

# Tutorial for NARROMI

## 1. Introduction

NARROMI is a Matlab program for inferring Gene Regulatory Networks (GRN) from gene expression dataset by combining ordinary differential equation based recursive optimization (RO) and information-theory based mutual information (MI).

## 2. Matlab Code description

### 2.1 narromi

```
[net,net_value,sig]=narromi(y,X,lamda,alpha,
beta,t)
```

#### 2.1.1 Input

Code	Description
<b>y</b>	Expression of target gene.
<b>X</b>	Expressions of regulators (TFs).
<b>lamda</b>	Regularization parameter for optimization.
<b>alpha</b>	Parameter for filtering genes with low MI correlations.
<b>beta</b>	Parameter for filtering genes with low regulatory strength for RO.
<b>t</b>	Parameter for the integration of MI and RO.

### 2.1.2 Output

Code	Description
<b>net</b>	Inferred sparse network.
<b>net_value</b>	Inferred network with regulatory strength.
<b>sig</b>	Inferred network with statistic significance.

## 2.2 Connect\_for\_cytoscape\_pvalue

```
[table]=Connect_for_cytoscape_pvalue(G,Gval,Gsig,  
name_TF,name_gene)
```

### 2.2.1 Input

Code	Description
<b>G</b>	Network for network structure
<b>Gval</b>	Networks with strengthens of regulation
<b>Gsig</b>	Significance level/p-value of each edge/interaction.
<b>name_TF,name_gene</b>	Name of TF and gene, which are matched with G, Gval and Gsig.

### 2.2.2 Output

Code	Description
<b>table</b>	Table list with four columns: first and

	<p>second columns are gene pairs interaction with each other, third column is interaction strengthen, forth column is significance level /p-value of interaction.</p>
--	---

### 2.3 ControlCenterNarromi.m

As an example, '**ControlCenterNarromi.m**' is control center code for a dataset.

## 3 Operation for dataset

M-file '**ControlCenterNarromi.m**' controls the whole program to infer gene regulatory network from gene expression dataset.

Example one is for the inference of networks without division of TFs and target genes. The network type is gene-->gene interaction.

Example two is for the inference of networks with division of TFs and target genes. The network type is TF-->gene interaction.

The TXT file (\*.txt) of the networks, namely 'network\_inferred.txt', is output. In the TXT file, first column are TFs, second column are target genes, third column is value representing the regulatory strength, and forth column is significance level /p-value of interaction.

## 4 Example

M-file ' **ControlCenterNarromi.m** ' controls the whole program to infer gene regulatory network from gene expression dataset.

```
% ControlCenterNarromi
% Example one: For the expression data of TFs and target genes;
% Example two: For the expression data of genes(not divided for TFs and
% targets).
% Version Data: 2012-3-25

clear
clc

%% Example one
% The TFs and targets are not divided.

load Ecoli_Data.mat;
% computing tg-tf network using narromi
% Input: TF_list,TF_expression,TG_list,TG_expression.
lamda = 1;
alpha = 0.05; % parameter for MI correlation.
beta = 0.05; % parameter for RO.
t = 0.6; % parameter for the rate of RO in the integration.

% As an example, we choose part of the expression.
TF_list = TG_list(1:15,:);
TF_expression = TG_expression(1:15,:);

network = zeros(size(TF_list,1),size(TF_list,1));
network_v = network;
netsig = network;

for i=1:size(TF_list,1)
    y = TF_expression(i,:);
    X =
[TF_expression(1:i-1,:);TF_expression(i+1:size(TF_expression,1),:)]';
    [net,net_value,sig]=narromi(y',X',lamda,alpha, beta, t) ;
    network(i,1:i-1) = net(1:i-1);network(i,i+1:size(TF_expression,1))
= net(i:end);
    network_v(i,1:i-1) = net_value(1:i-1);
network_v(i,i+1:size(TF_expression,1)) = net(i:end);
```

```

        netsig(i,1:i-1) = sig(1:i-1); netsig(i,i+1:size(TF_expression,1)) =
sig(i:end);
        i
end

% Output the network
significance = 0.05;
network_sig = zeros(size(netsig)) ;

network_sig(find(netsig<=significance)) = 1 ;
network_sig(logical(eye(size(network_sig)))) = 0;
[testfile_network]=Connect_for_cytoscape_pvalue(network_sig',network_
v',netsig',TF_list,TF_list) ;

network_size=size(testfile_network,1);
fprintf('NOTICE:\nThe Size of the Inferred Network
is %d.\n',network_size);

a=testfile_network';
fid=fopen('network_inferred.txt','w');
fprintf(fid,'%s %s %.6f %.3e\n',a{:}) ;
fclose(fid);
fprintf('NOTICE:\nPlease Find the Network File in the Matlab Current
Folder.\n')

%% Example Two
% The TFs and targets are divided.

load Ecoli_Data.mat;
% computing tg-tf network using narromi
% Input: TF_list,TF_expression,TG_list,TG_expression.
lamda = 1;
alpha = 0.05; % parameter for MI correlation.
beta = 0.05; % parameter for RO.
t = 0.6; % parameter for the rate of RO in the integration.

% As an example, we choose part of the expression.
TG_list = TG_list(1:10,:);
TG_expression = TG_expression(1:10,:);

network = zeros(size(TG_list,1),size(TF_list,1));
network_v = network;

```

```

netsig = network;

for i=1:size(TG_list,1)
    y = TG_expression(i,:);
    X = TF_expression;
    [net,net_value,sig]=narromi(y',X',lamda,alpha, beta, t) ;
    network(i,:) = net; network_v(i,:) = net_value; netsig(i,:) = sig;
    i
end

% Output the network
significance = 0.05;
network_sig = zeros(size(netsig)) ;

network_sig(find(netsig<=significance)) = 1 ;

[testfile_network]=Connect_for_cytoscape_pvalue(network_sig',network_
v',netsig',TF_list,TG_list) ;

network_size=size(testfile_network,1);
fprintf('NOTICE:\nThe Size of the Inferred Network
is %d.\n',network_size);

a=testfile_network';
fid=fopen('network_inferred.txt','w');
fprintf(fid,'%s %s %.6f %.3e\n',a{:}) ;
fclose(fid);
fprintf('NOTICE:\nPlease Find the Network File in the Matlab Current
Folder.\n')

```