Shelby Thomas

Dr. Pawar

BIOL-341-01

September 29, 2023

In-Class-Assignment

The first line in the program is the comment and all comments are started with an “#”. The comment allows the programmer to provide important information such as their name, the date it was created, and their purpose. Next you will put in setwd which is setting the new working directory and directs the R program to files. After that you would put in something like library(affy), this line allows you to load external libraries. In this case affymetrics (affy) is the library. Then you’ll put in ReadAffy, allowing the program to read cel files. Next is rma( eset), eset is a variable, which allows information/ data to be stored in the computer. After that you would want to put in exprs (eset\_Norm) in order to extract expression values and normalize the information/ data. Then you would want to perform an apply function for each data set that you’re collecting, the apply() allows you to perform a function across a data frames rows or columns. Inside the arguments allows you to specify what you want. Then you’ll perform a transpose, which will switch your columns to rows and your rows to columns. Finally, we can try to make fold changes, but before we can do that we have to take the mean of the samples. After we have collected the means we can get the subtraction fold change of our samples. For example if our two samples were treatment and control, then we would perform subtraction fold change for treatment over control. Lastly, we would export our variable as a .csv format file.