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:
  
  \[
  \begin{matrix}
  0.1997 & 0.3763 & \ldots & -0.2085 \\
  -0.5078 & 0.0913 & \ldots & -1.1053 \\
  \ldots & \ldots & \ldots & \ldots \\
  -0.2372 & -0.8130 & \ldots & -0.1932 \\
  \end{matrix}
  \]

- \(N\): 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:
  
  \[
  \begin{matrix}
  1 & 1 & \ldots & 0 \\
  0 & 1 & \ldots & 0 \\
  \ldots & \ldots & \ldots & \ldots \\
  0 & 0 & \ldots & 0 \\
  \end{matrix}
  \]

- \(ncg\): Number of gene clusters.

- \(ncs\): Number of sample clusters (cancer subtypes).

- \(d\): Tuning parameter \(\alpha\) 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:
  
  \[
  \begin{matrix}
  0.1360 & 0.1089 & \ldots & 0.0019 \\
  \end{matrix}
  \]

- \(gc\): Gene clusters detected by NCIS.
  
  Example:
  
  \[
  \begin{matrix}
  5 & 3 & \ldots & 7 \\
  \end{matrix}
  \]

- \(sc\): Sample clusters (cancer subtypes) detected by NCIS.
  
  Example:
  
  \[
  \begin{matrix}
  2 & 4 & \ldots & 1 \\
  \end{matrix}
  \]

- \(res\): Values of the objective function. Can be used to check the convergence of the algorithm.
Example:
3.2810×10^5  3.2738×10^5  ...  3.2698×10^5