

Package ‘anacor’

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Title Simple and Canonical Correspondence Analysis.

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Description Performs simple and canonical CA (covariates on rows/columns) on a two-way frequency table (with missings) by means of SVD. Different scaling methods (standard, centroid, Benzecri, Goodman) as well as various plots including confidence ellipsoids are provided.

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anacor-package	<i>Simple and Canonical Correspondence Analysis</i>
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Description

This package performs simple and canonical CA on a two-way frequency table (with missings) by means of SVD. Different scaling methods (standard, centroid, Benzecri, Goodman) as well as various plots including confidence ellipsoids are provided.

Details

Package: anacor
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The main function of the package is `anacor()` which performs simple CA. The input dataset `tab` is a (incomplete) frequency table. Various scaling options in terms of standard, centroid, Benzecri, and Goodman scaling are provided. They can be specified using the `scaling` argument. If covariates for row/column scores are provided, canonical CA will be computed. Utility functions to create various types of indicator matrices are implemented.

Author(s)

Jan de Leeuw, Patrick Mair

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References

de Leeuw, J. and Mair, P. (2009). Simple and Canonical Correspondence Analysis Using the R Package anacor. *Journal of Statistical Software*, 31(5), 1-18.

See Also

[anacor](#)

Examples

```
data(tocher)
res <- anacor(tocher)
res
summary(res)
```

anacor

Simple and Canonical Correspondence Analysis

Description

This function performs simple and canonical CA for incomplete tables based on SVD. Different scaling methods for row and column scores are provided.

Usage

```
anacor(tab, ndim = 2, row.covariates, col.covariates,
        scaling = c("Benzecri", "Benzecri"), ellipse = TRUE, eps = 1e-06)
```

```
## S3 method for class 'anacor'
print(x, ...)
## S3 method for class 'anacor'
summary(object, ...)
```

Arguments

tab	Data frame of dimension n times m with frequencies. Missings are coded as NA.
ndim	Number of dimensions.
row.covariates	Matrix with n rows containing covariates for the row scores.
col.covariates	Matrix with m rows containing covariates for the column scores.
scaling	A vector with two elements. The first one corresponds to the method for row scaling, the second one for column scaling. Available scaling methods are "standard", "centroid", "Benzecri", "Goodman".
ellipse	If TRUE, confidence ellipses are computed.
eps	Convergence criterion for reconstitution algorithm.
x	Object of class "anacor" in print.anacor.
object	Object of class "anacor" in summary.anacor.
...	Additional arguments ignored.

Details

Missing values in `tab` are imputed using the reconstitution algorithm. Setting `scaling` to "standard" leads to standard coordinates. Principal coordinates can be computed by means of Benzecri decomposition. Furthermore, scores can be scaled around their centroid. Goodman scaling is based on Fisher-Maug decomposition.

For large datasets it is suggested to set `ellipse = FALSE`. If `conf = TRUE`, make sure that there are no rows and columns that have full 0 entries.

Value

<code>row.scores</code>	Scaled row scores.
<code>col.scores</code>	Scaled column scores.
<code>ndim</code>	Number of dimensions extracted.
<code>chisq</code>	Total chi-square value.
<code>chisq.decomp</code>	Chi-square decomposition across dimensions with p-values.
<code>singular.values</code>	Singular values without trivial solution.
<code>se.singular.values</code>	Standard errors for the singular values.
<code>left.singvec</code>	Left singular vectors without trivial solution.
<code>right.singvec</code>	Right singular vectors without trivial solution.
<code>eigen.values</code>	Eigenvalues without trivial solution.
<code>datname</code>	Name of the dataset.
<code>tab</code>	Table with imputed frequencies in case of missings.
<code>row.covariates</code>	Matrix with row covariates.
<code>col.covariates</code>	Matrix with column covariates.
<code>scaling</code>	Scaling Method.
<code>bdmat</code>	List of matrices with observed and fitted Benzecri distances for rows and columns.
<code>rmse</code>	Root mean squared error of Benzecri distances (rows and columns).
<code>row.acov</code>	Covariance matrix for row scores.
<code>col.acov</code>	Covariance matrix for column scores.
<code>cancoef</code>	List containing canonical coefficients (CCA only).
<code>sitescores</code>	List containing the site scores (CCA only).
<code>isetcor</code>	List containing the intraset correlations (CCA only).

