

Package ‘toscca’

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Title Thresholded Ordered Sparse CCA

Version 0.1.0

Description

Performs Thresholded Ordered Sparse Canonical Correlation Analysis (CCA). For more details see Senar, N. (2024) <[doi:10.1093/bioadv/vbae021](https://doi.org/10.1093/bioadv/vbae021)> and Senar, N. et al. (2025) <[doi:10.48550/arXiv.2503.15140](https://doi.org/10.48550/arXiv.2503.15140)>.

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(>= 3.0.0)

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Author Nuria Senar [aut, cre] (ORCID: <<https://orcid.org/0000-0002-1004-5785>>)

Maintainer Nuria Senar <n.senarvilladeamigo@amsterdamumc.nl>

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| | |
|-------------|------------------------|
| cpev.toscca | <i>Calculates cpev</i> |
|-------------|------------------------|

Description

This function calculates cpev w.r.t. a chosen origin.

Usage

cpev.toscca(mat, weights)

Arguments

- mat A matrix.
- weights A numeric vector of canonical weights.

Value

Returns cpev values for the kth or 1:K components.

| | |
|-----------|--|
| fastEigen | <i>Performs eigen decomposition of a matrix in PS space.</i> |
|-----------|--|

Description

Performs eigen decomposition of a matrix in PS space.

Usage

```
fastEigen(A)
```

Arguments

| | |
|---|----------------------|
| A | A square matrix nxn. |
|---|----------------------|

Value

Matrix. Positive definite matrix.

| | |
|----------------|--|
| getCanSubspace | <i>Performs matrix residualisation over estimated canonical vectors by using the null space of the estimated canonical vector to construct a new matrix.</i> |
|----------------|--|

Description

Performs matrix residualisation over estimated canonical vectors by using the null space of the estimated canonical vector to construct a new matrix.

Usage

```
getCanSubspace(mat, vec)
```

Arguments

| | |
|-----|-----------------------------|
| mat | An nxp matrix. |
| vec | A vector of dimensions nxk. |

Details

For nxp matrix

$$\mathbf{A}$$

and pxk vector

$$\alpha$$

, the canonical is compute as $\mathbf{A}_{sub} = \mathbf{A}\alpha(\alpha^T\alpha)\alpha^T$.

Value

An $n \times k$ matrix.

| | |
|----------|----------------------------------|
| getWhich | <i>Get location of required.</i> |
|----------|----------------------------------|

Description

Get location of required.

Usage

```
getWhich(data, fun)
```

Arguments

| | |
|------|--------------------------|
| data | Numeric matrix. |
| fun | Function to search data. |

Value

Returns value matching function fun.

Examples

```
getWhich(rnorm(100), max)
```

| | |
|------------------|---|
| initialiseCanVar | <i>Initialised the canonical vector for the iterative process based on positive eigen values. Then, SVD is performed on that PS matrix.</i> |
|------------------|---|

Description

Initialised the canonical vector for the iterative process based on positive eigen values. Then, SVD is performed on that PS matrix.

Usage

```
initialiseCanVar(A, B)
```

Arguments

| | |
|---|-------------------------|
| A | An $n \times p$ matrix. |
| B | An $n \times q$ matrix. |

Value

An pzp vector.

Examples

```
#sample size etc
N = 10
p = 25
q = 5
# noise
X0 = sapply(1:p, function(x) rnorm(N))
Y0 = sapply(1:q, function(x) rnorm(N))

colnames(X0) = paste0("x", 1:p)
colnames(Y0) = paste0("y", 1:q)

# signal
Z1 = rnorm(N,0,1)

#Some associations with the true signal
alpha = (6:10) / 10
beta = -(2:3) / 10

loc_alpha = 1:length(alpha)
loc_beta = 1:length(beta)

for(j in 1:length(alpha))
  X0[, loc_alpha[j]] = alpha[j] * Z1 + rnorm(N,0,0.3)

for(j in 1:length(beta))
  Y0[, loc_beta[j]] = beta[j] * Z1 + rnorm(N,0,0.3)
cv = initialiseCanVar(X0, Y0)
```

modes

Calculates mode.

Description

Calculates mode.

