

# Package ‘StructureMC’

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**Type** Package

**Title** Structured Matrix Completion

**Version** 1.0

**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.

**URL** <https://github.com/celehs/StructureMC>

**BugReports** <https://github.com/celehs/StructureMC/issues>

**License** GPL-2

**Encoding** UTF-8

**RoxygenNote** 6.1.1

**NeedsCompilation** no

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StructureMC-package      *Structured Matrix Completion*

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### 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  $A_{22}$  of an approximately low-rank matrix  $A$  given the other blocks  $A_{11}$ ,  $A_{12}$ ,  $A_{21}$ .

### Author(s)

Yifu Liu, Anru Zhang, Tianxi Cai and T. Tony Cai

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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*.

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mynorm                      *mynorm*

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### Description

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

### Usage

```
mynorm(x, type)
```

### Arguments

|                   |   |
|-------------------|---|
| <code>x</code>    | numeric matrix  |
| <code>type</code> | character string, specifying the type of matrix norm to be computed. Details see norm function in R base. |

### 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*.

**See Also**

norm

**Examples**

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

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)**

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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*.

**Examples**

```
##dimension of matrix A with row number p1 = 10 and column number p2 = 9
p1 = 10
p2 = 9
m1 = 6##row number of A11
m2 = 3##column number of A11
A = matrix(rnorm(10, mean = 0, sd = 0.1), p1, p2)
##find the approximation low-rank of A under singular value decomposition (SVD)
j1 = svd(A)$d
num<-length(which(j1!=0))
j2 = svd(A)$u
```

```
j3 = svd(A)$v
D<-diag(j1)
D[num, num] = 0
app_low_rank_A = j2
##consturct the matrix Arecovery that need to be recovered
A11 = app_low_rank_A[1:m1, 1:m2]
A12 = app_low_rank_A[1:m1, (1+m2):p2]
A21 = app_low_rank_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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