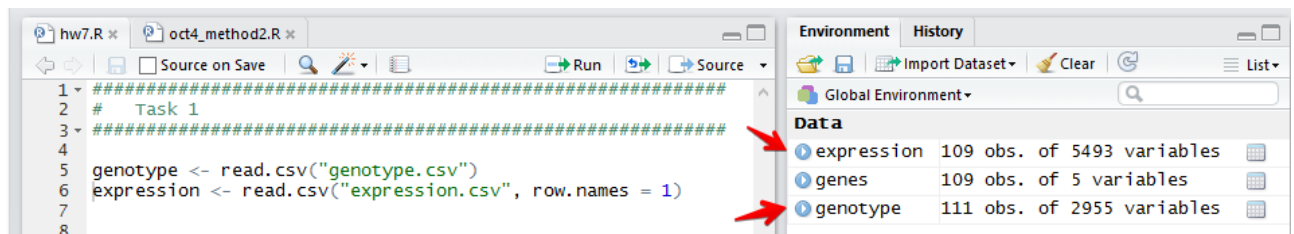


Homework #7

Anastasiia Konoplina

1. *read in the files.*

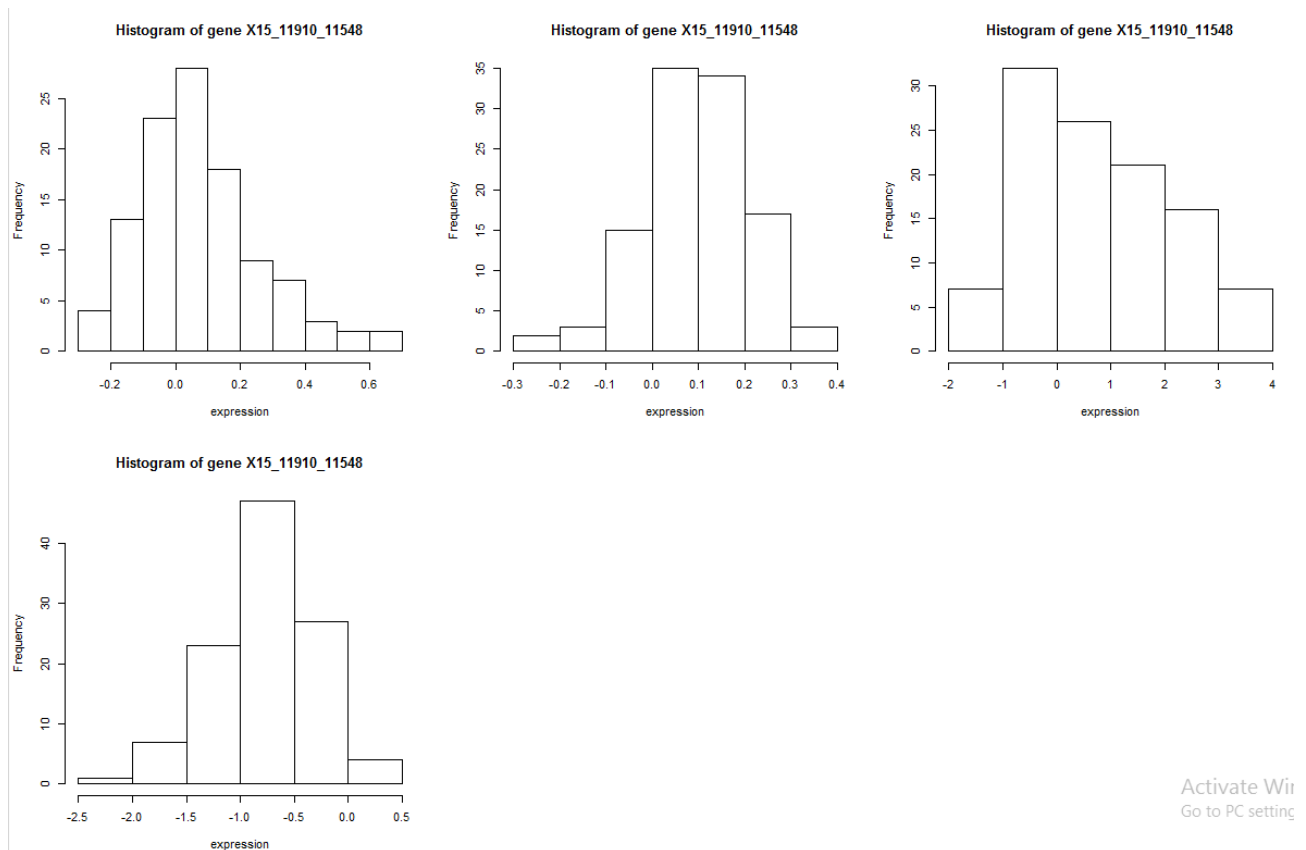
For this homework I used R instead of python.



