Bootstrapping MRF-based Subnetwork Identification Toolbox for Matlab

1. Introduction

Bootstrapping Markov Random Field (BMRF)-based method is specifically designed for subnetwork identification by integrating gene expression data and protein-protein interaction data. The detailed description of the BMRF approach can be found in the manuscript "A Bootstrapping Markov Random Field-based Method to Identify Protein-protein Interaction Subnetworks " by Li Chen, Jianhua Xuan, Rebecca B. Riggins, Robert Clarke and Yue Wang.

2. Usage

2.1 Syntax

To call netSVM use:

\[
\text{BMRF}_{\text{network ID}} \text{ BMRF}_{\text{network score}} = \text{BMRF}(\text{data, geneid, label, ppi, seed id, Distance, T})
\]

2.2 Description

The inputs to the BMRF function are:

- **data**: The training sample set. Each column is a sample and each row is a gene/feature. The gene id is listed in 'geneid'.
- **geneid**: The gene ids in the data set.
- **label**: Binary (1,2) labels for data samples.
- **ppi**: The protein-protein interaction data. n*2 matrix, where n is the number of interactions. First column is the gene id of start node and second column is the gene id of end node.
- **seed id**: seed gene ids.
- **Distance**: Parameter used in ‘search_network_MRF_SA2’, default is 2.
- **T**: Temperature parameter used in ‘search_network_MRF_SA2’, default is 1.

The outputs are:

- **BMRF_network_ID**: All subnetworks gene ids identified by BMRF.
- **BMRF_network_score**: All subnetworks scores identified by BMRF.

3. Demo

‘demo_bMRF.m’ shows an example of netSVM on simulation data. This demo shows how to call BMRF function and output the precision and recall of identified subnetwork.