GSE28619_RMA_normalization

2024-11-28

library(affy) library(GEOquery) library(tidyr) library(oligo) library(dplyr) library(tibble)

get supplementary files

getGEOSuppFiles("GSE28619")

untar files

untar("GSE28619/GSE28619_RAW.tar", exdir = 'data/')

reading in .cel files

raw.data <- ReadAffy(celfile.path = "data/")
raw.data

performing RMA normalization

rma.data <- affy::rma(raw.data) normalized.data <- rma.data

get expression estimates

normalized.expr <- as.data.frame(exprs(normalized.data))

map probe IDs to gene symbols

gse <- getGEO("GSE28619", GSEMatrix = TRUE)

fetch feature data to get ID - gene symbol mapping

feature.data <- gse\protect\T1\textdollarGSE28619_series_matrix.txt.gz@featureData@data

subset

feature.data <- feature.data[,c(1,11)]

normalized.expr <- normalized.expr %>% rownames_to_column(var = 'ID') %>% inner_join(., feature.data, by = 'ID')