Author(s)

Jan de Leeuw, Patrick Mair

References

De Leeuw, J. and Mair, P. (2009). Simple and Canonical Correspondence Analysis Using the R Package `anacor`. *Journal of Statistical Software*, 31(5), 1-18. <http://www.jstatsoft.org/v31/i05/>

See Also[plot.anacor](#)**Examples**

```
## simple CA on Tocher data, asymmetric coordinates
data(tocher)
res <- anacor(tocher, scaling = c("standard", "centroid"))
res
summary(res)

## 2- and 5-dimensional solutions for bitterling data, Benzecri scaling
data(bitterling)
res1 <- anacor(bitterling, ndim = 2, scaling = c("Benzecri", "Benzecri"))
res2 <- anacor(bitterling, ndim = 5, scaling = c("Benzecri", "Benzecri"))
res1
res2

## Canonical CA on Maxwell data, Goodman scaling
data(maxwell)
res <- anacor(maxwell$table, row.covariates = maxwell$row.covariates,
scaling = c("Goodman", "Goodman"))
res
summary(res)
```

bitterling

Bitterling

Description

This dataset concerns reproductive behavior of male bitterlings with data derived from 13 sequences using a moving time-window of size two.

Usage

```
data(bitterling)
```

Format

A frequency tables with bitterling reproductive behavior at time point 1 (rows) and at time point 2 (columns).

jk jerking

tu turning beats

hb head butting

chs chasing
ft fleeing
qu quivering
le leading
hdp head down posture
sk skimming
sn snapping
chf chafing
ffl finflickering

References

Wiepkema, P.R. (1961). An ethological analysis of the reproductive behavior of the bitterling (*rhodeus amarus bloch*). Archives Neerlandais Zoologique, 14, 103-199.

Examples

```
data(bitterling)
```

burtTable

Creates Burt Matrix

Description

Utility function to produce a Burt matrix out of a data-frame.

Usage

```
burtTable(data)
```

Arguments

data Data frame to be converted.

See Also

[expandFrame](#), [mkIndiList](#)

Examples

```
## sleeping bags
data(sleeping)
sleeping_cat <- sleeping
temp_cat <- cut(sleeping$Temperature, c(-20, -1, 7), labels = c("warm", "cold"))
sleeping_cat$Temperature <- temp_cat
weight_cat <- cut(sleeping$Weight, c(700, 1100, 2200), labels = c("light", "heavy"))
sleeping_cat$Weight <- weight_cat
price_cat <- cut(sleeping$Price, c(100, 250, 350, 700),
labels = c("cheap", "medium", "expensive"))
sleeping_cat$Price <- price_cat
sleeping_cat
burtTable(sleeping_cat)
```

expandFrame

Expand Matrix

Description

This utility function expands a matrix or data frame to an indicator supermatrix and optionally converts this to a data frame again. By default NA becomes zero and constant rows and columns are eliminated.

Usage

```
expandFrame(tab, clean = TRUE, zero = TRUE, returnFrame = TRUE)
```

Arguments

tab	Data frame (factors). Missings are coded as NA.
clean	If TRUE, rows and columns with 0 margins in data frame are deleted.
zero	If TRUE, NA's are replaced by 0.
returnFrame	If TRUE, a data frame is returned; if FALSE a matrix.

See Also

[burtTable](#), [mkIndiList](#)

Examples

```
## sleeping bags
data(sleeping)
sleeping_cat <- sleeping
temp_cat <- cut(sleeping$Temperature, c(-20, -1, 7), labels = c("warm", "cold"))
sleeping_cat$Temperature <- temp_cat
```

```
weight_cat <- cut(sleeping$Weight, c(700, 1100, 2200), labels = c("light", "heavy"))
sleeping_cat$Weight <- weight_cat
price_cat <- cut(sleeping$Price, c(100, 250, 350, 700),
labels = c("cheap", "medium", "expensive"))
sleeping_cat$Price <- price_cat
sleeping_cat
expandFrame(sleeping_cat)
```

galton

Galton's RFF data

Description

Records of family faculties cross-classification of midparent height and adult children height in inches.

