Package ‘DTHybrid’

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Title DT-Hybrid Algorithm
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Depends R (>= 3.0), methods, BiocGenerics, stats, gtools
Suggests parallel
LazyLoad yes
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Description An implementation of the DT-Hybrid algorithm which has been described in
Alaimo S, Pulvirenti A, Giugno R and Ferro A (2013). Drug-
target interaction prediction through domain-tuned network-
biocViews Bioinformatics, Networks, NetworkInference, NetworkAnalysis
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computeRecommendation Runs the DT-Hybrid algorithm on a bipartite network

Description
Compute the recommendations on a bipartite network by using the DT-Hybrid algorithm.

Usage
computeRecommendation(A, lambda=0.5, alpha=0.5, S=NA, S1=NA, cl=NA)
computeRecommendation

Arguments

A 
The adjacency matrix that represents the bipartite network. Given "n" nodes of type "X" and "m" nodes of type "Y", the adjacency matrix is an n by m matrix, where each element A[i,j] contains 1 if the X-node i interacts with the Y-node j, 0 otherwise.

alpha
Tuning parameter (value between 0 and 1) to adjust the performance of the algorithm.

lambda
Tuning parameter (value between 0 and 1) to adjust the performance of the algorithm.

S
A n by n similarity matrix where each element (value between 0 and 1) represents the similarity between two X-nodes.

S1
A m by m similarity matrix where each element (value between 0 and 1) represents the similarity between two Y-nodes.

c1
A cluster, generated with the function makeCluster available through packages snow or parallel, used to speed up the computation when the input matrices are too large.

Details

See cited document for more details.

Value

An n by m matrix where each element represents how much the interaction between an X-node and an Y-node is favorable.

Author(s)

Salvatore Alaimo

References


Examples

# Example using a Drug-Target Interaction dataset
data(enzyme)

# Compute recommendation
result <- computeRecommendation(enzyme_r)
## Not run: print(result)

# Compute recommendation using similarity informations
result1 <- computeRecommendation(enzyme_r, S=enzyme_ts, S1=enzyme_ds)
## Not run: print(result1)

# Speeds up the computation process through the use of multiple threads
library(parallel)
c1 <- makeCluster(detectCores())
result2 <- computeRecommendation(enzyme_r, S=enzyme_ts, S1=enzyme_ds, cl=c1)
An example Drug-Target interaction network dataset.

Description

The enzyme dataset consists: i) an n by m matrix enzyme_r, which represents the bipartite network built upon the known drug-target interactions; ii) an n by n matrix enzyme_ts where each element is the sequence similarity between all pairs of genes in the bipartite network, computed using a normalized Smith-Waterman score (Smith and Waterman, J.Mol.Bio, 1981); iii) an m by m matrix enzyme_ds where each element is the 2D chemical similarity between all pairs of drugs in the example network, computed using the SIMCOMP algorithm (Hattori et al, J.Ame.Chem.Soc, 2003).

Usage

data(enzyme)

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