**Data Download with CGDSR**

**1. Install and include in the library the cgdsr package and gene symbols**

install.packages("cgdsr")

library("cgdsr")

symbols = as.vector(read.csv("symbols.csv", header = T)[, 1])

**2. CGDS objects for download genetic data**

(a) CGDS(): Create a CGDS connection object

mycgds = CGDS("http://www.cbioportal.org/")

(b) getCancerStudies(): Retrieve a cancer study - ovarian cancer

mycancerstudy = getCancerStudies(mycgds)[155,1]

(c) getGeneticProfiles(): Retrieve a genetic profile - mutation profile

mygeneticprofile = getGeneticProfiles(mycgds,mycancerstudy)[14,1]

(d) getCaseLists(): Retrieve case lists for a specific cancer study

mycaselist = getCaseLists(mycgds,mycancerstudy)[2,1]

(e) getClinicalData(): Retrieve clinical data for a list of cases

myClinicalData = getClinicalData(mycgds,mycaselist)

**3. Download Data - Use gene symbols and getProfileData() function**

mRNA.df = lapply(gene\_name[1:length(symbols)], function(symbol){

df = getProfileData(mycgds, symbol, mygeneticprofile, mycaselist)

return(df)})

**4. Download Data - Check the patients' names**

check.patient.names = sapply(mRNA.df, rownames)

for(i in 1:dim(check.patient.names)[2]){

stopifnot(check.patient.names[,1] == check.patient.names[,i])}

**5. Combine the list and print the final result**

mRNA.comb.list = (do.call(cbind, mRNA.df))

write.csv(mRNA.comb.list, "FinalResult.csv")

**Installing the Bladder Cancer Toy Data**

**1. Install and include in the library the cgdsr package**

install.packages("cgdsr")

library("cgdsr")

symbols = as.vector(read.csv("symbols.csv", header = T)[,1])

**2. CGDS objects to download genetic data**

# (a) CGDS

mycgds = CGDS("http://www.cbioportal.org/")

# (b) Cancer Study

# Bladder cancer

mycancerstudy = getCancerStudies(mycgds)[22,1]

# (c) Genetic Variable

# mRNA Expression z-Scores (RNA Seq V2 RSEM)

mygeneticprofile = getGeneticProfiles(mycgds,mycancerstudy)[5,1]

# (d) Case List

# Tumor Samples with mRNA data (RNA Seq V2)

mycaselist = getCaseLists(mycgds,mycancerstudy)[7,1]

# (e) Clinical Data

myClinicalData = getClinicalData(mycgds,mycaselist)

write.csv(myClinicalData, "Blad\_TCGA\_mRNA\_Clinical\_Data.csv")

# If you can not get clinical data from the above code, use the following website to download.

<http://www.cbioportal.org/study?id=blca_tcga_pub_2017&tab=clinicalData>

**3. Download data**

# Use gene symbols and getProfileData() function

mRNA.df = lapply(gene\_name[1:length(symbols)], function(name){

df = getProfileData(mycgds, name, mygeneticprofile, mycaselist)

return(df)})

**4. Final result**

# (a) Combine the list

mRNA.comb.list = (do.call(cbind,mRNA.df))

# (b) Output the data

write.csv(mRNA.comb.list, "Blad\_TCGA\_mRNA\_RNA\_Seq\_Zscore.csv")

**5. CGDS objects to download genetic data**

# Mutations

mygeneticprofile = getGeneticProfiles(mycgds,mycancerstudy)[8,1]

# All Seq Tumors

mycaselist = getCaseLists(mycgds,mycancerstudy)[4,1] myClinicalData = getClinicalData(mycgds,mycaselist)

write.csv(myClinicalData, "Blad\_TCGA\_mutations\_Clinical\_Data.csv")

muta.df = lapply(gene\_name[1:length(symbols)], function(name){

df = getProfileData(mycgds, name, mygeneticprofile, mycaselist)

return(df)})

muta.comb.list = (do.call(cbind,muta.df))

write.csv(muta.comb.list, "Blad\_TCGA\_mutations.csv")