

NCIS Users' Guide

Syntax:

[*gw*, *gc*, *sc*, *res*] = *ncis* (*X*, *N*, *ncg*, *ncs*, *d*, *T*, *eps*).

Inputs:

X Gene expression matrix, with columns for samples and rows for genes.

Example:

0.1997	0.3763	...	-0.2085
-0.5078	0.0913	...	-1.1053
...
-0.2372	-0.8130	...	-0.1932

N Network adjacency matrix. We assume *X* and *N* have been preprocessed such that they have a same set of genes and the genes are arranged in a same order.

Example:

1	1	...	0
0	1	...	0
...
0	0	...	0

ncg Number of gene clusters.

ncs Number of sample clusters (cancer subtypes).

d Tuning parameter α in the weight-training algorithm.

T Number of iterations in co-clustering. Updating process will be terminated as the number of iterations reaches this pre-defined *T*.

eps Convergence threshold in co-clustering. Updating process will be terminated if the decreasing of the objective function is less than this pre-defined *eps*.

Outputs:

gw Weights trained for genes.

Example:

0.1360	0.1089	...	0.0019
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gc Gene clusters detected by NCIS.

Example:

5	3	...	7
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sc Sample clusters (cancer subtypes) detected by NCIS.

Example:

2	4	...	1
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res Values of the objective function. Can be used to check the convergence of the algorithm.

Example:

$$3.2810 \times 10^5$$

$$3.2738 \times 10^5$$

...

$$3.2698 \times 10^5$$