We need to rethink the algo for getting the submatrix and returning edges. Let’s write it from scratch and keep Venkata’s idea about filtering on the weights prior to doing anything else in mind.

Let’s write out some pseudocode for it:

1. We zero out anything in the correlation matrix that doesn’t fit our weight requirements
2. For each of the selected genes we:
   1. Get the top interactors for each gene. Let’s think of what this means. Say that a gene has 1000 interactors. We obviously only want to plot a maximum of 10 of them. We also want to be able to see the negative interactions as well. Then we need some additional parameters that a user can set on the client side because right now it is hard to decide from the R code alone what interacting genes to show.

We have a good example of the exclusions failing. So we choose VPS72-E and TBP-E.

firstNeighbours[[1]] = UBE2C-s, VPS72-S

firstNeighbours[[2]] = CDC45-S, UBE2C-s, EBNA1BP2-S, TBP-S

We need to have a general function that takes in an arbitrary list of nodes that are any mixture of epi and stroma, and then creates a bipartite positioning of those nodes.

Looks like we are getting quite a few duplicate nodes in our graph. They aren’t appearing because cytoscape hides them due to identical IDs, but they can be seen in the config, This implies something is wrong with our exclusions.

Fixed the exclusions.

Now let’s come up with our clustered layout. So let’s create a method that takes in a selected gene, its first and second neighbours, and