Package ‘FRCC’

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Title Fast Regularized Canonical Correlation Analysis
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custom.draw.circle  

Draws a circle

Description

Given a center, radius and color, this function draws a circle.

Usage

custom.draw.circle(x, y, r, col)

Arguments

x  
X coordinate of the center

y  
Y coordinate of the center

r  
Radius of the circle

col  
Color of the circle

Value

This function does not return a value, it just draws a circle.

Author(s)

Michael Bedward

References

http://www.r-bloggers.com/circle-packing-with-r/

frcc

This function implements the Fast Regularized Canonical Correlation Analysis

Description

This function implements the Fast Regularized Canonical Correlation algorithm described in [Cruz-Cano et al., 2014].

The main idea of the algorithm is using the minimum risk estimators of the correlation matrices described in [Schafer and Strimmer, 2008] during the calculation of the Canonical correlation Structure.

It can be considered an extension of the work for two set of variables (blocks) mentioned in [Tenenhaus and Tenenhaus, 2011].
Usage

frcc(X, Y)

Arguments

X numeric matrix (n by p) which contains the observations on the X variables.
Y numeric matrix (n by q) which contains the observations on the Y variables.

Value

A list with the following components of the Canonical Structure:

cor Canonical correlations.
p_values The corresponding p-values for each of the canonical correlations.
canonical_weights_X The canonical weights for the variables of the dataset X.
canonical_weights_Y The canonical weights for the variables of the dataset Y.
canonical_factor_loadings_X The inter-set canonical factor loadings for the variables of the dataset X.
canonical_factor_loadings_Y The inter-set canonical factor loadings for the variables of the dataset Y.

Author(s)

Raul Cruz-Cano

References


Examples

# Example # 1 Multivariate Normal Data
p<-10
q<-10
n<-50
res<-generate_multivariate_normal_sample(p,q,n)
X<-res$X
Y<-res$Y
rownames(X)<-c(1:n)
colnames(X)<-c(1:p)
generate_multivariate_normal_sample

It generates a sample from a multivariate normal distribution function

Description

It generates a sample from a multivariate normal distribution function with the cross-covariance matrix described in [Cruz-Cano et al. 2012].

Usage

generate_multivariate_normal_sample(p, q, n)

Arguments

- **p**: Number of desired variables in the dataset X.
- **q**: Number of desired variables in the dataset Y.
- **n**: Sample size desired.

Value

A list of n sample units with the values for the variables of the data sets X and Y.

Author(s)

Raul Cruz-Cano
References


Examples

```r
p<-10
q<-10
n<-50
res<-generate_multivariate_normal_sample(p,q,n)
X<-res$X
Y<-res$Y
rownames(X)<-c(1:n)
colnames(X)<-c(1:p)
colnames(Y)<-c(1:q)
my_res<-frcc(X,Y)
```

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**microRNA**

**Example data sets**

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**Description**

These are data sets used to demonstrate the functions in this package.

**Usage**

- microRNA
- soilspec
- Topoisomerase_II_Inhibitors

**Format**

Each is a dataframe.

**Examples**

- microRNA
- soilspec
- Topoisomerase_II_Inhibitors
off.diagonal.lambda  \textit{Calculates the value of the shrinkage coefficient for the off-diagonal matrices}

\section*{Description}
Calculates the value of the shrinkage coefficient for the off-diagonal matrices as described in [Cruz-Cano et al., 2012]

\section*{Usage}
\begin{verbatim}
off.diagonal.lambda(xs, p, q)
\end{verbatim}

\section*{Arguments}
\begin{itemize}
\item \texttt{xs} Matrix with the values for the datasets \textit{X} and \textit{Y}.
\item \texttt{p} Number of variables in the dataset \textit{X}.
\item \texttt{q} Number of variables in the dataset \textit{Y}.
\end{itemize}

\section*{Value}
Shrinkage coefficient for the off-diagonal matrices used to calculate the FRCC canonical structure.

\section*{Author(s)}
Raul Cruz-Cano

\section*{References}

\section*{plot_units  \textit{Plots the experimental units in the Canonical Variates Space}}

\section*{Description}
This function plots the experimental units used in the FRCCA as points in a two-dimensional plane in which the axis are the canonical variates selected by the user

\section*{Usage}
\begin{verbatim}
plot_units(X, Y, res.mrcc, i, text_size = 0.8, point_size = 2)
\end{verbatim}
plot_variables

Arguments

X numeric matrix (n by p) which contains the observations on the X variables.
Y numeric matrix (n by p) which contains the observations on the Y variables.
res.mrcc List containing a canonical structure provided by the function frcc for the dataset X and Y.
i Canonical Variate which will be used for the axes (X for horizontal and Y for vertical).
text_size Character expansion factor for the labels of the experimental units.
point_size Character expansion factor for the point representing the experimental units.

Value

This function just creates the units plot. It does not return a value.

Author(s)

Raul Cruz-Cano

References


Examples

#Example: NCI-60 micrRNA Data
data("Topoisomerase_II_Inhibitors")
data("microRNA")
my_res <- frcc(t(microRNA),-1*t(Topoisomerase_II_Inhibitors))
for( i in 1:dim(microRNA)[2])
{
  colnames(microRNA)[i]<-substr(colnames(microRNA)[i], 1, 2)
}#end for i
grDevices::dev.new()
plot_units(t(microRNA),-1*t(Topoisomerase_II_Inhibitors),my_res,1,1,text_size=0.01)

plot_variables

Plot variables in the Canonical Factor Loadings Space

Description

This function plots the variables used in the FRCCA as points in a two-dimensional plane in which the axis are the canonical factor loadings selected by the user.

Usage

plot_variables(res.mrcc, i, j, inner_circle_radius = 0.5, text_size = 0.8)
rearrange.frcc

Arguments

res.mrcc    List containing a canonical structure provided by the function frcc.
i          Canonical Factor Loadings which will be used as the horizontal axis.
j          Canonical Factor Loadings which will be used as the vertical axis.
inner_circle_radius    Radius of the circle which is used to determine which variables are significant.
                        Only the significant variables will be labeled.
text_size    Character expansion factor for the labels of the variables.

Value

This function just creates the variables plot. It does not return a value.

Author(s)

Raul Cruz-Cano

References


Examples

# Example: Multivariate Normal Data
p<-10
q<-10
n<-50
res<-generate_multivariate_normal_sample(p,q,n)
X<-res$X
Y<-res$Y
rownames(X)<-c(1:n)
colnames(X)<-c(1:p)
colnames(Y)<-c(1:q)
my_res<-frcc(X,Y)
grDevices::dev.new()
plot_variables(my_res,1,2,text_size=1.0)

rearrange.frcc    Rearranges the canonical structure according to the canonical correlations

Description

By using the minimum risk estimators of the correlation matrices instead of the sample correlation matrices the FRCC algorithm might disrupt the order of the canonical correlations and hence of the canonical structure. This is unacceptable for the algorithm used to calculate the p-values which requires the canonical correlations to be ordered in a descending order. This function rearranges the canonical structure according to the canonical correlations from largest to smallest.
Usage

`rearrange.frcc(res.frcc)`

Arguments

- `res.frcc`: List containing a canonical structure produced by the function `frcc`.

Value

A list containing the sorted canonical structure.

Author(s)

Raul Cruz-Cano

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