**Guide for running the code:**

We provided two programs: (1) Network\_ propagation.r for conducting network propagation; and (2) MSS\_modify.r for identifying gene signatures using netProfiles.

We also provided several sample datasets for running the programs.

***Running the Network\_ propagation.r***

1. Put the input files and the program in a same fold or define the paths for the files in the Network\_ propagation.r
2. Input files are: Interactions matrix (0s and 1s with gene name). 1 is for a known interaction and 0 if not (TCGA-A8-A09R\_founding\_int.csv). Adjacency matrix (TCGA-A8-A09R\_founding\_adj.csv) and the seed file. The seed file is text file containing all functional mutations listed using geneId (TCGA-A8-A09R\_founding\_seeds.csv).
3. Change the path to the files in the first few lines of the R script.
4. Run the program: Example: R --no-save < Network\_ propagation.r

***Running the* MSS\_modify.r**

1. Put the input files and the program in a same fold or define the paths for the files in the MSS\_modify.r
2. Input files are: Propagation file containing all the genes and the samples in the network and their heating scores after normalization (all\_scaled\_prop\_within.csv), the goTerm, dataset file and geneset file which will be used for identifying gene signatures. The dataset file has 4 columns: DatasetId, Sample ID, Group (recurred vs non-recurred group) and order (index in the propagation file). In the geneset file, the first column is the geneset Id and all the other columns are the genes’ row number from the propagation file (all of them are separated by a comma). Also, make sure to change the working directory and all the paths to the files, the dataset number and the minimum p-value and minimum percentage of a geneset to be significant in all random datasets.
3. R --no-save < MSS\_modify.r goTerm DataSetFile GeneSetFile runX

where runX equals to the run number (e.g run1).