Usage

```
data(galton)
```

Format

A frequency table with 11 times 14 height classifications in inches.

References

Galton, F. (1889). *Natural Inheritance*. London: MacMillan.

Examples

```
data(galton)
```

glass

Glass data

Description

Table with occupational status of fathers versus occupational status of their sons for a sample of 3497 British families.

Usage

```
data(glass)
```


Format

Rows represent occupation of fathers, columns occupation of sons.

PROF professional and high administrative
EXEC managerial and executive
HSUP higher supervisory
LSUP lower supervisory
SKIL skilled manual and routine nonmanual
SEMI semi-skilled manual
UNSK unskilled manual

References

Glass, D.V. (1954). Social Mobility in Britain. Glencoe: Free Press.

Examples

```
data(glass)
## maybe str(glass) ; plot(glass) ...
```

maxwell

Maxwell's data

Description

This data set is a hypothetical data set originally contrived by Maxwell (1961) for demonstrating his method of discriminant analysis. The data consist of three criterion groups, schizophrenic, manic-depressive and anxiety state, and four binary predictor variables each indicating either presence (1) or absence (0) of a certain symptom. The four symptoms are anxiety suspicion, schizophrenic type of thought disorders, and delusions of guilt. These four binary variables were factorially combined to form 16 distinct patterns of symptoms (predictor patterns), and each of these patterns is identified with a row of the table, which contains the cross-classification of 620 patients according to the 16 patterns of symptoms and the three criterion groups.

Usage

```
data(maxwell)
```

Format

A list with the frequency table as the first element and the row covariates as the second.

Details

This dataset can be used for canonical CA. The binary predictor variables can be considered as row covariates.

References

Maxwell, A.E. (1961). Canonical variate analysis when the variables are dichotomous. *Educational and Psychological Measurement*, 21,259-271.

Examples

```
data(maxwell)
## maybe str(maxwell) ; plot(maxwell) ...
```

mkIndiList

Converts Data Frame to Indicator Matrix

Description

This function takes a data frame, a vector of types, a list of knot vectors, and a vector of orders. It returns a list of codings for the variables, i.e., crisp indicator, numerical version, or fuzzy indicator.

Usage

```
mkIndiList(data, type = rep("C",dim(data)[2]), knots, ord)
```

Arguments

data	Data frame to be converted.
type	If "C", a crisp indicator is returned; if "A", a numerical version; if "F", the b-spline basis as a fuzzy indicator.
knots	List of knot sequences for type-F coding.
ord	Vector with b-spline order for type-F coding.

Details

For the fuzzy coding, the variable values need to be provided as integers. Each list element contains a vector with knots (breaks) for each variable separately. The order is defined through the ord argument as vector (again, for each variable). See bsplines help file for more details.

See Also

[expandFrame](#), [burtTable](#)

Examples

```

## sleeping bags crisp and numeric
data(sleeping)
sleeping_cat <- sleeping
temp_cat <- cut(sleeping$Temperature, c(-20, -1, 7), labels = c("warm", "cold"))
sleeping_cat$Temperature <- temp_cat
weight_cat <- cut(sleeping$Weight, c(700, 1100, 2200), labels = c("light", "heavy"))
sleeping_cat$Weight <- weight_cat
price_cat <- cut(sleeping$Price, c(100, 250, 350, 700),
labels = c("cheap", "medium", "expensive"))
sleeping_cat$Price <- price_cat
sleeping_cat
mkIndiList(sleeping_cat)      ## crisp
mkIndiList(sleeping_cat, type = rep("A", ncol(sleeping_cat)))      ## numeric
mkIndiList(sleeping_cat, type = c("A","A","A","C"))      ## mixed

## artificial data fuzzy coding
x1 <- sample(1:6, 20, replace = TRUE)
x2 <- sample(1:3, 20, replace = TRUE)
data <- data.frame(x1,x2)
knots <- list(c(1,3,5,6), c(1,2,3))
ord <- c(2,1)
mkIndiList(data, type = c("F","F"), knots = knots, ord = ord)

## Also mixed indicator versions are possible
mkIndiList(data, type = c("C","F"), knots = knots, ord = ord)

