Package ‘fabia’

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Title  FABIA: Factor Analysis for Bicluster Acquisition
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Depends  R (>= 2.8.0), Biobase
Imports  methods, graphics, grDevices, stats, utils

Description  Biclustering by "Factor Analysis for Bicluster Acquisition" (FABIA). FABIA is a model-based technique for biclustering, that is clustering rows and columns simultaneously. Biclusters are found by factor analysis where both the factors and the loading matrix are sparse. FABIA is a multiplicative model that extracts linear dependencies between samples and feature patterns. It captures realistic non-Gaussian data distributions with heavy tails as observed in gene expression measurements. FABIA utilizes well understood model selection techniques like the EM algorithm and variational approaches and is embedded into a Bayesian framework. FABIA ranks biclusters according to their information content and separates spurious biclusters from true biclusters. The code is written in C.

License  LGPL (>= 2.1)

Collate  AllClasses.R AllGenerics.R fabia.R
         methods-Factorization-class.R zzz.R

URL  http://www.bioinf.jku.at/software/fabia/fabia.html

biocViews  StatisticalMethod, Microarray, DifferentialExpression,
            MultipleComparison, Clustering, Visualization

NeedsCompilation  yes
estimateMode

Description

estimateMode: R implementation of estimateMode.

Usage

estimateMode(X, maxiter=50, tol=0.001, alpha=0.1, a1=4.0, G1=FALSE)
**estimateMode**

**Arguments**

- `X` matrix of which the modes of the rows are estimated.
- `maxiter` maximal number of iterations; default = 50.
- `tol` tolerance for stopping; default = 0.001.
- `alpha` learning rate; default = 0.1.
- `a1` parameter of the width of the given distribution; default = 4.
- `G1` kind of distribution, TRUE: G1, FALSE: G2; default = FALSE.

**Details**

The mode is estimated by contrast functions G1

\[
(1/a_1) \times \ln(\cosh(a_1 \times x))
\]

or G2

\[-(1/a_1) \times \exp(-1/2 \times x \times x)\]

The estimation is performed by gradient descent initialized by the median.

Implementation in R.

**Value**

- `u` the vector of estimated modes.
- `xu` `X - u` the mode centered data.

**Author(s)**

Sepp Hochreiter

**References**


**See Also**

`fabi`, `fabias`, `fabiap`, `fabi`, `fabiasp`, `mfsc`, `nmfdiv`, `nmfeu`, `nmfsc`, `extractPlot`, `extractBic`, `plotBicluster`, `Factorization`, `projFuncPos`, `projFunc`, `estimateMode`, `makeFabiaData`, `makeFabiaDataBlocks`, `makeFabiaDataPos`, `makeFabiaDataBlocksPos`, `matrixImagePlot`, `fabiaDemo`, `fabiaVersion`

**Examples**

```r
# DEMO

dat <- makeFabiaDataBlocksPos(n = 100, l = 50, p = 10, f1 = 5, f2 = 5, of1 = 5, of2 = 10, sd_noise = 2.0, sd_z_noise = 0.2, mean_z = 2.0,
```
extractBic

**Description**

extractBic: R implementation of extractBic.

**Usage**

`extractBic(fact, thresZ=0.5, thresL=NULL)`

**Arguments**

- `fact`: object of the class `Factorization`.
- `thresZ`: threshold for sample belonging to bicluster; default 0.5.
- `thresL`: threshold for loading belonging to bicluster (if not given it is estimated).

**Details**

Essentially the model is the sum of outer products of vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X, U \) from \( R^{n \times l} \).

\( U \) is the Gaussian noise with a diagonal covariance matrix which entries are given by \( \Psi_i \).

The \( Z \) is locally approximated by a Gaussian with inverse variance given by \( \text{lapla} \).

Using these values we can computer for each \( j \) the variance \( z_i \) given \( x_j \).

\[ x_j = Lz_j + u_j \]
This variance can be used to determine the information content of a bicluster.

The \( \lambda_i \) and \( z_i \) are used to extract the bicluster \( i \), where a threshold determines which observations and which samples belong the bicluster.

In bic the biclusters are extracted according to the largest absolute values of the component \( i \), i.e. the largest values of \( \lambda_i \) and the largest values of \( z_i \). The factors \( z_i \) are normalized to variance 1.

The components of bic are \( \text{binp} \), \( \text{bixv} \), \( \text{bixn} \), \( \text{biypv} \), and \( \text{biypn} \).

\( \text{binp} \) give the size of the bicluster: number observations and number samples. \( \text{bixv} \) gives the values of the extracted observations that have absolute values above a threshold. They are sorted. \( \text{bixn} \) gives the extracted observation names (e.g. gene names). \( \text{biypv} \) gives the values of the extracted samples that have absolute values above a threshold. They are sorted. \( \text{biypn} \) gives the names of the extracted samples (e.g. sample names).

In bicopp the opposite clusters to the biclusters are given. Opposite means that the negative pattern is present.

The components of opposite clusters bicopp are \( \text{binn} \), \( \text{bixv} \), \( \text{bixn} \), \( \text{biypnv} \), and \( \text{biynn} \).

\( \text{binn} \) give the size of the opposite bicluster: number observations and number samples. \( \text{bixv} \) gives the values of the extracted observations that have absolute values above a threshold. They are sorted. \( \text{bixn} \) gives the extracted observation names (e.g. gene names). \( \text{biypnv} \) gives the values of the opposite extracted samples that have absolute values above a threshold. They are sorted. \( \text{biynn} \) gives the names of the opposite extracted samples (e.g. sample names).

That means the samples are divided into two groups where one group shows large positive values and the other group has negative values with large absolute values. That means a observation pattern can be switched on or switched off relative to the average value.

\( \text{numn} \) gives the indices of bic with components: \( \text{numng} = \text{bix} \) and \( \text{numnp} = \text{biypn} \).

\( \text{numn} \) gives the indices of bicopp with components: \( \text{numng} = \text{bix} \) and \( \text{numnn} = \text{biynn} \).

Implementation in R.

**Value**

- bic: extracted biclusters.
- numn: indexes for the extracted biclusters.
- bicopp: extracted opposite biclusters.
- numnopp: indexes for the extracted opposite biclusters.
- x: scaled and centered data matrix.
- np: number of biclusters.

**Author(s)**

Sepp Hochreiter

**See Also**

fabia, fabias, fabiap, fabi, fabiasp, mfsc, nmfdiv, mmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion
Examples

# TEST

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
    sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resEx <- fabia(X, 3, 0.01, 20)
rEx <- extractBic(resEx)
rEx$bic[1,]
rEx$bic[2,]
rEx$bic[3,]

## Not run:

## DEMO1

dat <- makeFabiaDataBlocks(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
    sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resToy <- fabia(X, 13, 0.01, 200)
rToy <- extractBic(resToy)
avini(resToy)
rToy$bic[1,]
rToy$bic[2,]
rToy$bic[3,]

## DEMO2

avail <- require(fabiaData)
if (HAavail) {
message(""
message(""
message("#aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa"
message("Package 'fabiadata' is not available: please install.")
message("#aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa"
} else {

data(Breast_A)

X <- as.matrix(XBreast)

resBreast <- fabia(X,5,0.1,200)

rBreast <- extractBic(resBreast)

avini(resBreast)

rBreast$bic[1,]

rBreast$bic[2,]

rBreast$bic[3,]

}

## End(Not run)

---

**extractPlot**  

*Plotting of BiclusterinG Results*

**Description**

extractPlot: R implementation of `extractPlot`.

**Usage**

`extractPlot(fact, thresZ=0.5, ti="", thresL=NULL, Y=NULL, which=c(1,2,3,4,5,6))`

**Arguments**

- `fact` object of the class Factorization.
- `thresZ` threshold for sample belonging to bicluster; default 0.5.
- `thresL` threshold for loading belonging to bicluster (estimated if not given).
- `ti` plot title; default "".
- `Y` noise free data matrix.
- `which` which plot is shown: 1=noise free data (if available), 2=data, 3=reconstructed data, 4=error, 5=absolute factors, 6=absolute loadings; default c(1,2,3,4,5,6).
Details

Essentially the model is the sum of outer products of vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X, U \) from \( R^{n \times l} \).

The hidden dimension \( p \) is used for kmeans clustering of \( \lambda_i \) and \( z_i \).

The \( \lambda_i \) and \( z_i \) are used to extract the bicluster \( i \), where a threshold determines which observations and which samples belong the the bicluster.

The method produces following plots depending what plots are chosen by the "which" variable:

- "Y": noise free data (if available),
- "X": data,
- "LZ": reconstructed data,
- "LZ-X": error,
- "abs(Z)": absolute factors,
- "abs(L)": absolute loadings.

Implementation in \( R \).

Author(s)

Sepp Hochreiter

See Also

`fabi`, `fabias`, `fabiap`, `fabi`, `fabiasp`, `spfabi`, `mfsc`, `nmfdiv`, `nmfeu`, `nmfsc`, `extractPlot`, `extractBic`, `plotBicluster`, `Factorization`, `projFuncPos`, `projFunc`, `estimateMode`, `makeFabiaData`, `makeFabiaDataBlocks`, `makeFabiaDataPos`, `makeFabiaDataBlocksPos`, `matrixImagePlot`, `fabiDemo`, `fabiVersion`

Examples

```r
# TEST

dat <- makeFabiaDataBlocks(n = 100,l = 50,p = 3,f1 = 5,f2 = 5,
of1 = 5,of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
 sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resEx <- fabia(X,3,0.1,20)

extractPlot(resEx,ti="FABIA",Y=Y)
```
```r
## Not run:
#----------------------
# DEMO1
#----------------------

dat <- makeFabiaDataBlocks(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
 sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resToy <- fabia(X, 13, 0.01, 200)
extractPlot(resToy, ti="FABIA", Y = Y)

#----------------------
# DEMO2
#----------------------

avail <- require(fabiaData)

if (!avail) {
    message("")
    message("")
    message("########################################################################")
    message("Package 'fabiaData' is not available: please install.")
    message("########################################################################")
} else {

data(Breast_A)

X <- as.matrix(XBreast)

resBreast <- fabia(X, 5, 0.1, 200)
extractPlot(resBreast, ti="FABIA Breast cancer (Veer)")

# sorting of predefined labels
CBreast
}

## End(Not run)
```

---

**Fabi**  
*Factor Analysis for Bicluster Acquisition: Laplace Prior (FABI)*
Description

fabi: R implementation of fabia, therefore it is slow.

Usage

fabi(X, p=13, alpha=0.01, cyc=500, spl=0, spz=0.5, center=2, norm=1, lap=1.0)

Arguments

X         the data matrix.
p         number of hidden factors = number of biclusters; default = 13.
alpha     sparseness loadings (0-1.0); default = 0.01.
cyc       number of iterations; default = 500.
spl       sparseness prior loadings (0 - 2.0); default = 0 (Laplace).
spz       sparseness factors (0.5-2.0); default = 0.5 (Laplace).
center    data centering: 1 (mean), 2 (median), > 2 (mode), 0 (no); default = 2.
norm      data normalization: 1 (0.75-0.25 quantile), >1 (var=1), 0 (no); default = 1.
lap       minimal value of the variational parameter; default = 1.0.

Details

Biclusters are found by sparse factor analysis where both the factors and the loadings are sparse.
Essentially the model is the sum of outer products of vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X, U \) from \( R^{n \times l} \).
If the nonzero components of the sparse vectors are grouped together then the outer product results in a matrix with a nonzero block and zeros elsewhere.
We recommend to normalize the components to variance one in order to make the signal and noise comparable across components.
The model selection is performed by a variational approach according to Girolami 2001 and Palmer et al. 2006.
We included a prior on the parameters and minimize a lower bound on the posterior of the parameters given the data. The update of the loadings includes an additive term which pushes the loadings toward zero (Gaussian prior leads to an multiplicative factor).
The code is implemented in R, therefore it is slow.
Value

object of the class Factorization. Containing LZ (estimated noise free data L Z), L (loadings L), Z (factors Z), U (noise X − L Z), center (centering vector), scaleData (scaling vector), X (centered and scaled data X), Psi (noise variance σ), lapla (variational parameter), avini (the information which the factor z_{ij} contains about x_j averaged over j) xavini (the information which the factor z_j contains about x_j) ini (for each j the information which the factor z_{ij} contains about x_j).

Author(s)

Sepp Hochreiter

References


See Also

fabi, fabias, fabiap, spfabia, fabi, fabiasp, mfsc, nmfdiv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

```r
# TEST
#---------

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resEx <- fabi(X, 3, 0.01, 20)

## Not run:
#---------
# DEMO1
#---------
```
dat <- makeFabiaDataBlocks(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5, of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0, sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resToy <- fabi(X, 13, 0.01, 200)
extractPlot(resToy, ti = "FABI", Y = Y)

#-------------
# DEMO2
#-------------

avail <- require(fabiaData)

if (!avail) {
  message(""
  message(""
  message(""!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!")
  message("Package 'fabiaData' is not available: please install.")
  message(""!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!")
} else {

data(Breast_A)
X <- as.matrix(XBreast)
resBreast <- fabi(X, 5, 0.1, 200)
extractPlot(resBreast, ti = "FABI Breast cancer (Veer)")

# sorting of predefined labels
CBreast
}

#-------------
# DEMO3
#-------------

avail <- require(fabiaData)

if (!avail) {
  message(""
  message(""
  message(""!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!")
  message("Package 'fabiaData' is not available: please install.")
  message(""!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!")
} else {


data(Multi_A)
X <- as.matrix(XMulti)
resMulti <- fabi(X, 5, 0.1, 200)
extractPlot(resMulti, ti="FABI Multiple tissues(Su)")

# sorting of predefined labels
CMulti
}

-------------------
# DEMO4
-------------------

avail <- require(fabiaData)
if (!avail) {
  message(""
  message(""
  message(""Package 'fabiaData' is not available: please install."))
} else {

data(DLBCL_B)
X <- as.matrix(XDLBCL)
resDLBCL <- fabi(X, 5, 0.1, 200)
extractPlot(resDLBCL, ti="FABI Lymphoma(Rosenwald)")

# sorting of predefined labels
CDLBCL
}

## End(Not run)
Description

fabia: C implementation of fabia.