Usage

```
modes(d)
```

Arguments

d density object.

myHeatmap*Plot heatmap of cv w.r.t. the penalty parameter performance.*

Description

This function plots cca for different thresholds

Usage

```
myHeatmap(  
  mat,  
  palette_values = mpalette,  
  blue = NULL,  
  xlab = "",  
  ylab = "",  
  show_axes = TRUE,  
  show_labels = TRUE,  
  K = NULL  
)
```

Arguments

| | |
|-----------------------------|--|
| <code>mat</code> | A matrix. |
| <code>palette_values</code> | Character string. Vector of colour values for the heatmap. Default is package's palette. |
| <code>blue</code> | Logical. If TRUE, use only scale of blues from palette. |
| <code>xlab</code> | Character. Label for x axis. |
| <code>ylab</code> | Character. Label for y axis. |
| <code>show_axes</code> | Logic. Default is True. |
| <code>show_labels</code> | Logic. Default is True. |
| <code>K</code> | Numeric. Number of components. |

Value

No return value, called for plotting heatmap.

Examples

```
mat <- matrix(rexp(200, rate=.1), ncol=20)/200  
myHeatmap(mat)
```


plt.selstab

*Plot slection stability for penalty parameter performance.***Description**

This function plots cv for different thresholds

Usage

```
plt.selstab(
  object,
  X,
  Y,
  nonz_x,
  nonz_y,
  palette_values = mpalette,
  blue = TRUE,
  mm = TRUE,
  k = 1
)
```

Arguments

| | |
|----------------|---|
| object | A toscca object. |
| X | nxp matrix. Observation matrix. |
| Y | A nxq matrix. Observation matrix. |
| nonz_x | Numeric vector. Sparsity levels of X. |
| nonz_y | Numeric vector. Sparsity levels of Y. |
| palette_values | Character. Name of a palette for the heatmap. Default is "Teal". |
| blue | Logical. If TRUE, use only scale of blues from palette. |
| mm | Logic. Indicates whether there are multiple measurements or not. Default is True. |
| k | Numeric. Component, default k =1. |

Value

No return value, called for selection stability pot.

Examples

```
# example code
#sample size etc
N = 10
p = 25
q = 5
```



```

# noise
X0 = sapply(1:p, function(x) rnorm(N))
Y0 = sapply(1:q, function(x) rnorm(N))

colnames(X0) = paste0("x", 1:p)
colnames(Y0) = paste0("y", 1:q)

# signal
Z1 = rnorm(N,0,10)

#Some associations with the true signal
alpha = (6:10) / 10
beta = -(2:3) / 10

loc_alpha = 1:length(alpha)
loc_beta = 1:length(beta)

for(j in 1:length(alpha))
  X0[, loc_alpha[j]] = alpha[j] * Z1 + rnorm(N,0,0.03)

for(j in 1:length(beta))
  Y0[, loc_beta[j]] = beta[j] * Z1 + rnorm(N,0,0.03)

# performa toscca
X = standardVar(X0)
Y = standardVar(Y0)
K = 2 # number of components to be estimated
nonz_x = c(2,5, 10, 20) # number of nonzero variables for X
nonz_y = c(2, 3, 4) # number of nonzero variables for Y
init = "uniform" # type of initialisation
cca_toscca = toscca(X, Y, nonz_x, nonz_y, K, alpha_init = init,
combination = TRUE, K=1, silent = TRUE, toPlot = FALSE)
plt <- plt.selstab(cca_toscca,X, Y, nonz_x = nonz_x, nonz_y = nonz_y, mm=FALSE)

```

powerMethod

Performs power method.

Description

Performs power method.

Usage

```
powerMethod(mat, vec, tol = 10-6, maxIter = 500, silent = TRUE)
```


Arguments

| | |
|---------|--|
| mat | A square matrix nxn. |
| vec | A vector of dimensions nx1. |
| tol | Convergence criterion. Default is 10^{-6} . |
| maxIter | Maximum iterations. Default is 500. |
| silent | Logical. If TRUE, convergence performance will be printed. |

Value

List: vec: eigen vector; lambda: eigen value; t: total iterations.

| | |
|-------------|---------------------|
| progressBar | <i>Progress bar</i> |
|-------------|---------------------|

Description

Shows progress of a process.

Usage

```
progressBar(end, round)
```

Arguments

| | |
|-------|---|
| end | maximum number of times a process will run. |
| round | current round |

Value

Display in consol of current status.

| | |
|-----------------|--|
| residualisation | <i>Performs matrix residualisation over estimated canonical vectors. There are three types: basic (subtracts scaled estimated latent variable from data), null (uses the null space of the estimated canonical vector to construct a new matrix) and LV (uses SVD to residualise).</i> |
|-----------------|--|

Description

Performs matrix residualisation over estimated canonical vectors. There are three types: basic (subtracts scaled estimated latent variable from data), null (uses the null space of the estimated canonical vector to construct a new matrix) and LV (uses SVD to residualise).