```

plot.anacor

2-D and 3D plots for anacor solution

Description

These functions produce various 2- and 3-dimensional plots for objects of class "anacor"

Usage

```

## S3 method for class 'anacor'
plot(x, plot.type, plot.dim = c(1,2), legpos = "top", arrows = FALSE, conf = 0.95,
wlines = 0, xlab, ylab, main, type, xlim, ylim, cex.axis2, ...)

## S3 method for class 'anacor'
plot3d(x, plot.type, plot.dim = c(1,2,3), col.r = "RED", col.c = "BLUE",
arrows = TRUE, xlab, ylab, zlab, main, ...)

## S3 method for class 'anacor'
plot3dstatic(x, plot.type, plot.dim = c(1,2,3), col.r = "RED", col.c = "BLUE",
arrows = TRUE, main, xlab, ylab, zlab, xlim, ylim, zlim, ...)

```

Arguments

x	Object of class "anacor".
plot.type	Type of plot to be produced (details see below): 2-D and 3-D for "jointplot", "rowplot", and "colplot"; 2-D for "regplot", "graphplot", "benzplot", "transplot", and "orddiag".
plot.dim	Vector of length 2 with Dimensions to be plotted. For "regplot" a single value should be provided, for "transplot" more than two dimensions are allowed, and for "benzplot" this argument is ignored.
legpos	Position of the legend (for "transplot" only)
conf	Ellipsoid confidence level for "jointplot", "rowplot", and "colplot", assuming that the ellipse where computed in anacor(). If NULL, no ellipsoids are drawn.
arrows	If TRUE the points in "jointplot", "rowplot", and "colplot" are connected with the origin.
wlines	For "graphplot" only: If 0, all lines are of the same thickness. For values > 0 line thickness indicates the strength of the pull
col.r	Color for row score plots
col.c	Color for column score plots
xlab	Label x-axis.
ylab	Label y-axis.
zlab	Label z-axis.
xlim	Scale x-axis.
ylim	Scale y-axis.
zlim	Scale z-axis.
main	Plot title.
type	Whether points, lines or both should be plotted; for "regplot" and "transplot" only.
cex.axis2	For "regplot" only. The magnification to be used for the category labels in the scaled solution relative to the current setting of cex.
...	Additional graphical parameters.

Details

The following plot types are provided: "jointplot" plots row and column scores into the same device, "rowplot" and "colplot" plot the row scores and column scores, respectively, in separate devices. For these types of plots 3-dimensional versions are provided. The graph plot is an unlabeled version of the joint plot where the points are connected by lines. Options are provided (wlines) to steer the line thickness indicating the connection strength.

The regression plot ("regplot") provides two plots. First, the unscaled solution is plotted. A frequency grid for the row categories (x-axis) and column categories (y-axis) is produced. The regression line is based on the category weighted means of the relative frequencies: the blue line on the column-wise means on the x-axis and the column category on the y-axis, the red line is based

on the row categories on the x-axis and the row-wise means on the y-axis. In a second device the scaled solution is plotted. The frequency grid is determined by the row scores (x-axis) and the column scores (y-axis). Now, instead of the row/column categories, the column scores (black line y-axis) and the row scores (red line x-axis) are used.

The transformation plot ("transplot") plots the row/column categories against the row/column scores. The Benzecri plot ("benzplot") plots the observed distances against the fitted distances. It is assumed that the CA result is Benzecri scaled. The ordination diagram ("orddiag") for CCA produces a joint plot and includes the column and row covariates based on intraset correlations.

