Università degli Studi di Padova

Computer Engeneering

Learning From Networks
Mid Term Report

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Title

Human and mouse similarities in gene regulatory networks.

Motivation

We are interested in finding similarities and differences between human and mouse genes regulatory networks.

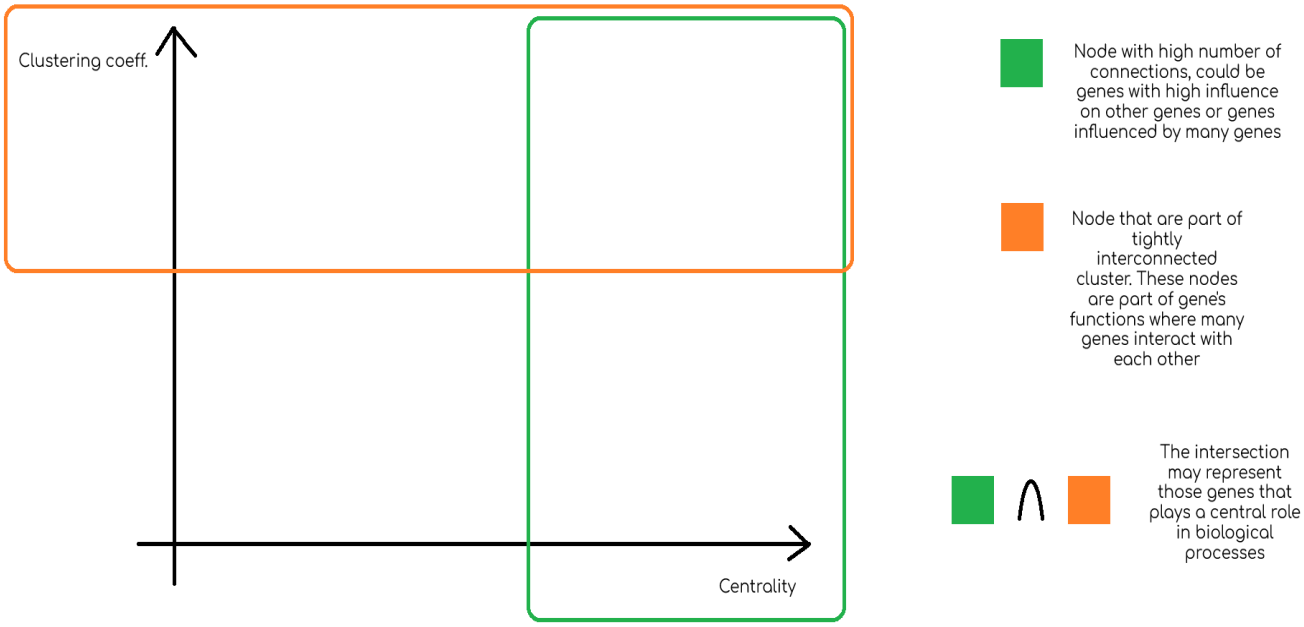
It could be relevant to medicine in order to find parallelisms between the two organisms.

In the regulatory network a node is a gene, and an edge is the interaction between two genes.
We want to find a similarity between human and mice biological processes by looking at gene's importance and influence in the network.

Centralities and Clustering coefficient analysis

We will plot centralities and cluster coefficients for each node in a scatter chart and highlight nodes that have major impact on biological processes.

The first idea is to look at the intersection of the two areas described in the following figure:



Graphlets

Our initial idea was to look at graphlets structure to find similar patterns in gene interactions between the two networks.

However, we couldn't find already implemented algorithms that compute graphlet.

We will continue our research and eventually we will try to implement an approximate algorithm to compute graphlets.

Similarities and differences

Our idea of similarities is a gene that interacts in a similar structure of genes in both networks and with almost the same influence.

For example, we expect two genes with high centrality and clustering coefficient that appear in the same structure in both networks to be similar.

We are focusing our research on similarities as we have understood them above because, in the biological context, it would be useful to experiment on mice once the similarity between certain regulatory genes is confirmed.

We do not intend to identify the differences explicitly, and the "nodes" that we do not consider similar should not necessarily be regarded as different, as they might be similar in other aspects that we are not taking into consideration.