Project 2 – Signature creation and iLINCS API

This assignment builds upon the R/shiny class and expands the API example.

1. For the assignment use the dataset TCGA_breast_cancer_ERstatus_allGenes.tsv. You may choose to "debug" your code with a smaller dataset TCGA_breast_cancer_ERpositive_vs_ERnegative_PAM50.tsv or TCGA_breast_cancer_LumA_vs_Basal_PAM50.tsv.
2. Your assignment is to develop code using R Shiny to present user interface that allows a user to upload a tsv file, presents an option to split the samples into two groups based on the available metadata and create a signature. The signature is then submitted to the iLincs API which retrieves concordant signatures.
3. Template is provided in the Project 2 github project (https://github.uc.edu/uc-datascience/Project2.git).
4. The template is missing the calculation of the differential expression – please use t-test to calculate t-statistic / p-value.
5. Expand the template to allow users to filter the input file to L1000 genes only (See the include L1000.txt file).
6. Further expand the template to allow users to submit only top 100 differentially expressed genes.
7. Compare results with iLincs
8. Extra credit for a heatmap or other visualizations.

The assignment is due on – March 9, 2023 midnight.

The submission should be zip compressed file named "project2-[*your UC username*].zip" (e.g. "project2-lastnfi.zip") which includes any supporting R files. The zip file should be uploaded canopy. The assignment entry in Canopy will be created shortly.