Module 2 Homework

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Question 1

```r
source("http://www.bioconductor.org/biocLite.R")
biocLite()
library(multtest)
data("golub")
```

(a)

```r
gol.fac <- factor(golub.cl, levels=0:1, labels = c("ALL","AML"))
meanALL <- apply(golub[,gol.fac=="ALL"], 1, mean)
```

(b)

```r
meanAML <- apply(golub[,gol.fac=="AML"], 1, mean)
```

(c)

```r
sortedALL <- order(abs(meanALL), decreasing = TRUE)
print(golub.gnames[sortedALL[1:3],2])
```

```
## [1] "GB DEF = Chromosome 1q subtelomeric sequence D1S553"
## [2] "37 kD laminin receptor precursor/p40 ribosome associated protein gene"
## [3] "RPS14 gene (ribosomal protein S14) extracted from Human ribosomal protein S14 gene"
```

(d)

```r
sortedAML <- order(abs(meanAML), decreasing = TRUE)
print(golub.gnames[sortedAML[1:3],2])
```

```
## [1] "GB DEF = mRNA fragment for elongation factor TU (N-terminus)"
## [2] "GB DEF = HLA-B null allele mRNA"
## [3] "Globin, Beta"
```

Question 2

(a)

```r
AML5 <- golub[1:5, gol.fac=="AML"]
write.csv(AML5, file = "AML5.csv")
```

(b)

```r
ALL5 <- golub[1:5, gol.fac=="ALL"]
write.csv(ALL5, file = "ALL5.txt")
```

(c)

```r
dataC <- golub[100:200, 1]
print(sd(dataC))
```
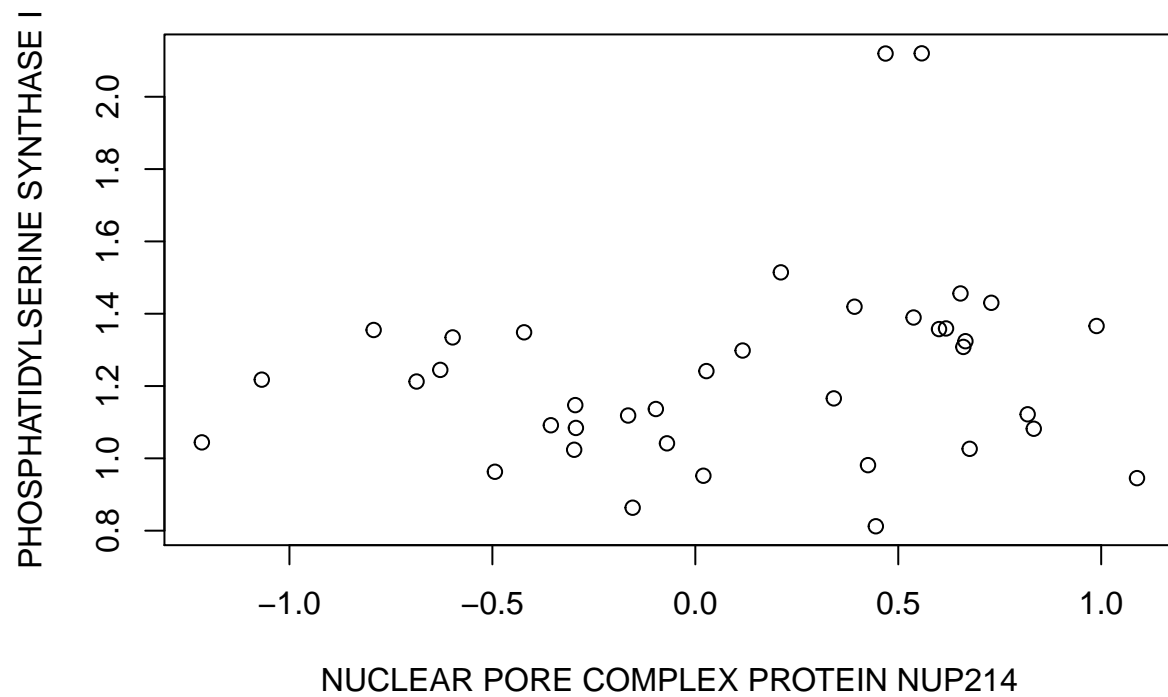
```
## [1] 0.9174976
```

