

Package: **acca** (via **r-universe**)

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Title A Canonical Correlation Analysis with Inferential Guaranties

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Description It performs Canonical Correlation Analysis and provides inferential guaranties on the correlation components. The p-values are computed following the resampling method developed in Winkler, A. M., Renaud, O., Smith, S. M., & Nichols, T. E. (2020). Permutation inference for canonical correlation analysis. *NeuroImage*, <doi:10.1016/j.neuroimage.2020.117065>. Furthermore, it provides plotting tools to visualize the results.

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Imports methods, stats, ggplot2, plyr

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acca-package

A Canonical Correlation Analysis with Inferential Guaranties

Description

It performs Canonical Correlation Analysis and provides inferential guaranties on the correlation components. The p-values are computed following the resampling method developed in Winkler, A. M., Renaud, O., Smith, S. M., & Nichols, T. E. (2020). Permutation inference for canonical correlation analysis. *NeuroImage*, <doi:10.1016/j.neuroimage.2020.117065>. Furthermore, it provides plotting tools to visualize the results.

Author(s)

Livio Finos

Examples

```
set.seed(1)
X=matrix(rnorm(500),100,5)
Y=matrix(rnorm(700),100,7)
Z=matrix(rnorm(200),100,2)
mod=cc(X,Y,Z)
mod

ccbiplot(mod)

mod=cc_inference(mod, B = 100, numb_cc = 3)
mod
```

acca-method

Methods for acca objects

Description

Methods for acca objects. The following are methods to extract and manipulate relevant information from a acca object.

Usage

```
## S3 method for class 'acca'
print(x, ...)

## S3 method for class 'acca'
summary(object, ...)
```

Arguments

x	an acca object
...	additional arguments to be passed
object	an acca

cc	cc
----	----

Description

Very similar `cancor()` of package `stats`, but 1) it allows for X and Y to be rank deficient, 2) it allows for categorical variables and 3) it allows for covariates, 4) more (see below).

Usage

```
cc(X, Y, Zx = NULL, Zy = Zx, numb_cc = NULL, fill.na = FALSE)
```

Arguments

X	See x in cancor for a proper documentation.
Y	See y in cancor for a proper documentation.
Zx	(=NULL by default) covariates (i.e. nuisance) of X. If different from NULL, the X are residualized by Zx before entering <code>cc()</code> . IMPORTANT: if Zx is not NULL, include the intercept (if appropriate!)
Zy	(=Zx by default) covariates of Y. Same use of Zx.
numb_cc	number of (pairs of) canonical correlations to be extracted
fill.na	replace NA in X and Y with column mean before enter <code>cc()</code> .

Value

It returns an acca object. This object contains the same list as returned by `cc`, while it also contains `prop_expl_var` which is a list reporting the proportion of explained (total) variance of X and Y by each component (i.e. mode).

```
L=matrix(rnorm(10),10,1) X=matrix(rnorm(50),10,5) Y=matrix(rnorm(70),10,7) Z=matrix(rnorm(20),10,2)
```

```
X[,1]=X[,1]+2*L Y[,1]=Y[,1]+2*L mod=cc(X,Y,Z) mod
```

```
ccbiplot(mod)
```

 ccbiplot

ccbiplot

Description

The function adapts the `ggbiplot::ggbiplot()` function to an `acca`-object.

Usage

```
ccbiplot(
  pcobj,
  choices = 1:2,
  scale = 1,
  pc.biplot = TRUE,
  obs.scale = 1 - scale,
  var.scale = scale,
  groups = NULL,
  shapes = NULL,
  ellipse = FALSE,
  ellipse.prob = 0.68,
  labels = NULL,
  labels.size = 3,
  alpha = 1,
  var.axes = TRUE,
  circle = FALSE,
  circle.prob = 0.69,
  varname.size = 3,
  varname.adjust = 1.5,
  varname.abbrev = FALSE,
  arrows.color = NULL,
  ...
)
```

Arguments

<code>pcobj</code>	an object returned by <code>acca:cc()</code>
<code>choices</code>	which PCs to plot
<code>scale</code>	covariance biplot (<code>scale = 1</code>), form biplot (<code>scale = 0</code>). When <code>scale = 1</code> , the inner product between the variables approximates the covariance and the distance between the points approximates the Mahalanobis distance.
<code>pc.biplot</code>	for compatibility with <code>biplot.princomp()</code>
<code>obs.scale</code>	scale factor to apply to observations
<code>var.scale</code>	scale factor to apply to variables
<code>groups</code>	optional factor variable indicating the groups that the observations belong to. If provided the points will be colored according to groups

shapes	which shapes to use when plotting observations
ellipse	draw a normal data ellipse for each group?
ellipse.prob	size of the ellipse in Normal probability
labels	optional vector of labels for the observations
labels.size	size of the text used for the labels
alpha	alpha transparency value for the points (0 = transparent, 1 = opaque)
var.axes	draw arrows for the variables?
circle	draw a correlation circle?
circle.prob	size of the circle in <code>qchisq(circle.prob, df = 2)</code>
varname.size	size of the text for variable names
varname.adjust	adjustment factor the placement of the variable names, ≥ 1 means farther from the arrow
varname.abbrev	whether or not to abbreviate the variable names
arrows.color	color of the arrows
...	not used yet

Value

It returns a `ggplot` object.

cc_inference	<i>cc_inference</i>
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Description

For each pairs of components, it computes p-values to test the null hypothesis of no correlation between components. The p-values are computed following the resampling method developed in Winkler, A. M., Renaud, O., Smith, S. M., & Nichols, T. E. (2020). Permutation inference for canonical correlation analysis. *NeuroImage*, 220, 117065. <https://doi.org/10.1016/j.neuroimage.2020.117065>.

Usage

```
cc_inference(
  mod,
  B = 100,
  alpha_max = 0.5,
  numb_cc = NULL,
  resamp_type = "sign-flip",
  light = FALSE
)
```

Arguments

mod	an acca object.
B	(100 by default) number of random sampling
alpha_max	stop if p-value > alpha_max (alpha_max=0.5 by default).
numb_cc	stop after computing p-values for the first numb_cc are computed (numb_cc=NULL - the default - means compute all).
resamp_type	"sign-flip" (by default) or "permutation"
light	If TRUE the orthogonalization of the residuals of the projection on Z is not performed. For large sample size the two methods tend to overlap.

Value

It returns an acca object (see `cc`) with p-values for each pair of the numb_cc components.

Examples

```
set.seed(1)
X=matrix(rnorm(500),100,5)
Y=matrix(rnorm(700),100,7)
Z=matrix(rnorm(200),100,2)
mod=cc(X,Y,Z)
mod

ccbiplot(mod)

mod=cc_inference(mod, B = 100, numb_cc = 3)
mod
```

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