinates are translated or scaled symmetrically.

Author(s)

Dave Jones

References

Feldman, M. 1997. The Win95 Game Programmer's Encyclopedia. Available from:

`http://www.geocities.com/SiliconValley/2151/win95gpe.html`

See Also

`f_vecAngle`, `f_vecMagDir`, `f_vecTrans3d`, `f_vecUV`

Examples

```
>> x = [0 10]';
>> y = [-10 -10]';
>> [tx,ty] = f_vecTrans(x,y,45,2,0.5,0)
tx =
       3.5355
       7.0711
ty =
     -0.70711
       2.8284
```

`f_vecTrans3d` *Transform 3-d vector coordinates*

Description

This function is used to rotate, translate, and/or scale 3 dimensional Cartesian coordinates. If the input coordinates specify the heads of (velocity) vectors, they may additionally be converted to unit length.

Usage

```
[tx,ty,tz] = f_vecTrans3d(x,y,z,xrot,yrot,zrot,transl,scale,unit);
```

Arguments

`x,y,z`	column vectors specifying coordinate triplets
`xrot`	rotation about X-axis in degrees (default = 0)
`yrot`	rotation about Y-axis in degrees (default = 0)
`zrot`	rotation about Z-axis in degrees (default = 0)
`transl`	translation `[dx dy dz]` (default = [0 0 0])
`scale`	scaling factor `[sx sy sz]` (default = [1 1 1])
`unit`	convert vectors to unit length (default = 0)

Details

This function uses the following matrices for transforming coordinates:

Rotation Matrices (θ is in radians):

X-axis:

$$\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & \cos(\theta) & -\sin(\theta) & 0 \\ 0 & \sin(\theta) & \cos(\theta) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Y-axis:

$$\begin{pmatrix} \cos(\theta) & 0 & \sin(\theta) & 0 \\ 0 & 1 & 0 & 0 \\ -\sin(\theta) & 0 & \cos(\theta) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Z-axis:

$$\begin{pmatrix} \cos(\theta) & -\sin(\theta) & 0 & 0 \\ \sin(\theta) & \cos(\theta) & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Translation matrix:

$$\begin{pmatrix} 1 & 0 & 0 & tx \\ 0 & 1 & 0 & ty \\ 0 & 0 & 1 & tz \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Scaling matrix:

$$\begin{pmatrix} sx & 0 & 0 & 0 \\ 0 & sy & 0 & 0 \\ 0 & 0 & sz & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Value

The function returns the following values:

`tx,ty`	transformed coordinates

Note

X, Y, & Z coordinates can be translated or scaled asymmetrically if 3 values are specified for these parameters. If only 1 value is provided, coordinates are translated or scaled symmetrically.

Author(s)

Dave Jones

References

Feldman, M. 1997. The Win95 Game Programmer's Encyclopedia. Available from:

`http://www.geocities.com/SiliconValley/2151/win95gpe.html`

See Also

`f_vecAngle`, `f_vecMagDir`, `f_vecTrans`, `f_vecUV` `f_vecUV` *U, V vector components from Magnitude & Direction*

Description

This function is used to obtain Cartesian coordinates (the U,V vector components) of a vector given its Polar coordinates (Magnitude & Direction).

Usage

```
[u,v] = f_vecUV(mag,dir);
```

Arguments

`mag`	column vector specifying magnitude of vectors (in arbitrary units)
`dir`	column vector indicating angle of rotation (in degrees from 0–360)

Details

This function is used to obtain Cartesian coordinates (the U,V vector components) of a vector given its Polar coordinates (magnitude & direction). Direction is the counter-clockwise angle of rotation.

