

Package ‘candisc’

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Description Functions for computing and graphing canonical discriminant analyses.

License GPL (>= 2)

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candisc-package *Generalized Canonical Discriminant Analysis*

Description

This package includes functions for computing and visualizing generalized canonical discriminant analyses for a multivariate linear model. They are designed to provide low-rank visualizations of terms in a `mlm` via the `plot` method and the **heplots** package.

Details

Package: candisc
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Version: 0.5-16
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License: GPL (>= 2)

The organization of functions in this package and the **heplots** package may change in a later version.

Author(s)

Michael Friendly and John Fox

Maintainer: Michael Friendly <friendly@yorku.ca>

References

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, 16 (2), 421-444. <http://www.math.yorku.ca/SCS/Papers/jcgs-heplots.pdf>

Gittins, R. (1985). *Canonical Analysis: A Review with Applications in Ecology*, Berlin: Springer.

See Also

[heplot](#)

candisc *Canonical discriminant analysis*

Description

`candisc` performs a generalized canonical discriminant analysis for one term in a multivariate linear model (i.e., an `mlm` object), computing canonical scores and vectors. It represents a transformation of the original variables into a canonical space of maximal differences for the term, controlling for other model terms. To be of any use, the term should be a factor or interaction corresponding to a multivariate test with 2 or more degrees of freedom for the null hypothesis.

Usage

```
candisc(mod, ...)

## S3 method for class 'mlm':
candisc(mod, term, type = "2", manova, ndim = rank, ...)

## S3 method for class 'candisc':
coef(object, type = c("std", "raw", "structure"), ...)

## S3 method for class 'candisc':
plot(x, which = 1:2, conf = 0.95, col, pch, scale, asp = 1,
      var.col = "blue", var.lwd = par("lwd"), prefix = "Can", suffix=TRUE,
      titles.ld = c("Canonical scores", "Structure"), ...)

## S3 method for class 'candisc':
print(x, digits=max(getOption("digits") - 2, 3), ...)

## S3 method for class 'candisc':
summary(object, means = TRUE, scores = FALSE, coef = c("std"),
         ndim, digits = max(getOption("digits") - 2, 4), ...)
```

Arguments

<code>mod</code>	An <code>mlm</code> object, such as computed by <code>lm()</code> with a multivariate response
<code>term</code>	the name of one term from <code>mod</code>
<code>type</code>	type of test for the model <code>term</code> , one of: "II", "III", "2", or "3"
<code>manova</code>	the <code>Anova.mlm</code> object corresponding to <code>mod</code> . Normally, this is computed internally by <code>Anova(mod)</code>
<code>ndim</code>	Number of dimensions to store in (or retrieve from, for the <code>summary</code> method) the means, structure, scores and <code>coeffs.*</code> components. The default is the rank of the H matrix for the hypothesis term.
<code>object, x</code>	A <code>candisc</code> object
<code>which</code>	A vector of two integers, selecting the canonical dimensions to plot
<code>conf</code>	Confidence coefficient for the confidence circles plotted in the <code>plot</code> method
<code>col</code>	A vector of colors to be used for the levels of the term in the <code>plot</code> method. In this version, you should assign colors and point symbols explicitly, rather than relying on the somewhat arbitrary defaults.

<code>pch</code>	A vector of point symbols to be used for the levels of the term in the <code>plot</code> method
<code>scale</code>	Scale factor for the variable vectors in canonical space. If not specified, a scale factor is calculated to make the variable vectors approximately fill the plot space.
<code>asp</code>	Aspect ratio for the <code>plot</code> method. The <code>asp=1</code> (the default) assures that the units on the horizontal and vertical axes are the same, so that lengths and angles of the variable vectors are interpretable.
<code>var.col</code>	Color used to plot variable vectors
<code>var.lwd</code>	Line width used to plot variable vectors
<code>prefix</code>	Prefix used to label the canonical dimensions plotted
<code>suffix</code>	Suffix for labels of canonical dimensions. If <code>suffix=TRUE</code> the percent of hypothesis (H) variance accounted for by each canonical dimension is added to the axis label.
<code>titles.1d</code>	A character vector of length 2, containing titles for the panels used to plot the canonical scores and structure vectors, for the case in which there is only one canonical dimension.
<code>means</code>	Logical value used to determine if canonical means are printed
<code>scores</code>	Logical value used to determine if canonical scores are printed
<code>coef</code>	Type of coefficients printed by the summary method. Any one or more of "std", "raw", or "structure"
<code>digits</code>	significant digits to print.
<code>...</code>	arguments to be passed down. In particular, <code>type="n"</code> can be used with the <code>plot</code> method to suppress the display of canonical scores.