Usage

```
fabia(X,p=13,alpha=0.01,cyc=500,sp1=0,spz=0.5,non_negative=0,random=1.0,center=2,norm=1, scale=0.0,lap=1.0,nl=0,1l=0)
```

Arguments

- **x**: the data matrix.
- **p**: number of hidden factors = number of biclusters; default = 13.
- **alpha**: sparseness loadings (0 - 1.0); default = 0.01.
- **cyc**: number of iterations; default = 500.
- **sp1**: sparseness prior loadings (0 - 2.0); default = 0 (Laplace).
- **spz**: sparseness factors (0.5 - 2.0); default = 0.5 (Laplace).
- **non_negative**: Non-negative factors and loadings if non_negative > 0; default = 0.
- **random**: <=0: by SVD, >0: random initialization of loadings in [-random,random]; default = 1.0.
- **center**: data centering: 1 (mean), 2 (median), > 2 (mode), 0 (no); default = 2.
- **norm**: data normalization: 1 (0.75-0.25 quantile), >1 (var=1), 0 (no); default = 1.
- **scale**: loading vectors are scaled in each iteration to the given variance. 0.0 indicates non scaling; default = 0.0.
- **lap**: minimal value of the variational parameter; default = 1.0
- **nl**: maximal number of biclusters at which a row element can participate; default = 0 (no limit)
- **1l**: maximal number of row elements per bicluster; default = 0 (no limit)
- **bl**: cycle at which the nl or 1l maximum starts; default = 0 (start at the beginning)

Details

Biclusters are found by sparse factor analysis where both the factors and the loadings are sparse. Essentially the model is the sum of outer products of vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X, U \) from \( R^{n \times l} \).
If the nonzero components of the sparse vectors are grouped together then the outer product results in a matrix with a nonzero block and zeros elsewhere.

The model selection is performed by a variational approach according to Girolami 2001 and Palmer et al. 2006.

We included a prior on the parameters and minimize a lower bound on the posterior of the parameters given the data. The update of the loadings includes an additive term which pushes the loadings toward zero (Gaussian prior leads to an multiplicative factor).

The code is implemented in C.

Value

object of the class Factorization. Containing LZ (estimated noise free data $LZ$), L (loadings $L$), Z (factors $Z$), U (noise: $X - LZ$), center (centering vector), scaleData (scaling vector), X (centered and scaled data $X$), Psi (noise variance $\sigma$), lapla (variational parameter), avini (the information which the factor $z_{ij}$ contains about $x_j$ averaged over $j$) xavini (the information which the factor $z_j$ contains about $x_j$) ini (for each $j$ the information which the factor $z_{ij}$ contains about $x_j$).

Author(s)

Sepp Hochreiter

References


See Also

fabia, fabias, fabiap, spfabia, readSpfabiaResult, fabi, fabiasp, mfsce, nmfdiv, nmfeu, mfsce, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projfunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiDemo, fabiaVersion

Examples

```R
# TEST

dat <- makeFabiaDataBlocks(n = 100, l= 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)
```
X <- dat[[1]]
Y <- dat[[2]]

resEx <- fabia(X,3,0.01,50)

### Not run:
#-----------------
# DEMO1: Toy Data
#-----------------

n = 1000
l= 100
p = 10

dat <- makeFabiaDataBlocks(n = n,l= l,p = p,f1 = 5,f2 = 5,
of1 = 5,of2 = 10,sd_noise = 3.0,sd_z_noise = 0.2,mean_z = 2.0,
     sd_z = 1.0,sd_l_noise = 0.2,mean_l = 3.0,sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
ZC <- dat[[3]]
LC <- dat[[4]]

gclab <- rep.int(0,l)
gllab <- rep.int(0,n)
clab <- as.character(1:l)
llab <- as.character(1:n)
for (i in 1:p){
    for (j in ZC[i]){ 
        clab[j] <- paste(as.character(i),"_",clab[j],sep="") 
    }
    for (j in LC[i]){ 
        llab[j] <- paste(as.character(i),"_",llab[j],sep="") 
    }
gclab[unlist(ZC[i])] <- gclab[unlist(ZC[i])] + p*i
gllab[unlist(LC[i])] <- gllab[unlist(LC[i])] + p*i
}

groups <- gclab

#### FABIA
resToy1 <- fabia(X,13,0.01,400)
extractPlot(resToy1,ti="FABIA",Y=Y)
raToy1 <- extractBic(resToy1)
if ((raToy1$bic[[1]][1]>1) && (raToy1$bic[[1]][2]>1)) {
  plotBicluster(raToy1,1)
} else {
  message("")
  message("")
  message("Package 'fabiaData' is not available: please install.")
  message("")
} else {
  data(Breast_A)
  X <- as.matrix(XBreast)

  resBreast1 <- fabia(X,5,0.1,400)
  extractPlot(resBreast1,ti="FABIA Breast cancer(Veer)"

  raBreast1 <- extractBic(resBreast1)
if ((raBreast1$bic[[1]]$1]$1 > 1) & (raBreast1$bic[[1]]$2]$1 > 1) {
  plotBicluste(raBreast1, 1)
}
if ((raBreast1$bic[[2]]$1]$1 > 1) & (raBreast1$bic[[2]]$2]$1 > 1) {
  plotBicluste(raBreast1, 2)
}
if ((raBreast1$bic[[3]]$1]$1 > 1) & (raBreast1$bic[[3]]$2]$1 > 1) {
  plotBicluste(raBreast1, 3)
}
if ((raBreast1$bic[[4]]$1]$1 > 1) & (raBreast1$bic[[4]]$2]$1 > 1) {
  plotBicluste(raBreast1, 4)
}

plot(resBreast1,dim=c(1,2),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(1,3),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(1,4),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(1,5),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(2,3),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(2,4),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(2,5),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(3,4),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(3,5),label.tol=0.03,col.group=CBreast,label.size=0.6)
plot(resBreast1,dim=c(4,5),label.tol=0.03,col.group=CBreast,label.size=0.6)

#------------------------------------------------------
# DEMO3: Su's multiple tissue types
# gene expression data set
#------------------------------------------------------

avail <- require(fabiaData)
if (!avail) {
  message(""
  message(""
  message("#+++++++++++++++++++++++++++++++++++++++++++++++++++++
  message("Package 'fabiaData' is not available: please install.
  message("#+++++++++++++++++++++++++++++++++++++++++++++++++++++
} else {

data(Multi_A)
X <- as.matrix(XMulti)
resMulti1 <- fabia(X, 5, 0.06, 300, norm=2)
extractPlot(resMulti1, ti="FABIA Multiple tissues(Su)"
raMulti1 <- extractBic(resMulti1)

if ((raMulti1$bic[[1]][1]>1) & (raMulti1$bic[[1]][2]>1)) {
  plotBicluster(raMulti1,1)
}
if ((raMulti1$bic[[2]][1]>1) & (raMulti1$bic[[2]][2]>1)) {
  plotBicluster(raMulti1,2)
}
if ((raMulti1$bic[[3]][1]>1) & (raMulti1$bic[[3]][2]>1)) {
  plotBicluster(raMulti1,3)
}
if ((raMulti1$bic[[4]][1]>1) & (raMulti1$bic[[4]][2]>1)) {
  plotBicluster(raMulti1,4)
}

plot(resMulti1,dim=c(1,2),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(1,3),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(1,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(1,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(2,3),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(2,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(2,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(3,4),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(3,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)
plot(resMulti1,dim=c(4,5),label.tol=0.01,col.group=CMulti,lab.size=0.6)

# DEMO4: Rosenwald’s diffuse large-B-cell
# lymphoma gene expression data set

avail <- require(fabiaData)

if (!avail) {
  message("")
  message("")
  message(""""""""""""""")
  message("Package 'fabiaData' is not available: please install.")
  message(""""""""""""""")
} else {

data(DLBCL_B)
X <- as.matrix(DLBCL)
resDLBCL1 <- fabia(X,5,0.1,400,norm=2)
extractPlot(resLBCL1,ti="FABIA Lymphoma(Rosenwald)")
raLBCL1 <- extractBic(resLBCL1)
if ((raLBCL1$bic[[1]][1]>1) & (raLBCL1$bic[[1]][2]>1)) {
  plotBiccluster(raLBCL1,1)
}
if ((raLBCL1$bic[[2]][1]>1) & (raLBCL1$bic[[2]][2]>1)) {
  plotBiccluster(raLBCL1,2)
}
if ((raLBCL1$bic[[3]][1]>1) & (raLBCL1$bic[[3]][2]>1)) {
  plotBiccluster(raLBCL1,3)
}
if ((raLBCL1$bic[[4]][1]>1) & (raLBCL1$bic[[4]][2]>1)) {
  plotBiccluster(raLBCL1,4)
}
plot(resLBCL1,dim=c(1,2),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(1,3),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(1,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(1,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(2,3),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(2,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(2,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(3,4),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(3,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)
plot(resLBCL1,dim=c(4,5),label.tol=0.03,col.group=CDLBCL,lab.size=0.6)

## End(Not run)

---

**Description**

fabiaDemo calls the demo codes for fabia.

**Usage**

fabiaDemo()

**Author(s)**

Sepp Hochreiter
fabiap

See Also

fabi, fabias, fabiap, fabi, fabiasp, mfsc, nmfdiv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

## Not run:
# interactive
fabiademo()

## End(Not run)

fabiap

Factor Analysis for Bicluster Acquisition: Post-Projection (FABIAP)

Description

fabiap: C implementation of fabiap.

Usage

fabiap(X, p=13, alpha=0.01, cyc=500, spl=0, spz=0.5, sL=0.6, sZ=0.6, non_negative=0, random=1.0, center=2, norm=1, scale=0.0)

Arguments

X
the data matrix.

p
number of hidden factors = number of biclusters; default = 13.

alpha
sparseness loadings (0-1.0); default = 0.01.

cyc
number of iterations; default = 500.

spl
sparseness prior loadings (0 - 2.0); default = 0 (Laplace).

spz
sparseness factors (0.5 - 2.0); default = 0.5 (Laplace).

sL
final sparseness loadings; default = 0.6.

sZ
final sparseness factors; default = 0.6.

non_negative
Non-negative factors and loadings if non_negative > 0; default = 0.

random
<=0: by SVD, >0: random initialization of loadings in [-random,random]; default = 1.0.

center
data centering: 1 (mean), 2 (median), > 2 (mode), 0 (no); default = 2.

norm
data normalization: 1 (0.75-0.25 quantile), >1 (var=1), 0 (no); default = 1.

scale
loading vectors are scaled in each iteration to the given variance. 0.0 indicates non scaling; default = 0.0.
lap

minimal value of the variational parameter; default = 1.0.

nL

maximal number of biclusters at which a row element can participate; default = 0 (no limit)

lL

maximal number of row elements per bicluster; default = 0 (no limit)

dL

cycle at which the nL or lL maximum starts; default = 0 (start at the beginning)

Details

Biclusters are found by sparse factor analysis where both the factors and the loadings are sparse.
Post-processing by projecting the final results to a given sparseness criterion.

Essentially the model is the sum of outer products of vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X \), \( U \) from \( R^{n \times l} \).

If the nonzero components of the sparse vectors are grouped together then the outer product results in a matrix with a nonzero block and zeros elsewhere.

The model selection is performed by a variational approach according to Girolami 2001 and Palmer et al. 2006.

We included a prior on the parameters and minimize a lower bound on the posterior of the parameters given the data. The update of the loadings includes an additive term which pushes the loadings toward zero (Gaussian prior leads to an multiplicative factor).

**Post-processing:** The final results of the loadings and the factors are projected to a sparse vector according to Hoyer, 2004: given an \( l_1 \)-norm and an \( l_2 \)-norm minimize the Euclidean distance to the original vector (currently the \( l_2 \)-norm is fixed to 1). The projection is a convex quadratic problem which is solved iteratively where at each iteration at least one component is set to zero. Instead of the \( l_1 \)-norm a sparseness measurement is used which relates the \( l_1 \)-norm to the \( l_2 \)-norm:

The code is implemented in C and the projection in R.

Value

object of the class Factorization. Containing \( LZ \) (estimated noise free data \( LZ \)), \( L \) (loadings \( L \)), \( Z \) (factors \( Z \)), \( U \) (noise \( X - LZ \)), center (centering vector), scaleData (scaling vector), \( X \) (centered and scaled data \( X \)), \( \Psi \) (noise variance \( \sigma \)), \( \lambda \) (variational parameter), \( \alpha \) (the information which the factor \( z_{ij} \) contains about \( x_{ij} \) averaged over \( j \)) \( \beta \) (the information which the factor \( z_j \) contains about \( x_{ij} \) for each \( j \) the information which the factor \( z_{ij} \) contains about \( x_{ij} \)).