Value

The function returns the following values:

`u,v`	Cartesian coordinates of heads of vector components

Author(s)

Dave Jones

See Also

`f_vecAngle`, `f_vecMagDir`, `f_vecTrans`

Examples

```
>> mag = [10 14.142]';
>> dir = [90 225]';
>> [u,v] = f_vecUV(mag,dir)
u =
  6.1232e-016
      -9.9999
v =
           10
      -9.9999
```

`Appendix A` *(M)ANOVA Examples*

Description

Here are a number of ANOVA Examples using f_npManova. These are provided to help the user become familiar with the syntax used for running the function and for coding of ANOVA factors. Note that f_npManova uses a GLM approach to ANOVA and relies on the *unrestricted* model for constructing proper F-ratios, so output may differ from that found in textbook examples, which typically use the restricted model with balanced designs. The GLM approach used here should provide output similar to that given by SAS and MINITAB.

Remember that the true power of this function is utilized when the response variable consists of a symmetric distance matrix based one of the metrics commonly used in community ecology (e.g., Bray-Curtis, etc.).

References

K. A. Brownlee. 1960. Statistical theory and methodology in science and engineering, John Wiley & Sons, Inc., New York.

Neter, J., M. H. Kutner, C. J. Nachtsheim, & W. Wasserman. 1996. Applied linear statistical models, 4th Edition, Richard D. Irwin, Inc., Burr Ridge, Illinois.

Sokal, R. R. & F. J. Rohlf. 1995. Biometry — The principles and practice of statistics in biological research. 3rd ed. W. H. Freeman, New York. xix + 887 pp.

Zar, J. H. 1999. Biostatistical analysis. 4th ed. Prentice Hall, Upper Saddle River, NJ.

Winer, B. J. 1971. Statistical Principles in Experimental Design, Second Edition, McGraw-Hill.

Examples

1. For an example of a *Two-Way Model I ANOVA with replication*, load the file, `sr_11p1.mat`, in the `data` folder. This data is from Table 11.1 of Sokal & Rohlf (1995) and has 1 response variable, `food`, and 2 fixed factors: `fat` and `sex`.

```
>> load sr_11p1.mat
>> dis = f_euclid(food');
>> result = f_npManova(dis,[sex fat],0,0,1000,1);

========================================
```

```
  Please specify the ANOVA model
  for 2-way ANOVA factors 1 & 2:
-----------------------------------------
1 & 2 are fixed                     [21]
1 is fixed or random, 2 is random   [22]
1 is fixed or random, 2 is nested   [23]

Select model...[0 will cancel]
21

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'        'df'    'SS'        'MS'        'F'         'p'
    'factor 1'      [ 1]    [3780.8]    [3780.8]    [2.5925]    [0.139]
    'factor 2'      [ 1]    [ 61204]    [ 61204]    [41.969]    [0.001]
    'factor 1x2'    [ 1]    [918.75]    [918.75]    [  0.63]    [0.446]
    'residual'      [ 8]    [ 11667]    [1458.3]    [   NaN]    [  NaN]
    'total'         [11]    [ 77570]    [   NaN]    [   NaN]    [  NaN]

      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

2. For an example of a *Two-Way Mixed-Model ANOVA without replication*, load the file, `sr_11p3.mat`, in the `data` folder. This data is from Box 11.3 of Sokal & Rohlf (1995) and has 1 response variable, `temp`, and 2 factors: `depth` (fixed), and `day` (random).

```
>> load sr_11p3.mat
>> dis = {f_euclid}(temp');
>> result = f_npManova(dis,[depth day],0,0,1000,1);

========================================
  Please specify the ANOVA model
  for 2-way ANOVA factors 1 & 2:
-----------------------------------------
1 & 2 are fixed                     [21]
1 is fixed or random, 2 is random   [22]
1 is fixed or random, 2 is nested   [23]

Select model...[0 will cancel]
22
```

```
Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'      'df'    'SS'        'MS'          'F'        'p'
    'factor 1'    [ 9]    [2119.7]    [  235.52]    [ 2835]    [0.001]
    'factor 2'    [ 3]    [ 0.562]    [ 0.18733]    [2.255]    [0.134]
    'residual'    [27]    [ 2.243]    [0.083074]    [  NaN]    [  NaN]
    'total'       [39]    [2122.5]    [     NaN]    [  NaN]    [  NaN]

      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data has NO replication)
```

3. For an example of a *Two-Way Model II Nested ANOVA (balanced)*, load the file, `sr_10p1.mat`, in the `data` folder. This data is from Box 10.1 of Sokal & Rohlf (1995) and has 1 response variable, `wing`, and 2 factors: `cage` (random), and `female` (nested).

