Thesis Outlines

Methology

1. **Construct the network**
   a. Select the data
   b. Review the networks constructed so far for these data
   c. Construct the net using Pearson cor and MI :
      i. pearson correlations absolute value (measuring connectance only, not the nature of the connection) ,
      ii. pearson correlation (includes the nature of the connection, negative or positive),
      iii. MI,
      iv. IV sign(r)*MI ,
      v. time series network (transfer entropy),
      vi. VI conditional entropy,
      vii. VII sign(r)*conditional entropy
   d. **compare b with c**
2. **compute centralities**
   a. compute for : I ,II, III, IV nets the following centralities :
      degree, betweenness, closeness, PageRank, eigencentrality, K-shell decomposition, entropy of each centrality, motifs?, modules?

3. **compute vitalities of centralities**
   a. vitality is the change of the centrality measure after the deletion of a node: $Vitality_s = (S_{terminal} - S_{initial})/S_{initial}$
4. **evaluate the essentiality of the nodes with the highest vitality**
   a. gene enrichment, gene ontology
5. **recommend the best net construction and the best vitality for the assessment of the biological essentiality**

Master Thesis Structure

Chapter 1
Research question
Why it is important?
Who did what so far? Review of literature!

Master Thesis Structure

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Research question
Why it is important?
Who did what so far? Review of literature!
What remains to be done? Why the biologist is not satisfied?

Chapter 2
Methodology for addressing the problem
Necessary theoretical concepts and results

Chapter 3
Data (origin, reliability, size)
Computations Results
Mathematical meaning of the results

Chapter 4
Biological significance of the results

Chapter 5
Conclusions
1. Mathematical comparison with available results (what is new)
2. Biological comparison with available results (what is new)
3. General comparison with available results (what is new)
4. Perspectives for future work