

Package ‘PMA2’

May 12, 2022

Type Package

Title Penalized Multivariate Analysis

Version 2.1

Date 2022-05-04

URL <https://github.com/Ali-Mahzarnia/PMA2>

BugReports <https://github.com/Ali-Mahzarnia/PMA2>

Author Ali Mahzarnia

Maintainer Ali Mhazarnia <ali.mahzarnia@duke.edu>

Description

A modified version of PMA. The `CCA()` and `CCA.permute()` functions can also compute the component-wise standard deviations of estimated U and V through permutations in addition to standardize them. Furthermore, it computes the non-parametric p-values for each components. Performs Penalized Multivariate Analysis: a penalized matrix decomposition, sparse principal components analysis, and sparse canonical correlation analysis, described in Ali Mahzarnia, Alexander Badea (2022), "Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation" at bioRxiv.

Depends R (>= 2.10)

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 7.0.2

NeedsCompilation yes

Repository CRAN

Date/Publication 2022-05-12 07:00:05 UTC

R topics documented:

PMA-package	2
breastdata	2

CCA	3
CCA.permute	8
MultiCCA	12
MultiCCA.permute	14
PlotCGH	16
PMD	18
PMD.cv	22
SPC	24
SPC.cv	27

Index	31
--------------	-----------

PMA-package	<i>Penalized Multivariate Analysis</i>
-------------	--

Description

This package is called **PMA**, for **P**enalized **M**ultivariate **A**alysis. It implements three methods: A penalized matrix decomposition, sparse principal components analysis, and sparse canonical correlations analysis. All are described in the reference below. The main functions are: PMD, CCA and SPC.

Details

The first, PMD, performs a penalized matrix decomposition. CCA performs sparse canonical correlation analysis. SPC performs sparse principal components analysis.

There also are cross-validation functions for tuning parameter selection for each of the above methods: SPC.cv, PMD.cv, CCA.permute. And PlotCGH produces nice plots for DNA copy number data.

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

breastdata	<i>Breast cancer gene expression + DNA copy number data set from Chin et. al. and used in Witten, et. al. See references below.</i>
------------	---

Description

This data set consists of gene expression and DNA copy number measurements on a set of 89 samples. The data set can be used to perform integrative analysis of gene expression and DNA copy number data, as in . That is, we can look for sets of genes that are associated with regions of chromosomal gain/loss.

Must be downloaded from <https://github.com/Ali-Mahzarnia/PMA2/> and put into the folder PMA/data

Format

The format is a list containing the following elements: - dna: a 2149x89 matrix of CGH spots x Samples - rna: a 19672x89 matrix of Genes x Samples - chrom: a 2149-vector of chromosomal location of each CGH spot - nuc: a 2149-vector of nucleotide position for each CGH spot - gene: a 19672-vector with an accession number for each gene - genenames: a 19672-vector with a name for each gene - genechr: a 19672-vector with a chromosomal location for each gene - genedesc: a 19672-vector with a description for each gene - genepos: a 19672-vector with a nucleotide position for each gene

Details

Missing values were imputed using 5-nearest neighbors (see library pamr).

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

Examples

```
data(breastdata)
attach(breastdata)
PlotCGH(dna[,1], chrom=chrom, main="Sample 1", nuc=nuc)
detach(breastdata)
```

CCA

Perform sparse canonical correlation analysis using the penalized matrix decomposition.

Description

This is a function of a modification version of the PMA package. Given matrices X and Z , which represent two sets of features on the same set of samples, find sparse u and v such that $u'X'Zv$ is large. For X and Z , the samples are on the rows and the features are on the columns. X and Z must have same number of rows, but may (and usually will) have different numbers of columns. The columns of X and/or Z can be unordered or ordered. If unordered, then a lasso penalty will be used to obtain the corresponding canonical vector. If ordered, then a fused lasso penalty will be used; this will result in smoothness. In addition, this function would report the component-wise estimated standard deviation of each U and V component and standardize them accordingly. The package also computes the non-parametric p-values of the components of u and v based on the permutations.

Usage

```
CCA(
  x,
  z,
  typex = c("standard", "ordered"),
  typez = c("standard", "ordered"),
  penaltyx = NULL,
  penaltyz = NULL,
  K = 1,
  niter = 15,
  v = NULL,
  trace = TRUE,
  standardize = TRUE,
  xnames = NULL,
  znames = NULL,
  chromx = NULL,
  chromz = NULL,
  upos = FALSE,
  uneg = FALSE,
  vpos = FALSE,
  vneg = FALSE,
  outcome = NULL,
  y = NULL,
  cens = NULL,
  UVperms=NA,
  allpenaltyxs=NA
)
```

Arguments

x	Data matrix; samples are rows and columns are features. Cannot contain missing values.
z	Data matrix; samples are rows and columns are features. Cannot contain missing values.
typex	Are the columns of x unordered (type="standard") or ordered (type="ordered")? If "standard", then a lasso penalty is applied to u, to enforce sparsity. If "ordered" (generally used for CGH data), then a fused lasso penalty is applied, to enforce both sparsity and smoothness.
typez	Are the columns of z unordered (type="standard") or ordered (type="ordered")? If "standard", then a lasso penalty is applied to v, to enforce sparsity. If "ordered" (generally used for CGH data), then a fused lasso penalty is applied, to enforce both sparsity and smoothness.
penaltyx	The penalty to be applied to the matrix x, i.e. the penalty that results in the canonical vector u. If typex is "standard" then the L1 bound on u is $\text{penaltyx} \cdot \sqrt{\text{ncol}(x)}$. In this case penaltyx must be between 0 and 1 (larger L1 bound corresponds to less penalization). If "ordered" then it's the fused lasso

	penalty lambda, which must be non-negative (larger lambda corresponds to more penalization).
penaltyz	The penalty to be applied to the matrix z, i.e. the penalty that results in the canonical vector v. If typez is "standard" then the L1 bound on v is penaltyz*sqrt(ncol(z)). In this case penaltyz must be between 0 and 1 (larger L1 bound corresponds to less penalization). If "ordered" then it's the fused lasso penalty lambda, which must be non-negative (larger lambda corresponds to more penalization).
K	The number of u's and v's desired; that is, the number of canonical vectors to be obtained.
niter	How many iterations should be performed? Default is 15.
v	The first K columns of the v matrix of the SVD of X'Z. If NULL, then the SVD of X'Z will be computed inside the CCA function. However, if you plan to run this function multiple times, then save a copy of this argument so that it does not need to be re-computed (since that process can be time-consuming if X and Z both have high dimension).
trace	Print out progress?
standardize	Should the columns of x and z be centered (to have mean zero) and scaled (to have standard deviation 1)? Default is TRUE.
xnames	An optional vector of column names for x.
znames	An optional vector of column names for z.
chromx	Used only if typex is "ordered"; allows user to specify a vector of length ncol(x) giving the chromosomal location of each CGH spot. This is so that smoothness will be enforced within each chromosome, but not between chromosomes.
chromz	Used only if typez is "ordered"; allows user to specify a vector of length ncol(z) giving the chromosomal location of each CGH spot. This is so that smoothness will be enforced within each chromosome, but not between chromosomes.
upos	If TRUE, then require elements of u to be positive. FALSE by default. Can only be used if type is "standard".
uneg	If TRUE, then require elements of u to be negative. FALSE by default. Can only be used if type is "standard".
vpos	If TRUE, require elements of v to be positive. FALSE by default. Can only be used if type is "standard".
vneg	If TRUE, require elements of v to be negative. FALSE by default. Can only be used if type is "standard".
outcome	If you would like to incorporate a phenotype into CCA analysis - that is, you wish to find features that are correlated across the two data sets and also correlated with a phenotype - then use one of "survival", "multiclass", or "quantitative" to indicate outcome type. Default is NULL.
y	If outcome is not NULL, then this is a vector of phenotypes - one for each row of x and z. If outcome is "survival" then these are survival times; must be non-negative. If outcome is "multiclass" then these are class labels (1,2,3,...). Default NULL.

cens	If outcome is "survival" then these are censoring statuses for each observation. 1 is complete, 0 is censored. Default NULL.
UVperms	A list of U and V generated by CCA.permute function. It must include all of the estimated Us and Vs for all of the regularization parameters and all of the permutations. Read the CCA.permute for the format of this list. Check the example below.
allpenaltyxs	A vector of all of the x regularization parameters generated by the CCA.permute function. Check the example below for more information.