Details

Canonical discriminant analysis is typically carried out in conjunction with a one-way MANOVA design. It represents a linear transformation of the response variables into a canonical space in which (a) each successive canonical variate produces maximal separation among the groups (e.g., maximum univariate F statistics), and (b) all canonical variates are mutually uncorrelated. For a one-way MANOVA with g groups and p responses, there are $df_h = \min(g-1, p)$ such canonical dimensions, and tests, initially stated by Bartlett (1938) allow one to determine the number of significant canonical dimensions. Computational details for the one-way case are described in Cooley & Lohnes (1971), and in the SAS/STAT User's Guide, "The CANDISC procedure: Computational Details," http://support.sas.com/onlinedoc/913/getDoc/en/statug.hlp/candisc_sect12.htm.

A generalized canonical discriminant analysis extends this idea to a general multivariate linear model. Analysis of each term in the `m1m` produces a rank df_h H matrix sum of squares and crossproducts matrix that is tested against the rank df_e E matrix by the standard multivariate tests (Wilks' Lambda, Hotelling-Lawley trace, Pillai trace, Roy's maximum root test). For any given term in the `m1m`, the generalized canonical discriminant analysis amounts to a standard discriminant analysis based on the H matrix for that term in relation to the full-model E matrix.

Value

An object of class `candisc` with the following components:

<code>dfh</code>	hypothesis degrees of freedom for <code>term</code>
<code>dfe</code>	error degrees of freedom for the <code>mlm</code>
<code>rank</code>	number of non-zero eigenvalues of HE^{-1}
<code>eigenvalues</code>	eigenvalues of HE^{-1}
<code>canrsq</code>	squared canonical correlations
<code>pct</code>	A vector containing the percentages of the <code>canrsq</code> of their total.
<code>ndim</code>	Number of canonical dimensions stored in the <code>means</code> , <code>structure</code> and <code>coeffs.*</code> components
<code>means</code>	A data.frame containing the class means for the levels of the factor(s) in the <code>term</code>
<code>factors</code>	A data frame containing the levels of the factor(s) in the <code>term</code>
<code>term</code>	name of the <code>term</code>
<code>terms</code>	A character vector containing the names of the terms in the <code>mlm</code> object
<code>coeffs.raw</code>	A matrix containing the raw canonical coefficients
<code>coeffs.std</code>	A matrix containing the standardized canonical coefficients
<code>structure</code>	A matrix containing the canonical structure coefficients on <code>ndim</code> dimensions, i.e., the correlations between the original variates and the canonical scores. These are sometimes referred to as Total Structure Coefficients.
<code>scores</code>	A data frame containing the predictors in the <code>mlm</code> model and the canonical scores on <code>ndim</code> dimensions. These are calculated as $Y \%*\% coeffs.raw$, where <code>Y</code> contains the standardized response variables.

Author(s)

Michael Friendly and John Fox

References

- Bartlett, M. S. (1938). Further aspects of the theory of multiple regression. *Proc. Camb. Phil. Soc.* 34, 33-34.
- Cooley, W.W. & Lohnes, P.R. (1971). *Multivariate Data Analysis*, New York: Wiley.
- Gittins, R. (1985). *Canonical Analysis: A Review with Applications in Ecology*, Berlin: Springer.

