########### download data from GEO using GEO query ####

source("<https://bioconductor.org/biocLite.R>")

biocLite("GEOquery")

######### download GEO processed data matrix ####

##gse <- getGEO("GSE21653",  destdir = getwd(),GSEMatrix = TRUE)

getGEO("GSE21653",  destdir = getwd(),GSEMatrix = TRUE)  
###show(gse)

#### Download Raw Supplementary data ####

getGEOSuppFiles(GSE45267) ####  series you want to download GSE45267

### set path of series data

setwd( "GSE45267")

# unpack raw files

zipF <- list.files(pattern="RAW.tar", full.names = T)

untar(zipF, exdir = "data")

## unzip or gunzip files

files = list.files("data/", pattern = NULL)

sapply(paste("data", files, sep = "/"), gunzip)

#################### processing of Raw affymetrix array data from GEO ###########

############ using affy package ####

#### install packages ####

source("<https://bioconductor.org/biocLite.R>")

biocLite("GEOquery")

biocLite("affy")

biocLite("oligo")

##### Load packages or libraries

library(GEOquery)

library(affy)

####Set working directory for download

setwd(path)

##### download raw data

getGEOSuppFiles(series\_id) ####  series you want to download GSE45267

### set path of series data

setwd(series)

# unpack raw files

zipF <- list.files(pattern="RAW.tar", full.names = T)

untar(zipF, exdir = "data")

## unzip or gunzip files

files = list.files("data/", pattern = NULL)

sapply(paste("data", files, sep = "/"), gunzip)

### set path for data directory

setwd("data")

#load data

raw.data = ReadAffy()

# perform RMA normalization (or any normalization method depends upon choice and availability in affy package)

data\_rma.norm = rma(raw.data)

############ write data into a matrix file

write.exprs(data\_rma.norm, file="mydata\_rma.txt")

#### command to know annotation database name

annot<-annotation(raw.data)

db <-paste0(annot, ".db" )

#### write name of annotation database in a file

write.table(db, file = "annoatation\_db", quote = FALSE, sep = "\t")

#### install and load annotation database

source("https://bioconductor.org/biocLite.R")

biocLite(db,character.only=TRUE)

library(db,character.only=TRUE)

####### extract genes symbols and IDs corresponds to probe IDs ###

Ids\_gene1<-select(get(db), rownames(raw.data), columns=c("SYMBOL", "ENTREZID", "GENENAME"), keytype="PROBEID")

######## write probe id and corresponding  gene symbols in a files

write.table(Ids\_gene1, file = "Ids\_gene\_affy", quote = FALSE, sep = "\t")

#################### using Oligo packages ###########3

######################### oligo package #########

**library(oligo)**

**library(oligo)**

**library(affycoretools)**

**library(hugene20sttranscriptcluster.db)**

**library(limma)**

# Read in the CEL files in the directory

**celFiles <- list.celfiles()**

**affyRaw <- read.celfiles(celFiles)**

# You might need to install and load a package for the specific array you are using (this example is mouse gene 2.0 ST)

# It may try to load it automatically, but may fail.  Install & load the library manually if this happens.

**library(pd.mogene.2.0.st)**

**eset <- rma(affyRaw)**

# Finally, save the data to an output file to be used by other programs, etc (Data will be log2 transformed and normalized)

**write.exprs(eset,file="rma\_data.txt")**