Details

This function is useful for performing an integrative analysis of two sets of measurements taken on the same set of samples: for instance, gene expression and CGH measurements on the same set of patients. It takes in two data sets, called x and z , each of which have (the same set of) samples on the rows. If z is a matrix of CGH data with *ordered* CGH spots on the columns, then use `typez="ordered"`. If z consists of unordered columns, then use `typez="standard"`. Similarly for `typex`.

This function performs the penalized matrix decomposition on the data matrix $X'Z$. Therefore, the results should be the same as running the PMD function on $t(x)$ using the CCA function is much faster because it avoids computation of $X'Z$.

The CCA criterion is as follows: find unit vectors u and v such that $u'X'Zv$ is maximized subject to constraints on u and v . If `typex="standard"` and `typez="standard"` then the constraints on u and v are lasso (L_1). If `typex="ordered"` then the constraint on u is a fused lasso penalty (promoting sparsity and smoothness). Similarly if `typez="ordered"`.

When `type x` is "standard": the L_1 bound of u is `penaltyx*sqrt(ncol(x))`.

When `typex` is "ordered": `penaltyx` controls the amount of sparsity and smoothness in u , via the fused lasso penalty: $\lambda \sum_j |u_j| + \lambda \sum_j |u_j - u_{(j-1)}|$. If NULL, then it will be chosen adaptively from the data.

Value

<code>u</code>	u is output. If you asked for multiple factors then each column of u is a factor. u has dimension $n \times K$ if you asked for K factors.
<code>v</code>	v is output. If you asked for multiple factors then each column of v is a factor. v has dimension $p \times K$ if you asked for K factors.
<code>d</code>	A vector of length K , which can alternatively be computed as the diagonal of the matrix $u'X'Zv$.
<code>v.init</code>	The first K factors of the v matrix of the SVD of $x'z$. This is saved in case this function will be re-run later.
<code>SDu</code>	Standard deviations of the components of U through the permutations for the given joint regularization parameter <code>penaltyx</code> and <code>penaltyz</code> .
<code>SDv</code>	Similar to <code>SDu</code> .
<code>standardu</code>	Standardized U using the estimated U and the component-wise standard deviation of U through permutations, <code>SDu</code> . There would be the following message if Inf values are created: The "Inf" in standardized U or V i.e. "standardu" or "standardv" indicates that the estimated U or V for that component

is nonzero and that its estimated standard deviation through all permutations is zero. Therefore, that component is the most significant among all. If a component of U or V is estimated zero, the associated “standardu” or “standardv” component is zero.

standardv	Similar to SDv.
pvalsu	No-parametric p-values associated to the components of u for the hypothesis testing with the null that each component is zero. If the estimated component is positive, the alternative would be that the true component is positive. Note that under the null hypothesis the permutation is zero, so in this scenario, the non-parametric p-value is the proportion that the permutations resulted in a greater value than that of the component of u. If you need the p-value of the opposite direction of simply subtract this value from 1.
pvalsv	Similar to pvalsu.

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer’s Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[PMD,CCA.permute](#)

Examples

```
set.seed(3128) # for replicating the result
n=100 # sample size
q=20 # base size
S=100*matrix(rnorm(100),n,q) # base matrix
u=c(rep(0,5),rep(1,3),rep(0,2) ) # True u
v=c(rep(1,5),rep(0,5),rep(1,5) ) # True v
p1=length(u) # length of true u
p2=length(v) #length of true v
U=matrix(rep(u, q),p1,q) # coefficients of base matrix for constructing X
V=matrix(rep(v, q),p2,q) # coefficients of base matrix for constructing Z
x=S%*%t(U) # constructing U
x=x+matrix(rnorm(dim(x)[1]*dim(x)[2]),dim(x)[1],dim(x)[2]); # adding noise
z=S%*%t(V) # constructing V
z=z+matrix(rnorm(dim(z)[1]*dim(z)[2]),dim(z)[1],dim(z)[2]); # adding noise
library(PMA2)
#for beter estimations try with more permutations,
# such as nperms=1000
perm.out <- CCA.permute(x,z,typex="standard",typez="standard",
                       nperms=10, SD=TRUE, upos = TRUE, vpos = TRUE)
# by SD=TRUE we estimate SD of U and V components too.
# by upos and vpos we restrict the estimations to only
# positive values but this isn't necessary generally
print(perm.out)
```

```

out <- CCA(x,z,typex="standard",typez="standard",K=1,
          penaltyx=perm.out$bestpenaltyx,penaltyz=perm.out$bestpenaltyz,
          v=perm.out$v.init, UVperms = perm.out$UVperms,
          allpenaltyxs = perm.out$penaltyxs , upos = TRUE, vpos = TRUE)
print(out)
# results of projection for u
# respectively:True U, Estimated U, Standard deviations, Zscores, nonparametric-Pvalues
utable=base::cbind(u,out$u, out$SDu, out$standardu, out$pvalsu)
colnames(utable)=c("True U", "Estimated U", "SDs", "Zscores", "nonpar-Pvals")
utable
# results of projection for v
# respectively:True V, Estimated V, Standard deviations, Zscores, nonparametric-Pvalues
vtable=base::cbind(v,out$v, out$SDv, out$standardv, out$pvalsv)
colnames(vtable)=c("True V", "Estimated V", "SDs", "Zscores", "nonpar-Pvals")
vtable

```

CCA.permute

Select tuning parameters for sparse canonical correlation analysis using the penalized matrix decomposition.

Description

This is a function of a modification version of the PMA package. This function can be used to automatically select tuning parameters for sparse CCA using the penalized matrix decomposition. For each data set x and z , two types are possible: (1) type "standard", which does not assume any ordering of the columns of the data set, and (2) type "ordered", which assumes that columns of the data set are ordered and thus that corresponding canonical vector should be both sparse and smooth (e.g. CGH data). In addition, this function would report the stored U s and V s for all lambdas through all permutations for standard deviation estimations.