```
>> load sr_10p1.mat
>> dis = f_euclid(wing');
>> result = f_npManova(dis,[cage female],0,0,1000,1);

========================================
  Please specify the ANOVA model
  for 2-way ANOVA factors 1 & 2:
-----------------------------------------
1 & 2 are fixed                     [21]
1 is fixed or random, 2 is random  [22]
1 is fixed or random, 2 is nested  [23]

Select model...[0 will cancel]
23

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'      'df'    'SS'        'MS'        'F'         'p'
    'factor 1'    [ 2]    [665.68]    [332.84]    [1.7409]    [0.252]
    'factor 2'    [ 9]    [1720.7]    [191.19]    [146.88]    [0.001]
    'residual'    [12]    [ 15.62]    [1.3017]    [   NaN]    [  NaN]
    'total'       [23]    [  2402]    [   NaN]    [   NaN]    [  NaN]
```

```
      # iterations =       1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

4. For an example of a *Two-Way Model II Nested ANOVA (unbalanced)*, load the file, `sr_10p6.mat`, in the `data` folder. This data is from Box 10.6 of Sokal & Rohlf (1995) and has 1 response variable, `ph`, and 2 factors: `dam` (random), and `sire` (nested).

```
>> load sr_10p6.mat
>> dis = f_euclid(ph');
>> result = f_npManova(dis,[dam sire],0,0,1000,1);

==========================================
  Please specify the ANOVA model
  for 2-way ANOVA factors 1 & 2:
------------------------------------------
1 & 2 are fixed                    [21]
1 is fixed or random, 2 is random  [22]
1 is fixed or random, 2 is nested  [23]

Select model...[0 will cancel]
23

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'      'df'     'SS'        'MS'        'F'         'p'
    'factor 1'    [ 14]    [1780.2]    [127.16]    [3.5383]    [0.003]
    'factor 2'    [ 22]    [ 790.6]    [35.937]    [1.4482]    [0.107]
    'residual'    [123]    [3052.2]    [24.814]    [   NaN]    [  NaN]
    'total'       [159]    [5622.9]    [   NaN]    [   NaN]    [  NaN]

      # iterations =       1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

5. For an example of a *Two-Way Model III ANOVA with no replication*, load the file, `zar_12p4.mat`, in the `data` folder. This data is from Example 12.4 of Zar (1999) and has 1 response variable, `gain`, and 2 random factors: `diet`, and `block`. This is also know as a *randomized block design*.

```
>> load zar_12p4.mat
>> dis = f_euclid(gain');
>> result = f_npManova(dis,[diet block],0,0,1000,1);

========================================
  Please specify the ANOVA model
  for 2-way ANOVA factors 1 & 2:
-----------------------------------------
1 & 2 are fixed                     [21]
1 is fixed or random, 2 is random  [22]
1 is fixed or random, 2 is nested  [23]

Select model...[0 will cancel]
22

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'      'df'    'SS'        'MS'         'F'         'p'
    'factor 1'    [ 3]    [27.425]    [ 9.1418]    [11.825]    [0.004]
    'factor 2'    [ 4]    [62.647]    [ 15.662]    [20.259]    [0.001]
    'residual'    [12]    [ 9.277]    [0.77308]    [   NaN]    [  NaN]
    'total'       [19]    [ 99.35]    [    NaN]    [   NaN]    [  NaN]

      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data has NO replication)
```

6. For an example of a *Three-Way Model I ANOVA with replication*, load the file, `zar_14p1.mat`, in the `data` folder. This data is from Example 14.1 of Zar (1999) and has 1 response variable, `rate`, and 3 fixed factors: `species`, `temp`, and `sex`.