Usage

```
residualisation(
  mat,
  vec,
  spaceMat = NULL,
  type = c("LV", "null", "basic"),
  na.allow = TRUE
)
```

Arguments

| | |
|----------|--|
| mat | An nxp matrix. |
| vec | A vector of dimensions nxk. |
| spaceMat | Only for "null" type residualisation. Default is NULL. |
| type | Character. It can be LV, null or basic depending on which type of residualisation will be performed. |
| na.allow | Logical. If TRUE, NAs will be allowed. |

Value

Matrix.

| | |
|-------------------|---|
| scaledResidualMat | <i>Performs scalling for matrix residualisation based on calculated coefficients.</i> |
|-------------------|---|

Description

Performs scalling for matrix residualisation based on calculated coefficients.

Usage

```
scaledResidualMat(A)
```

Arguments

| | |
|---|----------------|
| A | An nxp matrix. |
|---|----------------|

Value

scaled matrix.

| | |
|----------|---|
| scale_rm | <i>Standardises matrices with multiple measurements per individual.</i> |
|----------|---|

Description

This function standardises matrices with multiple measurements w.r.t. a chosen origin.

Usage

```
scale_rm(mat, origin = NULL, centre = FALSE)
```

Arguments

| | |
|--------|---|
| mat | A matrix. |
| origin | Measurement of reference for standardisation. |
| centre | Logical. TRUE to centre data. Default is FALSE. |

Value

Returns scaled and/or centred values for repeated measurements.

Examples

```
#sample size etc
N = 10
p = 25
q = 5
# noise
X0 = sapply(1:p, function(x) rnorm(N))
Y0 = sapply(1:q, function(x) rnorm(N))

colnames(X0) = paste0("x", 1:p)
colnames(Y0) = paste0("y", 1:q)

# signal
Z1 = rnorm(N,0,1)

#Some associations with the true signal
alpha = (6:10) / 10
beta = -(2:3) / 10

loc_alpha = 1:length(alpha)
loc_beta = 1:length(beta)

for(j in 1:length(alpha))
  X0[, loc_alpha[j]] = alpha[j] * Z1 + rnorm(N,0,0.3)

for(j in 1:length(beta))
```



```

Y0[, loc_beta[j]] = beta[j] * Z1 + rnorm(N,0,0.3)

X = standardVar(X0)
Y = standardVar(Y0)

```

standardVar

Standardise a matrix

Description

This function standardises a matrix or a vector and gives the option to centre or normalise (only vectors).

Usage

```
standardVar(mat, centre = TRUE, normalise = FALSE)
```

Arguments

| | |
|-----------|--|
| mat | Matrix or vector to be standardise. |
| centre | Logical, if true, centre to mean zero. |
| normalise | Logical, if true, performs vector normalisation. |

Value

A matrix or vector with the preferred standardisation

Examples

```

#sample size etc
N = 10
p = 25
q = 5
# noise
X0 = sapply(1:p, function(x) rnorm(N))
Y0 = sapply(1:q, function(x) rnorm(N))

colnames(X0) = paste0("x", 1:p)
colnames(Y0) = paste0("y", 1:q)

# signal
Z1 = rnorm(N,0,1)

#Some associations with the true signal
alpha = (6:10) / 10
beta = -(2:3) / 10

loc_alpha = 1:length(alpha)

```



```

loc_beta = 1:length(beta)

for(j in 1:length(alpha))
  X0[, loc_alpha[j]] = alpha[j] * Z1 + rnorm(N,0,0.3)

for(j in 1:length(beta))
  Y0[, loc_beta[j]] = beta[j] * Z1 + rnorm(N,0,0.3)

X = standardVar(X0)
Y = standardVar(Y0)

```

toscamm.perm

Computes permutatied cc fot TOSCCA-MM

Description

This function estimates sparse canonical vectors for permuted matrices with multiple measurements.