Usage

```

CCA.permute(
  x,
  z,
  typex = c("standard", "ordered"),
  typez = c("standard", "ordered"),
  penaltyxs = NULL,
  penaltyzs = NULL,
  niter = 3,
  v = NULL,
  trace = TRUE,
  nperms = 25,
  standardize = TRUE,
  chromx = NULL,
  chromz = NULL,
  upos = FALSE,

```

```

    uneg = FALSE,
    vpos = FALSE,
    vneg = FALSE,
    outcome = NULL,
    y = NULL,
    cens = NULL,
    SD=FALSE
)

```

Arguments

x	Data matrix; samples are rows and columns are features.
z	Data matrix; samples are rows and columns are features. Note that x and z must have the same number of rows, but may (and generally will) have different numbers of columns.
typex	Are the columns of x unordered (type="standard") or ordered (type="ordered")? If "standard", then a lasso penalty is applied to v, to enforce sparsity. If "ordered" (generally used for CGH data), then a fused lasso penalty is applied, to enforce both sparsity and smoothness.
typez	Are the columns of z unordered (type="standard") or ordered (type="ordered")? If "standard", then a lasso penalty is applied to v, to enforce sparsity. If "ordered" (generally used for CGH data), then a fused lasso penalty is applied, to enforce both sparsity and smoothness.
penaltyxs	The set of x penalties to be considered. If typex="standard", then the L1 bound on u is $\text{penaltyxs} \cdot \sqrt{\text{ncol}(x)}$. If "ordered", then it's the lambda for the fused lasso penalty. The user can specify a single value or a vector of values. If penaltyxs is a vector and penaltyzs is a vector, then the vectors must have the same length. If NULL, then the software will automatically choose a single lambda value if type is "ordered", or a grid of (L1 bounds)/ $\sqrt{\text{ncol}(x)}$ if type is "standard".
penaltyzs	The set of z penalties to be considered. If typez="standard", then the L1 bound on v is $\text{penaltyzs} \cdot \sqrt{\text{ncol}(z)}$. If "ordered", then it's the lambda for the fused lasso penalty. The user can specify a single value or a vector of values. If penaltyzs is a vector and penaltyzs is a vector, then the vectors must have the same length. If NULL, then the software will automatically choose a single lambda value if type is "ordered", or a grid of (L1 bounds)/ $\sqrt{\text{ncol}(z)}$ if type is "standard".
niter	How many iterations should be performed each time CCA is called? Default is 3, since an approximate estimate of u and v is acceptable in this case, and otherwise this function can be quite time-consuming.
v	The first K columns of the v matrix of the SVD of X'Z. If NULL, then the SVD of X'Z will be computed inside this function. However, if you plan to run this function multiple times, then save a copy of this argument so that it does not need to be re-computed (since that process can be time-consuming if X and Z both have high dimension).
trace	Print out progress?

nperms	How many times should the data be permuted? Default is 25. A large value of nperms is very important here, since the formula for computing the z-statistics requires a standard deviation estimate for the correlations obtained via permutation, which will not be accurate if nperms is very small.
standardize	Should the columns of X and Z be centered (to have mean zero) and scaled (to have standard deviation 1)? Default is TRUE.
chromx	Used only if typex="ordered"; a vector of length ncol(x) that allows you to specify which chromosome each CGH spot is on. If NULL, then it is assumed that all CGH spots are on same chromosome.
chromz	Used only if typex="ordered"; a vector of length ncol(z) that allows you to specify which chromosome each CGH spot is on. If NULL, then it is assumed that all CGH spots are on same chromosome.
upos	If TRUE, then require all elements of u to be positive in sign. Default is FALSE. Can only be used if type is standard.
uneg	If TRUE, then require all elements of u to be negative in sign. Default is FALSE. Can only be used if type is standard.
vpos	If TRUE, then require all elements of v to be positive in sign. Default is FALSE. Can only be used if type is standard.
vneg	If TRUE, then require all elements of v to be negative in sign. Default is FALSE. Can only be used if type is standard.
outcome	If you would like to incorporate a phenotype into CCA analysis - that is, you wish to find features that are correlated across the two data sets and also correlated with a phenotype - then use one of "survival", "multiclass", or "quantitative" to indicate outcome type. Default is NULL.
y	If outcome is not NULL, then this is a vector of phenotypes - one for each row of x and z. If outcome is "survival" then these are survival times; must be non-negative. If outcome is "multiclass" then these are class labels. Default NULL.
cens	If outcome is "survival" then these are censoring statuses for each observation. 1 is complete, 0 is censored. Default NULL.
SD	If TRUE, the output would include a non-empty list UVperms which is the stored Us, and Vs for the regularization parameters through permutations. This list can be used to estimate the standard deviations of the components of U and V, and finally standardizing these components.

Details

For X and Z, the samples are on the rows and the features are on the columns.

The tuning parameters are selected using a permutation scheme. For each candidate tuning parameter value, the following is performed: (1) The samples in X are randomly permuted nperms times, to obtain matrices X^*_1, X^*_2, \dots . (2) Sparse CCA is run on each permuted data set (X^*_i, Z) to obtain factors (u^*_i, v^*_i) . (3) Sparse CCA is run on the original data (X, Z) to obtain factors u and v. (4) Compute $c^*_i = \text{cor}(X^*_i, u^*_i, Z, v^*_i)$ and $c = \text{cor}(Xu, Zv)$. (5) Use Fisher's transformation to convert these correlations into random variables that are approximately normally distributed. Let Fisher(c) denote the Fisher transformation of c. (6) Compute a z-statistic for Fisher(c),

using $(\text{Fisher}(c) - \text{mean}(\text{Fisher}(c^*))) / \text{sd}(\text{Fisher}(c^*))$. The larger the z-statistic, the "better" the corresponding tuning parameter value.

This function also gives the p-value for each pair of canonical variates (u,v) resulting from a given tuning parameter value. This p-value is computed as the fraction of c^*_i 's that exceed c (using the notation of the previous paragraph).

Using this function, only the first left and right canonical variates are considered in selection of the tuning parameter.

Note that x and z must have same number of rows. This function performs just a one-dimensional search in tuning parameter space, even if penaltyxs and penaltyzs both are vectors: the pairs (penaltyxs[1], penaltyzs[1]), (penaltyxs[2], penaltyzs[2]),.... are considered.

Value

zstat	The vector of z-statistics, one per element of sumabss.
pvals	The vector of p-values, one per element of sumabss.
bestpenaltyx	The x penalty that resulted in the highest z-statistic.
bestpenaltyz	The z penalty that resulted in the highest z-statistic.
cors	The value of $\text{cor}(Xu, Zv)$ obtained for each value of sumabss.
corperms	The nperms values of $\text{cor}(Xu, Zv^*)$ obtained for each value of sumabss, where X^* indicates the X matrix with permuted rows, and u^* and v^* are the output of CCA using data (X^*, Z) .
ft.cors	The result of applying Fisher transformation to cors.
ft.corperms	The result of applying Fisher transformation to corperms.
nnonzerous	Number of non-zero u's resulting from applying CCA to data (X,Z) for each value of sumabss.
nnonzerouv	Number of non-zero v's resulting from applying CCA to data (X,Z) for each value of sumabss.
v.init	The first factor of the v matrix of the SVD of $x'z$. This is saved in case this function (or the CCA function) will be re-run later.
UVperms	A list of nperms i.e. number of permutations. Each object of this list is a list with the size of penaltyxs i.e. number of joint regularized parameters used in all permutations. Each of these lists is itself a list of two matrices, that are Us and Vs associated with the permutation and the joint regularized parameters.

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[PMD,CCA](#)

Examples

```
# See examples in CCA function
```

MultiCCA

Perform sparse multiple canonical correlation analysis.

Description

Given matrices X_1, \dots, X_K , which represent K sets of features on the same set of samples, find sparse w_1, \dots, w_K such that $\sum_{(i < j)} (w_i' X_i' X_j w_j)$ is large. If the columns of X_k are ordered (and `type="ordered"`) then w_k will also be smooth. For X_1, \dots, X_K , the samples are on the rows and the features are on the columns. X_1, \dots, X_K must have same number of rows, but may (and usually will) have different numbers of columns.

