

# NETWORK MOTIFS EMERGE FROM INTERCONNECTION THAT FAVOR STABILITY

## **A Mathematica package to calculate the motifs from real and condensed networks**

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Last update: March 21, 2015

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**Description:** This package has the Mathematica script and data files required to reproduce the results of our paper. It is organized in four folders:

1. [Yeast] Contains the complete mathematica script and data files necessary to reproduce the results of our paper for the Yeast network. In particular, this folder has
  - 1.1. The mathematica package MotifCollapsePackage.wl implementing functions to interpret the output of mfinder, functions to produce the condensed networks, functions to compute the mean contraction loss, among other things. The use of each function is documented in the package itself.
  - 1.2. Two mathematica notebooks Yeast-RandCondensation1.nb and Yeast-RandCondensation1.nb used to condense the network.
  - 1.3. The mathematica notebook Analyze-Randomizations1.nb used to analyze the contractions loss of motifs in the original and condensed networks.
  - 1.4. Two files subgraphs3nodes.wdx and subgraphs4nodes.wdx containing all 3- and 4-node subgraphs.

1.5. Two folders cond1/ and cond2/ containing 10 realizations for the first and second condensation of the network.

1.6. Several \_MEMBERS\*.txt and \_OUT\*.txt files obtained using mfinder. They contain the enumeration of all subgraphs of the networks, and the motifs found.

1.7. The file TRN-Yeast\_netNoMutual.dat containing the edge-list of the Yeast Transcription-Regulation network, in mfinder format. It also contains several other .dat files corresponding to the condensed networks.

2. [CElegans] Contains the results of our analysis applied to the C.elegans network. This folder has

2.1. The edge-list of the neuron network of C.elegans neuralCElegans\_net.dat in mfinder format. It also contains the corresponding \_MEMBERS\*.txt and \_OUT\*.txt files obtained using mfinder.

2.2. Three folders cond1, cond2 and cond3 containing the condensed networks in condensation 1, 2 and 3, respectively. These folders also contain \_MEMBERS\*.txt and \_OUT\*.txt files obtained using mfinder.

3. [EColi] Contains the results of our analysis applied to the E.coli network. This folder has

3.1. The edge-list of the neuron network of E.coli EColiAlon\_net.dat in mfinder format. It also contains the corresponding \_MEMBERS\*.txt and \_OUT\*.txt files obtained using mfinder.

3.2. Three folders cond1, cond2 and cond3 containing the condensed networks in condensation 1, 2 and 3, respectively. These folders also contain \_MEMBERS\*.txt and \_OUT\*.txt files obtained using mfinder.

4. [SaintMartin] Contains the results of our analysis applied to the Saint Martin network. This folder has

3.1. The edge-list of the food web at Saint Martin FW-StMartin\_net.dat in mfinder format. It also contains the corresponding \_MEMBERS\*.txt and \_OUT\*.txt files obtained using mfinder.

3.2. One folder cond1 containing the condensed network in first step. This folders also contains \_MEMBERS\*.txt and \_OUT\*.txt files obtained using mfinder.

The mathematica notebooks and package in the Yeast folder can be directly applied to analyze all other networks as well.