Things the Cat’s Cradle package should do:

* Create the transposed Seurat object from a given Seurat object. I have been referring to these two as f and fPrime.
  + Perform the usual scaling, PCA, UMAP, clustering, etc. on fPrime.
* Make various figures, including hoverable versions of UMAP, etc.
* Comparison of gene clusters to pre-fabricated gene sets, e.g., Hallmark, GO, etc.
* Compute mean (scaled) gene expression for each gene cluster / cell cluster pair.
* Cat’s Cradle graphs of mean expression for the gene cluster / cell cluster pairs.
  + This calls for something that will display relationships between cell clusters when two cell clusters share an interest in a common gene cluster.
* Comparison of the DE genes for cell clusters with gene clusters.
* Gene nearest neighbor attribute investigation. We consider the nearest neighbor graph of fPrime together with a list of attributes for some subset of genes. For each gene, we can then get a “neighborhood profile” by considering a neighborhood of that gene and asking how common different attributes are in that neighborhood. This profile can also be based on the entire graph if the edges are weighted in a way which gives edges between distant vertices low weights.