Usage

```
MultiCCA(
  xlist,
  penalty = NULL,
  ws = NULL,
  niter = 25,
  type = "standard",
  ncomponents = 1,
  trace = TRUE,
  standardize = TRUE
)
```

Arguments

<code>xlist</code>	A list of length K , where K is the number of data sets on which to perform sparse multiple CCA. Data set k should be a matrix of dimension $n \times p_k$ where p_k is the number of features in data set k .
<code>penalty</code>	The penalty terms to be used. Can be a single value (if the same penalty term is to be applied to each data set) or a K -vector, indicating a different penalty term for each data set. There are 2 possible interpretations for the penalty terms: If <code>type="standard"</code> then this is an L1 bound on w_k , and it must be between 1 and $\sqrt{p_k}$ (p_k is the number of features in matrix X_k). If <code>type="ordered"</code> then this is the parameter for the fused lasso penalty on w_k .
<code>ws</code>	A list of length K . The k th element contains the first <code>ncomponents</code> columns of the v matrix of the SVD of X_k . If <code>NULL</code> , then the SVD of X_1, \dots, X_K will be computed inside the <code>MultiCCA</code> function. However, if you plan to run this function multiple times, then save a copy of this argument so that it does not need to be re-computed.
<code>niter</code>	How many iterations should be performed? Default is 25.

type	Are the columns of X_1, \dots, X_K unordered (type="standard") or ordered (type="ordered")? If "standard", then a lasso penalty is applied to v , to enforce sparsity. If "ordered" (generally used for CGH data), then a fused lasso penalty is applied, to enforce both sparsity and smoothness. This argument can be a vector of length K (if different data sets are of different types) or it can be a single value "ordered"/"standard" (if all data sets are of the same type).
ncomponents	How many factors do you want? Default is 1.
trace	Print out progress?
standardize	Should the columns of X_1, \dots, X_K be centered (to have mean zero) and scaled (to have standard deviation 1)? Default is TRUE.

Value

ws	A list of length K , containing the sparse canonical variates found (element k is a $p_k \times n_{\text{components}}$ matrix).
ws.init	A list of length K containing the initial values of w_s used, by default these are the v vector of the svd of matrix X_k .

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[MultiCCA.permute](#), [CCA](#), [CCA.permute](#)

Examples

```
# Generate 3 data sets so that first 25 features are correlated across
# the data sets...
set.seed(123)
u <- matrix(rnorm(50),ncol=1)
v1 <- matrix(c(rep(.5,25),rep(0,75)),ncol=1)
v2 <- matrix(c(rep(1,25),rep(0,25)),ncol=1)
v3 <- matrix(c(rep(.5,25),rep(0,175)),ncol=1)

x1 <- u%*%t(v1) + matrix(rnorm(50*100),ncol=100)
x2 <- u%*%t(v2) + matrix(rnorm(50*50),ncol=50)
x3 <- u%*%t(v3) + matrix(rnorm(50*200),ncol=200)

xlist <- list(x1, x2, x3)

# Run MultiCCA.permute w/o specifying values of tuning parameters to
# try.
# The function will choose the lambda for the ordered data set.
# Then permutations will be used to select optimal sum(abs(w)) for
# standard data sets.
```

```

# We assume that x1 is standard, x2 is ordered, x3 is standard:
perm.out <- MultiCCA.permute(xlist, type=c("standard", "ordered",
"standard"))
print(perm.out)
plot(perm.out)
out <- MultiCCA(xlist, type=c("standard", "ordered", "standard"),
penalty=perm.out$bestpenalties, ncomponents=2, ws=perm.out$ws.init)
print(out)
# Or if you want to specify tuning parameters by hand:
# this time, assume all data sets are standard:
perm.out <- MultiCCA.permute(xlist, type="standard",
penalties=cbind(c(1.1,1.1,1.1),c(2,3,4),c(5,7,10)), ws=perm.out$ws.init)
print(perm.out)
oldpar <- par(mfrow = c(1,1))
plot(perm.out)

# Making use of the fact that the features are ordered:
out <- MultiCCA(xlist, type="ordered", penalty=.6)
par(mfrow=c(3,1))
PlotCGH(out$ws[[1]], chrom=rep(1,ncol(x1)))
PlotCGH(out$ws[[2]], chrom=rep(2,ncol(x2)))
PlotCGH(out$ws[[3]], chrom=rep(3,ncol(x3)))
par(oldpar)

```

MultiCCA.permute

Select tuning parameters for sparse multiple canonical correlation analysis using the penalized matrix decomposition.

Description

This function can be used to automatically select tuning parameters for sparse multiple CCA. This is the analog of sparse CCA, when >2 data sets are available. Each data set may have features of type="standard" or type="ordered" (e.g. CGH data). Assume that there are K data sets, called \$X1,...,XK\$.

Usage

```

MultiCCA.permute(
  xlist,
  penalties = NULL,
  ws = NULL,
  type = "standard",
  nperms = 10,
  niter = 3,
  trace = TRUE,
  standardize = TRUE
)

```

Arguments

xlist	A list of length K, where K is the number of data sets on which to perform sparse multiple CCA. Data set k should be a matrix of dimension $n \times p_k$ where p_k is the number of features in data set k.
penalties	The penalty terms to be considered in the cross-validation. If the same penalty term is desired for each data set, then this should be a vector of length equal to the number of penalty terms to be considered. If different penalty terms are desired for each data set, then this should be a matrix with rows equal to the number of data sets, and columns equal to the number of penalty terms to be considered. For a given data set X_k , if type is "standard" then the penalty term should be a number between 1 and $\sqrt{p_k}$ (the number of features in data set k); it is a L1 bound on w_k . If type is "ordered", on the other hand, the penalty term is of the form λ in the fused lasso penalty. Therefore, the interpretation of the argument depends on whether type is "ordered" or "standard" for this data set.
ws	A list of length K; the kth element contains the first n components columns of the v matrix of the SVD of X_k . If NULL, then the SVD of X_k will be computed inside this function. However, if you plan to run this function multiple times, then save a copy of this argument so that it does not need to be re-computed.
type	A K-vector containing elements "standard" or "ordered" - or a single value. If a single value, then it is assumed that all elements are the same (either "standard" or "ordered"). If columns of v are ordered (e.g. CGH spots ordered along the chromosome) then "ordered", otherwise use "standard". "standard" will result in a lasso (L_1) penalty on v, which will result in smoothness. "ordered" will result in a fused lasso penalty on v, yielding both sparsity and smoothness.
nperms	How many times should the data be permuted? Default is 25. A large value of nperms is very important here, since the formula for computing the z-statistics requires a standard deviation estimate for the correlations obtained via permutation, which will not be accurate if nperms is very small.
niter	How many iterations should be performed each time CCA is called? Default is 3, since an approximate estimate of u and v is acceptable in this case, and otherwise this function can be quite time-consuming.
trace	Print out progress?
standardize	Should the columns of X and Z be centered (to have mean zero) and scaled (to have standard deviation 1)? Default is TRUE.