See Also

[candiscList](#), [heplot](#), [heplot3d](#)

Examples

```

grass.mod <- lm(cbind(N1,N9,N27,N81,N243) ~ Block + Species, data=Grass)
Anova(grass.mod,test="Wilks")

grass.can1 <-candisc(grass.mod, term="Species")
plot(grass.can1, type="n")

# library(heplots)
heplot(grass.can1, scale=6)

# iris data
iris.mod <- lm(cbind(Petal.Length, Sepal.Length, Petal.Width, Sepal.Width) ~ Species, data=iris)
iris.can <- candisc(iris.mod, data=iris)
#-- assign colors and symbols corresponding to species
col <- rep(c("red", "black", "blue"), each=50)
pch <- rep(1:3, each=50)
plot(iris.can, col=col, pch=pch)

heplot(iris.can)

# 1-dim plot
iris.can1 <- candisc(iris.mod, data=iris, ndim=1)
plot(iris.can1)

```

candiscList

Canonical discriminant analyses

Description

candiscList performs a generalized canonical discriminant analysis for all terms in a multivariate linear model (i.e., an `mlm` object), computing canonical scores and vectors.

Usage

```

candiscList(mod, ...)

## S3 method for class 'mlm':
candiscList(mod, type = "2", manova, ndim, ...)

## S3 method for class 'candiscList':
plot(x, term, ask = interactive(), graphics = TRUE, ...)

## S3 method for class 'candiscList':
print(x, ...)

## S3 method for class 'candiscList':
summary(object, ...)

```

Arguments

<code>mod</code>	An <code>mlm</code> object, such as computed by <code>lm()</code> with a multivariate response
<code>type</code>	type of test for the model term, one of: "II", "III", "2", or "3"
<code>manova</code>	the <code>Anova.mlm</code> object corresponding to <code>mod</code> . Normally, this is computed internally by <code>Anova(mod)</code>
<code>ndim</code>	Number of dimensions to store in the means, structure, scores and <code>coeffs.*</code> components. The default is the rank of the H matrix for the hypothesis term.
<code>object, x</code>	A <code>candiscList</code> object
<code>term</code>	The name of one term to be plotted for the <code>plot</code> method. If not specified, one <code>candisc</code> plot is produced for each term in the <code>mlm</code> object.
<code>ask</code>	If <code>TRUE</code> (the default, when running interactively), a menu of terms is presented; if <code>ask</code> is <code>FALSE</code> , canonical plots for all terms are produced.
<code>graphics</code>	if <code>TRUE</code> (the default, when running interactively), then the menu of terms to plot is presented in a dialog box rather than as a text menu.
<code>...</code>	arguments to be passed down.

Value

An object of class `candiscList` which is a list of `candisc` objects for the terms in the `mlm`.

Author(s)

Michael Friendly and John Fox

See Also

[candisc](#), [heplot](#), [heplot3d](#)

Examples

```
grass.mod <- lm(cbind(N1,N9,N27,N81,N243) ~ Block + Species, data=Grass)

grass.canL <-candiscList(grass.mod)
print(grass.canL)
plot(grass.canL, type="n", ask=FALSE)
```

`dataIndex`*Indices of observations in a model data frame*

Description

Find sequential indices for observations in a data frame corresponding to the unique combinations of the levels of a given model term from a model object or a data frame

Usage

```
dataIndex(x, term)
```

Arguments

<code>x</code>	Either a data frame or a model object
<code>term</code>	The name of one term in the model, consisting only of factors

Value

A vector of indices.

Author(s)

Michael Friendly

Examples

```
factors <- expand.grid(A=factor(1:3), B=factor(1:2), C=factor(1:2))
n <- nrow(factors)
responses <- data.frame(Y1=10+round(10*rnorm(n)), Y2=10+round(10*rnorm(n)))

test <- data.frame(factors, responses)
mod <- lm(cbind(Y1, Y2) ~ A*B, data=test)

dataIndex(mod, "A")
dataIndex(mod, "A:B")
```

Grass

*Yields from Nitrogen nutrition of grass species***Description**

The data frame `Grass` gives the yield ($10 * \log_{10}$ dry-weight (g)) of eight grass Species in five replicates (Block) grown in sand culture at five levels of nitrogen.

Usage

```
data(Grass)
```

Format

A data frame with 40 observations on the following 7 variables.