Author(s)

Jan de Leeuw, Patrick Mair

References

de Leeuw, J., & Mair, P. (2007). Simple and canonical correspondence analysis using the R package anacor. Preprint available at <http://gifi.stat.ucla.edu/anacor.pdf>

See Also

[anacor](#)

Examples

```
##Regression plots using Glass data
data(glass)
res <- anacor(glass)
plot(res, plot.type = "regplot", xlab = "fathers occupation", ylab = "sons occupation")

## Benzecri Plots for bitterling data
data(bitterling)
res1 <- anacor(bitterling, ndim = 2, scaling = c("Benzecri", "Benzecri"))
res2 <- anacor(bitterling, ndim = 5, scaling = c("Benzecri", "Benzecri"))
res2
plot(res1, plot.type = "benzplot", main = "Benzecri Distances (2D)")
plot(res2, plot.type = "benzplot", main = "Benzecri Distances (5D)")

## Column score plot, transformation plot, and ordination diagram for canonical CA
data(maxwell)
res <- anacor(maxwell$table, row.covariates = maxwell$row.covariates,
scaling = c("Goodman", "Goodman"))
res
plot(res, plot.type = "colplot", xlim = c(-1.5,1), conf = NULL)
plot(res, plot.type = "transplot", legpos = "topright")
plot(res, plot.type = "orddiag")
```

sleeping	<i>Sleeping Bags</i>
----------	----------------------

Description

This data set provides 4 variables measured on 21 sleeping bags. The variables are temperature, weight, price, and material.

Usage

```
sleeping
```

Format

A data frame of dimension 21 times 4.

References

Prediger, S. (1997). Symbolic objects in formal concept analysis. In G. Mineau, and A. Fall (eds.), Proceedings of the 2nd International Symposium on Knowledge, Retrieval, Use, and Storage for Efficiency.

Examples

```
data(sleeping)
sleeping
```

spider	<i>Hunting spider data</i>
--------	----------------------------

Description

Abundance of hunting spiders in a Dutch dune area.

Usage

```
data(glass)
```

Format

A list of data frames containing the frequency table (28 observations) and the row covariates.

Table:

Alopacce Abundance of *Alopecosa accentuata*.

Alopcune Abundance of *Alopecosa cuneata*.

Alopfabr Abundance of *Alopecosa fabrilis*.

Arctlute Abundance of *Arctosa lutetiana*.
 Arctperi Abundance of *Arctosa perita*.
 Auloalbi Abundance of *Aulonia albimana*.
 Pardlugu Abundance of *Pardosa lugubris*.
 Pardmont Abundance of *Pardosa monticola*.
 Pardnigr Abundance of *Pardosa nigriceps*.
 Pardpull Abundance of *Pardosa pullata*.
 Trocterr Abundance of *Trochosa terricola*.
 Zoraspin Abundance of *Zora spinimana*.

Row covariates:

WaterCon Log percentage of soil dry mass.
 BareSand Log percentage cover of bare sand.
 FallTwig Log percentage cover of fallen leaves and twigs.
 CoveMoss Log percentage cover of the moss layer.
 CoveHerb Log percentage cover of the herb layer.
 ReflLux Reflection of the soil surface with cloudless sky.

References

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

Examples

```
data(spider)
str(spider)
```

srole

Srole Data

Description

This dataset provides a cross-classification of subjects according to their mental health status and parents' socio-economic status.

Usage

```
data(srole)
```

Format

Mental health has four categories (rows): well, mild symptom formation, moderate symptom formation, and impaired. There are six categories of socio-economic status in the columns.

References

Srole, L., Langner, T.S., Michael, S.T., Opler, M.K., \& Rennie, T.A.C. (1962). Mental health in the metropolis: The midtown Manhattan study. New York: McGraw-Hill.

Examples

```
data(srole)
## maybe str(srole) ; plot(srole) ...
```

tocher	<i>Tocher's eye/hair color data.</i>
--------	--------------------------------------

Description

Eye color and hair color cross-classification of 5387 Scottish school children.

Usage

```
data(tocher)
```

Format

Frequency table with eye color in the rows (blue, light, medium, dark) and hair color in the columns (fair, red, medium, dark, black).

References

Maung, K. (1941). Discriminant analysis of Tocher's eye colour data for Scottish school children. *Annals of Eugenics*, 11, 64-67.

Examples

```
data(tocher)
## maybe str(tocher) ; plot(tocher) ...
```


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