Details

The tuning parameters are selected using a permutation scheme. For each candidate tuning parameter value, the following is performed: (1) Repeat the following n times, for n large: (a) The samples in (X_1, \dots, X_K) are randomly permuted to obtain data sets (X_1^*, \dots, X_K^*) . (b) Sparse multiple CCA is run on the permuted data sets (X_1^*, \dots, X_K^*) to get canonical variates (w_1^*, \dots, w_K^*) . (c) Record $t^* = \sum_{(i < j)} \text{Cor}(X_i^* w_i^*, X_j^* w_j^*)$. (2) Sparse CCA is run on the original data (X_1, \dots, X_K) to obtain canonical variates (w_1, \dots, w_K) . (3) Record $t = \sum_{(i < j)} \text{Cor}(X_i w_i, X_j w_j)$. (4) The resulting p-value is given by $\text{mean}(t^* > t)$; that is, the fraction of permuted

totals that exceed the total on the real data. Then, choose the tuning parameter value that gives the smallest value in Step 4.

This function only selects tuning parameters for the FIRST sparse multiple CCA factors.

Note that x_1, \dots, x_K must have same number of rows. This function performs just a one-dimensional search in tuning parameter space.

Value

zstat	The vector of z-statistics, one per element of penalties.
pvals	The vector of p-values, one per element of penalties.
bestpenalties	The best set of penalties (the one with the highest zstat).
cors	The value of $\sum_{(j < k)} \text{cor}(X_k w_k, X_j w_j)$ obtained for each value of penalties.
corperms	The nperms values of $\sum_{(j < k)} \text{cor}(X_k^* w_k^*, X_j^* w_j^*)$ obtained for each value of penalties, where X_k^* indicates the X_k matrix with permuted rows, and w_k^* is the canonical variate corresponding to the permuted data.
ws.init	Initial values used for ws in sparse multiple CCA algorithm.

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[MultiCCA](#), [CCA.permute](#), [CCA](#)

Examples

```
# See examples in MultiCCA function
```

PlotCGH

Plot CGH data

Description

Given a vector of gains/losses at CGH spots, this makes a plot of gain/loss on each chromosome.

Usage

```
PlotCGH(array, chrom = NULL, nuc = NULL, main = "", scaleEachChrom = TRUE)
```

Arguments

array	A vector containing the chromosomal location of each CGH spot.
chrom	A numeric vector of the same length as "array"; its values should indicate the chromosome that each CGH spot is on (for instance, for human genomic data, values of chrom should range from 1 to 24). If NULL, then it is assumed that all elements of 'array' are on the same chromosome.
nuc	A numeric vector of same length as "array", indicating the nucleotide position of each CGH spot. If NULL, then the function assumes that each CGH spot corresponds to a consecutive position. E.g. if there are 200 CGH spots on chromosome 1, then they are located at positions 1,2,...,199,200.
main	Give your plot a title.
scaleEachChrom	Default is TRUE. This means that each chromosomes CGH spots are divided by 1.1 times the max of the CGH spots on that chromosome. This way, the CGH spots on each chromosome of the plot are as big as possible (i.e. easy to see). If FALSE, then all of the CGH spots are divided by 1.1 times the max of ALL the CGH spots. This means that on some chromosomes CGH spots might be hard to see, but has the advantage that now relative magnitudes of CGH spots on different chromosomes can be seen from figure.

Details

This function makes a plot of regions of genomic gain/loss.

Value

No return value, called for plot

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[PMD](#), [PMD.cv](#), [CCA](#), [CCA.permute](#)

Examples

```
# Use breast data
data(breastdata)
attach(breastdata)

# dna contains CGH data and chrom contains chromosome of each CGH spot;
# nuc contains position of each CGH spot.
dna <- t(dna)
PlotCGH(dna[1,],chrom=chrom,nuc=nuc,main="Sample 1: All Chromosomes")
```

```

PlotCGH(dna[1,chrom==1], chrom=chrom[chrom==1], nuc=nuc[chrom==1],
main= "Sample 1: Chrom 1")
PlotCGH(dna[1,chrom<=3], chrom=chrom[chrom<=3], nuc=nuc[chrom<=3],
main="Sample 1: Chroms 1, 2, and 3")
detach(breastdata)

```

PMD

Get a penalized matrix decomposition for a data matrix.

Description

Performs a penalized matrix decomposition for a data matrix. Finds factors u and v that summarize the data matrix well. u and v will both be sparse, and v can optionally also be smooth.

Usage

```

PMD(
  x,
  type = c("standard", "ordered"),
  sumabs = 0.4,
  sumabsu = 5,
  sumabsv = NULL,
  lambda = NULL,
  niter = 20,
  K = 1,
  v = NULL,
  trace = TRUE,
  center = TRUE,
  chrom = NULL,
  rnames = NULL,
  cnames = NULL,
  upos = FALSE,
  uneg = FALSE,
  vpos = FALSE,
  vneg = FALSE
)

```

Arguments

<code>x</code>	Data matrix of dimension $n \times p$, which can contain NA for missing values.
<code>type</code>	"standard" or "ordered": Do we want v to simply be sparse, or should it also be smooth? If the columns of x are ordered (e.g. CGH spots along a chromosome) then choose "ordered". Default is "standard". If "standard", then the PMD function will make use of <code>sumabs</code> OR <code>sumabsu</code> & <code>sumabsv</code> . If "ordered", then the function will make use of <code>sumabsu</code> and <code>lambda</code> .

sumabs	Used only if type is "standard". A measure of sparsity for u and v vectors, between 0 and 1. When sumabs is specified, and sumabsu and sumabsv are NULL, then sumabsu is set to $\sqrt{n} \cdot \text{sumabs}$ and sumabsv is set to $\sqrt{p} \cdot \text{sumabs}$. If sumabs is specified, then sumabsu and sumabsv should be NULL. Or if sumabsu and sumabsv are specified, then sumabs should be NULL.
sumabsu	Used for types "ordered" AND "standard". How sparse do you want u to be? This is the sum of absolute values of elements of u. It must be between 1 and the square root of the number of rows in data matrix. The smaller it is, the sparser u will be.
sumabsv	Used only if type is "standard". How sparse do you want v to be? This is the sum of absolute values of elements of v. It must be between 1 and square root of number of columns of data. The smaller it is, the sparser v will be.
lambda	Used only if type is "ordered". This is the tuning parameter for the fused lasso penalty on v, which takes the form $\lambda \ v\ _1 + \lambda \sum v_j - v_{j-1} $. λ must be non-negative. If NULL, then it is chosen adaptively from the data.
niter	How many iterations should be performed. It is best to run at least 20 of so. Default is 20.
K	The number of factors in the PMD to be returned; default is 1.
v	The first right singular vector(s) of the data. (If missing data is present, then the missing values are imputed before the singular vectors are calculated.) v is used as the initial value for the iterative PMD algorithm. If x is large, then this step can be time-consuming; therefore, if PMD is to be run multiple times, then v should be computed once and saved.
trace	Print out progress as iterations are performed? Default is TRUE.
center	Subtract out mean of x? Default is TRUE.
chrom	If type is "ordered", then this gives the option to specify that some columns of x (corresponding to CGH spots) are on different chromosomes. Then v will be sparse, and smooth <i>within</i> each chromosome but not <i>between</i> chromosomes. Length of chrom should equal number of columns of x, and each entry in chrom should be a number corresponding to which chromosome the CGH spot is on.
rnames	An optional vector containing a name for each row of x.
cnames	An optional vector containing a name for each column of x.
upos	Constrain the elements of u to be positive? TRUE or FALSE.
uneg	Constrain the elements of u to be negative? TRUE or FALSE.
vpos	Constrain the elements of v to be positive? TRUE or FALSE. Cannot be used if type is "ordered".
vneg	Constrain the elements of v to be negative? TRUE or FALSE. Cannot be used if type is "ordered."