Author(s)

Sepp Hochreiter
References


See Also

fabiap, fabias, fabiap, spfabia, fabi, fabiasp, nmfsc, nmfdiv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

```r
#------------------------
# TEST
#------------------------

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
   sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resEx <- fabiap(X, 3, 0.1, 50)

## Not run:

#------------------------
# DEMO1: Toy Data
#------------------------

n = 1000
l = 100
p = 10

dat <- makeFabiaDataBlocks(n = n, l = 1, p = p, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
   sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
```
```r
ZC <- dat[[3]]
LC <- dat[[4]]

gclab <- rep.int(0,1)
gllab <- rep.int(0,n)
clab <- as.character(1:1)
llab <- as.character(1:n)
for (i in 1:p){
  for (j in ZC[i]){  
    clab[j] <- paste(as.character(i),"\_",clab[j],sep="")  
  }
  for (j in LC[i]){  
    llab[j] <- paste(as.character(i),"\_",llab[j],sep="")  
  }
gclab[unlist(ZC[i])] <- gclab[unlist(ZC[i])] + p^i
  gllab[unlist(LC[i])] <- gllab[unlist(LC[i])] + p^i
}

groups <- gclab

### FABIAP
resToy3 <- fabiap(X,13,0.1,400)
extractPlot(resToy3,ti="FABIAP",Y=Y)

raToy3 <- extractBic(resToy3)
if ((raToy3$bic[[1]][1]>1) & (raToy3$bic[[1]][2]>1) {  
  plotBicluster(raToy3,1)
}
if ((raToy3$bic[[2]][1]>1) & (raToy3$bic[[2]][2]>1) {  
  plotBicluster(raToy3,2)
}
if ((raToy3$bic[[3]][1]>1) & (raToy3$bic[[3]][2]>1) {  
  plotBicluster(raToy3,3)
}
if ((raToy3$bic[[4]][1]>1) & (raToy3$bic[[4]][2]>1) {  
  plotBicluster(raToy3,4)
}

colnames(X(resToy3)) <- clab
rownames(X(resToy3)) <- llab

plot(resToy3,dim=c(1,2),label.tol=0.1,col.group = groups,lab.size=0.6)
plot(resToy3,dim=c(1,3),label.tol=0.1,col.group = groups,lab.size=0.6)
plot(resToy3,dim=c(2,3),label.tol=0.1,col.group = groups,lab.size=0.6)

#-----------------------------------
```
# DEMO2: Laura van't Veer's gene expression data set for breast cancer

avail <- require(fabiaData)

if (!avail) {
  message("")
  message("")
  message("############################################")
  message("Package 'fabiaData' is not available: please install.")
  message("############################################")
} else {

  data(Breast_A)

  X <- as.matrix(XBreast)

  resBreast3 <- fabiap(X, 5, 0.1, 400)

  extractPlot(resBreast3, ti="FABIAP Breast cancer (Veer)")

  raBreast3 <- extractBic(resBreast3)

  if (raBreast3$bic[[1]][1]>1) & (raBreast3$bic[[1]][2]>1) {
    plotBicluster(raBreast3, 1)
  }
  if (raBreast3$bic[[2]][1]>1) & (raBreast3$bic[[2]][2]>1) {
    plotBicluster(raBreast3, 2)
  }
  if (raBreast3$bic[[3]][1]>1) & (raBreast3$bic[[3]][2]>1) {
    plotBicluster(raBreast3, 3)
  }
  if (raBreast3$bic[[4]][1]>1) & (raBreast3$bic[[4]][2]>1) {
    plotBicluster(raBreast3, 4)
  }

  plot(resBreast3, dim=c(1, 2), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(1, 3), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(1, 4), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(1, 5), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(2, 3), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(2, 4), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(2, 5), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(3, 4), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(3, 5), label.tol=0.03, col.group=CBreast, lab.size=0.6)
  plot(resBreast3, dim=c(4, 5), label.tol=0.03, col.group=CBreast, lab.size=0.6)
}


# DEMO3: Su's multiple tissue types
# gene expression data set
#

avail <- require(fabiaData)

if (!avail) {
  message(""")
  message(""")
  message("""""""""""""""""""""""""""""""""""""""")
  message("Package 'fabiaData' is not available: please install.")
  message("""""""""""""""""""""""""""""""""""""""")
} else {

data(Multi_A)

X <- as.matrix(XMulti)

resMulti3 <- fabiap(X, S, 1, 300)

extractPlot(resMulti3, ti="FABIAP Multiple tissues(Su)"

raMulti3 <- extractBic(resMulti3)

if ((raMulti3$bic[[1]][1]>1) && (raMulti3$bic[[1]][2]>1) {
  plotBicCluster(raMulti3, 1)
}
if ((raMulti3$bic[[2]][1]>1) && (raMulti3$bic[[2]][2]>1) {
  plotBicCluster(raMulti3, 2)
}
if ((raMulti3$bic[[3]][1]>1) && (raMulti3$bic[[3]][2]>1) {
  plotBicCluster(raMulti3, 3)
}
if ((raMulti3$bic[[4]][1]>1) && (raMulti3$bic[[4]][2]>1) {
  plotBicCluster(raMulti3, 4)
}

plot(resMulti3, dim=c(1,2), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(1,3), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(1,4), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(1,5), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(2,3), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(2,4), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(2,5), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(3,4), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(3,5), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti3, dim=c(4,5), label.tol=0.01, col.group=CMulti, lab.size=0.6)
# DEMO4: Rosenwald's diffuse large-B-cell lymphoma gene expression data set

```r
avail <- require(fabiaData)
if (!avail) {
  message(""
  message(""
  message("###############################################")
  message("Package 'fabiaData' is not available: please install.")
  message("###############################################")
} else {

data(DLBCL_B)
X <- as.matrix(XDLBCL)

resDLBCL3 <- fabiap(X, 5, 0.1, 400)

extractPlot(resDLBCL3, ti="FABIAP Lymphoma(Rosenwald)"
raDLBCL3 <- extractBic(resDLBCL3)

if (raDLBCL3$bic[[1]][1]>1) & (raDLBCL3$bic[[1]][2]>1) {
  plotBicluster(raDLBCL3,1)
} if (raDLBCL3$bic[[2]][1]>1) & (raDLBCL3$bic[[2]][2]>1) {
  plotBicluster(raDLBCL3,2)
} if (raDLBCL3$bic[[3]][1]>1) & (raDLBCL3$bic[[3]][2]>1) {
  plotBicluster(raDLBCL3,3)
} if (raDLBCL3$bic[[4]][1]>1) & (raDLBCL3$bic[[4]][2]>1) {
  plotBicluster(raDLBCL3,4)
}

plot(resDLBCL3, dim=c(1,2), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(1,3), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(1,4), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(1,5), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(2,3), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(2,4), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(2,5), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(3,4), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(3,5), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL3, dim=c(4,5), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
```
```
**fabias**  
*Factor Analysis for Bicluster Acquisition: Sparseness Projection (FABIAS)*

**Description**

fabias: C implementation of fabias.

**Usage**

```
fabias(X,p=13,alpha=0.6,cyc=500,spz=0.5,non_negative=0,random=1.0,center=2,norm=1,lap=1.0,nL=0,lL=0)
```

**Arguments**

- **X**  
  the data matrix.
- **p**  
  number of hidden factors = number of biclusters; default = 13.
- **alpha**  
  sparseness loadings (0.1 - 1.0); default = 0.1.
- **cyc**  
  number of iterations; default = 500.
- **spz**  
  sparseness factors (0.5 - 2.0); default = 0.5 (Laplace).
- **non_negative**  
  Non-negative factors and loadings if non_negative > 0; default = 0.
- **random**  
  <=0: by SVD, >0: random initialization of loadings in [-random,random]; default = 1.0.
- **center**  
  data centering: 1 (mean), 2 (median), > 2 (mode), 0 (no); default = 2.
- **norm**  
  data normalization: 1 (0.75-0.25 quantile), >1 (var=1), 0 (no); default = 1.
- **lap**  
  minimal value of the variational parameter; default = 1.0.
- **nL**  
  maximal number of biclusters at which a row element can participate; default = 0 (no limit)
- **lL**  
  maximal number of row elements per bicluster; default = 0 (no limit)
- **bL**  
  cycle at which the nL or lL maximum starts; default = 0 (start at the beginning)

**Details**

Biclusters are found by sparse factor analysis where *both* the factors and the loadings are sparse. Essentially the model is the sum of outer products of vectors:

\[
X = \sum_{i=1}^{p} \lambda_i z_i^T + U
\]
where the number of summands $p$ is the number of biclusters. The matrix factorization is

$$X = L Z + U$$

Here $\lambda_i$ are from $R^n$, $z_i$ from $R^l$, $L$ from $R^{n \times p}$, $Z$ from $R^{d \times l}$, and $X$, $U$ from $R^{n \times l}$.

If the nonzero components of the sparse vectors are grouped together then the outer product results in a matrix with a nonzero block and zeros elsewhere.

The model selection is performed by a variational approach according to Girolami 2001 and Palmer et al. 2006.

The prior has finite support, therefore after each update of the loadings they are projected to the finite support. The projection is done according to Hoyer, 2004: given an $l_1$-norm and an $l_2$-norm minimize the Euclidean distance to the original vector (currently the $l_2$-norm is fixed to 1). The projection is a convex quadratic problem which is solved iteratively where at each iteration at least one component is set to zero. Instead of the $l_1$-norm a sparseness measurement is used which relates the $l_1$-norm to the $l_2$-norm.

The code is implemented in C.

**Value**

Object of the class `Factorization`. Containing LZ (estimated noise free data $L Z$), L (loadings $L$), Z (factors $Z$), U (noise $X - L Z$), center (centering vector), scaleData (scaling vector), X (centered and scaled data $X$), Psi (noise variance $\sigma$), lapla (variational parameter), avini (the information which the factor $z_{ij}$ contains about $x_j$ averaged over $j$), xavini (the information which the factor $z_j$ contains about $x_j$), ini (for each $j$ the information which the factor $z_{ij}$ contains about $x_j$).

**Author(s)**

Sepp Hochreiter

**References**


**See Also**

fabia, fabias, fabiap, spfabia, fabi, fabiasp, mfsc, nmfd, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion
Examples

#-----------------
# TEST
#-----------------

dat <- makeFabiaDataBlocks(n = 1000, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resEx <- fabias(X, 3, 0.6, 50)

## Not run:
#-----------------
# DEMO1: Toy Data
#-----------------

n = 1000
l = 100
p = 10

dat <- makeFabiaDataBlocks(n = n, l = l, p = p, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
ZC <- dat[[3]]
LC <- dat[[4]]

gclab <- rep.int(0, l)
gllab <- rep.int(0, n)
clab <- as.character(1:1)
llab <- as.character(1:n)
for (i in 1:p){
  for (j in ZC[i]){
    clab[j] <- paste(as.character(i), "\", clab[j], sep="")
  }
  for (j in LC[i]){
    llab[j] <- paste(as.character(i), "\", llab[j], sep="")
  }

gclab[unlist(ZC[i])] <- gclab[unlist(ZC[i])] + p * i
gllab[unlist(LC[i])] <- gllab[unlist(LC[i])] + p * i
}
fabias

groups <- gclab

### FABIAS

```
resToy2 <- fabias(X,13,0.6,400)
extractPlot(resToy2,ti="FABIAS",Y=Y)
```

```
raToy2 <- extractBic(resToy2)

if ((raToy2$bic[[1]][1]>1) && (raToy2$bic[[1]][2]>1) { plotBicuster(raToy2,1) }
if ((raToy2$bic[[2]][1]>1) && (raToy2$bic[[2]][2]>1) { plotBicuster(raToy2,2) }
if ((raToy2$bic[[3]][1]>1) && (raToy2$bic[[3]][2]>1) { plotBicuster(raToy2,3) }
if ((raToy2$bic[[4]][1]>1) && (raToy2$bic[[4]][2]>1) { plotBicuster(raToy2,4) }
```

```
colnames(X(resToy2)) <- clab
rownames(X(resToy2)) <- llab
```

```
plot(resToy2,dim=c(1,2),label.tol=0.1,col.group = groups,lab.size=0.6)
plot(resToy2,dim=c(1,3),label.tol=0.1,col.group = groups,lab.size=0.6)
plot(resToy2,dim=c(2,3),label.tol=0.1,col.group = groups,lab.size=0.6)
```

#-------------------------------
# DEMO2: Laura van't Veer's gene expression
# data set for breast cancer
#-------------------------------