```
>> load zar_14p1.mat
>> dis = f_euclid(rate');
>> result = f_npManova(dis,[species temp sex],0,0,1000,1);

===========================================================
  Please specify the ANOVA model
  for 3-way ANOVA factors 1, 2, & 3:
-----------------------------------------------------------
All factors fixed                                   [31]
1 & 2 are fixed, 3 is random                        [32]
1 is fixed or random, 2 & 3 are random              [33]
```

```
1 & 2 fixed,     3 nested in 1        (Cross-Nested)  [34]
1 &/or 2 random, 3 nested in 1        (Cross-Nested)  [35]
3 nested in 2 nested in 1             (Fully Nested)  [36]

Select model...[0 will cancel]
31

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'          'df'    'SS'           'MS'           'F'         'p'
    'factor 1'        [ 2]    [   1.8175]    [  0.90875]    [24.475]    [0.001]
    'factor 2'        [ 2]    [   24.656]    [   12.328]    [332.02]    [0.001]
    'factor 3'        [ 1]    [0.0088889]    [0.0088889]    [0.2394]    [0.626]
    'factor 1x2'      [ 4]    [   1.1017]    [  0.27542]    [7.4177]    [0.002]
    'factor 1x3'      [ 2]    [  0.37028]    [  0.18514]    [4.9863]    [0.013]
    'factor 2x3'      [ 2]    [  0.17528]    [ 0.087639]    [2.3603]    [0.114]
    'factor 1x2x3'    [ 4]    [  0.22056]    [ 0.055139]    [ 1.485]    [0.233]
    'residual'        [54]    [    2.005]    [  0.03713]    [   NaN]    [  NaN]
    'total'           [71]    [   30.355]    [      NaN]    [   NaN]    [  NaN]

      # iterations =       1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

7. For an example of a *Three-Way Model I ANOVA with no replication*, load the file, `sr_12p1.mat`, in the `data` folder. This data is from Box 12.1 of Zar (1999) and has 1 response variable, `time`, and 3 fixed factors: `temp`, `cn`, and `o2`.

```
>> load zar_14p1.mat
>> dis = f_euclid(rate');
>> result = f_npManova(dis,[species temp sex],0,0,1000,1);

===========================================================
  Please specify the ANOVA model
  for 3-way ANOVA factors 1, 2, & 3:
-----------------------------------------------------------
All factors fixed                                     [31]
1 & 2 are fixed, 3 is random                          [32]
1 is fixed or random, 2 & 3 are random                [33]

1 & 2 fixed,     3 nested in 1        (Cross-Nested)  [34]
1 &/or 2 random, 3 nested in 1        (Cross-Nested)  [35]
3 nested in 2 nested in 1             (Fully Nested)  [36]
```

```
Select model...[0 will cancel]
31

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'          'df'    'SS'            'MS'            'F'         'p'
    'factor 1'        [ 2]    [    1.8175]    [   0.90875]    [24.475]    [0.001]
    'factor 2'        [ 2]    [    24.656]    [    12.328]    [332.02]    [0.001]
    'factor 3'        [ 1]    [0.0088889]     [0.0088889]     [0.2394]    [0.612]
    'factor 1x2'      [ 4]    [    1.1017]    [   0.27542]    [7.4177]    [0.001]
    'factor 1x3'      [ 2]    [   0.37028]    [   0.18514]    [4.9863]    [0.012]
    'factor 2x3'      [ 2]    [   0.17528]    [  0.087639]    [2.3603]    [0.093]
    'factor 1x2x3'    [ 4]    [   0.22056]    [  0.055139]    [ 1.485]    [0.221]
    'residual'        [54]    [     2.005]    [   0.03713]    [   NaN]    [  NaN]
    'total'           [71]    [    30.355]    [       NaN]    [   NaN]    [  NaN]

      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

8. For an example of a *Three-Way Model II ANOVA with replication*, load the file, `thick.mat`, in the `data` folder. This data ships with MINITAB and has 1 response variable, `thickness`, 2 fixed factors: `time` and `setting`, and 1 random factor: `operator`.