Details

The criterion for the PMD is as follows: we seek vectors u and v such that $u'Xv$ is large, subject to $\|u\|_2=1$, $\|v\|_2=1$ and additional penalties on u and v . These additional penalties

are as follows: If type is "standard", then lasso (L_1) penalties (promoting sparsity) are placed on u and v . If type is "ordered", then lasso penalty is placed on u and a fused lasso penalty (promoting sparsity and smoothness) is placed on v .

If type is "standard", then arguments `sumabs` OR `sumabsu`&`sumabsv` are used. If type is "ordered", then `sumabsu` AND `lambda` are used. `sumabsu` is the bound of absolute value of elements of u . `sumabsv` is bound of absolute value of elements of v . If `sumabs` is given, then `sumabsu` is set to $\sqrt{\text{nrow}(x)} * \text{sumabs}$ and `sumabsv` is set to $\sqrt{\text{ncol}(x)} * \text{sumabs}$. `lambda` is the parameter for the fused lasso penalty on v when type is "ordered": $\lambda(\|v\|_1 + \sum_j |v_j - v_{(j-1)})$.

Value

<code>u</code>	u is output. If you asked for multiple factors then each column of u is a factor. u has dimension $n \times K$ if you asked for K factors.
<code>v</code>	v is output. If you asked for multiple factors then each column of v is a factor. v has dimension $p \times K$ if you asked for K factors.
<code>d</code>	d is output. Computationally, $d = u'Xv$ where u and v are the sparse factors output by the PMD function and X is the data matrix input to the PMD function. When $K=1$, the residuals of the rank-1 PMD are given by $X - duv'$.
<code>v.init</code>	The first right singular vector(s) of the data; these are returned to save on computation time if PMD will be run again.
<code>meanx</code>	Mean of x that was subtracted out before PMD was performed.

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[PMD.cv](#), [SPC](#)

Examples

```
# Try PMD with L1 penalty on rows and columns: type="standard"
# A simple simulated example
set.seed(1)
# Our data is a rank-one matrix, plus noise. The underlying components
# contain 50 and 75 non-zero elements, respectively.
u <- matrix(c(rnorm(50), rep(0,150)),
ncol=1)
v <- matrix(c(rnorm(75),rep(0,225)), ncol=1)
x <- u*%t(v)+
matrix(rnorm(200*300),ncol=300)
# We can use cross-validation to try to find optimal value of sumabs
cv.out <- PMD.cv(x, type="standard", sumabss=seq(0.1, 0.6, len=20))
print(cv.out)
```

```

plot(cv.out)
# The optimal value of sumabs is 0.4157, but we can get within one
# standard error of that CV error using sumabs=0.337, which corresponds to
# an average of 45.8 and 71.8 non-zero elements in each component - pretty
# close to the true model.
# We can fit the model corresponding to the lowest cross-validation error:
out <- PMD(x, type="standard", sumabs=cv.out$bestsumabs, K=1, v=cv.out$v.init)
print(out)
oldpar <- par(mfrow = c(1,1))
par(mfrow=c(2,2))
par(mar=c(2,2,2,2))
plot(out$u[,1], main="Est. u")
plot(out$v[,1], main="Est. v")
plot(u, main="True u")
plot(v, main="True v")
# And if we want to control sumabsu and sumabsv separately, we can do
# that too. Let's get 2 components while we're at it:
out2 <- PMD(x, type="standard", K=2, sumabsu=6, sumabsv=8, v=out$v.init,
cnames=paste("v", sep=" ", 1:ncol(x)), rnames=paste("u", sep=" ", 1:nrow(x)))
print(out2)

# Now check out PMD with L1 penalty on rows and fused lasso penalty on
# columns: type="ordered". We'll use the Chin et al (2006) Cancer Cell
# data set; try "?breastdata" for more info.

data(breastdata)
attach(breastdata)
# dna contains CGH data and chrom contains chromosome of each CGH spot;
# nuc contains position of each CGH spot.
dna <- t(dna) # Need samples on rows and CGH spots on columns
# First, look for shared regions of gain/loss on chromosome 1.
# Use cross-validation to choose tuning parameter value

par(mar=c(2,2,2,2))
cv.out <- PMD.cv(dna[,chrom==1], type="ordered", chrom=chrom[chrom==1],
nuc=nuc[chrom==1],
sumabsus=seq(1, sqrt(nrow(dna)), len=15))
print(cv.out)
plot(cv.out)
out <- PMD(dna[,chrom==1], type="ordered",
sumabsu=cv.out$bestsumabsu, chrom=chrom[chrom==1], K=1, v=cv.out$v.init,
cnames=paste("Pos", sep=" ",
nuc[chrom==1]), rnames=paste("Sample", sep=" ", 1:nrow(dna)))
print(out, verbose=TRUE)
# Which samples actually have that region of gain/loss?
par(mfrow=c(3,1))
par(mar=c(2,2,2,2))
PlotCGH(dna[which.min(out$u[,1]),chrom==1], chrom=chrom[chrom==1],
main=paste(paste(paste("Sample ", sep=" ", which.min(out$u[,1])),
sep="; u=", round(min(out$u[,1]),3))), nuc=nuc[chrom==1])
PlotCGH(dna[88,chrom==1], chrom=chrom[chrom==1],
main=paste("Sample 88; u=", sep=" ", round(out$u[88,1],3)),
nuc=nuc[chrom==1])

```

```

PlotCGH(out$v[,1],chrom=chrom[chrom==1], main="v",nuc=nuc[chrom==1])

detach(breastdata)
par(oldpar)

```

PMD.cv

Do tuning parameter selection for PMD via cross-validation

Description

Performs cross-validation to select tuning parameters for rank-1 PMD, the penalized matrix decomposition for a data matrix.

Usage

```

PMD.cv(
  x,
  type = c("standard", "ordered"),
  sumabss = seq(0.1, 0.7, len = 10),
  sumabsus = NULL,
  lambda = NULL,
  nfold = 5,
  niter = 5,
  v = NULL,
  chrom = NULL,
  nuc = NULL,
  trace = TRUE,
  center = TRUE,
  upos = FALSE,
  uneg = FALSE,
  vpos = FALSE,
  vneg = FALSE
)

```

Arguments

x	Data matrix of dimension $n \times p$, which can contain NA for missing values.
type	"standard" or "ordered": Do we want v to simply be sparse, or should it also be smooth? If the columns of x are ordered (e.g. CGH spots along a chromosome) then choose "ordered". Default is "standard". If "standard", then the PMD function will make use of sumabs OR sumabsu&sumabsv. If "ordered", then the function will make use of sumabsu and lambda.