```
avail <- require(fabiaData)

if (!avail) {
  message(""
  message(""
  message(""Package 'fabiaData' is not available: please install."')
  message(""
} else {

data(Breast_A)
```
X <- as.matrix(XBreast)
resBreast2 <- fabias(X,5,0.6,300)

extractPlot(resBreast2,ti="FABIAS Breast cancer(Veer)")

raBreast2 <- extractBic(resBreast2)

if ((raBreast2$bic[[1]][1]>1) && (raBreast2$bic[[1]][2]>1) { plotBicluster(raBreast2,1) } if ((raBreast2$bic[[2]][1]>1) && (raBreast2$bic[[2]][2]>1) { plotBicluster(raBreast2,2) } if ((raBreast2$bic[[3]][1]>1) && (raBreast2$bic[[3]][2]>1) { plotBicluster(raBreast2,3) } if ((raBreast2$bic[[4]][1]>1) && (raBreast2$bic[[4]][2]>1) { plotBicluster(raBreast2,4) }

plot(resBreast2, dim=c(1,2), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(1,3), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(1,4), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(1,5), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(2,3), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(2,4), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(2,5), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(3,4), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(3,5), label.tol=0.03, col.group=CBreast, lab.size=0.6) plot(resBreast2, dim=c(4,5), label.tol=0.03, col.group=CBreast, lab.size=0.6)

# DEMO3: Su's multiple tissue types
# gene expression data set
# avail <- require(fabiaData)

if (!avail) {
  message("")
  message("")
  message("Package 'fabiaData' is not available: please install.")
} else {

data(Multi_A)

X <- as.matrix(XMulti)
resMulti2 <- fabias(X, 5, 0.6, 300)

extractPlot(resMulti2, ti="FABIAS Multiple tissues(Su)"

raMulti2 <- extractBic(resMulti2)

if ((raMulti2$bic[[1]][1])>1) && (raMulti2$bic[[1]][2])>1) {
  plotBicluster(raMulti2, 1)
}

if ((raMulti2$bic[[2]][1])>1) && (raMulti2$bic[[2]][2])>1) {
  plotBicluster(raMulti2, 2)
}

if ((raMulti2$bic[[3]][1])>1) && (raMulti2$bic[[3]][2])>1) {
  plotBicluster(raMulti2, 3)
}

if ((raMulti2$bic[[4]][1])>1) && (raMulti2$bic[[4]][2])>1) {
  plotBicluster(raMulti2, 4)
}

plot(resMulti2, dim=c(1, 2), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(1, 3), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(1, 4), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(1, 5), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(2, 3), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(2, 4), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(2, 5), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(3, 4), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(3, 5), label.tol=0.01, col.group=CMulti, lab.size=0.6)
plot(resMulti2, dim=c(4, 5), label.tol=0.01, col.group=CMulti, lab.size=0.6)

# Demo: Rosenwald's diffuse large-B-cell lymphoma gene expression data set

avail <- require(fabiaData)

if (!avail) {
  message("")
  message("")
  message(""# Demo: Rosenwald's diffuse large-B-cell lymphoma gene expression data set
  message("")
  message("")
} else {

data(DLBCL_B)

X <- as.matrix(XDLBCL)
fabiasp <- fabias(X, 5, 0.6, 300)

extractPlot(resDLBCL2, ti="FABIAS Lymphoma(Rosenwald)")

raDLBCL2 <- extractBic(resDLBCL2)

if ((raDLBCL2$bic[[1]])[1] > 1) & (raDLBCL2$bic[[1]])[2] > 1) {
    plotBicluster(raDLBCL2, 1)
}
if ((raDLBCL2$bic[[2]])[1] > 1) & (raDLBCL2$bic[[2]])[2] > 1) {
    plotBicluster(raDLBCL2, 2)
}
if ((raDLBCL2$bic[[3]])[1] > 1) & (raDLBCL2$bic[[3]])[2] > 1) {
    plotBicluster(raDLBCL2, 3)
}
if ((raDLBCL2$bic[[4]])[1] > 1) & (raDLBCL2$bic[[4]])[2] > 1) {
    plotBicluster(raDLBCL2, 4)
}

plot(resDLBCL2, dim=c(1, 2), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(1, 3), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(1, 4), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(1, 5), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(2, 3), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(2, 4), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(2, 5), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(3, 4), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(3, 5), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)
plot(resDLBCL2, dim=c(4, 5), label.tol=0.03, col.group=CDLBCL, lab.size=0.6)

## End(Not run)

---

fabiasp

**Factor Analysis for Bicluster Acquisition: Sparseness Projection (FABIASP)**

**Description**

fabiasp: R implementation of fabias, therefore it is slow.

**Usage**

fabiasp(X, p=13, alpha=0.6, cyc=500, spz=0.5, center=2, norm=1, lap=1.0)
Arguments

- **X**: the data matrix.
- **p**: number of hidden factors = number of biclusters; default = 13.
- **alpha**: sparseness loadings (0.1 - 1.0); default = 0.6.
- **cyc**: number of iterations; default = 500.
- **spz**: sparseness factors (0.5 - 2.0); default = 0.5 (Laplace).
- **center**: data centering: 1 (mean), 2 (median), > 2 (mode), 0 (no); default = 2.
- **norm**: data normalization: 1 (0.75-0.25 quantile), >1 (var=1), 0 (no); default = 1.
- **lap**: minimal value of the variational parameter; default = 1.0.

Details

Biclusters are found by sparse factor analysis where both the factors and the loadings are sparse. Essentially the model is the sum of outer products of vectors:

\[
X = \sum_{i=1}^{p} \lambda_i z_i^T + U
\]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[
X = LZ + U
\]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X, U \) from \( R^{n \times l} \).

If the nonzero components of the sparse vectors are grouped together then the outer product results in a matrix with a nonzero block and zeros elsewhere.

The model selection is performed by a variational approach according to Girolami 2001 and Palmer et al. 2006.

The prior has finite support, therefore after each update of the loadings they are projected to the finite support. The projection is done according to Hoyer, 2004: given an \( l_1 \)-norm and an \( l_2 \)-norm minimize the Euclidean distance to the original vector (currently the \( l_2 \)-norm is fixed to 1). The projection is a convex quadratic problem which is solved iteratively where at each iteration at least one component is set to zero. Instead of the \( l_1 \)-norm a sparseness measurement is used which relates the \( l_1 \)-norm to the \( l_2 \)-norm.

The code is implemented in R, therefore it is slow.

Value

Object of the class `Factorization`. Containing \( LZ \) (estimated noise free data \( LZ \)), \( L \) (loadings \( L \)), \( Z \) (factors \( Z \)), \( U \) (noise \( X - LZ \)), center (centering vector), scaleData (scaling vector), \( X \) (centered and scaled data \( X \)), Psi (noise variance \( \sigma \)), lapla (variational parameter), avini (the information which the factor \( z_{ij} \) contains about \( x_j \) averaged over \( j \)), xavini (the information which the factor \( z_j \) contains about \( x_j \)), ini (for each \( j \) the information which the factor \( z_{ij} \) contains about \( x_j \)).
Author(s)
Sepp Hochreiter

References

See Also
fabilia, fabias, fabiap, spfabia, fabi, fabiasp, mfsc, nmfdv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

### Not run:
#### DEMO1

```
dat <- makeFabiaDataBlocks(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
SD_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)
X <- dat[[1]]
Y <- dat[[2]]

resEx <- fabiasp(X, 3, 0.6, 50)
```
Y <- dat[[2]]

resToy <- fabiasp(X, 13.0, 6, 200)

extractPlot(resToy, "ti=FABIASP", Y=Y)

#-----------
# DEMO2
#-----------

avail <- require(fabiaData)

if (!avail) {
  message(""
  message(""
  message("#_________________________________________________________"
  message("Package 'fabiaData' is not available: please install."
  message("#_________________________________________________________"
} else {

data(Breast_A)

X <- as.matrix(XBreast)

resBreast <- fabiasp(X, 5.0, 6, 200)

extractPlot(resBreast, "ti="FABIASP Breast cancer(Veer)"

#sorting of predefined labels
CBreast

}

#-----------
# DEMO3
#-----------

avail <- require(fabiaData)

if (!avail) {
  message(""
  message(""
  message("#_________________________________________________________"
  message("Package 'fabiaData' is not available: please install."
  message("#_________________________________________________________"
} else {

data(Multi_A)
X <- as.matrix(XMulti)
resMulti <- fabiasp(X,5,0.6,200)

extractPlot(resMulti, "ti=FABIASP Multiple tissues(Su)")

# sorting of predefined labels
CMulti

#-----------------
# DEMO4
#-----------------

avail <- require(fabiaData)
if (!avail) {
  message"
  message"
  message"Package 'fabiaData' is not available: please install.""
} else {
  data(DLBCL_B)
  X <- as.matrix(XDLBCL)

  resDLBCL <- fabiasp(X,5,0.6,200)
  extractPlot(resDLBCL, "ti=FABIASP Lymphoma(Rosenwald)"

  # sorting of predefined labels
  CDLBCL
}

## End(Not run)

---

fabiaVersion  Display version info for package and for FABIA

**Description**

fabiaVersion displays version information about the package.
Usage

fabiaVersion()

Author(s)

Sepp Hochreiter

See Also

fabia, fabias, fabiap, spfabia, readSpfabiaResult, fabi, fabiasp, mfsc, nmfdm, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

fabiaVersion()

---

Factorization-class  Factorization instances

Description

Factorization is a class to store results of matrix factorization algorithms. It has been designed for biclustering but can be used for "principal component analysis", "singular value decomposition", "independent component analysis", "factor analysis", and "non-negative matrix factorization".

Usage

```r
## S4 method for signature 'Factorization'
plot(x, Rm=NULL, Cm=NULL, dim = c(1, 2),
    zoom = rep(1, 2), col.group = NULL,
    colors = c("orange", "red", rainbow(length(unique(col.group))),
    start=2/6, end=4/6)),
    col.areas = TRUE, col.symbols = c(1, rep(2, length(unique(col.group)))),
    sampleNames = TRUE, rot = rep(-1, length(dim)),
    labels = NULL, label.tol = 0.1, lab.size = 0.725, col.size = 10,
    row.size = 10, do.smoothScatter = FALSE,
    do.plot = TRUE, ... )

