

Assignment 1
Deadline - 25 March 2023

- 1) Download any microarray data of interest from GEO with at least 100 samples and two classes.
- 2) After performing EDA and preprocessing, list the data attributes, including pdata and fdata.
- 3) State the effects after completing the log transformation of microarray data.
- 4) Perform differential expression analysis using simple t-test, log fold change, and correct p values using Holm correction. Draw a volcano plot.
- 5) Perform differential expression analysis using the limma package. Draw a volcano plot.
- 6) Choose a significant cutoff based on log(FC) and p-values and justify why you chose those values as the cutoff.
- 7) Perform Enrichment analysis using the set of genes that you have obtained using the Gene set enrichment analysis method.
- 8) Explain the meaning of different parameters in your Gene set enrichment analysis code. Show the results of enrichment in various plots and make observations.
- 9) Observe and analyze the pathways which you obtained.