Species a factor with levels B.media D.glomerata F.ovina F.rubra H.pubesens
K.cristata L.perenne P.bertolonii

Block a factor with levels 1 2 3 4 5

N1 species yield at 1 ppm Nitrogen

N9 species yield at 9 ppm Nitrogen

N27 species yield at 27 ppm Nitrogen

N81 species yield at 81 ppm Nitrogen

N243 species yield at 243 ppm Nitrogen

Details

Nitrogen (NaNO_3) levels were chosen to vary from what was expected to be from critically low to almost toxic. The amount of Nitrogen can be considered on a \log_3 scale, with levels 0, 2, 3, 4, 5. Gittins (1985, Ch. 11) treats these as equally spaced for the purpose of testing polynomial trends in Nitrogen level.

The data are also not truly multivariate, but rather a split-plot experimental design. For the purpose of exposition, he regards Species as the experimental unit, so that correlations among the responses refer to a composite representative of a species rather than to an individual exemplar.

Source

Gittins, R. (1985), *Canonical Analysis: A Review with Applications in Ecology*, Berlin: Springer-Verlag, Table A-5.

Examples

```
str(Grass)
grass.mod <- lm(cbind(N1,N9,N27,N81,N243) ~ Block + Species, data=Grass)
```

heplot.candisc *Canonical Discriminant HE plots*

Description

These functions plot ellipses (or ellipsoids in 3D) in canonical discriminant space representing the hypothesis and error sums-of-squares-and-products matrices for terms in a multivariate linear model. They provide a low-rank 2D (or 3D) view of the effects for that term in the space of maximum discrimination.

Usage

```
## S3 method for class 'candisc':
heplot(mod, which = 1:2, scale, asp = 1, var.col = "blue",
       var.lwd = par("lwd"), prefix = "Can", suffix = TRUE, terms = mod$term, ...)

## S3 method for class 'candisc':
heplot3d(mod, which = 1:3, scale, asp="iso", var.col = "blue", var.lwd=par("lwd"),
         prefix = "Can", suffix = FALSE, terms = mod$term,
         ...)
```

Arguments

mod	A <code>candisc</code> object for one term in a <code>mlm</code>
which	A numeric vector containing the indices of the canonical dimensions to plot.
scale	Scale factor for the variable vectors in canonical space. If not specified, the function calculates one to make the variable vectors approximately fill the plot window.
asp	Aspect ratio for the horizontal and vertical dimensions. The defaults, <code>asp=1</code> for <code>heplot.candisc</code> and <code>asp="iso"</code> for <code>heplot3d.candisc</code> ensure equal units on all axes, so that angles and lengths of variable vectors are interpretable. As well, the standardized canonical scores are uncorrelated, so the Error ellipse (ellipsoid) should plot as a circle (sphere) in canonical space. For <code>heplot3d.candisc</code> , use <code>asp=NULL</code> to suppress this transformation to iso-scaled axes.
var.col	Color for variable vectors and labels
var.lwd	Line width for variable vectors
prefix	Prefix for labels of canonical dimensions.
suffix	Suffix for labels of canonical dimensions. If <code>suffix=TRUE</code> the percent of hypothesis (H) variance accounted for by each canonical dimension is added to the axis label.
terms	Terms from the original <code>mlm</code> whose H ellipses are to be plotted in canonical space. The default is the one term for which the canonical scores were computed. If <code>terms=TRUE</code> , all terms are plotted.
...	Arguments to be passed down to <code>heplot</code> or <code>heplot3d</code>

Details

The generalized canonical discriminant analysis for on term in a `mlm` is based on the eigenvalues, λ_i , and eigenvectors, V , of the H and E matrices for that term. This produces uncorrelated canonical scores which give the maximum univariate F statistics. The canonical HE plot is then just the HE plot of the canonical scores for the given term.

For `heplot3d.candisc`, the default `asp="iso"` now gives a geometrically correct plot, but the third dimension, `CAN3`, is often small. Passing an expanded range in `zlim` to `heplot3d` usually helps.

Value

No useful value; used for the side-effect of producing a canonical HE plot.