## S4 method for signature 'Factorization'
show(object)

## S4 method for signature 'Factorization'
showSelected(object, which=c(1,2,3,4))
```
## S4 method for signature 'Factorization'

`summary(object, ...)`

### Arguments

**PLOT:**

- **x**
  - object of the class `Factorization`.
- **Rm**
  - row weighting vector. If `NULL`, it defaults to `rep(1,nrow(L(x)))`.
- **Cm**
  - column weighting vector. If `NULL`, it defaults to `rep(1,ncol(Z(x)))`.
- **dim**
  - optional principal factors that are plotted along the horizontal and vertical axis. Defaults to `c(1,2)`.
- **zoom**
  - optional zoom factor for row and column items. Defaults to `c(1,1)`.
- **col.group**
  - optional vector (character or numeric) indicating the different groupings of the columns. Defaults to 1.
- **colors**
  - vector specifying the colors for the annotation of the plot; the first two elements concern the rows; the third till the last element concern the columns; the first element will be used to color the unlabeled rows; the second element for the labeled rows and the remaining elements to give different colors to different groups of columns. Defaults to `c("orange", "red", rainbow(length(unique(col.group)))[1], start=2/6)`.
- **col.areas**
  - logical value indicating whether columns should be plotted as squares with areas proportional to their marginal mean and colors representing the different groups (TRUE), or with symbols representing the groupings and identical size (FALSE). Defaults to TRUE.
- **col.symbols**
  - vector of symbols when `col.areas=FALSE` corresponds to the `pch` argument of the function `plot`. Defaults to `c(1, rep(2, length(unique(col.group)))))`.
- **sampleNames**
  - either a logical vector of length one or a character vector of length equal to the number of samples in the dataset. If a logical is provided, sample names will be displayed on the plot (TRUE; default) or not (FALSE); if a character vector is provided, the names provided will be used to label the samples instead of the default column names.
- **rot**
  - rotation of plot. Defaults to `c(-1,-1)`.
- **labels**
  - character vector to be used for labeling points on the graph; if `NULL` (default), the row names of `x` are used instead.
- **label.tol**
  - numerical value specifying either the percentile (`label.tol<=1`) of rows or the number of rows (`label.tol>1`) most distant from the plot-center (0,0) that are labeled and are plotted as circles with area proportional to the marginal means of the original data. Defaults to 1.
- **lab.size**
  - size of identifying labels for row- and column-items as `cex` parameter of the `text` function. Defaults to 0.725.
- **col.size**
  - size of the column symbols in mm. Defaults to 10.
- **row.size**
  - size of the row symbols in mm. Defaults to 10.
do.smoothScatter
use smoothScatter or not instead of plotting individual points. Defaults to FALSE.
do.plot
produce a plot or not. Defaults to TRUE.
... further arguments are passed on to eqscaleplotLoc which draws the canvas for
the plot; useful for adding a main or a custom sub.
SHOW:

object
An instance of Factorization-class.

SHOWSELECTED:
see object at show.

which
used to provide a list of which plots should be generated: 1=the information
content of biclusters, 2=the information content of samples, 3=the loadings per
bicluster, 4=the factors per bicluster, default c(1,2,3,4).

SUMMARY:
see object at show.
... further arguments.

Details

Plot Produces a biplot of a matrix factorization result stored in an instance of the Factorization
class.
The function plot is based on the function plot.mpm in the R package mpm (Version: 1.0-
16, Date: 2009-08-26, Title: Multivariate Projection Methods, Maintainer: Tobias Verbeke
<tobias.verbeke@openanalytics.be>, Author: Luc Wouters <wouters_luc@telenet.be>.
Biclusters are found by sparse factor analysis where both the factors and the loadings are
sparse.
Essentially the model is the sum of outer products of vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^n \times p \), \( Z \) from \( R^p \times l \), and \( X, U \) from \( R^n \times l \).
For noise free projection like independent component analysis we set the noise term to zero:
\( U = 0 \).
The argument label.tol can be used to select the most informative rows, i.e. rows that are
most distant from the center of the plot (smaller 1: percentage of rows, larger 1: number of
rows).
Only these row-items are then labeled and represented as circles with their areas proportional
to the row weighting.
If the column-items are grouped these groups can be visualized by colors given by col.group.
Show  Statistics of a matrix factorization result stored in an instance of the Factorization class.
This function supplies statistics on a matrix factorization result which is stored as an instance of `Factorization-class`.
The following is plotted:
1. the information content of biclusters.
2. the information content of samples.
3. the loadings per bicluster.
4. the factors per bicluster.

ShowSelected  Lists selected statistics of a matrix factorization result stored in an instance of the Factorization class.
This function supplies selected statistics on a matrix factorization result which is stored as an instance of `Factorization-class`.
The following is plotted depending on the display selection variable `which`:
1. the information content of biclusters.
2. the information content of samples.
3. the loadings per bicluster.
4. the factors per bicluster.

Summary  Summary of matrix factorization result stored in an instance of the Factorization class.
This function gives information on a matrix factorization result which is stored as an instance of `Factorization-class`.
The summary consists of following items:
1. the number or rows and columns of the original matrix.
2. the number of clusters for rows and columns is given.
3. for the row cluster the information content is given.
4. for each column its information is given.
5. for each column cluster a summary is given.
6. for each row cluster a summary is given.

Value

**FACTORIZATION:**
An instance of `Factorization-class`.

**PLOT:**

**Rows**  a list with the X and Y coordinates of the rows and an indication `Select` of whether the row was selected according to `label_tol`.

**Columns**  a list with the X and Y coordinates of the columns.

**SHOW:**  no value.

**SHOWSELECTED:**  no value.

**SUMMARY:**  no value.
Slots

Objects of class Factorization have the following slots:

parameters: Saves parameters of the factorization method in a list: ("method","number of cycles","sparseness weight","sparseness prior for loadings","sparseness prior for factors","number biclusters","projection sparseness loadings","projection sparseness factors","initialization range","are loadings rescaled after each iterations","normalization = scaling of rows","centering method of rows","parameter for method").

n: number of rows, left dimension.
p1: right dimension of left matrix.
p2: left dimension of right matrix.
l: number of columns, right dimension.
center: vector of the centers.
scaleData: vector of the scaling factors.
X: centered and scaled data matrix n x l.
L: left matrix n x p1.
Z: right matrix p2 x l.
M: middle matrix p1 x p2.
LZ: matrix L x M x Z.
u: noise matrix.
avini: information of each bicluster, vector of length p2.
Xavini: information extracted from each sample, vector of length l.
in: information of each bicluster in each sample, matrix p2 x l.
Psi: noise variance per row, vector of length n.
lapla: prior information for each sample, vector of length l.

Constructor

Constructor of class Factorization.

Factorization(parameters=list(),n=1,p1=1,p2=1,l=1,center=as.vector(1),scaleData=as.vector(1),X=as.matrix(matrix(rnorm(100),10,10)),Y=as.matrix(matrix(rnorm(100),10,10)),...)

Accessors

In the following x denotes a Factorization object.

parameters(x), parameters(x) <- value: Returns or sets parameters, where the return value and value are both an instance of list. Parameters of the factorization method are stored in a list: ("method","number of cycles","sparseness weight","sparseness prior for loadings","sparseness prior for factors","number biclusters","projection sparseness loadings","projection sparseness factors","initialization range","are loadings rescaled after each iterations","normalization = scaling of rows","centering method of rows","parameter for method").

n(x), n(x) <- value: Returns or sets n, where the return value and value are both an instance of numeric. Number of rows, left dimension.
p1(x), p1(x) <- value: Returns or sets p1, where the return value and value are both an instance of numeric. Right dimension of left matrix.

p2(x), p2(x) <- value: Returns or sets p2, where the return value and value are both an instance of numeric. Left dimension of right matrix.

l(x), l(x) <- value: Returns or sets l, where the return value and value are both an instance of numeric. Number of columns, right dimension.

center(x), center(x) <- value: Returns or sets center, where the return value and value are both an instance of numeric. Vector of the centers.

scaleData(x), scaleData(x) <- value: Returns or sets scaleData, where the return value and value are both an instance of numeric. Vector of the scaling factors.

X(x), X(x) <- value: Returns or sets X, where the return value and value are both an instance of matrix. Centered and scaled data matrix n x l.

L(x), L(x) <- value: Returns or sets L, where the return value and value are both an instance of matrix. Left matrix n x p1.

Z(x), Z(x) <- value: Returns or sets Z, where the return value and value are both an instance of matrix. Right matrix p2 x l.

M(x), M(x) <- value: Returns or sets M, where the return value and value are both an instance of matrix. Middle matrix p1 x p2.

LZ(x), LZ(x) <- value: Returns or sets LZ, where the return value and value are both an instance of matrix. Matrix L x M x Z.

U(x), U(x) <- value: Returns or sets U, where the return value and value are both an instance of matrix. Noise matrix.

avini(x), avini(x) <- value: Returns or sets avini, where the return value and value are both an instance of numeric. Information of each bicluster, vector of length p2.

xavini(x), xavini(x) <- value: Returns or sets xavini, where the return value and value are both an instance of numeric. Information extracted from each sample, vector of length l.

ini(x), ini(x) <- value: Returns or sets ini, where the return value and value are both an instance of matrix. Information of each bicluster in each sample, matrix p2 x l.

Psi(x), Psi(x) <- value: Returns or sets Psi, where the return value and value are both an instance of numeric. Noise variance per row, vector of length n.

lapla(x), lapla(x) <- value: Returns or sets lapla, where the return value and value are both an instance of matrix. Prior information for each sample, vector of length l.

Signatures

plot signature(x = "Factorization", y = "missing") Plot of a matrix factorization result
show signature(object = "Factorization") Display statistics of a matrix factorization result
showSelected signature(object = "Factorization", which = "numeric") Display particular statistics of a matrix factorization result
summary signature(object = "Factorization") Summary of matrix factorization result

Functions that return objects of this class

Factorization objects are returned by fabia, fabias, fabiap, fabiapsp, mfsc, nmfsc, nmfdiv, and nmfeu.
Extension to store results of other methods

The class Factorization may contain the result of different matrix factorization methods. The methods may be generative or not.

Methods may be "singular value decomposition" (M contains singular values as well as avini, L and Z are orthonormal matrices), "independent component analysis" (Z contains the projection/sources, L is the mixing matrix, M is unity), "factor analysis" (Z contains factors, L the loadings, M is unity, U the noise, Psi the noise covariance, lapla is a variational parameter for non-Gaussian factors, avini and ini are the information the factors convey about the observations).

Author(s)

Sepp Hochreiter

See Also

fabia, fabias, fabiap, fabisp, fabiasp, mfsc, nmfdiv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

```r
# TEST

# PLOT

#---------------------

n=200
l=100
p=4

dat <- makeFabiaDataBlocks(n = n,l= l,p = p,f1 = 5,f2 = 5,
of1 = 5,of2 = 10,sd_noise = 3.0,sd_z_noise = 0.2,mean_z = 2.0,
sd_z = 1.0,sd_l_noise = 0.2,mean_l = 3.0,sd_l = 1.0)

X <- dat[[1]]
ZC <- dat[[3]]
LC <- dat[[4]]

resEx <- fabia(X,p,0.01,400)

gclab <- rep.int(0,1)
gllab <- rep.int(0,n)
```
clab <- as.character(1:l)
llab <- as.character(1:n)
for (i in 1:p){
    for (j in ZC[i]){  
        clab[j] <- paste(as.character(i),"_",lab[j],sep="")
    }
    for (j in LC[i]){  
        llab[j] <- paste(as.character(i),"_",lab[j],sep="")
    }
    gclab[unlist(ZC[i])] <- gclab[unlist(ZC[i])] + p^i
    gllab[unlist(LC[i])] <- gllab[unlist(LC[i])] + p^i
}
grp <- gclab
colnames(X(resEx)) <- clab
rownames(X(resEx)) <- llab

plot(resEx,dim=c(1,2),label.tol=0.1,col.group = groups,lab.size=0.6)
plot(resEx,dim=c(1,3),label.tol=0.1,col.group = groups,lab.size=0.6)
plot(resEx,dim=c(2,3),label.tol=0.1,col.group = groups,lab.size=0.6)

#-------------------------
#  SHOW
#-------------------------

dat <- makeFabiaDataBlocks(n = 100,l= 50,p = 3,f1 = 5,f2 = 5,
of1 = 5,of2 = 10,sd_noise = 3.0,sd_z_noise = 0.2,mean_z = 2.0,
    sd_z = 1.0,sd_l_noise = 0.2,mean_l = 3.0,sd_l = 1.0)
X <- dat[[1]]

resEx <- fabia(X,3,0.01,100)
show(resEx)

#-------------------------
#  SHOWSELECTED
#-------------------------

dat <- makeFabiaDataBlocks(n = 100,l= 50,p = 3,f1 = 5,f2 = 5,
of1 = 5,of2 = 10,sd_noise = 3.0,sd_z_noise = 0.2,mean_z = 2.0,
    sd_z = 1.0,sd_l_noise = 0.2,mean_l = 3.0,sd_l = 1.0)
**makeFabiaData**

*Generation of Bicluster Data*

**Description**

`makeFabiaData`: R implementation of makeFabiaData.

**Usage**

```r
makeFabiaData(n, l, p, f1, f2, of1, of2, sd_noise, sd_z_noise, mean_z, sd_z, sd_l_noise, mean_l, sd_l)
```

**Arguments**

- `n`: number of observations.
- `l`: number of samples.
- `p`: number of biclusters.
- `f1`: `n/f1` max. additional samples are active in a bicluster.
- `f2`: `n/f2` max. additional observations that form a pattern in a bicluster.
of1 minimal active samples in a bicluster.
of2 minimal observations that form a pattern in a bicluster.
sd_noise Gaussian zero mean noise std on data matrix.
sd_z_noise Gaussian zero mean noise std for deactivated hidden factors.
mean_z Gaussian mean for activated factors.
sd_z Gaussian std for activated factors.
sd_l_noise Gaussian zero mean noise std if no observation patterns are present.
mean_l Gaussian mean for observation patterns.
sd_l Gaussian std for observation patterns.

Details

Essentially the data generation model is the sum of outer products of sparse vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

and noise free

\[ Y = LZ \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X, U, Y \) from \( R^{n \times l} \).

Sequentially \( L_i \) are generated using \( n, f2, \) of2, \( \text{sd}_l\_\text{noise}, \text{mean}_l, \text{sd}_l \). of2 gives the minimal observations participating in a bicluster to which between 0 and \( n / f2 \) observations are added, where the number is uniformly chosen. \( \text{sd}_l\_\text{noise} \) gives the noise of observations not participating in the bicluster. \( \text{mean}_l \) and \( \text{sd}_l \) determines the Gaussian from which the values are drawn for the observations that participate in the bicluster. The sign of the mean is randomly chosen for each component.

Sequentially \( Z_i \) are generated using \( l, f1, \) of1, \( \text{sd}_z\_\text{noise}, \text{mean}_z, \text{sd}_z \). of1 gives the minimal samples participating in a bicluster to which between 0 and \( l / f1 \) samples are added, where the number is uniformly chosen. \( \text{sd}_z\_\text{noise} \) gives the noise of samples not participating in the bicluster. \( \text{mean}_z \) and \( \text{sd}_z \) determines the Gaussian from which the values are drawn for the samples that participate in the bicluster.

\( U \) is the overall Gaussian zero mean noise generated by \( \text{sd}_\text{noise} \).

Implementation in \( R \).

Value

- \( X \) the noise data from \( R^{n \times l} \).
- \( Y \) the noise free data from \( R^{n \times l} \).
- \( ZC \) list where i-th element gives samples belonging to i-th bicluster.
- \( LC \) list where i-th element gives observations belonging to i-th bicluster.
Author(s)

Sepp Hochreiter

See Also

fabia, fabias, fabiap, fabi, fabiasp, mfsc, nmfdiv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

```r
# TEST
# TEST
# TEST

dat <- makeFabiaData(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
   sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

matrixImagePlot(Y)
dev.new()
matrixImagePlot(X)

## Not run:
# DEMO
# DEMO
# DEMO

dat <- makeFabiaData(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
   sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

matrixImagePlot(Y)
dev.new()
matrixImagePlot(X)

## End(Not run)
```
**makeFabiaDataBlocks**  
*Generation of Bicluster Data with Bicluster Blocks*

**Description**

`makeFabiaDataBlocks`: R implementation of `makeFabiaDataBlocks`.

**Usage**

```r
makeFabiaDataBlocks(n, l, p, f1, f2, of1, of2, sd_noise, sd_z_noise, mean_z, sd_z, sd_l_noise, mean_l, sd_l)
```

**Arguments**

- `n`: number of observations.
- `l`: number of samples.
- `p`: number of biclusters.
- `f1`: `n/f1` max. additional samples are active in a bicluster.
- `f2`: `n/f2` max. additional observations that form a pattern in a bicluster.
- `of1`: minimal active samples in a bicluster.
- `of2`: minimal observations that form a pattern in a bicluster.
- `sd_noise`: Gaussian zero mean noise std on data matrix.
- `sd_z_noise`: Gaussian zero mean noise std for deactivated hidden factors.
- `mean_z`: Gaussian mean for activated factors.
- `sd_z`: Gaussian std for activated factors.
- `sd_l_noise`: Gaussian zero mean noise std if no observation patterns are present.
- `mean_l`: Gaussian mean for observation patterns.
- `sd_l`: Gaussian std for observation patterns.

**Details**

Bicluster data is generated for visualization because the biclusters are now in block format. That means observations and samples that belong to a bicluster are consecutive. This allows visual inspection because the user can identify blocks and whether they have been found or reconstructed.

Essentially the data generation model is the sum of outer products of sparse vectors:

$$X = \sum_{i=1}^{p} \lambda_i z_i^T + U$$
where the number of summands $p$ is the number of biclusters. The matrix factorization is

$$X = LZ + U$$

and noise free

$$Y = LZ$$

Here $\lambda_i$ are from $\mathbb{R}^n$, $z_i$ from $\mathbb{R}^l$, $L$ from $\mathbb{R}^{n \times p}$, $Z$ from $\mathbb{R}^{p \times l}$, and $X, U, Y$ from $\mathbb{R}^{n \times l}$.

Sequentially $L_i$ are generated using $n, f2, \text{of2, sd\_l\_noise, mean\_l, sd\_l}$. of2 gives the minimal observations participating in a bicluster to which between 0 and $n/f2$ observations are added, where the number is uniformly chosen. sd\_l\_noise gives the noise of observations not participating in the bicluster. mean\_l and sd\_l determines the Gaussian from which the values are drawn for the observations that participate in the bicluster. The sign of the mean is randomly chosen for each component.

Sequentially $Z_i$ are generated using $1, f1, \text{of1, sd\_z\_noise, mean\_z, sd\_z}$. of1 gives the minimal samples participating in a bicluster to which between 0 and $l/f1$ samples are added, where the number is uniformly chosen. sd\_z\_noise gives the noise of samples not participating in the bicluster. mean\_z and sd\_z determines the Gaussian from which the values are drawn for the samples that participate in the bicluster.

$U$ is the overall Gaussian zero mean noise generated by sd\_noise.

Implementation in $\mathbb{R}$.

**Value**

- $Y$ the noise data from $\mathbb{R}^{n \times l}$.
- $X$ the noise free data from $\mathbb{R}^{n \times l}$.
- $ZC$ list where i-th element gives samples belonging to i-th bicluster.
- $LC$ list where i-th element gives observations belonging to i-th bicluster.

**Author(s)**

Sepp Hochreiter

**See Also**

- fabia, fabias, fabiap, fabi, fabiasp, mfsc, nmfdsv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

**Examples**

