Package: DFSMTF

Type: Package

Title: Prediction of RNA-binding protein and alternative splicing event associations: a sparse non-negative matrix tri-factorization method

Version: 1.0

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Description: This package implements the DFSMTF algorithm with a matrix tri-factorization framework, which integrates the sparseness constraint to predict novel lncRNA-disease associations.

Depends:

MATLAB (>= 2012a)

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To operate:

\* for the example of DFSMTF:

we have provided some pre-data for DFSMTF, if you want to run DFSMTF framwork, please run the script "DFSMTF\_Init\_RBP\_AS" directly.

\*\* All data loading processes are included in script "DFSMTF\_Init\_RBP\_AS"

Files:

Simulation\_Init.m: The entry to the DFSMTF simulation framework, for randomly generated data and doing preprocessing.

DFSMTF\_Demo\_simulation.m: The main function for the simulation algorithm.

lernVector2.m: Init the basis matrix factor G with SVD

- If you have any problem, please contact Yushan Qiu (yushan.qiu@szu.edu.cn) and Xiaoqing Cheng (xiaoqing9054@xjtu.edu.cn)!