Package: StructureMC (via r-universe)

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Type Package

Title Structured Matrix Completion

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Depends R (>= 3.1.0), MASS, matrixcalc

Description Current literature on matrix completion focuses primarily on independent sampling models under which the individual observed entries are sampled independently. Motivated by applications in genomic data integration, we propose a new framework of structured matrix completion (SMC) to treat structured missingness by design. Specifically, our proposed method aims at efficient matrix recovery when a subset of the rows and columns of an approximately low-rank matrix are observed. The main function in our package, smc.FUN, is for recovery of the missing block A22 of an approximately low-rank matrix A given the other blocks A11, A12, A21.

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Repository https://yifuliu.r-universe.dev

RemoteUrl https://github.com/yifuliu/structuremc

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Contents

`StructureMC-package` *Structured Matrix Completion*

Description

Current literature on matrix completion focuses primarily on independent sampling models under which the individual observed entries are sampled independently. Motivated by applications in genomic data integration, we propose a new framework of structured matrix completion (SMC) to treat structured missingness by design. Specifically, our proposed method aims at efficient matrix recovery when a subset of the rows and columns of an approximately low-rank matrix are observed. The main function in our package, smc.FUN, is for recovery of the missing block A22 of an approximately low-rank matrix A given the other blocks A11, A12, A21.

Author(s)

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References

Cai, T., Cai, T. T., & Zhang, A. (2015). Structured Matrix Completion with Applications to Genomic Data Integration. *Journal of the American Statistical Association*.

`mynorm` *mynorm*

Description

This function returns the spectral norm of a real matrix if type is 2. Otherwise, it returns the matirx norm of the "norm" function using LAPACK.

Usage

```
mynorm(x, type = c("O", "I", "F", "M", "2"))
```

Arguments

`x`	numeric matrix
`type`	character string, specifying the type of matrix norm to be computed. Details see norm function in R base.

Author(s)

Yifu Liu and Anru Zhang

References

Cai, T., Cai, T. T., & Zhang, A. (2015). Structured Matrix Completion with Applications to Genomic Data Integration. *Journal of the American Statistical Association*.

See Also

norm

Examples

```
A = matrix(rnorm(10, mean = 0, sd = 0.1), 10, 10)
mynorm(A, "2")
mynorm(A, "O")
```

`smc.FUN` *Structured Matrix Completion*

Description

The main function in our package, smc.FUN, is for recovery of the missing block A22 of an approximately low-rank matrix A given the other blocks A11, A12, A21.

Usage

```
smc.FUN(A.mat, c_T, col_thresh, m1, m2)
```

Arguments

`A.mat`	The approximately low-rank matrix that we want to recover
`c_T`	c_T is the thresholding level, the default value is 2.
`col_thresh`	is column thresholding
`m1`	number of rows of block A11
`m2`	number of columns of block A11

Author(s)

Yifu Liu and Anru Zhang

References

Cai, T., Cai, T. T., & Zhang, A. (2015). Structured Matrix Completion with Applications to Genomic Data Integration. *Journal of the American Statistical Association*.

Examples

```
##dimension of matrix A with row number p1 = 10 and column number p2 = 9
p1 = 60
p2 = 50
m1 = 55##row number of A11
m2 = 45##column number of A11
A = matrix(rnorm(300, mean = 0.05, sd = 0.1), p1, p2)
#different blocks of our matrix A
A11 = A[1:m1, 1:m2]
A12 = A[1:m1, (1+m2):p2]
A21 = A[(1+m1):p1, 1:m2]
Arecovery = rbind(cbind(A11,A12),cbind(A21,matrix(NA,nrow=p1-m1,ncol=p2-m2)))
##recovery the block A22
A22 = smc.FUN(Arecovery, 2, ”True”, m1, m2)
```

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