```r
# TEST

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
```
makeFabiaDataBlocksPos

Generation of Bicluster Data with Bicluster Blocks

Description

makeFabiaDataBlocksPos: R implementation of makeFabiaDataBlocksPos.

Usage

makeFabiaDataBlocksPos(n, l, p, f1, f2, of1, of2, sd_noise, sd_z_noise, mean_z, sd_z, sd_l_noise, mean_l, sd_l)

Arguments

n number of observations.
makeFabiaDataBlocksPos

1 number of samples.
p number of biclusters.
f1 nn/f1 max. additional samples are active in a bicluster.
f2 n/f2 max. additional observations that form a pattern in a bicluster.
of1 minimal active samples in a bicluster.
of2 minimal observations that form a pattern in a bicluster.
sd_noise Gaussian zero mean noise std on data matrix.
sd_z_noise Gaussian zero mean noise std for deactivated hidden factors.
mean_z Gaussian mean for activated factors.
sd_z Gaussian std for activated factors.
sd_l_noise Gaussian zero mean noise std if no observation patterns are present.
mean_l Gaussian mean for observation patterns.
sd_l Gaussian std for observation patterns.

Details

Bicluster data is generated for visualization because the biclusters are now in block format. That means observations and samples that belong to a bicluster are consecutive. This allows visual inspection because the user can identify blocks and whether they have been found or reconstructed.

Essentially the data generation model is the sum of outer products of sparse vectors:

$$X = \sum_{i=1}^{p} \lambda_i z_i^T + U$$

where the number of summands $p$ is the number of biclusters. The matrix factorization is

$$X = LZ + U$$

and noise free

$$Y = LZ$$

Here $\lambda_i$ are from $R^n$, $z_i$ from $R^l$, $L$ from $R^{n \times p}$, $Z$ from $R^{p \times l}$, and $X, U, Y$ from $R^{n \times l}$.

Sequentially $L_i$ are generated using $n, f2, of2, sd_l_noise, mean_l, sd_l$. $of2$ gives the minimal observations participating in a bicluster to which between 0 and $n/f2$ observations are added, where the number is uniformly chosen. $sd_l_noise$ gives the noise of observations not participating in the bicluster. $mean_l$ and $sd_l$ determines the Gaussian from which the values are drawn for the observations that participate in the bicluster. "POS": The sign of the mean is fixed.

Sequentially $Z_i$ are generated using $l, f1, of1, sd_z_noise, mean_z, sd_z$. $of1$ gives the minimal samples participating in a bicluster to which between 0 and $l/f1$ samples are added, where the number is uniformly chosen. $sd_z_noise$ gives the noise of samples not participating in the bicluster. $mean_z$ and $sd_z$ determines the Gaussian from which the values are drawn for the samples that participate in the bicluster.

$U$ is the overall Gaussian zero mean noise generated by $sd_noise$.

Implementation in $R$. 

makeFabiaDataBlocksPos

Value

- **Y** the noise data from $R^{n \times l}$.
- **X** the noise free data from $R^{n \times l}$.
- **ZC** list where $i$-th element gives samples belonging to $i$-th bicluster.
- **LC** list where $i$-th element gives observations belonging to $i$-th bicluster.

Author(s)

Sepp Hochreiter

See Also

- fabia, fabias, fabiap, fabi, fabiasp, mfc, nnmfdiv, nnmfeu, nmfsc, extractPlot, extractBic, plotBicuster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

```r
# TEST

dat <- makeFabiaDataBlocksPos(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

matrixImagePlot(Y)
dev.new()
matrixImagePlot(X)

## Not run:
# DEMO


dat <- makeFabiaDataBlocksPos(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

Y <- dat[[1]]
X <- dat[[2]]

matrixImagePlot(Y)
dev.new()
```
Description

`makeFabiaDataPos`: R implementation of `makeFabiaDataPos`.

Usage

```r
description = matrixImagePlot(X)
## End(Not run)
```

Arguments

- `n`: number of observations.
- `l`: number of samples.
- `p`: number of biclusters.
- `f1`: \( n/f1 \) max. additional samples are active in a bicluster.
- `f2`: \( n/f2 \) max. additional observations that form a pattern in a bicluster.
- `of1`: minimal active samples in a bicluster.
- `of2`: minimal observations that form a pattern in a bicluster.
- `sd_noise`: Gaussian zero mean noise std on data matrix.
- `sd_z_noise`: Gaussian zero mean noise std for deactivated hidden factors.
- `mean_z`: Gaussian mean for activated factors.
- `sd_z`: Gaussian std for activated factors.
- `sd_l_noise`: Gaussian zero mean noise std if no observation patterns are present.
- `mean_l`: Gaussian mean for observation patterns.
- `sd_l`: Gaussian std for observation patterns.
Details

Essentially the data generation model is the sum of outer products of sparse vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

and noise free

\[ Y = LZ \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X, U, Y \) from \( R^{n \times l} \).

Sequentially \( L_i \) are generated using \( n, f1, of1, sd_{l\_noise}, mean_{l}, sd_{l} \). \( of1 \) gives the minimal observations participating in a bicluster to which between 0 and \( n/f1 \) observations are added, where the number is uniformly chosen. \( sd_{l\_noise} \) gives the noise of observations not participating in the bicluster. \( mean_{l} \) and \( sd_{l} \) determines the Gaussian from which the values are drawn for the observations that participate in the bicluster. "POS": The sign of the mean is fixed.

Sequentially \( Z_i \) are generated using \( 1, f1, of1, sd_{z\_noise}, mean_{z}, sd_{z} \). \( of1 \) gives the minimal samples participating in a bicluster to which between 0 and \( l/f1 \) samples are added, where the number is uniformly chosen. \( sd_{z\_noise} \) gives the noise of samples not participating in the bicluster. \( mean_{z} \) and \( sd_{z} \) determines the Gaussian from which the values are drawn for the samples that participate in the bicluster.

\( U \) is the overall Gaussian zero mean noise generated by \( sd_{noise} \).

Implementation in \( R \).

Value

- \( X \): the noise data from \( R^{n \times l} \).
- \( Y \): the noise free data from \( R^{n \times l} \).
- \( ZC \): list where i-th element gives samples belonging to i-th bicluster.
- \( LC \): list where i-th element gives observations belonging to i-th bicluster.

Author(s)

Sepp Hochreiter

See Also

- fabia, fabias, fabiap, fabi, fabiasp, mfsc, nmfdv, nmfeu, nmfsc, extractPlot, extractBic, plotBicCluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion
Examples

#------------------
# TEST
#------------------

dat <- makeFabiaDataPos(n = 100, l= 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

matrixImagePlot(Y)
dev.new()
matrixImagePlot(X)

## Not run:
#------------------
# DEMO
#------------------

dat <- makeFabiaDataPos(n = 1000, l= 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

matrixImagePlot(Y)
dev.new()
matrixImagePlot(X)

## End(Not run)

matrixImagePlot | Plotting of a Matrix

Description

matrixImagePlot: R implementation of myImagePlot.

Usage

matrixImagePlot(x, xLabels=NULL, yLabels=NULL, zlim=NULL, title=NULL)
matrixImagePlot

Arguments

- **x**: the matrix.
- **xLabels**: vector of strings to label the columns (default "colnames(x)").
- **yLabels**: vector of strings to label the rows (default "rownames(x)").
- **zlim**: vector containing a low and high value to use for the color scale.
- **title**: title of the plot.

Details

Plotting a table of numbers as an image using R.

The color scale is based on the highest and lowest values in the matrix.

The original R code has been obtained by [http://www.phaget4.org/R/myImagePlot.R](http://www.phaget4.org/R/myImagePlot.R) and then has been modified.

References


See Also

- fabia, fabias, fabiap, fabi, fabiasp, mfsc, nmfdvi, nmfeu, nmfsc, extractPlot, extractBic,
- plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks,
- makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

```r
# TEST

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5, of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0, sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)
X <- dat[[1]]
Y <- dat[[2]]

matrixImagePlot(Y)
dev.new()
matrixImagePlot(X)
```

## Not run:

```r
# DEMO
```
**mfsc**

**Sparse Matrix Factorization for Bicluster Analysis (MFSC)**

### Description

**mfsc**: R implementation of mfsc.

### Usage

```r
mfsc(X, p=5, cyc=100, sL=0.6, sZ=0.6, center=2, norm=1)
```

### Arguments

- **X**: the data matrix.
- **p**: number of hidden factors = number of biclusters; default = 5.
- **cyc**: maximal number of iterations; default = 100.
- **sL**: final sparseness loadings; default = 0.6.
- **sZ**: final sparseness factors; default = 0.6.
- **center**: data centering: 1 (mean), 2 (median), > 2 (mode), 0 (no); default = 2.
- **norm**: data normalization: 1 (0.75-0.25 quantile), >1 (var=1), 0 (no); default = 1.

### Details

Biclusters are found by sparse matrix factorization where both factors are sparse.

Essentially the model is the sum of outer products of vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T \]
where the number of summands $p$ is the number of biclusters. The matrix factorization is

$$X = LZ$$

Here $\lambda_i$ are from $R^n$, $z_i$ from $R^l$, $L$ from $R^{n \times p}$, $Z$ from $R^{p \times l}$, and $X$ from $R^{n \times l}$.

**No noise assumption:** In contrast to factor analysis there is no noise assumption.

If the nonzero components of the sparse vectors are grouped together then the outer product results in a matrix with a nonzero block and zeros elsewhere.

The model selection is performed by a constraint optimization according to Hoyer, 2004. The Euclidean distance (the Frobenius norm) is minimized subject to sparseness constraints.

Model selection is done by gradient descent on the Euclidean objective and thereafter projection of single vectors of $L$ and single vectors of $Z$ to fulfill the sparseness constraints.

The projection minimize the Euclidean distance to the original vector given an $l_1$-norm and an $l_2$-norm.

The projection is a convex quadratic problem which is solved iteratively where at each iteration at least one component is set to zero. Instead of the $l_1$-norm a sparseness measurement is used which relates the $l_1$-norm to the $l_2$-norm.

The code is implemented in R.

**Value**

Object of the class `Factorization`. Containing $LZ$ (estimated noise free data $LZ$), $L$ (loadings $L$), $Z$ (factors $Z$), $U$ (noise $X - LZ$), center (centering vector), `scaleData` (scaling vector), $X$ (centered and scaled data $X$)

**Author(s)**

Sepp Hochreiter

**References**


**See Also**

`fabia`, `fabias`, `fabiap`, `fabi`, `fabiasp`, `mfsc`, `nmfdiv`, `nmfzu`, `nmfsc`, `extractPlot`, `extractBic`, `plotBicluster`, `Factorization`, `projFuncPos`, `projFunc`, `estimateMode`, `makeFabiaData`, `makeFabiaDataBlocks`, `makeFabiaDataPos`, `makeFabiaDataBlocksPos`, `matrixImagePlot`, `fabiaDemo`, `fabiaVersion`
Examples

```
#TEST

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5, 
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0, 
    sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resEx <- mfsc(X, 3, 30, 0.6, 0.6)