```
>> load thick.mat
>> dis = f_euclid(thickness');
>> result = f_npManova(dis,[time setting operator],0,0,1000,1);

===========================================================
  Please specify the ANOVA model
  for 3-way ANOVA factors 1, 2, & 3:
-----------------------------------------------------------
All factors fixed                                    [31]
1 & 2 are fixed, 3 is random                         [32]
1 is fixed or random, 2 & 3 are random               [33]

1 & 2 fixed,     3 nested in 1        (Cross-Nested)  [34]
1 &/or 2 random, 3 nested in 1        (Cross-Nested)  [35]
3 nested in 2 nested in 1             (Fully Nested)  [36]

Select model...[0 will cancel]
```

```
32

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'          'df'    'SS'         'MS'         'F'          'p'
    'factor 1'        [ 1]    [     9]     [     9]     [0.29032]    [0.648]
    'factor 2'        [ 2]    [ 15676]     [7838.2]     [ 73.178]    [0.001]
    'factor 3'        [ 2]    [1120.9]     [560.44]     [ 4.9114]    [0.052]
    'factor 1x2'      [ 2]    [ 114.5]     [ 57.25]     [ 2.3854]    [0.209]
    'factor 1x3'      [ 2]    [    62]     [    31]     [ 1.2917]    [0.363]
    'factor 2x3'      [ 4]    [428.44]     [107.11]     [  4.463]    [0.088]
    'factor 1x2x3'    [ 4]    [    96]     [    24]     [  7.082]    [0.004]
    'residual'        [18]    [    61]     [3.3889]     [    NaN]    [  NaN]
    'total'           [35]    [ 17568]     [   NaN]     [    NaN]    [  NaN]

      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

9. For an example of a *Three-Way Model II ANOVA with no replication*, load the file, `milk.mat`, in the `data` folder. This is from Brownlee (1960:p.516) and has 1 response variable, `counts`, 2 fixed factors: `bottle` and `tube`, and 1 random factor: `sample`.

```
>> load milk.mat
>> dis = f_euclid(counts');
>> result = f_npManova(dis,[bottle tube sample],0,0,1000,1);

===========================================================
  Please specify the ANOVA model
  for 3-way ANOVA factors 1, 2, & 3:
-----------------------------------------------------------
All factors fixed                                    [31]
1 & 2 are fixed, 3 is random                         [32]
1 is fixed or random, 2 & 3 are random               [33]

1 & 2 fixed,     3 nested in 1        (Cross-Nested)  [34]
1 &/or 2 random, 3 nested in 1        (Cross-Nested)  [35]
3 nested in 2 nested in 1             (Fully Nested)  [36]

Select model...[0 will cancel]
32
```

```
Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'        'df'    'SS'         'MS'         'F'          'p'
    'factor 1'      [ 1]    [0.34722]    [0.34722]    [0.14066]    [0.736]
    'factor 2'      [ 2]    [ 15.361]    [ 7.6806]    [ 7.6903]    [0.003]
    'factor 3'      [11]    [ 93.486]    [ 8.4987]    [ 3.6208]    [ 0.08]
    'factor 1x2'    [ 2]    [ 1.3611]    [0.68056]    [0.60767]    [0.572]
    'factor 1x3'    [11]    [ 27.153]    [ 2.4684]    [ 2.2041]    [0.048]
    'factor 2x3'    [22]    [ 21.972]    [0.99874]    [0.89177]    [0.616]
    'residual'      [22]    [ 24.639]    [ 1.1199]    [    NaN]    [  NaN]
    'total'         [71]    [ 184.32]    [    NaN]    [    NaN]    [  NaN]

      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data has NO replication)
```

