

# 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:

```
[BMRF_network_ID BMRF_network_score] = BMRF(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.