Homework #7

Anastasiia Konoplina

1. read in the files.

For this homework I used R instead of python.

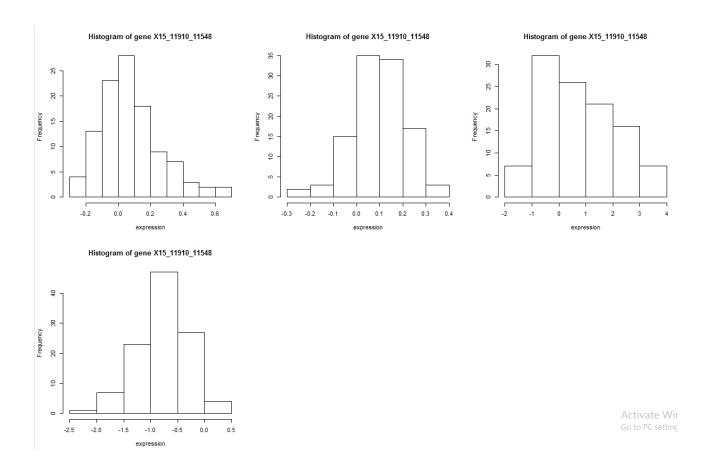
```
Environment History
hw7.R × Oct4_method2.R ×

☐ Import Dataset ▼ 
☐ Clear 
☐
                        Run 🕦 Source 🔻
 Global Environment →
     Task 1
                                              Data
 ① expression 109 obs. of 5493 variables
 genotype <- read.csv("genotype.csv")
genotype <- read.csv("expression.csv", row.names = 1)</pre>
                                              genes
                                                      109 obs. of 5 variables
                                                                         genotype
                                                      111 obs. of 2955 variables 🔠
```

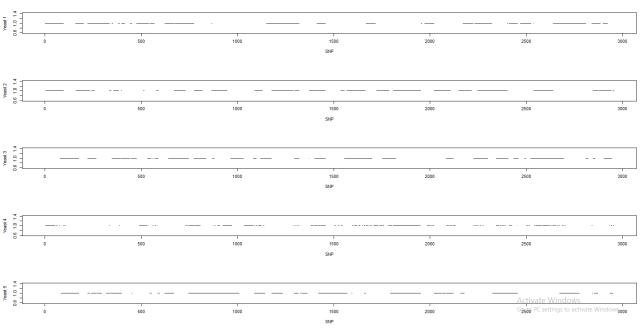
The code of implementation of all the tasks can be found on <u>Github</u>. The code for first task can be find under appropriate comment ("Task 1").

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.