**Partial Correlation Problem Discussion**

Looking at the package we were trying before, GeneNet, I cannot find anyone who used it to find the p-values for partial correlation coefficients. Lots of people using it for partial correlation coefficients, but no p-values. Looking at the methods utilized by the package, the problem we are running into, is that the function is based on shrinkage estimators, which makes it hard to calculate p-values.

One paper I found talked about partial correlations as functionally similar to coefficients from multiple linear regression. Given this, I’ve considered some alternatives. I could run a LASSO comparing each TES protein-coding gene to each target tissue gene, and then using the function boot.lasso.proj to get p-values. Alternatively, I could do stepwise forward selection based on BIC values, and then pull out p-values from the final model.

It seems the biggest issues are T1E inflation and overfitting data. I’m not quite sure where this analysis is on the inference/prediction dichotomy, so I’m not quite sure about how seriously we should be concerned about these problems.