Usage

```

toscamm.perm(
  A,
  B,
  nonzero_a,
  nonzero_b,
  K = 1,
  folds = 1,
  toPlot = FALSE,
  draws = 1000,
  cancel,
  bootCCA = NULL,
  silent = TRUE,
  parallel_logic = TRUE,
  nuisanceVar = 0,
  testStatType = "CC",
  model = "lme",
  lmeformula = " ~ 0 + poly(time,3) + (1|id)",
  arformula = NULL,
  ncores = NULL
)

```

Arguments

| | |
|-----------|-------------------------------------|
| A | A matrix. |
| B | A matrix. |
| nonzero_a | Integer. Threshold parameter for A. |

| | |
|----------------|--|
| nonzero_b | Integer. Threshold parameter for B. |
| K | Integer. Number of components. |
| folds | Integer. Indicates number of folds to perform. |
| toPlot | Logical. Indicates if plots will be produced. Default is FALSE. |
| draws | Integer. Number of draws in permutation. |
| cancor | Numeric vector of length K with estimated canonical correlations. |
| bootCCA | deprecated. |
| silent | Logical. TRUE to keep silent output messages. Default is FALSE. |
| parallel_logic | Logical. TRUE to parallelise folds. Default is FALSE. |
| nuisanceVar | Numeric. Number of nuisance variables. |
| testStatType | Character. Choice of test-statistic c("CC", "Wilks", "Roy"). |
| model | Character. c("lme", "ar"). Model to fit longitudinal latent space. |
| lmeformula | Character. LME formula. Default is " $\sim -1 + \text{time} + (1 \text{id})$ ". |
| arformula | Numeric vector. Choice of ARIMA. Default is c(1,0,0). |
| ncores | numeric. Number of cores to use in parallelisation. Default is detectCores() -1. |

Value

Permuted canonical correlation for ell K and p-values.

List with permuted correlations and p-values.

Examples

```
# example code

# dont run due to parallel processes
#sample size etc
N = 10
p = 25
q = 5
X0 = list()
Y0 = list()

#Some associations with the true signal
cwa = (6:10) / 10
cwb = -(2:3) / 10

alpha = rep(0, p)
beta = rep(0, q)

loc_alpha = 1:length(alpha)
loc_beta = 1:length(beta)

alpha[loc_alpha] = cwa
beta[loc_beta] = cwb
```



```

sg = matrix(c(1, 0.6, 0.3, rep(0, 2),
              0.6, 1, 0.6, 0.3, rep(0, 1),
              0.3, 0.6, 1, 0.6, 0.3,
              rep(0,1), 0.3, 0.6, 1, 0.6,
              rep(0,2), 0.3, 0.6, 1), ncol = 5)

for(i in 1:N)
{
  times = 1:5
  Zi1 = (sin(100*times))^times + times * 0.65 + rnorm(1,0,0.95)
  Zi = cbind(Zi1)
  #Simulate data and add some noise
  X0i = sapply(1:p, function(a) MASS::mvrnorm(1, (Zi %*% t(alpha))[a], Sigma = sg))
  Y0i = sapply(1:q, function(a) MASS::mvrnorm(1, (Zi %*% t(beta))[a], Sigma = sg))

  colnames(X0i) = paste0("X", 1:ncol(X0i))
  colnames(Y0i) = paste0("Y", 1:ncol(Y0i))
  #Check the simulated cross correlation
  #image(cor(X0i, Y0i))

  #Remove some observations
  # p_observed = 1
  X0i = cbind(id=i, time=times, X0i)#[rbinom(length(times),1,p_observed)==1,]
  Y0i = cbind(id=i, time=times, Y0i)#[rbinom(length(times),1,p_observed)==1,]

  X0[[i]] = X0i
  Y0[[i]] = Y0i
}

X0 = do.call("rbind", X0)
Y0 = do.call("rbind", Y0)

X = data.frame(X0); Y = data.frame(Y0)
nonz_a = c(2, 5, 10, 20)
nonz_b = c(2, 3, 4)

mod <- toscamm(X, Y, folds = 2, nonzero_a = nonz_a, nonzero_b = nonz_b, silent = TRUE)
nza <- mod$nonzero_a
nzb <- mod$nonzero_b
cc <- mod$cancor
perm_cc <- toscamm.perm(X,Y, nonzero_a=nza, nonzero_b=nzb,cancor=cc, ncores=2, draws = 10)

```

toscca

Sparse Canonical Correlation Analysis. Computation of CC via NIPALS with soft thresholding.

Description

Sparse Canonical Correlation Analysis. Computation of CC via NIPALS with soft thresholding.

