```
# --------------------------------------------------------
# HW1 Problem 4b
#
# Script by: Mohammad Abdulqader
#
# this shell script is used to solve problem 4b in
# the HW1 assignment for BME 230B
# --------------------------------------------------------

let a=0

# create these files
echo log_likelihood > experiment_1.txt
echo log_likelihood > experiment_2.txt
tail -3850 data.txt | awk -F '\t' '{print $1}' > y2.txt

while [ $a -lt 200 ]
do

    # shuf to get 10 random Y values.
    shuf -n 10 y.txt > sample_Y.txt
    shuf -n 10 y2.txt > sample_Y2.txt

    # now run pathy.jar for first experiment
    java -jar pathy.jar sample_Y.txt data.txt modela.bif >> experiment_1.txt

    # now run pathy.jar for second experiment
    java -jar pathy.jar sample_Y2.txt data.txt modela.bif >> experiment_2.txt

    # increment a (number of iterations)
    let a=a+1

done

# remove excess files
rm sample_Y.txt ReadMe.txt YgenesIndScore.txt y2.txt sample_Y2.txt

# done
```

```
# ---------------------------------------------------------
# HW1 Problem 4c
#
# Script by: Mohammad Abdulqader
#
# this shell script is used to solve problem 4c in
# the HW1 assignment for BME 230B
# ---------------------------------------------------------

let a=0

# create these files
echo log_likelihood > experiment_3.txt
echo log_likelihood > experiment_4.txt
tail -3850 data.txt | awk -F '\t' '{print $1}' > y2.txt

while [ $a -lt 200 ]
do

    # shuf to get 10 random Y values.
    shuf -n 10 y.txt > sample_Y.txt
    shuf -n 10 y2.txt > sample_Y2.txt

    # now run pathy.jar for first experiment
    java -jar pathy.jar sample_Y.txt data.txt modelb.bif >> experiment_3.txt

    # now run pathy.jar for second experiment
    java -jar pathy.jar sample_Y2.txt data.txt modelb.bif >> experiment_4.txt

    # increment a (number of iterations)
    let a=a+1

done

# remove excess files
rm sample_Y.txt ReadMe.txt YgenesIndScore.txt y2.txt sample_Y2.txt


# done
```

```r
# --------------------------------------------------------
# HW1 Problem 4
#
# Script by: Mohammad Abdulqader
#
# this R script is used to solve problem 4b and 4c in
# the HW1 assignment for BME 230B
# --------------------------------------------------------

# read data
data1 <-read.csv('experiment_1.txt')
data2 <-read.csv('experiment_2.txt')
data3 <-read.csv('experiment_3.txt')
data4 <-read.csv('experiment_4.txt')


# Model A
pdf('Problem_4b.pdf')
par(mfrow = c(2, 1))

hist(data1$log_likelihood, main='Log-Likelihood from 10 Genes in y.txt - Model A',
     col = 'blue', xlab = 'Log-Likelihood')
hist(data2$log_likelihood, main='Log-Likelihood from 10 Random Genes - Model A',
     col = 'blue', xlab = 'Log-Likelihood')

dev.off()

# Model B
pdf('Problem_4c.pdf')
par(mfrow = c(2, 1))

hist(data3$log_likelihood, main='Log-Likelihood from 10 Genes in y.txt - Model B',
     col = 'blue', xlab = 'Log-Likelihood')
hist(data4$log_likelihood, main='Log-Likelihood from 10 Random Genes - Model B',
     col = 'blue', xlab = 'Log-Likelihood')

dev.off()

par(mfrow = c(1, 1))
```