# To Do Sunday May 15

Rewrite some of the R scripts to make them more dynamic. This applies especially to the findCorrelations complete and getRelevantSubmatrix. We need to extract some methods out of those scripts so that it is easier to see what is going on. Right now we are using random if statements here and there and then just alternating indices for epi and stroma. Turning these into methods will make code much cleaner and extendable. Our findCorrelations script does not return a weight matrix but rather a vector of weights

For now, it seems reasonable to continue returning the weight matrix to the user. I’m not sure if it makes sense to return edges from R. Performance wise, it’s hard to say whether or not R is faster than node in making the edges. The issue on the server side now is that if we return a sparse weight matrix from R, the server will waste time iterating over a bunch of entries that are zeros. If we were to return actual edges that specify the start node, end node, and interaction strength from R, this would no longer be a problem. However, this means that the R script would have to be the one to do the iterating

Lastly, we need to reorganize everything so that the matrices themselves contain rownames and colnames with the appropriate –E or –S added to them. We should stay away from doing this on the server since a lot of the decision making when it comes to whether or not we are indexing in rows or columns is based on the side flag. And finally, we need to figure out a way to make everything more generalizable to when we will be dealing with epi-epi and stroma-stroma matrices. Our current logic breaks for these cases since it runs under the assumption that we are dealing with only epi-stroma.