Usage

```
toscca(
  A,
  B,
  nonzero_a,
  nonzero_b,
  K = 1,
  alpha_init = c("eigen", "random", "uniform"),
  folds = 1,
  silent = FALSE,
  toPlot = TRUE,
  typeResid = "basic",
  combination = FALSE,
  parallel_logic = FALSE
)
```

Arguments

| | |
|----------------------|---|
| A, B | Data matrices. |
| nonzero_a, nonzero_b | Numeric. Scalar or vector over the number of nonzeros allowed for a correlation estimate. |
| K | Numeric. Number of components to be computed. |
| alpha_init | Character. Type initialisation for α . Default is "eigen". |
| folds | Numeric. Number of folds for the cross-validation process. |
| silent | Logical. If FALSE, a progress bar will appear on the console. Default is FALSE. |
| toPlot | Logical. If TRUE, plot will be generated automatically showing the estimated canonical weights. Default is TRUE. |
| typeResid | Character. Choice of residualisation technique. Options are basic (default), null and LV. |
| combination | Logical. If TRUE, the algorithm will search for the best combination of sparsity choice nonzero_a and nonzero_b for each component. This should be used for exploratory analysis. Default is FALSE. |
| parallel_logic | Logical. If TRUE, cross-validation is done in parallel. Default is FALSE. |

Value

a list with the following elements:

List with estimated toscca parameters.

Examples

```

#sample size etc
N = 10
p = 25
q = 5
# noise
X0 = sapply(1:p, function(x) rnorm(N))
Y0 = sapply(1:q, function(x) rnorm(N))

colnames(X0) = paste0("x", 1:p)
colnames(Y0) = paste0("y", 1:q)

# signal
Z1 = rnorm(N,0,1)

#Some associations with the true signal
alpha = (6:10) / 10
beta = -(2:3) / 10

loc_alpha = 1:length(alpha)
loc_beta = 1:length(beta)

for(j in 1:length(alpha))
  X0[, loc_alpha[j]] = alpha[j] * Z1 + rnorm(N,0,0.3)

for(j in 1:length(beta))
  Y0[, loc_beta[j]] = beta[j] * Z1 + rnorm(N,0,0.3)

X = standardVar(X0)
Y = standardVar(Y0)
K = 2                                # number of components to be estimated
nonz_x = c(2,5, 10, 20)              # number of nonzero variables for X
nonz_y = c(2, 3, 4)                  # number of nonzero variables for Y
init = "uniform"                     # type of initialisation
cca_toscca = toscca(X, Y, nonz_x, nonz_y, K, alpha_init = init, silent = TRUE, toPlot = FALSE)

```

toscca.core

Sparse Canonical Correlation Analysis. Computation of CC via NIPALS with soft thresholding.

Description

Sparse Canonical Correlation Analysis. Computation of CC via NIPALS with soft thresholding.

Usage

```
toscca.core(
```



```

    alphaInit,
    A,
    B,
    nonzero_a,
    nonzero_b,
    iter = 20,
    tol = 10^(-6),
    silent = FALSE
  )

```

Arguments

| | |
|----------------------|---|
| alphaInit | Character. Type initialisation for α . |
| A, B | Data matrices. |
| nonzero_a, nonzero_b | Numeric. Scalar or vector over the number of non zeroes allowed for a correlation estimate. |
| iter | Numeric. Maximum number of iterations. Default is 20. |
| tol | Numeric. Tolerance threshold. Default is 10^{-6} . |
| silent | Logical. If FALSE, a progress bar will appear on the console. Default is FALSE. |

Value

a list with the following elements:

| | |
|--------------|--|
| toscca.folds | <i>Sparse Canonical Correlation Analysis. Computation of CC via NIPALS with soft thresholding.</i> |
|--------------|--|

Description

Sparse Canonical Correlation Analysis. Computation of CC via NIPALS with soft thresholding.

Usage

```

toscca.folds(
  A,
  B,
  nonzero_a,
  nonzero_b,
  alpha_init,
  folds = 1,
  parallel_logic = FALSE,

```



```

    silent = FALSE,
    toPlot = TRUE,
    ATest_res = NULL,
    BTest_res = NULL
  )

```

Arguments

| | |
|----------------------|---|
| A, B | Data matrices. |
| nonzero_a, nonzero_b | Numeric. Scalar or vector over the number of nonzeros allowed for a correlation estimate. |
| alpha_init | Character. Type initialisation for α . Default is "eigen". |
| folds | Integer. Indicates number of folds to perform. |
| parallel_logic | Logical. TRUE to parallelise folds. Default is FALSE. |
| silent | Logical. TRUE to keep silent output messages. Default is FALSE. |
| toPlot | Logical. TRUE to plot results. |
| ATest_res | NULL. Keep NULL. |
| BTest_res | NULL. Keep NULL. |

Value

a list with the following elements:

| | |
|-----------|-----------------------------|
| toscca.lv | <i>Get latent variables</i> |
|-----------|-----------------------------|

Description

Gets latent variables from data and estimates.

