

Participation of microRNAs in human interactome: extraction of microRNA-microRNA regulations

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1. Comparing the microRNA-TF network with some real networks:

The microRNA-TF network is compared with the human transcription factor networks: (Rodriguez-Caso *et al.*, 2005), the yeast proteome (Jeong *et al.*, 2001) and world wide web (Vazquez *et al.*, 2002).

table 1. comparison of microRNA-TF network with some real networks.

Description	N	I	k	C	L
miRNA-TF network	771	8043	10.43	0.0239	1.59
HTFN	230	851	3.70	0.17	4.50
Yeast proteome	1870	4488	2.40	0.07	6.81
Internet	10100	38380	3.80	0.24	3.70

The parameters we used are: total number of nodes N; total number of links I, average degree k; clustering coefficient of the network C and average path length L. Some parameters are defined in the next section. MicroRNA-TF network exhibited a strong liner relationship with the rest.

2. Description of topological parameters:

2.1 Strongly Connected Component (SCC): A directed sub-graph is called a strongly connected component if there is a path from each vertex in the sub-graph to every other vertex.

2.2 Average degree of the network (k): Average degree k of the network is defined as follows:

$$k = \frac{I}{N}$$

2.3 Clustering coefficient of network (C): Clustering coefficient of any directed network is formally defined as follows:

$$C = \frac{1}{N} \sum_{i=1}^N \frac{l_i}{k_i(k_i - 1)}$$

where l_i denotes the number of links N_i has got with its neighboring nodes and k_i , degree of node N_i .

3. TOMWDG hands out

3.1 Example:

$$GTOM_m = \frac{4 + 1}{\min(6, 6) + 1 - 1} = 0.83$$

$$CR_m = \frac{\frac{1}{2}[(0.8 + 0.6) + (0.5 + 0.7)] + \frac{1}{2} \times 0.6}{\max[(0.5 + 0.6), (0.6 + 0.7 + 0.4 + 0.8)] + 1 - \frac{1}{2} \times 0.6} = 0.5$$

$$BCR_m = \frac{\frac{1}{2}[(0.7 + 0.7) + (0.3 + 0.9)] + \frac{1}{2} \times 0.6}{\max[(0.9 + 0.9 + 0.7 + 0.6), (0.7 + 0.3)] + 1 - \frac{1}{2} \times 0.6} = 0.42$$

$$TOMWDG_m(i, j) = \frac{1}{2}(0.5 + 0.42) = 0.46$$

3.2 Additional properties of TOMWDG:

- Rear part of the denominators in both CR and BCR measures ensure that the denominator will never score a zero.
- The rear part of the numerators ensures that direct connection(s) between the nodes is (are) also given priority.
- Depending upon the requirement of cluster size the value of m can be chosen.

References:

Rodriguez-Caso, C. *et al.*, (2005) Topology, tinkering and evolution of the human transcription factor network, *FEBS*, doi:10.1111/j.1742-4658.2005.05041.x

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Jeong, H., Mason, S.P., Barabasi, A.L., Oltvai, Z.N., (2001) Lethality and centrality in protein networks. *Nature* 411, 41–42.