Author(s)

Michael Friendly and John Fox

References

Friendly, M. (2006). Data Ellipses, HE Plots and Reduced-Rank Displays for Multivariate Linear Models: SAS Software and Examples *Journal of Statistical Software*, 17(6), 1-42. <http://www.jstatsoft.org/v17/i06/>

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, 16 (2), 421-444. <http://www.math.yorku.ca/SCS/Papers/jcgs-heplots.pdf>

See Also

[candisc](#), [candiscList](#), [heplot](#), [heplot3d](#), [aspect3d](#)

Examples

```
grass.mod <- lm(cbind(N1,N9,N27,N81,N243) ~ Block + Species, data=Grass)

grass.can1 <-candisc(grass.mod, term="Species")
grass.canL <-candiscList(grass.mod)

heplot(grass.can1, scale=6)
heplot(grass.can1, scale=6, terms=TRUE)
heplot(grass.canL, terms=TRUE, ask=FALSE)

heplot3d(grass.can1)
# compare with non-iso scaling
aspect3d(x=1,y=1,z=1)
# or,
# heplot3d(grass.can1, asp=NULL)

## Pottery data, from car package
pottery.mod <- lm(cbind(Al, Fe, Mg, Ca, Na) ~ Site, data=Pottery)
```

```
(pottery.can <-candisc(pottery.mod))

heplot(pottery.can, var.lwd=3)
heplot3d(pottery.can, var.lwd=3, scale=10, zlim=c(-3,3))

## Not run:
play3d(spin3d(axis = c(1, 0, 0), rpm = 5), duration=12)

## End(Not run)

## FootHead data, from heplots package
library(heplots)
data(FootHead)

# use Helmert contrasts for group
contrasts(FootHead$group) <- contr.helmert

foot.mod <- lm(cbind(width, circum,front.back,eye.top,ear.top,jaw)~group, data=FootHead)
foot.can <- candisc(foot.mod)
heplot(foot.can, main="Candisc HE plot",
  hypotheses=list("group.1"="group1","group.2"="group2"),
  col=c("red", "blue", "green3", "green3" ), var.col="red")
```

heplot.candiscList *Canonical Discriminant HE plots*

Description

These functions plot ellipses (or ellipsoids in 3D) in canonical discriminant space representing the hypothesis and error sums-of-squares-and-products matrices for terms in a multivariate linear model. They provide a low-rank 2D (or 3D) view of the effects for that term in the space of maximum discrimination.

Usage

```
## S3 method for class 'candiscList':
heplot(mod, term, ask = interactive(), graphics = TRUE, ...)

## S3 method for class 'candiscList':
heplot3d(mod, term, ask = interactive(), graphics = TRUE, ...)
```

Arguments

mod	A <code>candiscList</code> object for terms in a <code>mlm</code>
term	The name of one term to be plotted for the <code>heplot</code> and <code>heplot3d</code> methods. If not specified, one plot is produced for each term in the <code>mlm</code> object.
ask	If <code>TRUE</code> (the default), a menu of terms is presented; if <code>ask</code> is <code>FALSE</code> , canonical HE plots for all terms are produced.

graphics if TRUE (the default, when running interactively), then the menu of terms to plot is presented in a dialog box rather than as a text menu.

... Arguments to be passed down

Value

No useful value; used for the side-effect of producing canonical HE plots.

Author(s)

Michael Friendly and John Fox

References

Friendly, M. (2006). Data Ellipses, HE Plots and Reduced-Rank Displays for Multivariate Linear Models: SAS Software and Examples *Journal of Statistical Software*, 17(6), 1-42. <http://www.jstatsoft.org/v17/i06/>

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, 16(2) 421-444. <http://www.math.yorku.ca/SCS/Papers/jcgs-heplots.pdf>

See Also

[candisc](#), [candiscList](#), [heplot](#), [heplot3d](#)

HSB

High School and Beyond Data

Description

The High School and Beyond Project was a longitudinal study of students in the U.S. carried out in 1980 by the National Center for Education Statistics. Data were collected from 58,270 high school students (28,240 seniors and 30,030 sophomores) and 1,015 secondary schools. The HSB data frame is sample of 600 observations, of unknown characteristics, originally taken from Tatsuoka (1988).

Usage

```
data(HSB)
```

Format

A data frame with 600 observations on the following 15 variables. There is no missing data.