## Not run:

# DEMO1: Toy Data

n = 1000
l = 100
p = 10

dat <- makeFabiaDataBlocks(n = n, l = l, p = p, f1 = 5, f2 = 5, 
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0, 
    sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
ZC <- dat[[3]]
LC <- dat[[4]]

gclab <- rep.int(0, l)
gllab <- rep.int(0, n)
clab <- as.character(1:l)
llab <- as.character(1:n)

for (i in 1:p){
    for (j in ZC[i]){ 
        clab[j] <- paste(as.character(i),"\",clab[j],sep="")
    }
    for (j in LC[i]){ 
        llab[j] <- paste(as.character(i),"\",llab[j],sep="")
    }
    gclab[unlist(ZC[i])] <- gclab[unlist(ZC[i])] + p^i
    gllab[unlist(LC[i])] <- gllab[unlist(LC[i])] + p^i
}

groups <- gclab
```
### MFSC

resToy4 <- mfsc(X,13,100,0.6,0.6)

extractPlot(resToy4,ti="MFSC",Y=Y)

raToy4 <- extractBic(resToy4,thresZ=0.01,thresL=0.05)

if ((raToy4$bic[[1]][1][1]>1) & (raToy4$bic[[1]][2][2]>1)) {
  plotBicluster(raToy4,1)
} if ((raToy4$bic[[2]][1][1]>1) & (raToy4$bic[[2]][2][2]>1)) {
  plotBicluster(raToy4,2)
} if ((raToy4$bic[[3]][1][1]>1) & (raToy4$bic[[3]][2][2]>1)) {
  plotBicluster(raToy4,3)
} if ((raToy4$bic[[4]][1][1]>1) & (raToy4$bic[[4]][2][2]>1)) {
  plotBicluster(raToy4,4)
}

colnames(X(resToy4)) <- clab
rownames(X(resToy4)) <- llab

plot(resToy4,dim=c(1,2),label.tol=0.1,col.group = groups,lab.size=0.6) plot(resToy4,dim=c(1,3),label.tol=0.1,col.group = groups,lab.size=0.6) plot(resToy4,dim=c(2,3),label.tol=0.1,col.group = groups,lab.size=0.6)

# DEMO2: Laura van't Veer's gene expression data set for breast cancer

avail <- require(fabiaData)

if (!avail) {
  message(""
  message(""
  message(""Package 'fabiaData' is not available: please install."
  message(""
} else {

data(Breast_A)

X <- as.matrix(XBreast)

resBreast4 <- mfsc(X,5,100,0.6,0.6)
extractPlot(resBreast4,ti="MFSC Breast cancer (Veer)")

raBreast4 <- extractBic(resBreast4,thresZ=0.01,thresL=0.05)

if ((raBreast4$bic[[1]][1]>1) && (raBreast4$bic[[1]][2]>1) ) {
  plotBicluster(raBreast4,1)
}
if ((raBreast4$bic[[2]][1]>1) && (raBreast4$bic[[2]][2]>1) ) {
  plotBicluster(raBreast4,2)
}
if ((raBreast4$bic[[3]][1]>1) && (raBreast4$bic[[3]][2]>1) ) {
  plotBicluster(raBreast4,3)
}
if ((raBreast4$bic[[4]][1]>1) && (raBreast4$bic[[4]][2]>1) ) {
  plotBicluster(raBreast4,4)
}

plot(resBreast4,dim=c(1,2),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(1,3),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(1,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(1,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(2,3),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(2,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(2,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(3,4),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(3,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)
plot(resBreast4,dim=c(4,5),label.tol=0.03,col.group=CBreast,lab.size=0.6)

# DEM03: Su's multiple tissue types
# gene expression data set

avail <- require(fabiaData)

if (!avail) {
  message(""")
  message(""")
  message("****************************************")
  message("Package 'fabiaData' is not available: please install.")
  message("****************************************")
} else {

data(Multi_A)

X <- as.matrix(XMulti)
resMulti4 <- mfsc(X,5,100,0.6,0.6)
extractPlot(resMulti4,ti="MFSC Multiple tissues(Su)")

raMulti4 <- extractBic(resMulti4,thresZ=0.01,thresL=0.05)
if ( (raMulti4$bic[[1]][1]>1) & (raMulti4$bic[[1]][2]>1) ) {
  plotBicluster(raMulti4,1)
} if ( (raMulti4$bic[[2]][1]>1) & (raMulti4$bic[[2]][2]>1) ) {
  plotBicluster(raMulti4,2)
} if ( (raMulti4$bic[[3]][1]>1) & (raMulti4$bic[[3]][2]>1) ) {
  plotBicluster(raMulti4,3)
} if ( (raMulti4$bic[[4]][1]>1) & (raMulti4$bic[[4]][2]>1) ) {
  plotBicluster(raMulti4,4)
}

plot(resMulti4, dim=c(1,2), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(1,3), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(1,4), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(1,5), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(2,3), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(2,4), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(2,5), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(3,4), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(3,5), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)
plot(resMulti4, dim=c(4,5), label.tol = 0.01, col.group = CMulti, lab.size = 0.6)

# DEMO4: Rosenwald’s diffuse large-B-cell lymphoma gene expression data set

avail <- require(fabiaData)
if (!avail) {
  message(""
  message(""
  message("-------------------------------------------------------------------------------------------------------------------------------------")
  message("Package 'fabiaData' is not available: please install.")
  message("-------------------------------------------------------------------------------------------------------------------------------------")
} else {

data(DLBCL_B)
X <- as.matrix(XDLBCL)

resDLBCL4 <- mfsc(X, 5, 100, 0.6, 0.6)

extractPlot(resDLBCL4, ti = "MFSC Lymphoma (Rosenwald)"

raDLBCL4 <- extractBic(resDLBCL4, thresZ = 0.01, thresL = 0.05)

if ((raDLBCL4$bic[[1]][1] > 1) && (raDLBCL4$bic[[1]][2] > 1)) {
  plotBicluster(raDLBCL4, 1)
}

if ((raDLBCL4$bic[[2]][1] > 1) && (raDLBCL4$bic[[2]][2] > 1)) {
  plotBicluster(raDLBCL4, 2)
}

if ((raDLBCL4$bic[[3]][1] > 1) && (raDLBCL4$bic[[3]][2] > 1)) {
  plotBicluster(raDLBCL4, 3)
}

if ((raDLBCL4$bic[[4]][1] > 1) && (raDLBCL4$bic[[4]][2] > 1)) {
  plotBicluster(raDLBCL4, 4)
}

plot(resDLBCL4, dim = c(1, 2), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(1, 3), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(1, 4), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(1, 5), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(2, 3), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(2, 4), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(2, 5), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(3, 4), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(3, 5), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)
plot(resDLBCL4, dim = c(4, 5), label.tol = 0.03, col.group = CDLBCL, lab.size = 0.6)

## End(Not run)

---

**nmfdiv**

*Non-negative Matrix Factorization: Kullback-Leibler Divergence*

**Description**

nmfdiv: R implementation of nmfdiv.

**Usage**
nmfdiv(X,p=5,cyc=100)

Arguments

X  the data matrix.

p  number of hidden factors = number of biclusters; default = 5.

cyc  maximal number of iterations; default = 100.

Details

Non-negative Matrix Factorization represents positive matrix \( X \) by positive matrices \( L \) and \( Z \).  
Objective for reconstruction is Kullback-Leibler divergence.  
Essentially the model is the sum of outer products of vectors:

\[
X = \sum_{i=1}^{p} \lambda_i z_i^T
\]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[
X = LZ
\]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n\times p} \), \( Z \) from \( R^{p\times l} \), and \( X \) from \( R^{n\times l} \).

The model selection is performed according to D. D. Lee and H. S. Seung, 1999, 2001.

The code is implemented in \( R \).

Value

object of the class Factorization. Containing \( LZ \) (estimated noise free data \( LZ \)), \( L \) (loading \( L \)), \( Z \) (factors \( Z \)), \( U \) (noise \( X - LZ \)), \( X \) (scaled data \( X \)).

Author(s)

Sepp Hochreiter

References


See Also

fabi, fabias, fabiap, fabi, fabiasp, mfsc, nmfdiv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion
nmfeu: R implementation of nmfeu.

Example:

```r
#-----------------  
# TEST           
#-----------------

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5, 
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0, 
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
X <- abs(X)

resEx <- nmfdiv(X,3)

## Not run:
#-----------------  
# DEMO           
#-----------------

dat <- makeFabiaDataBlocks(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5, 
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0, 
sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
X <- abs(X)

resToy <- nmfdiv(X,13)

extractPlot(resToy, ti="NMFDIV", Y=Y)

## End(Not run)
```

nmfeu: Non-negative Matrix Factorization: Euclidean Distance

Description

nmfeu: R implementation of nmfeu.
Usage

\[ \text{nmefu}(X, p=5, \text{cyc}=100) \]

Arguments

- \( X \): the data matrix.
- \( p \): number of hidden factors = number of biclusters; default = 5.
- \( \text{cyc} \): maximal number of iterations; default = 100.

Details

Non-negative Matrix Factorization represents positive matrix \( X \) by positive matrices \( L \) and \( Z \).
Objective for reconstruction is Euclidean distance.
Essentially the model is the sum of outer products of vectors:
\[
X = \sum_{i=1}^{p} \lambda_i z_i^T
\]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is
\[
X = LZ
\]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X \) from \( R^{n \times l} \).
The model selection is performed according to D. D. Lee and H. S. Seung, 2001.
The code is implemented in R.

Value

object of the class Factorization. Containing \( LZ \) (estimated noise free data \( LZ \)), \( L \) (loadings \( L \)), \( Z \) (factors \( Z \)), \( U \) (noise \( X - LZ \)), \( \hat{X} \) (scaled data \( X \)).

Author(s)

Sepp Hochreiter

References


nmfsc

See Also

fabi, fabias, fabiap, fabi, fabiasp, mfc, nmfdiv, nmfeu, nmfsc, extractPlot, extractBic,
plotBicluster, Factorization, projFuncPos, projfunc, estimateMode, makeFabiaData, makeFabiaDataBlocks,
makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

#-----------------
# TEST
#-----------------

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
 sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
X <- abs(X)

resEx <- nmfeu(X, 3)

## Not run:
#-----------------
# DEMO
#-----------------

dat <- makeFabiaDataBlocks(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
 sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
X <- abs(X)

resToy <- nmfeu(X, 13)

extractPlot(resToy, ti = "NMFEU", Y = Y)

## End(Not run)

---

nmfsc

Non-negative Sparse Matrix Factorization

---
Description

**nmfsc**: R implementation of *nmfsc*.

Usage

```r
nmfsc(x, p=5, cyc=100, sL=0.6, sZ=0.6)
```

Arguments

- **x**: the data matrix.
- **p**: number of hidden factors = number of biclusters; default = 5.
- **cyc**: maximal number of iterations; default = 100.
- **sL**: sparseness loadings; default = 0.6.
- **sZ**: sparseness factors; default = 0.6.

Details

Non-negative Matrix Factorization represents positive matrix $X$ by positive matrices $L$ and $Z$ that are sparse. Objective for reconstruction is Euclidean distance and sparseness constraints. Essentially the model is the sum of outer products of vectors:

$$X = \sum_{i=1}^{p} \lambda_i z_i^T$$

where the number of summands $p$ is the number of biclusters. The matrix factorization is

$$X = LZ$$

Here $\lambda_i$ are from $\mathbb{R}^n$, $z_i$ from $\mathbb{R}^l$, $L$ from $\mathbb{R}^{n \times p}$, $Z$ from $\mathbb{R}^{p \times l}$, and $X$ from $\mathbb{R}^{n \times l}$.

If the nonzero components of the sparse vectors are grouped together then the outer product results in a matrix with a nonzero block and zeros elsewhere.

The model selection is performed by a constraint optimization according to Hoyer, 2004. The Euclidean distance (the Frobenius norm) is minimized subject to sparseness and non-negativity constraints.

Model selection is done by gradient descent on the Euclidean objective and thereafter projection of single vectors of $L$ and single vectors of $Z$ to fulfill the sparseness and non-negativity constraints.

The projection minimize the Euclidean distance to the original vector given an $l_1$-norm and an $l_2$-norm and enforcing non-negativity.

The projection is a convex quadratic problem which is solved iteratively where at each iteration at least one component is set to zero. Instead of the $l_1$-norm a sparseness measurement is used which relates the $l_1$-norm to the $l_2$-norm.

The code is implemented in R.
nmfsc

Value

object of the class Factorization. Containing LZ (estimated noise free data \(LZ\)), L (loadings \(L\)), Z (factors \(Z\)), U (noise \(X - LZ\)), X (data \(X\)).

Author(s)

Sepp Hochreiter

References


See Also

fabi, fabias, fabiap, fabi, fabiasp, mfsc, nmfd, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, FabiaVersion

Examples

#------------
# TEST
#------------

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
   sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
X <- abs(X)

resEx <- nmfsc(X, 3, 30, 0.6, 0.6)

## Not run:
#------------
# DEMO
#------------

dat <- makeFabiaDataBlocks(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
   sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]
plotBicluster

Description

plotBicluster: \texttt{R} implementation of plotBicluster.

Usage

\begin{verbatim}
plotBicluster(r, p, opp=FALSE, zlim=NULL, title=NULL, which=c(1, 2))
\end{verbatim}

Arguments

\begin{verbatim}
\begin{itemize}
\item r: the result of extract_bic.
\item p: the bicluster to plot.
\item opp: plot opposite bicluster, default = FALSE.
\item zlim: vector containing a low and high value to use for the color scale.
\item title: title of the plot.
\item which: which plots are shown: 1=data matrix with bicluster on upper left, 2=plot of the bicluster; default c(1, 2).
\end{itemize}
\end{verbatim}

Details

One bicluster is visualized by two plots. The variable "which" indicates which plots should be shown.

Plot1 (which=1): The data matrix is sorted such that the bicluster appear at the upper left corner. The bicluster is marked by a rectangle.

Plot2 (which=2): Only the bicluster is plotted.

Implementation in \texttt{R}. 

X <- abs(X)

resToy <- nmfsc(X, 13, 100, 0.6, 0.6)

extractPlot(resToy, ti="NMFSC", Y=Y)

## End(Not run)
Author(s)
Sepp Hochreiter

See Also
fabia, fabias, fabiap, fabi, fabiasp, mfscc, nmfddiv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

#--------------
# TEST
#--------------

dat <- makeFabiaDataBlocks(n = 100, l = 50, p = 3, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
   sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resEx <- fabia(X, 0.01, 20)
rEx <- extractBic(resEx)
plotBicluster(rEx, p = 1)

## Not run:
#--------------
# DEMO1
#--------------

dat <- makeFabiaDataBlocks(n = 1000, l = 100, p = 10, f1 = 5, f2 = 5,
of1 = 5, of2 = 10, sd_noise = 3.0, sd_z_noise = 0.2, mean_z = 2.0,
   sd_z = 1.0, sd_l_noise = 0.2, mean_l = 3.0, sd_l = 1.0)

X <- dat[[1]]
Y <- dat[[2]]

resToy <- fabia(X, 0.01, 200)
rToy <- extractBic(resToy)
plotBicluster(rToy, p = 1)
# projFunc

Projection of a Vector to a Sparse Vector

Description

projFunc: R implementation of projFunc.

Usage

projFunc(s, k1, k2)

Arguments

- s: data vector.
- k1: sparseness, l1 norm constraint.
- k2: l2 norm constraint.
The projection is done according to Hoyer, 2004: given an $l_1$-norm and an $l_2$-norm minimize the Euclidean distance to the original vector. The projection is a convex quadratic problem which is solved iteratively where at each iteration at least one component is set to zero.

In the applications, instead of the $l_1$-norm a sparseness measurement is used which relates the $l_1$-norm to the $l_2$-norm.

Implementation in R.

Value

\[ v \] sparse projected vector.

Author(s)

Sepp Hochreiter

References


See Also

`fibia`, `fabias`, `fabiap`, `fabi`, `fabiasp`, `mfsc`, `nmfdiv`, `nmfeu`, `nmfsc`, `extractPlot`, `extractBic`, `plotBicluster`, `Factorization`, `projFuncPos`, `projfunc`, `estimateMode`, `makeFabiaData`, `makeFabiaDataBlocks`, `makeFabiaDataPos`, `makeFabiaDataBlocksPos`, `matrixImagePlot`, `fabiDemo`, `fabiVersion`

Examples