Usage

```
toscca.lv(data, alpha, beta)
```

Arguments

| | |
|-------|--|
| data | List containint both observation amtrices. |
| alpha | px1 numeric vector. canonical weights for X. |
| beta | qx1 numeric vector. canonical weights for Y. |

| | |
|-------------|---------------------------------------|
| toscca.perm | <i>Permutation testing for toscca</i> |
|-------------|---------------------------------------|

Description

This function performs permutation testing on CC estimates.

Usage

```
toscca.perm(
  A,
  B,
  nonzero_a,
  nonzero_b,
  K,
  alpha_init = c("eigen", "random", "uniform"),
  folds = 1,
  toPlot = FALSE,
  draws = 20,
  cancor,
  silent = TRUE,
  parallel_logic = TRUE,
  nuisanceVar = 0,
  testStatType = "CC",
  ncores = NULL
)
```

Arguments

| | |
|----------------------|--|
| A, B | Data matrices. |
| nonzero_a, nonzero_b | Numeric. Scalar or vector over the number of nonzeros allowed for a correlation estimate. |
| K | Numeric. Number of components to be computed. |
| alpha_init | Character. Type initialisation for α . Default is "eigen". |
| folds | Numeric. Number of folds for the cross-validation process. |
| toPlot | Logical. If TRUE, plot will be generated automatically showing the estimated canonical weights. Default is TRUE. |
| draws | Numeric. Number of permutations for each component. |
| cancor | Numeric. Scalar or vector: anonical correlation estimate(s). |
| silent | Logical. If FALSE, a progress bar will appear on the console. Default is FALSE. |
| parallel_logic | Logical. If TRUE, cross-validation is done in parallel. Default is FALSE. |

| | |
|--------------|--|
| nuisanceVar | Data with nuisance variables. For statistic type. |
| testStatType | Character. Choice of statistic. Options are CC (default), Wilks and Roy. |
| ncores | numeric. Number of cores to use in parallelisation. Default is detectCores() -1. |

Details

For an exploratory analysis `nonzero_a` and `nonzero_b` can be vectors. The algorithm will then search for the best combination of sparsity choice `nonzero_a` and `nonzero_b` for each component.

Value

Matrix with permutation estimates.

List with permuted correlations and p-values.

Examples

```
#sample size etc
N = 10
p = 25
q = 5
# noise
X0 = sapply(1:p, function(x) rnorm(N))
Y0 = sapply(1:q, function(x) rnorm(N))

colnames(X0) = paste0("x", 1:p)
colnames(Y0) = paste0("y", 1:q)

# signal
Z1 = rnorm(N,0,1)

#Some associations with the true signal
alpha = (6:10) / 10
beta = -(2:3) / 10

loc_alpha = 1:length(alpha)
loc_beta = 1:length(beta)

for(j in 1:length(alpha))
  X0[, loc_alpha[j]] = alpha[j] * Z1 + rnorm(N,0,0.3)

for(j in 1:length(beta))
  Y0[, loc_beta[j]] = beta[j] * Z1 + rnorm(N,0,0.3)

X = standardVar(X0)
Y = standardVar(Y0)
K = 2                                     # number of components to be estimated
nonz_x = c(2,5, 10, 20)                 # number of nonzero variables for X
nonz_y = c(1, 2, 3, 4)                   # number of nonzero variables for Y
init = "uniform"                         # type of initialisation
cca_toscca = toscca(X, Y, nonz_x, nonz_y, K, alpha_init = init, silent = TRUE, toPlot = FALSE)
```



```
#dont run due to parallelisation.
cc = cca_toscca$cancor
perm_toscca = toscca.perm(X, Y, nonz_x, nonz_y, K = K, init, draws = 10, cancor = cc, ncores = 2)
```

| | |
|---------------------------|---|
| <code>toscca.tStat</code> | <i>Get the estatistic for the permutations.</i> |
|---------------------------|---|

Description

Get the estatistic for the permutations.

