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% ========== NetICS test tutorial ===========
% This is a test of the NetICS algorithm using the source data. You can
% download all the supplementary files following the link in the readme
% file. Then you have to put all the FUN and data in the same folder.

% ====== Files like describe in the netisc fun ===========
%   INPUTS:
%   filenameMu(varargin{1}):        input file that contains the genetically
 aberrant genes of each sample.
%                                   It contains two columns that map every
 gene (1st column) to the samples that
%                                   it is genetically aberrant (2nd column)
%   adj(varargin{2}):               adjacency matrix of the directed
 interaction network
%   restart_prob(varargin{3}):      restart probability for the insulated
 diffusion. For (Wu et al., 2010) network use 0.4.
%   rank_method_str(varargin{4}):   'MEDIAN' uses the median of the sample-
specific ranks
%                                   'RRA' uses the Robust Rank Aggregation
 method to integrate sample-specific ranked lists
%                                   'SUM' uses the sum of the sample-specific
 ranks
%   filenameNet(varargin{5}):       input file that contains the list of the
 genes that are present in the network.
%                                   They should be in the same order as in
 the rows of the adjacency matrix adj.
%                                   An example file is given that contains
 the gene names of the network described in (Wu et al, 2010).
%   filenameRNA(varargin{6}):       tab delimited file with two columns.
 First column contains the genes for which differential expression
%                                   between the tumor and normal samples at
 the RNA level was measured. Second column contains the p-values
%                                   of these measurements. This file can be
 the result of a tool for differential expression analysis such as DESeq2.
%                                   Each gene in this file should have only
 one entry.
%   filenamePR(varargin{7}):        tab delimited file with two columns.
 First column contains the proteins for which differential expression between
%                                   the tumor and normal samples at the
 protein level was measured. Second column contains the p-values of these
%                                   measurements. Each gene in this file
 should have only one entry.

load('adj_lar_com');
restart_prob=0.4;
%%%%%ù
```

======== Running the NetICS fun ============

```
[ ranked_list_genes, ranked_scores ] = netics_fun( 'mutation_data_breast.txt',
 adj_lar_com,
 restart_prob, 'RANK_AGGREG=SUM', 'network_genes.txt', 'RNA_diff_expr_breast.txt', 'protei
%%%%

Computing diffused matrix...
Running NetICS...
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results

```
z = ranked_list_genes(1:10);
disp(z)

    {'TP53'  }
    {'UBA52' }
    {'UBB'   }
    {'GNB1'  }
    {'EP300' }
    {'RAC1'  }
    {'PIK3CA'}
    {'RPS27A'}
```

```
{'NFKB1' }
{'GNG2'  }
```

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