**Codes**

* “MainCode.R”

The document is used for searching networks initiated from each gene located on the human functional protein interaction (FI) database.

Input: the gene expression data of breast cancer patients; survival time of breast cancer patients; protein-protein interaction database;

Outut: subnetworks initiated from each gene; corresponding scores of subnetworks.

Other: Specially, the three 100 trials are also implemented through this code with the random permutation of data (please read the “MainCode.R” for detail).

* “SignificanceTest.R”

The document is used for selecting significant survival prognostic network markers (SPNs) through the results of three 100 trials.

Input: the results of three 100 trials; the subnetworks obtained from “MainCode.R” initiated from each gene; corresponding scores of subnetworks;

Output: significant survival prognostic network markers (SPNs).

* “SurvialAnalysis.R”

The document is used for survival analysis of patients based on identified subnetwork markes.

Input: SPNs identifed after the three tests; the gene expression data of breast cancer patients; survival time of breast cancer patients;

Output: the results of survival analysis including the survival curves, the classification of patients, and the P-value of log-rank test.

* “FisherTest.R”

The document is the program used for Fisher exact test in BP sets and KEGG pathway sets.

Input: significant survival prognostic network markers (SPNs); KEGG pathway sets; Biological process (BP) sets;

Output: enrichment of SPNs in KEGG pathway sets and BP sets.

* “MyImageFunction.R”

The document is used for plotting the enrichment results in BP sets and KEGG pathway sets.

Input: the enrichment result of SPNs in BP sets and KEGG sets;

Output: the plots showing the enrichment result of SPNs in BP sets and KEGG sets.

**Datasets used in Codes**

* Training set

The breast cancer patients dataset used as training set can be downloaded from the additional file 1 in paper PMID: 23618380.

* Test set

The breast cancer patients datasets used as test set can be downloaded from the GEO database, referenced by accession number GSE25066.

* “FIdatabase.txt”

The document of human functional protein interaction (FI) database can be downloaded from the paper PMID: 20482850.

* “ProlferationGene.txt”

The document of proliferation genes used for classifying patients into different proliferation tertile can be downloaded from the paper PMID: 23618380.

* “BP.txt” and “KEGG.txt”

The document of biological process sets and the KEGG pathway sets downloaded from the MSigDB database of GSEA website.