10. For an example of a *Three-Way Model III ANOVA with replication*, load the file, `exercise.mat`, in the `data` folder. This data is from Table 23.4 of Neter et al. (1996) and has 1 response variable, `tol`, and 3 random factors: `gender`, `fat`, and `smoke`.

```
>> load exercise.mat
>> dis = f_euclid(tol');
>> result = f_npManova(dis,[gender fat smoke],0,0,1000,1);

===========================================================
  Please specify the ANOVA model
  for 3-way ANOVA factors 1, 2, & 3:
-----------------------------------------------------------
All factors fixed                                     [31]
1 & 2 are fixed, 3 is random                          [32]
1 is fixed or random, 2 & 3 are random                [33]

1 & 2 fixed,     3 nested in 1        (Cross-Nested)  [34]
1 &/or 2 random, 3 nested in 1        (Cross-Nested)  [35]
3 nested in 2 nested in 1             (Fully Nested)  [36]

Select model...[0 will cancel]
33

Permuting the data 999 times...

==================================================
```

```
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'          'df'    'SS'        'MS'        'F'          'p'
    'factor 1'        [ 1]    [176.58]    [176.58]    [ 7.7278]    [0.037]
    'factor 2'        [ 1]    [242.57]    [242.57]    [ 2.8797]    [0.084]
    'factor 3'        [ 1]    [70.384]    [70.384]    [0.86198]    [0.187]
    'factor 1x2'      [ 1]    [ 13.65]    [ 13.65]    [ 7.2981]    [  0.2]
    'factor 1x3'      [ 1]    [ 11.07]    [ 11.07]    [ 5.9187]    [0.233]
    'factor 2x3'      [ 1]    [72.454]    [72.454]    [ 38.737]    [0.089]
    'factor 1x2x3'    [ 1]    [1.8704]    [1.8704]    [0.20036]    [0.694]
    'residual'        [16]    [149.37]    [9.3354]    [    NaN]    [  NaN]
    'total'           [23]    [737.95]    [   NaN]    [    NaN]    [  NaN]

      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

11. For an example of a *Three-Way Model III ANOVA with no replication*, load the file, `milk.mat`, in the `data` folder. This is from Brownlee (1960:p.516) and has 1 response variable, `counts` and 3 random factors: `bottle`, `tube`, and `sample`.

```
>> load milk.mat
>> dis = f_euclid(counts');
>> result = f_npManova(dis,[bottle tube sample],0,0,1000,1);

===========================================================
  Please specify the ANOVA model
  for 3-way ANOVA factors 1, 2, & 3:
-----------------------------------------------------------
All factors fixed                                    [31]
1 & 2 are fixed, 3 is random                         [32]
1 is fixed or random, 2 & 3 are random               [33]

1 & 2 fixed,     3 nested in 1        (Cross-Nested)  [34]
1 &/or 2 random, 3 nested in 1        (Cross-Nested)  [35]
3 nested in 2 nested in 1             (Fully Nested)  [36]

Select model...[0 will cancel]
33

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'        'df'    'SS'         'MS'         'F'          'p'
```

```
    'factor 1'      [ 1]    [0.34722]     [0.34722]     [0.17113]     [0.555]
    'factor 2'      [ 2]    [ 15.361]     [ 7.6806]     [ 13.731]     [0.025]
    'factor 3'      [11]    [ 93.486]     [ 8.4987]     [ 3.6208]     [0.062]
    'factor 1x2'    [ 2]    [ 1.3611]     [0.68056]     [0.60767]     [0.558]
    'factor 1x3'    [11]    [ 27.153]     [ 2.4684]     [ 2.2041]     [ 0.06]
    'factor 2x3'    [22]    [ 21.972]     [0.99874]     [0.89177]     [0.612]
    'residual'      [22]    [ 24.639]     [ 1.1199]     [    NaN]     [  NaN]
    'total'         [71]    [ 184.32]     [    NaN]     [    NaN]     [  NaN]

