Week May 16-20

1. Added the ability to search interactions and self-loops on the client side. This is needed when a graph with many interactions is returned and the user wants to focus on a specific gene.
2. Built an entirely new framework for returning graph data from R to the server. Before, there was a lack of consistency since one method would expect a correlation matrix to be returned, and another method would expect gene names and lists of correlations to be returned. For the sake of standardization, as well as more importantly being able to create more advanced layout by knowing which genes are first neighbours and which genes are second neighbours (this was not possible when retuning a correlation matrix), I made it so that the R scripts now return a list of gene names, their degrees, as well as a list of edges to the server. This made things much more extendable since the scripts now all share a lot of common methods located in the helpers.R file. This new framework not only required changing the R scripts, but it also required changing the server side code quite a bit.
3. Changed the way in which the neighbor-general method works on the server. We used to create edges only from selected genes to their neighbours. When exploring 3rd and 4th neighbours, this method failed to add some edges since it is possible that some of the edges for a selected gene at the 4th neighbor state could have needed to originate from a previous neighbor which was not a selected gene. This essentially gives the user the ability to drill down into any level of neighbours that they want to see.
4. Created a clustered layout display for the genes of interest graph. This view is more condensed than the panel layout, and it allows for more structural relationships to be seen than the random layout. The new layout also shows when nodes share the same first neighbours which might be relevant biologically.
5. Added a more dynamic user interface for filtering based on correlation. In fact, for the genes of interest graph, there are now two stages of filtering that can be done. First, the user can choose some genes of interest and get back a graph of first neighbours. They can then filter the correlations happening between the genes of interest and the first neighbours. Afterwards, they can retrieve the second neighbours of the genes of interest. Finally, they can filter the interactions happening between first neighbours and second neighbours. This allows a user to focus on correlations of a certain strength at multiple levels thereby greatly reducing the complexity and size of the graph.
6. Added the ability for users to click on a node in the graph and have the edges associated with that node be highlighted while all other edges disappear. This is very useful for dense graph.
7. Made the tabs more dynamic based on the controller that is being used for the tab. This allows for the sidebar to have completely different controls in the main tab as opposed to the neighbours tab.