(d)

```r
sdAllPatient <- apply(golub, 1, sd)
print(sum(sdAllPatient>1))
```

```
## [1] 123
```

(e)

```r
g101 <- golub[101,]
g102 <- golub[102,]
gname101 <- golub.gnames[101,2]
gname102 <- golub.gnames[102,2]
plot(g101, g102, xlab = gname101, ylab = gname102)
```
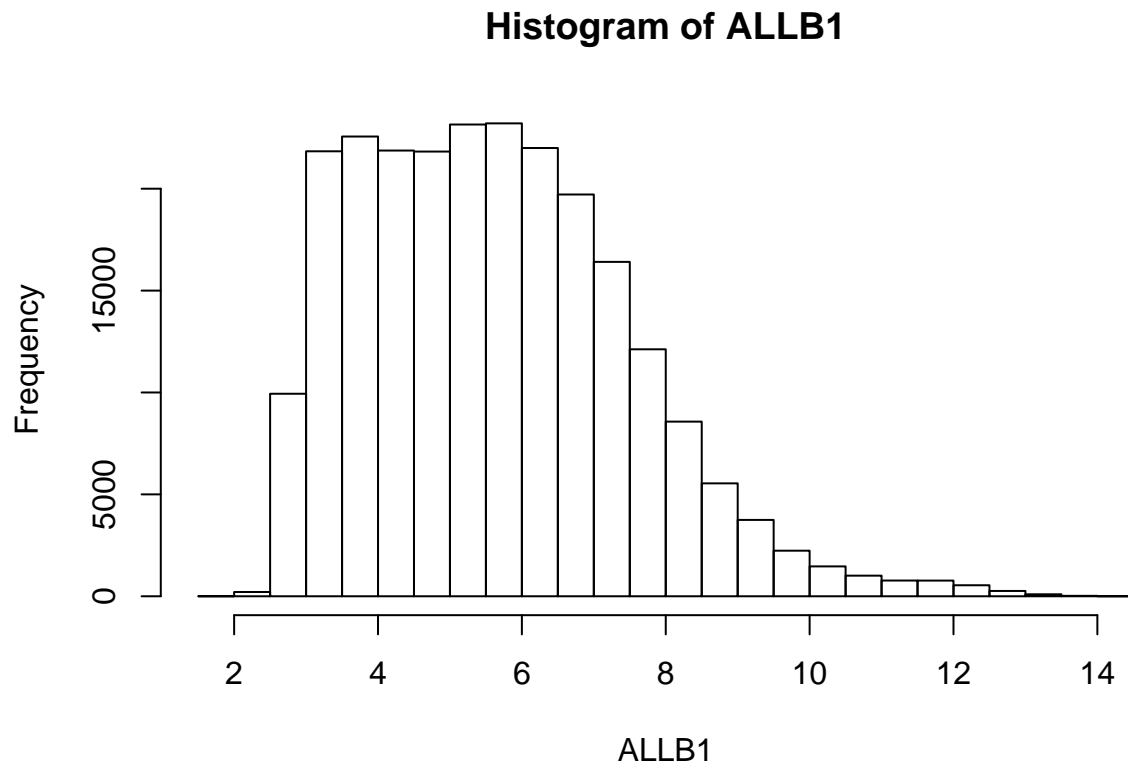
Question 3

```
library(ALL)
data("ALL")
str(ALL)
```

(a)

```
ALLB1 <- exprs(ALL[,ALL$BT=="B1"])
hist(ALLB1)
```

Histogram of ALLB1

(b)

```
meanB1 <- apply(ALLB1, 1, mean)
```

(c)

```
sortedMeanB1 <- order(abs(meanB1), decreasing = TRUE)
print(meanB1[sortedMeanB1[1:3]])
```

```
## AFFX-hum_alu_at        31962_at        31957_r_at
##        13.41648        13.16671           13.15995
```

Question 4

(a)

```
data("trees")
print(typeof(trees))
```

```
## [1] "list"
```

(b)

```
plot(trees$Girth,trees$Height, col = "blue", type = "o", pch = "+", xlab = "Girth", ylab= "Height&Valume
lines(trees$Girth, trees$Volume, col = "red", type = "o")
legend("bottomright", c("Height", "Valume"), col = c("blue", "red"), lty = c(1,1))
```