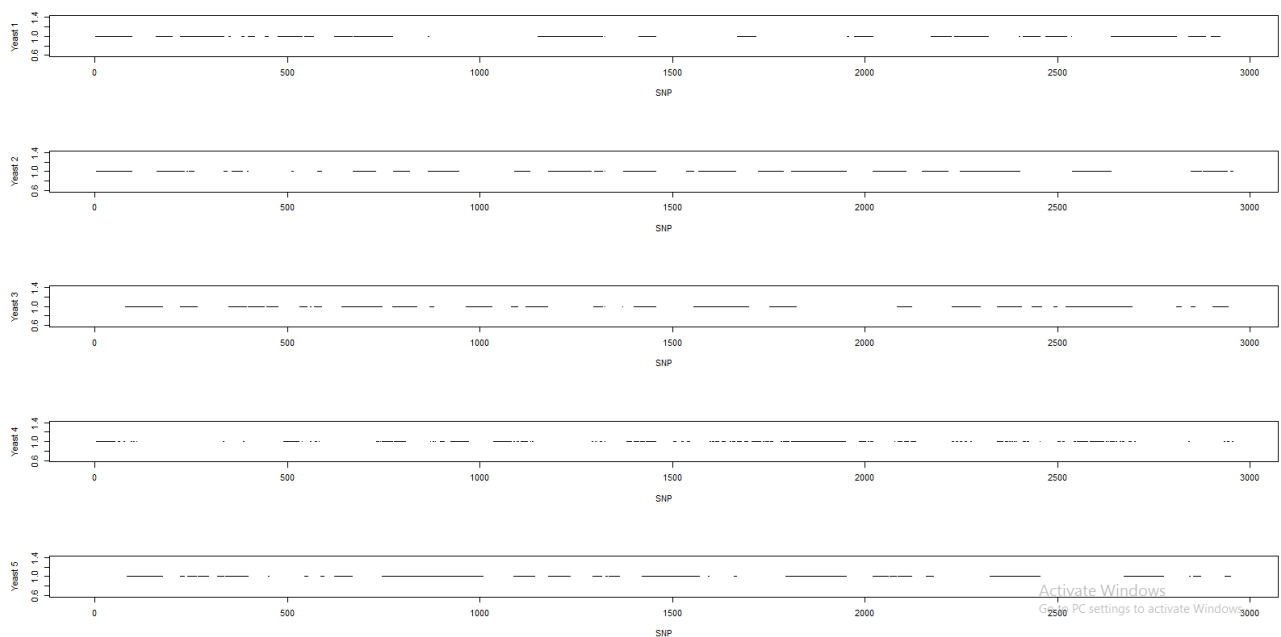
The code of implementation of all the tasks can be found on [Github](#). The code for first task can be find under appropriate comment ("Task 1").

2. *choose 2 - 5 genes (columns in expression.csv file) and plot their expression distribution.*

Code of implementation can be found [here](#) under Task 2



3. choose 2 - 5 individual yeast IDs (rows in genotype.csv file) and plot SNP values.



The code can be found [here](#).