Readme for Supplementary R Codes

The R scripts in this folder are not currently used. Some of them are easy to tell from the file names, but still some of them are not quite clear. Thus, I will note information about those scripts as much as possible. If I do not mention a particular file below, either it has been clear enough of its file names or not being important and less useful.

* “After CCP” series are former versions of main codes “Kmean Pipe”. However, After CCP series also contain the codes that are previously used, such as finding stamps of cluster tree or computing the overlapping genes from parent view (It differs from current child view).
* “HALLMARK” and “3 system” scripts are associated with breast cancer case that I was using HALLMARK gene sets to evaluate it with 3 different type of labeling, patient identity, clinical subtype, and molecular subtype.
* “Compare” and “Ovlap” series are related to the across comparison among output of resulting candidate GO terms using our methods.
* “GOterms\_State\_Correction” series are the scripts I was using to rectify the linage status of kmeans cluster nodes. We once wanted to confirm the inheritance of those cluster nodes, but we hardly can fix the parameters at that time. Thus, I created these series to correct the state of cluster nodes under a certain criteria. Anyway, it seems that Dr. Yeang had implemented his methods and solved the problem. (Notes are written in the script.)
* “MigDB\_Binary” and “NMF” series are the methods we tested previously. If there is anything you want try using NMF method. You can have a check here.
* “Screen” series are former version of main codes “NegSilhoutte Score Pipe”. They both contain silhouette computation part and tsne plotting section.
* Others are much or less clear itself by its file name. You can just survey these if there is anything relevant to what its titles.