      # iterations =       1000
---------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data has NO replication)
```

12. For an example of a *Three-Way, Fully Nested, Mixed Model ANOVA (balanced)*, load the file, `sr_10p5.mat`, in the `data` folder. This is from Box 10.5 of Sokal Rohlf (1995) has 1 response variable, `gly`, 1 fixed factor, `rx` and 2 nested factors: `rat` (nested in `rx`) and `prep` (nested in `rat`).

```
>> load sr_10p5.mat
>> dis = f_euclid(gly');
>> result = f_npManova(dis,[rx rat prep],0,0,5000,1);

============================================================
  Please specify the ANOVA model
  for 3-way ANOVA factors 1, 2, & 3:
------------------------------------------------------------
All factors fixed                                      [31]
1 & 2 are fixed, 3 is random                           [32]
1 is fixed or random, 2 & 3 are random                 [33]

1 & 2 fixed,     3 nested in 1        (Cross-Nested)  [34]
1 &/or 2 random, 3 nested in 1        (Cross-Nested)  [35]
3 nested in 2 nested in 1             (Fully Nested)  [36]

Select model...[0 will cancel]
36

Permuting the data 4999 times...

===================================================
    Nonparametric (Permutation-based) MANOVA:
---------------------------------------------------
    'Source'      'df'    'SS'        'MS'        'F'         'p'
    'factor 1'    [ 2]    [1557.6]    [778.78]    [ 2.929]    [ 0.192]
    'factor 2'    [ 3]    [797.67]    [265.89]    [5.3715]    [0.0148]
    'factor 3'    [12]    [   594]    [  49.5]    [2.3386]    [0.0484]
```

```
    'residual'    [18]    [   381]    [21.167]    [   NaN]    [   NaN]
    'total'       [35]    [3330.2]    [   NaN]    [   NaN]    [   NaN]

      # iterations =        5000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

13. For an example of a *Three-Way Cross-Nested ANOVA with replication*, load the file, `steel.mat`, in the `data` folder. This is from Brownlee (1960:p.530) and has 1 response variable, `qual`, 2 fixed factors: `ann` and `loc`, and 1 nested factor: `coil` (nested in `ann`. This design is also know as *partially nested* or *partially hierarchical*.

```
>> load steel.mat
>> dis = f_euclid(qual');
>> result = f_npManova(dis,[ann loc coil],0,0,1000,1);

===========================================================
  Please specify the ANOVA model
  for 3-way ANOVA factors 1, 2, & 3:
-----------------------------------------------------------
All factors fixed                                    [31]
1 & 2 are fixed, 3 is random                         [32]
1 is fixed or random, 2 & 3 are random               [33]

1 & 2 fixed,     3 nested in 1        (Cross-Nested)  [34]
1 &/or 2 random, 3 nested in 1        (Cross-Nested)  [35]
3 nested in 2 nested in 1             (Fully Nested)  [36]

Select model...[0 will cancel]
34

Permuting the data 999 times...

==================================================
    Nonparametric (Permutation-based) MANOVA:
--------------------------------------------------
    'Source'        'df'    'SS'        'MS'        'F'          'p'
    'factor 1'      [ 1]    [  2646]    [  2646]    [  1.091]    [0.346]
    'factor 2'      [ 1]    [1872.7]    [1872.7]    [ 35.389]    [0.004]
    'factor 3'      [ 4]    [9701.3]    [2425.3]    [ 45.833]    [0.001]
    'factor 1x2'    [ 1]    [16.667]    [16.667]    [0.31496]    [0.606]
    'factor 2x3'    [ 4]    [211.67]    [52.917]    [0.50039]    [0.718]
    'residual'      [12]    [  1269]    [105.75]    [    NaN]    [  NaN]
    'total'         [23]    [ 15717]    [   NaN]    [    NaN]    [  NaN]
```

```
      # iterations =        1000
--------------------------------------------------
(Note: NaNs are placeholders for the ANOVA table)

(Data with replication)
```

`Appendix B` *F-ratios used by f_npManova*

Description

Here are the F-ratios used in the various ANOVA designs supported by f_npManova.