sumabss	Used only if type is "standard". A vector of sumabs values to be used. Sumabs is a measure of sparsity for u and v vectors, between 0 and <ol style="list-style-type: none"> When sumabss is specified, and sumabsus and sumabsvs are NULL, then sumabsus is set to $\sqrt{n} \cdot \text{sumabss}$ and sumabsvs is set to $\sqrt{p} \cdot \text{sumabss}$. If sumabss is specified, then sumabsus and sumabsvs should be NULL. Or if sumabsus and sumabsvs are specified, then sumabss should be NULL.
sumabsus	Used only for type "ordered". A vector of sumabsu values to be used. Sumabsu measures sparseness of u - it is the sum of absolute values of elements of u. Must be between 1 and \sqrt{n} .
lambda	Used only if type is "ordered". This is the tuning parameter for the fused lasso penalty on v, which takes the form $\lambda \ v\ _1 + \lambda v_j - v_{(j-1)} $. λ must be non-negative. If NULL, then it is chosen adaptively from the data.
nfolds	How many cross-validation folds should be performed? Default is 5.
niter	How many iterations should be performed. For speed, only 5 are performed by default.
v	The first right singular vector(s) of the data. (If missing data is present, then the missing values are imputed before the singular vectors are calculated.) v is used as the initial value for the iterative PMD algorithm. If x is large, then this step can be time-consuming; therefore, if PMD is to be run multiple times, then v should be computed once and saved.
chrom	If type is "ordered", then this gives the option to specify that some columns of x (corresponding to CGH spots) are on different chromosomes. Then v will be sparse, and smooth <i>within</i> each chromosome but not <i>between</i> chromosomes. Length of chrom should equal number of columns of x, and each entry in chrom should be a number corresponding to which chromosome the CGH spot is on.
nuc	If type is "ordered", can specify the nucleotide position of each CGH spot (column of x), to be used in plotting. If NULL, then it is assumed that CGH spots are equally spaced.
trace	Print out progress as iterations are performed? Default is TRUE.
center	Subtract out mean of x? Default is TRUE
upos	Constrain the elements of u to be positive? TRUE or FALSE.
uneg	Constrain the elements of u to be negative? TRUE or FALSE.
vpos	Constrain the elements of v to be positive? TRUE or FALSE. Cannot be used if type is "ordered".
vneg	Constrain the elements of v to be negative? TRUE or FALSE. Cannot be used if type is "ordered."

Details

If type is "standard", then lasso (λ_1) penalties (promoting sparsity) are placed on u and v. If type is "ordered", then lasso penalty is placed on u and a fused lasso penalty (promoting sparsity and smoothness) is placed on v.

Cross-validation of the rank-1 PMD is performed over `sumabss` (if type is "standard") or over `sumabsu` (if type is "ordered"). If type is "ordered", then `lambda` is chosen from the data without cross-validation.

The cross-validation works as follows: Some percent of the elements of X is removed at random from the data matrix. The PMD is performed for a range of tuning parameter values on this partially-missing data matrix; then, missing values are imputed using the decomposition obtained. The value of the tuning parameter that results in the lowest sum of squared errors of the missing values is "best".

To do cross-validation on the rank-2 PMD, first the rank-1 PMD should be computed, and then this function should be performed on the residuals, given by $X - udv'$.

Value

<code>cv</code>	Average sum of squared errors obtained over cross-validation folds.
<code>cv.error</code>	Standard error of average sum of squared errors obtained over cross-validation folds.
<code>bestsumabs</code>	If <code>type="standard"</code> , then value of <code>sumabss</code> resulting in smallest CV error is returned.
<code>bestsumabsu</code>	If <code>type="ordered"</code> , then value of <code>sumabsu</code> resulting in smallest CV error is returned.
<code>v.init</code>	The first right singular vector(s) of the data; these are returned to save on computation time if PMD will be run again.

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[PMD](#), [SPC](#)

Examples

```
# See examples in PMD help file
```

SPC

Perform sparse principal component analysis

Description

Performs sparse principal components analysis by applying PMD to a data matrix with lasso (L_1) penalty on the columns and no penalty on the rows.

Usage

```
SPC(
  x,
  sumabsv = 4,
  niter = 20,
  K = 1,
  orth = FALSE,
  trace = TRUE,
  v = NULL,
  center = TRUE,
  cnames = NULL,
  vpos = FALSE,
  vneg = FALSE,
  compute.pve = TRUE
)
```

Arguments

x	Data matrix of dimension $n \times p$, which can contain NA for missing values. We are interested in finding sparse principal components of dimension p .
sumabsv	How sparse do you want v to be? This is the sum of absolute values of elements of v . It must be between 1 and square root of number of columns of data. The smaller it is, the sparser v will be.
niter	How many iterations should be performed. It is best to run at least 20 of so. Default is 20.
K	The number of factors in the PMD to be returned; default is 1.
orth	If TRUE, then use method of Section 3.2 of Witten, Tibshirani and Hastie (2008) to obtain multiple sparse principal components. Default is FALSE.
trace	Print out progress as iterations are performed? Default is TRUE.
v	The first right singular vector(s) of the data. (If missing data is present, then the missing values are imputed before the singular vectors are calculated.) v is used as the initial value for the iterative PMD(L_1 , L_1) algorithm. If x is large, then this step can be time-consuming; therefore, if PMD is to be run multiple times, then v should be computed once and saved.
center	Subtract out mean of x ? Default is TRUE
cnames	An optional vector containing a name for each column.
vpos	Constrain the elements of v to be positive? TRUE or FALSE.
vneg	Constrain the elements of v to be negative? TRUE or FALSE.
compute.pve	Compute percent variance explained? Default TRUE. If not needed, then choose FALSE to save time.

Details

PMD(x ,sumabsu=sqrt(nrow(x)), sumabsv=3, K=1) and SPC(x ,sumabsv=3, K=1) give the same result, since the SPC method is simply PMD with an L_1 penalty on the columns and no penalty on the rows.

In Witten, Tibshirani, and Hastie (2008), two methods are presented for obtaining multiple factors for SPC. The methods are as follows:

(1) If one has already obtained factors u_{k-1} factors then one can compute residuals by subtracting out these factors. Then u_k and v_k can be obtained by applying the SPC/PMD algorithm to the residuals.

(2) One can require that u_k be orthogonal to u_i 's with $i < k$; the method is slightly more complicated, and is explained in WT&H(2008).

Method 1 is performed by running SPC with option `orth=FALSE` (the default) and Method 2 is performed using option `orth=TRUE`. Note that Methods 1 and 2 always give identical results for the first component, and often given quite similar results for later components.

Value

<code>u</code>	<code>u</code> is output. If you asked for multiple factors then each column of <code>u</code> is a factor. <code>u</code> has dimension $n \times K$ if you asked for K factors.
<code>v</code>	<code>v</code> is output. These are the sparse principal components. If you asked for multiple factors then each column of <code>v</code> is a factor. <code>v</code> has dimension $p \times K$ if you asked for K factors.
<code>d</code>	<code>d</code> is output; it is the diagonal of the matrix D in the penalized matrix decomposition. In the case of the rank-1 decomposition, it is given in the formulation $\ X - uv^T\ _F^2$ subject to $\ u\ _1 \leq \sum u_i $, $\ v\ _1 \leq \sum v_j $. Computationally, $d = u^T X v$ where <code>u</code> and <code>v</code> are the sparse factors output by the PMD function and X is the data matrix input to the PMD function.
<code>prop.var.explained</code>	A vector containing the proportion of variance explained by the first 1, 2, ..., K sparse principal components obtained. Formula for proportion of variance explained is on page 20 of Shen & Huang (2008), <i>Journal of Multivariate Analysis</i> 99: 1015-1034.
<code>v.init</code>	The first right singular vector(s) of the data; these are returned to save on computation time if PMD will be run again.
<code>meanx</code>	Mean of <code>x</code> that was subtracted out before SPC was performed.

