# Week of May 16

## Monday

### Morning

We will dedicate the morning to testing out the following functionalities:

1. Test first neighbours

2. Test second neighbours

3. Test the genes of interest

4. Test the filtering by edge weight

5. Test varying the layout

6. Test varying the p value

We need to do this for multiple choices of P Values.

### Afternoon

WE might want it to be the case that the edge weight filtering applies to not only the main graph, but the children, as well as the genes of interest graph.

In fact, it might be a good idea to slowly phase out the main graph since we will not be using it later on at all due to the complexity of the 20k by 20k matrix.

We have generalized the neighbor general method so that it now allows you to keep asking for neighbours and doesn’t limit you to only the 2nd neighbours. We need to extend the front end in order to permit the user to keep on exploring neighbours. It is still however made to work for only an epi-stroma correlation matrix. We need to come up with a scheme that will work got epi-epi as well.

IT would be nice to have the circular layouts done by the time that Venkata gets back.

In order to phase out the overall graph and start focusing on the graph that shows the genes of interest, we need to create a path on the server that is simply responsible for getting a list of genes as well as their degrees.

Okay so let’s create the R script and the necessary server side code in order to accomplish this.

Then we will move on to changing the front end so that the filtering happens on the graph that is returned to the client after they select a list of genes of interest.

Let’s see what the performance of the md-autocomplete control is like when it contains 20,000 genes