`id` Observation id: a numeric vector

`gender` a factor with levels `male` `female`

`race` Race or ethnicity: a factor with levels `hispanic` `asian` `african-amer` `white`

```

ses Socioeconomic status: a factor with levels low middle high
sch School type: a factor with levels public private
prog High school program: a factor with levels general academic vocation
locus Locus of control: a numeric vector
concept Self-concept: a numeric vector
mot Motivation: a numeric vector
career Career plan: a factor with levels clerical craftsman farmer homemaker laborer
  manager military operative prof1 prof2 proprietor protective sales
  school service technical not working
read Standardized reading score: a numeric vector
write Standardized writing score: a numeric vector
math Standardized math score: a numeric vector
sci Standardized science score: a numeric vector
ss Standardized social science (civics) score: a numeric vector

```

Source

Tatsuoka, M. M. (1988). *Multivariate Analysis: Techniques for Educational and Psychological Research* (2nd ed.). New York: Macmillan, Appendix F, 430-442.

Retrieved from: <http://www.gseis.ucla.edu/courses/data/hbs6.dta>

References

High School and Beyond data files: <http://www.sscnet.ucla.edu/issr/da/index/techinfo/I78961.HTM>

Examples

```

str(HSB)
# main effects model
hsb.mod <- lm( cbind(read, write, math, sci, ss) ~
  gender + race + ses + sch + prog, data=HSB)
Anova(hsb.mod)

# Add some interactions
hsb.mod1 <- update(hsb.mod, . ~ . + gender:race + ses:prog)
heplot(hsb.mod1, col=palette()[c(2,1,3:6)], variables=c("read", "math"))

hsb.can1 <- candisc(hsb.mod1, term="race")
heplot(hsb.can1, col=c("red", "black"))

# show canonical results for all terms
hsb.can <- candiscList(hsb.mod)
hsb.can

```

Wolves

Wolf skulls

Description

Skull morphometric data on Rocky Mountain and Arctic wolves (*Canis Lupus L.*) taken from Morrison (1990), originally from Jolicoeur (1959).

Usage

`data(Wolves)`

Format

A data frame with 25 observations on the following 11 variables.

`group` a factor with levels `ar:f ar:m rm:f rm:m`, comprising the combinations of `location` and `sex`

`location` a factor with levels `ar=Arctic, rm=Rocky Mountain`

`sex` a factor with levels `f=female, m=male`

`x1` palatal length, a numeric vector

`x2` postpalatal length, a numeric vector

`x3` zygomatic width, a numeric vector

`x4` palatal width outside first upper molars, a numeric vector

`x5` palatal width inside second upper molars, a numeric vector

`x6` postglenoid foramina width, a numeric vector

`x7` interorbital width, a numeric vector

`x8` braincase width, a numeric vector

`x9` crown length, a numeric vector

Details

All variables are expressed in millimeters.

The goal was to determine how geographic and sex differences among the wolf populations are determined by these skull measurements. For MANOVA or (canonical) discriminant analysis, the factors `group` or `location` and `sex` provide alternative parameterizations.

Source

Morrison, D. F. *Multivariate Statistical Methods*, (3rd ed.), 1990. New York: McGraw-Hill, p. 288-289.

References

Jolicoeur, P. "Multivariate geographical variation in the wolf *Canis lupis L.*", *Evolution*, XIII, 283–299.

Examples

```
data(Wolves)

# using group
wolf.mod <-lm(cbind(x1,x2,x3,x4,x5,x6,x7,x8,x9)~group, data=Wolves)
Anova(wolf.mod)

(wolf.can <-candisc(wolf.mod))
plot(wolf.can)
heplot(wolf.can)

# using location, sex
wolf.mod2 <-lm(cbind(x1,x2,x3,x4,x5,x6,x7,x8,x9)~location*sex, data=Wolves)
Anova(wolf.mod2)

(wolf.can2 <-candiscList(wolf.mod2))
plot(wolf.can2)
```

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print.candiscList(*candiscList*), 6

summary.candisc(*candisc*), 2
summary.candiscList
 (*candiscList*), 6

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