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[SPC.cv](#), [PMD](#), [PMD.cv](#)

Examples

```
#A simple simulated example
```

```

set.seed(1)
u <- matrix(c(rnorm(50), rep(0,150)),ncol=1)
v <- matrix(c(rnorm(75),rep(0,225)), ncol=1)
x <- u%*%t(v)+matrix(rnorm(200*300),ncol=300)
# Perform Sparse PCA - that is, decompose a matrix w/o penalty on rows
# and w/ L1 penalty on columns
# First, we perform sparse PCA and get 4 components, but we do not
# require subsequent components to be orthogonal to previous components
out <- SPC(x,sumabsv=3, K=4)
print(out,verbose=TRUE)
# We could have selected sumabsv by cross-validation, using function SPC.cv
# Now, we do sparse PCA using method in Section 3.2 of WT&H(2008) for getting
# multiple components - that is, we require components to be orthogonal
out.orth <- SPC(x,sumabsv=3, K=4, orth=TRUE)
print(out.orth,verbose=TRUE)
oldpar <- par(mfrow = c(1,1))
par(mfrow=c(1,1))
plot(out$u[,1], out.orth$u[,1], xlab="", ylab="")
# Note that the first components w/ and w/o orth option are identical,
# since the orth option only affects the way that subsequent components
# are found
print(round(t(out$u)%*%out$u,4)) # not orthogonal
print(round(t(out.orth$u)%*%out.orth$u,4)) # orthogonal

# Use SPC.cv to choose tuning parameters:
cv.out <- SPC.cv(x)
print(cv.out)
plot(cv.out)
out <- SPC(x, sumabsv=cv.out$bestsumabsv)
print(out)
# or we could do
out <- SPC(x, sumabsv=cv.out$bestsumabsv1se)
print(out)
par(oldpar)

```

SPC.cv

Perform cross-validation on sparse principal component analysis

Description

Selects tuning parameter for the sparse principal component analysis method of Witten, Tibshirani, and Hastie (2008), which involves applying PMD to a data matrix with lasso ($\$L_1$) penalty on the columns and no penalty on the rows. The tuning parameter controls the sum of absolute values - or $\$L_1$ norm - of the elements of the sparse principal component.

Usage

```
SPC.cv(
```

```

x,
sumabsvs = seq(1.2, 5, len = 10),
nfolds = 5,
niter = 5,
v = NULL,
trace = TRUE,
orth = FALSE,
center = TRUE,
vpos = FALSE,
vneg = FALSE
)

```

Arguments

x	Data matrix of dimension $n \times p$, which can contain NA for missing values. We are interested in finding sparse principal components of dimension p .
sumabsvs	Range of sumabsv values to be considered in cross-validation. Sumabsv is the sum of absolute values of elements of v. It must be between 1 and square root of number of columns of data. The smaller it is, the sparser v will be.
nfolds	Number of cross-validation folds performed.
niter	How many iterations should be performed. By default, perform only 5 for speed reasons.
v	The first right singular vector(s) of the data. (If missing data is present, then the missing values are imputed before the singular vectors are calculated.) v is used as the initial value for the iterative PMD(L_1 , L_1) algorithm. If x is large, then this step can be time-consuming; therefore, if PMD is to be run multiple times, then v should be computed once and saved.
trace	Print out progress as iterations are performed? Default is TRUE.
orth	If TRUE, then use method of Section 3.2 of Witten, Tibshirani and Hastie (2008) to obtain multiple sparse principal components. Default is FALSE.
center	Subtract out mean of x? Default is TRUE
vpos	Constrain elements of v to be positive? Default is FALSE.
vneg	Constrain elements of v to be negative? Default is FALSE.

Details

This method only performs cross-validation for the first sparse principal component. It does so by performing the following steps $nfolds$ times: (1) replace a fraction of the data with missing values, (2) perform SPC on this new data matrix using a range of tuning parameter values, each time getting a rank-1 approximation UdV' where V is sparse, (3) measure the mean squared error of the rank-1 estimate of the missing values created in step 1.

Then, the selected tuning parameter value is that which resulted in the lowest average mean squared error in step 3.

In order to perform cross-validation for the second sparse principal component, apply this function to $X - UdV'$ where UdV' are the output of running SPC on the raw data X .

Value

cv	Average sum of squared errors that results for each tuning parameter value.
cv.error	Standard error of the average sum of squared error that results for each tuning parameter value.
bestsumabsv	Value of sumabsv that resulted in lowest CV error.
nonzerovs	Average number of non-zero elements of v for each candidate value of sumabsv.
v.init	Initial value of v that was passed in. Or, if that was NULL, then first right singular vector of X.
bestsumabsv1se	The smallest value of sumabsv that is within 1 standard error of smallest CV error.

References

Ali Mahzarnia, Alexander Badea (2022), Joint Estimation of Vulnerable Brain Networks and Alzheimer's Disease Risk Via Novel Extension of Sparse Canonical Correlation at bioRxiv.

See Also

[SPC](#), [PMD](#), [PMD.cv](#)

Examples

```
#A simple simulated example
set.seed(1)
u <- matrix(c(rnorm(50), rep(0,150)),ncol=1)
v <- matrix(c(rnorm(75),rep(0,225)), ncol=1)
x <- u%*%t(v)+matrix(rnorm(200*300),ncol=300)
# Perform Sparse PCA - that is, decompose a matrix w/o penalty on rows
# and w/ L1 penalty on columns
# First, we perform sparse PCA and get 4 components, but we do not
# require subsequent components to be orthogonal to previous components
out <- SPC(x,sumabsv=3, K=4)
print(out,verbose=TRUE)
# We could have selected sumabsv by cross-validation, using function SPC.cv
# Now, we do sparse PCA using method in Section 3.2 of WT&H(2008) for getting
# multiple components - that is, we require components to be orthogonal
out.orth <- SPC(x,sumabsv=3, K=4, orth=TRUE)
print(out.orth,verbose=TRUE)
oldpar <- par(mfrow = c(1,1))
par(mfrow=c(1,1))
plot(out$u[,1], out.orth$u[,1], xlab="", ylab="")
# Note that the first components w/ and w/o orth option are identical,
# since the orth option only affects the way that subsequent components
# are found
print(round(t(out$u)%*%out$u,4)) # not orthogonal
print(round(t(out.orth$u)%*%out.orth$u,4)) # orthogonal
```

```
# Use SPC.cv to choose tuning parameters:
cv.out <- SPC.cv(x)
print(cv.out)
plot(cv.out)
out <- SPC(x, sumabsv=cv.out$bestsumabsv)
print(out)
# or we could do
out <- SPC(x, sumabsv=cv.out$bestsumabsv1se)
print(out)
par(oldpar)
```

Index

* datasets

breastdata, [2](#)

* package

PMA-package, [2](#)

breastdata, [2](#)

CCA, [3](#), [11](#), [13](#), [16](#), [17](#)

CCA.permute, [7](#), [8](#), [13](#), [16](#), [17](#)

MultiCCA, [12](#), [16](#)

MultiCCA.permute, [13](#), [14](#)

plot.MultiCCA.permute

(MultiCCA.permute), [14](#)

plot.SPC.cv (SPC.cv), [27](#)

PlotCGH, [16](#)

PMA (PMA-package), [2](#)

PMA-package, [2](#)

PMD, [7](#), [11](#), [17](#), [18](#), [24](#), [26](#), [29](#)

PMD.cv, [17](#), [20](#), [22](#), [26](#), [29](#)

print.CCA (CCA), [3](#)

print.MultiCCA (MultiCCA), [12](#)

print.MultiCCA.permute

(MultiCCA.permute), [14](#)

print.SPC (SPC), [24](#)

print.SPC.cv (SPC.cv), [27](#)

SPC, [20](#), [24](#), [24](#), [29](#)

SPC.cv, [26](#), [27](#)