```r
# DEMO
#
#
size <- 30
sparseness <- 0.7
s <- as.vector(rnorm(size))
sp <- sqrt(1.0*size)-(sqrt(1.0*size)-1.0)*sparseness
ss <- projFunc(s,k1=sp,k2=1)
s
ss
```
**projFuncPos**

*Projection of a Vector to a Non-negative Sparse Vector*

**Description**

projFuncPos: R implementation of projFuncPos.

**Usage**

projFuncPos(s, k1, k2)

**Arguments**

- s: data vector.
- k1: sparseness, l1 norm constraint.
- k2: l2 norm constraint.

**Details**

The projection minimize the Euclidean distance to the original vector given an \( l_1 \)-norm and an \( l_2 \)-norm and enforcing non-negativity.

The projection is a convex quadratic problem which is solved iteratively where at each iteration at least one component is set to zero.

In the applications, instead of the \( l_1 \)-norm a sparseness measurement is used which relates the \( l_1 \)-norm to the \( l_2 \)-norm:

Implementation in R.

**Value**

v: non-negative sparse projected vector.

**Author(s)**

Sepp Hochreiter

**References**


**See Also**

fabi, fabias, fabiap, fabi, fabiasp, mfs, nmfd, nmfe, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion
Examples

```r
# DEMO

size <- 30
sparseness <- 0.7

s <- as.vector(rnorm(size))
sp <- sqrt(1.0*size)-(sqrt(1.0*size)-1.0)*sparseness

ss <- projFuncPos(s, k1=sp, k2=1)

s

ss
```

readSamplesSpfabia: Factor Analysis for Bicluster Acquisition: Read Sparse Matrix Samples

Description

readSamplesSpfabia: C implementation of readSamplesSpfabia.

Usage

```r
readSamplesSpfabia(X, samples=0, lowerB=0.0, upperB=1000.0)
```

Arguments

- `X` the file name of the sparse matrix in sparse format.
- `samples` vector of samples which should be read; default = 0 (all samples)
- `lowerB` lower bound for filtering the inputs columns, the minimal column sum; default = 0.0.
- `upperB` upper bound for filtering the inputs columns, the maximal column sum; default = 1000.0.

Details

The data matrix is directly scanned by the C-code and must be in sparse matrix format.

Sparse matrix format: *first line: numer of rows (the samples). *second line: number of columns (the features). *following lines: for each sample (row) three lines with

1) number of nonzero row elements
II) indices of the nonzero row elements (ATTENTION: starts with 0!!)
III) values of the nonzero row elements (ATTENTION: floats with decimal point like 1.0 !!)
The code is implemented in C.

Value

X (data of the given samples)

Author(s)

Sepp Hochreiter

References


See Also

fabi, fabias, fabiap, spfabia, readSamplesSpfabia, readSpfabiaResult, fabi, fabiasp, mfsc, nmfdv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

Examples

```
#-----------------
# TEST
#-----------------
```

readSpfabiaResult  

Factor Analysis for Bicluster Acquisition: Read Results of SpFabia

Description

readSpfabiaResult: C implementation of readSpfabiaResult.

Usage

```
readSpfabiaResult(X)
```
samplesPerFeature

Arguments

X the file prefix name of the result files of spfabia.

Details

Read the results of spfabia.
The code is implemented in C.

Value

object of the class Factorization. Containing L (loadings \( L \)), \( Z \) (factors \( Z \)), \( \Psi \) (noise variance \( \sigma \)), lapla (variational parameter), avini (the information which the factor \( z_{ij} \) contains about \( x_j \) averaged over \( j \)), xavini (the information which the factor \( z_j \) contains about \( x_j \) ), xini (for each \( j \) the information which the factor \( z_{ij} \) contains about \( x_j \)).

Author(s)

Sepp Hochreiter

References


See Also

fabia, fabias, fabiap, spfabia, readSamplesSpfabia, readSpfabiaResult, fabi, fabiasp, mfsc, nmfdiv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion

samplesPerFeature  

Factor Analysis for Bicluster Acquisition: Supplies samples per feature.

Description

samplesPerFeature: C implementation of samplesPerFeature.

Usage

samplesPerFeature(X, samples=0, lowerB=0.0, upperB=1000.0)
**Arguments**

- **x**  
  the file name of the sparse matrix in sparse format.

- **samples**  
  vector of samples which should be read; default = 0 (all samples)

- **lowerB**  
  lower bound for filtering the inputs columns, the minimal column sum; default = 0.0.

- **upperB**  
  upper bound for filtering the inputs columns, the maximal column sum; default = 1000.0.

**Details**

Supplies the samples for which a feature is not zero.

The data matrix is directly scanned by the C-code and must be in sparse matrix format.

Sparse matrix format:  
- first line: numer of rows (the samples).
- second line: number of columns (the features).
- following lines: for each sample (rows) three lines with
  - I) number of nonzero row elements
  - II) indices of the nonzero row elements (ATTENTION: starts with 0!!)
  - III) values of the nonzero row elements (ATTENTION: floats with decimal point like 1.0 !!)

The code is implemented in C.

**Value**

list with elements:  
- **sl** (List with one element per feature: each element is a vector of samples where the feature is not zero.)
- **nsl** Vector of feature length containing number of samples having a non-zero feature value.

**Author(s)**

Sepp Hochreiter

**References**


**See Also**

- fabia, fabias, fabiap, spfabia, readSamplesSpfabia, samplesPerFeature, readSpfabiaResult
- fabi, fabiasp, mfsc, nmfdv, nmfeu, nmfsc, extractPlot, extractBic, plotBicluster, Factorization, projFuncPos, projFunc, estimateMode, makeFabiaData, makeFabiaDataBlocks, makeFabiaDataPos, makeFabiaDataBlocksPos, matrixImagePlot, fabiaDemo, fabiaVersion
spfabia

Factor Analysis for Bicluster Acquisition: SPARSE FABIA

Examples

#------------
# TEST
#------------

spfabia

Description

spfabia: C implementation of spfabia.

Usage

spfabia(X,p=13,alpha=0.01,cyc=500,sp1=0,spz=0.5,non_negative=0,random=1.0,write_file=1,norm=1,scale=0.0

Arguments

- **x**: the file name of the sparse matrix in sparse format.
- **p**: number of hidden factors = number of biclusters; default = 13.
- **alpha**: sparseness loadings (0 - 1.0); default = 0.01.
- **cyc**: number of iterations; default = 500.
- **sp1**: sparseness prior loadings (0 - 2.0); default = 0 (Laplace).
- **spz**: sparseness factors (0.5 - 2.0); default = 0.5 (Laplace).
- **non_negative**: Non-negative factors and loadings if non_negative > 0; default = 0.
- **random**: >0: random initialization of loadings in [0,random], <0: random initialization of loadings in [-random,random]; default = 1.0.
- **write_file**: >0: results are written to files (L in sparse format), default = 1.
- **norm**: data normalization: >0 (var=1), 0 (no); default = 1.
- **scale**: loading vectors are scaled in each iteration to the given variance. 0.0 indicates non scaling; default = 0.0.
- **lap**: minimal value of the variational parameter; default = 1.0.
- **nL**: maximal number of biclusters at which a row element can participate; default = 0 (no limit).
- **lL**: maximal number of row elements per bicluster; default = 0 (no limit).
- **bL**: cycle at which the nL or lL maximum starts; default = 0 (start at the beginning).
samples vector of samples which should be included into the analysis; default = 0 (all samples)
initL vector of indices of the selected samples which are used to initialize L; default = 0 (random initialization).
iter number of iterations; default = 1.
quant quantile of largest L values to remove in each iteration; default = 0.001.
lowerB lower bound for filtering the inputs columns, the minimal column sum; default = 0.0.
upperB upper bound for filtering the inputs columns, the maximal column sum; default = 1000.0.
dorescale rescale factors Z to variance 1 and consequently also L; logical; default: FALSE.
doini compute the information content of the biclusters and sort the biclusters according to their information content; logical, default: FALSE.
eps lower bound for variational parameter lapla; default: 1e-3.
eps1 lower bound for divisions to avoid division by zero; default: 1e-10.

Details

Version of fabia for a sparse data matrix. The data matrix is directly scanned by the C-code and must be in sparse matrix format.

Sparse matrix format: *first line: numer of rows (the samples). *second line: number of columns (the features). *following lines: for each sample (row) three lines with
I) number of nonzero row elements
II) indices of the nonzero row elements (ATTENTION: starts with 0!!)
III) values of the nonzero row elements (ATTENTION: floats with decimal point like 1.0 !!)

Biclusters are found by sparse factor analysis where both the factors and the loadings are sparse.
Essentially the model is the sum of outer products of vectors:

\[ X = \sum_{i=1}^{p} \lambda_i z_i^T + U \]

where the number of summands \( p \) is the number of biclusters. The matrix factorization is

\[ X = LZ + U \]

Here \( \lambda_i \) are from \( R^n \), \( z_i \) from \( R^l \), \( L \) from \( R^{n \times p} \), \( Z \) from \( R^{p \times l} \), and \( X \), \( U \) from \( R^{n \times l} \).

If the nonzero components of the sparse vectors are grouped together then the outer product results in a matrix with a nonzero block and zeros elsewhere.

The model selection is performed by a variational approach according to Girolami 2001 and Palmer et al. 2006.

We included a prior on the parameters and minimize a lower bound on the posterior of the parameters given the data. The update of the loadings includes an additive term which pushes the loadings toward zero (Gaussian prior leads to a multiplicative factor).

The code is implemented in C.
Value

object of the class `Factorization`. Containing `L` (loadings), `Z` (factors), `Psi` (noise variance `sigma`), `lapla` (variational parameter), `avini` (the information which the factor `z_{ij}` contains about `x_j` averaged over `j`) `xavini` (the information which the factor `z_j` contains about `x_j`), `ini` (for each `j` the information which the factor `z_{ij}` contains about `x_j`).

Author(s)

Sepp Hochreiter

References


See Also

`fabi`, `fabias`, `fabiap`, `spfabia`, `readSamplesSpfabia`, `samplesPerFeature`, `readSpfabiaResult`, `fabi`, `fabiasp`, `mfsc`, `nmfd`, `nmfeu`, `nmfsc`, `extractPlot`, `extractBic`, `plotBic`, `cluster`, `Factorization`, `projFuncPos`, `projFunc`, `estimateMode`, `makeFabiaData`, `makeFabiaDataBlocks`, `makeFabiaDataPos`, `makeFabiaDataBlocksPos`, `matrixImagePlot`, `fabiDemo`, `fabiVersion`

Examples

```r
# --------------------------
# TEST
# --------------------------

samples <- 20
features <- 200
sparseness <- 0.9
write(samples, file = "sparseFabiaTest.txt", ncolumns = features, append = FALSE, sep = " ")
write(features, file = "sparseFabiaTest.txt", ncolumns = features, append = TRUE, sep = " ")
for (i in 1:samples)
{
  ind <- which(runif(features)>sparseness)-1
  num <- length(ind)
  val <- abs(rnorm(num))
  write(num, file = "sparseFabiaTest.txt", ncolumns = features, append = TRUE, sep = " ")
  write(ind, file = "sparseFabiaTest.txt", ncolumns = features, append = TRUE, sep = " ")
  write(val, file = "sparseFabiaTest.txt", ncolumns = features, append = TRUE, sep = " ")
}
res <- spfabia("sparseFabiaTest",p=3,alpha=0.03,cyc=50,non_negative=1,write_file=0,norm=0)
```
unlink("sparseFabiaTest.txt")

plot(res, dim=c(1,2))
plot(res, dim=c(1,3))
plot(res, dim=c(2,3))
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