Usage

```
toscca.tStat(cancor, A, B, C = 0, type = c("CC", "Wilks", "Roy"))
```

Arguments

| | |
|---------------------|--|
| <code>cancor</code> | Numeric. Canonical Correlation estimate. |
| <code>A</code> | An nxp matrix. |
| <code>B</code> | An nxq matrix. |
| <code>C</code> | An nxs matrix. Confounding variables. |
| <code>type</code> | Character. Choice of statistic: Canonical correlation, Wilks's statistic or Roy's statistic. |

Value

Statistic

| | |
|-----------------------|---------------------------|
| <code>tosccamm</code> | <i>Computes TOSCCA-MM</i> |
|-----------------------|---------------------------|

Description

This function estimates sparse canonical vectors for matrices with multiple measurements and the trajectories of the latent variables.

Usage

```
tosccamm(
  A,
  B,
  nonzero_a,
  nonzero_b,
  folds = 1,
  parallel_logic = FALSE,
  silent = FALSE,
  ATest_res = NULL,
  BTest_res = NULL,
  model = "lme",
  lmeformula = "~ -1 + time + (1|id)",
  arformula = c(1, 0, 0)
)
```

Arguments

| | |
|----------------|--|
| A | A data.frame with id and time as first two columns. |
| B | A data.frame with id and time as first two columns. |
| nonzero_a | Integer. Threshold parameter for A. |
| nonzero_b | Integer. Threshold parameter for B. |
| folds | Integer. Indicates number of folds to perform. |
| parallel_logic | Logical. TRUE to parallelise folds. Default is FALSE. |
| silent | Logical. TRUE to keep silent output messages. Default is FALSE. |
| ATest_res | NULL. Keep NULL. |
| BTest_res | NULL. Keep NULL. |
| model | Character. c("lme", "ar"). Model to fit longitudinal latent space. |
| lmeformula | Character. LME formula. Default is "~ -1 + time + (1 id)". |
| arformula | Numeric vector. Choice of ARIMA. Default is c(1,0,0). |

Value

Canonical vectors for k components.

List with estimated tosccamm parameters.

Examples

```
# example code
#sample size etc
N = 10
p = 25
q = 5
X0 = list()
Y0 = list()
```



```

#Some associations with the true signal
cwa = (6:10) / 10
cwb = -(2:3) / 10

alpha = rep(0, p)
beta = rep(0, q)

loc_alpha = 1:length(alpha)
loc_beta = 1:length(beta)

alpha[loc_alpha] = cwa
beta[loc_beta] = cwb

sg = matrix(c(1, 0.6, 0.3, rep(0, 2),
              0.6, 1, 0.6, 0.3, rep(0, 1),
              0.3, 0.6, 1, 0.6, 0.3,
              rep(0,1), 0.3, 0.6, 1, 0.6,
              rep(0,2), 0.3, 0.6, 1), ncol = 5)

for(i in 1:N)
{
  times = 1:5
  Zi1 = (sin(100*times))^times + times * 0.65 + rnorm(1,0,0.95)
  Zi = cbind(Zi1)
  #Simulate data and add some noise
  X0i = sapply(1:p, function(a) MASS::mvrnorm(1, (Zi %*% t(alpha))[a], Sigma = sg))
  Y0i = sapply(1:q, function(a) MASS::mvrnorm(1, (Zi %*% t(beta))[a], Sigma = sg))

  colnames(X0i) = paste0("X", 1:ncol(X0i))
  colnames(Y0i) = paste0("Y", 1:ncol(Y0i))
  #Check the simulated cross correlation
  #image(cor(X0i, Y0i))

  #Remove some observations
  # p_observed = 1
  X0i = cbind(id=i, time=times, X0i)[rbinom(length(times),1,p_observed)==1,]
  Y0i = cbind(id=i, time=times, Y0i)[rbinom(length(times),1,p_observed)==1,]

  X0[[i]] = X0i
  Y0[[i]] = Y0i
}

X0 = do.call("rbind", X0)
Y0 = do.call("rbind", Y0)

X = data.frame(X0); Y = data.frame(Y0)
nonz_a = c(2, 5, 10, 20)
nonz_b = c(2, 3, 4)

mod <- tosccamm(X, Y, folds = 2, nonzero_a = nonz_a, nonzero_b = nonz_b, silent = TRUE)

```


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