References

Zar, J. H. 1999. Biostatistical analysis. 4th ed. Prentice Hall, Upper Saddle River, NJ.

This program uses a GLM-approach to (M)ANOVA, so for mixed models (when there are both fixed and random factors) an unrestricted model is used.

Two-way ANOVA's:

A = fixed, B = fixed: [*f_npManova2*]

Source	F-ratio
A	MS_A/MS_{error}
B	MS_B/MS_{error}
AB	MS_{AB}/MS_{error}

A = fixed, B = random:
A = random, B = random: [*f_npManova2*]

Source	F-ratio
A	MS_A/MS_{AB}
B	MS_B/MS_{AB}
AB	MS_{AB}/MS_{error}

Two-way Nested ANOVA's:

A = fixed, B = nested in A
A = random, B = nested in A: [*f_npManova2n*]

Source	F-ratio
A	MS_A/MS_B
B	MS_B/MS_{error}

Three-way ANOVA's:

A = fixed, B = fixed, C = fixed: [*f_npManova3*]

Source	F-ratio
A	MS_A/MS_{error}
B	MS_B/MS_{error}
C	MS_c/MS_{error}
AB	MS_{AB}/MS_{error}
AC	MS_{AC}/MS_{error}
BC	MS_{BC}/MS_{error}
ABC	MS_{ABC}/MS_{error}

A = fixed, B = fixed, C = random: [*f_npManova3*]

Source	F-ratio
A	MS_A/MS_{AC}
B	MS_B/MS_{BC}
C	$MS_c/(MS_{AC} + MS_{BC} - MS_{ABC})$
AB	MS_{AB}/MS_{ABC}

AC	MS_{AC}/MS_{ABC}
BC	MS_{BC}/MS_{ABC}
ABC	MS_{ABC}/MS_{error}

A = fixed, B = random, C = random:
A = random, B = random, C = random: [*f_npManova3*]

Source	F-ratio
A	$MS_A/(MS_{AB} + MS_{AC} - MS_{ABC})$
B	$MS_B/(MS_{AB} + MS_{BC} - MS_{ABC})$
C	$MS_c/(MS_{AC} + MS_{BC} - MS_{ABC})$
AB	MS_{AB}/MS_{ABC}
AC	MS_{AC}/MS_{ABC}
BC	MS_{BC}/MS_{ABC}
ABC	MS_{ABC}/MS_{error}

Three-way Cross-Nested ANOVA's:

A = fixed, B = fixed, C = nested in A: [*f_npManova3Nest1*]

Source	F-ratio
A	MS_A/MS_C
B	MS_B/MS_{BC}
C	MS_C/MS_{BC}
AB	MS_{AB}/MS_{BC}
BC	MS_{BC}/MS_{error}

A = fixed, B = random, C = nested in A
A = random, B = fixed, C = nested in A
A = fixed, B = fixed, C = nested in A: [*f_npManova3Nest1*]

Source	F-ratio
A	$MS_A/MS_C + MS_{AB} - MS_{BC}$
B	MS_B/MS_{AB}
C	MS_C/MS_{BC}
AB	MS_{AB}/MS_{BC}
BC	MS_{BC}/MS_{error}

Three-way Fully-Nested ANOVA's:

A = fixed, B = nested in A, C = nested in B:
A = random, B = nested in A, C = nested in B: [*f_npManova3Nest2*]

Source	F-ratio
A	MS_A/MS_B
B	MS_B/MS_C
C	MS_C/MS_{error}