Package 'SFAmix'

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Type	Package
Title	SFAmix
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Description SFAmix is a bayesian statistical method that decomposes a normally distributed matrix into the product of a sparse loading matrix, and a dense factor matrix. The method employs a three parameter beta distribution that act as a spike and slab prior to induce sparsity to the loading matrix. The method further consider the loading to be drawn from a mixture of sparse and dense component, which allows it to model the hidden confounding (in its dense component). The method is especially suitable for deriving context informed functional gene modules, where the context can be inferred from the factor matrix, and the sparse gene modules can be found on the corresponding loadings. Please refer to our paper for more details (https://arxiv.org/abs/1310.4792).

License GPL (>= 2)

Depends R (>= 2.14)

Collate SFAmixWrapper.R

NeedsCompilation yes

RoxygenNote 6.0.1

R topics documented:

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Description

Simulate matrix with dimension of 500 x 200, number of factors is set to 15, where 10 of them being sparse. The sparse loading matrix cotains mostly zeros, and random blocks of nonzero values generated from N(0,std). The dense loading matrix is generated from N(0,std), the factor matrix and the error matrix are generated from N(0,1).

Usage

```
gen_SFAmix_data(std = 1)
```

Arguments

std

standard deviation for the normal distribution

Value

a list containing the following lams: the sparse loading matrix lamd: the dense loading matrix

ex: the factors matrix

y: the y matrix calculated as y = lam * ex + err

SFAmixR

An algorithm for decomposing a high dimensional matrix into the product of a sparse loading matrix, and a dense factor matrix.

Description

An algorithm for decomposing a high dimensional matrix into the product of a sparse loading matrix, and a dense factor matrix.

Usage

```
SFAmixR(y = y, nf = 50, a = 0.5, b = 0.5, itr = 500, out_itr = 20,
  out_dir = NULL)
```

Arguments

У	matrix to be decmoposed, no missing values are allowed
nf	the number of factors for the algorithm to start with, will be shrank to a smaller number reflecting the number of factors needed to explain the variance, default to 50
а	paramater one for the three parameter beta distribution, default to 0.5 to recapitulate horseshoe
b	paramater two for the three parameter beta distribution, default to 0.5 to recapitulate horseshoe
itr	The maximum number of iterations the algorithm is allowed to run, default to 500

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out_itr (Optional) Iteration number out_itr, the algorithm will write temporary results into the specified directory (see below) every out_itr number of iterations.

out_dir (Optional) Directory where the algorithm will write temporary results into at the specified iteration number(see above)

Value

lam: the sparse loading matrix
ex: the factor matrix
z: a vector indicating whether the corresponding loading is sparse (value of 1)
nf: the number of factors learned by the model
exx: the expected value of the covarance matrix, E(XX^T)
itr: the number of iterations for the algorithm to converge

Author(s)

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References

https://arxiv.org/abs/1310.4792

Examples

```
library(SFAmix)
## simulate data
data = gen_SFAmix_data(std=2)
## run algorithm on the simulated data
result = SFAmixR(data$y,nf=50,a=0.5,b=0.5,itr=1000)
## calculate a correlation matrix of the estimated loading matrix
## and the true loading matrix. Ideally, there should be one and
## only one big correlation value for a given row and column of the
## correlation matrix
cor.est.real = cor(result$lam[,result$z==1],data$lams)
## visulize the correlation matrix
image(cor.est.real)
```

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