```
#1
library(multtest)
data(golub)
#A
gene_name <- "MSN Moesin"
gene_row_index <- grep(gene_name, golub.gnames[, 2])

if (length(gene_row_index) == 0) {
  cat("Gene", gene_name, "not found in golub.gnames.\n")
} else {
  cat("Gene", gene_name, "found at row index:", gene_row_index, "\n")

  gene_expression <- golub[gene_row_index, ]
  effect_size_a <- mean(gene_expression) / sd(gene_expression)
  cat("Effect size for gene MSN Moesin:", effect_size_a, "\n")
}
```

Gene MSN Moesin found at row index: 969
Effect size for gene MSN Moesin: 6.475913

```
#B
if (!exists("gol.fac")) {
  gol.fac <- factor(golub.cl, levels = 0:1, labels = c("ALL", "AML"))
}
effect_size_b <- apply(golub[1:2000, gol.fac == "AML"], 2, function(x)
mean(x, na.rm = TRUE) / sd(x, na.rm = TRUE))
print(effect_size_b)


#C
hist(effect_size_b, main = "Histogram of Effect Sizes for AML Patients",
xlab = "Effect Size")
```
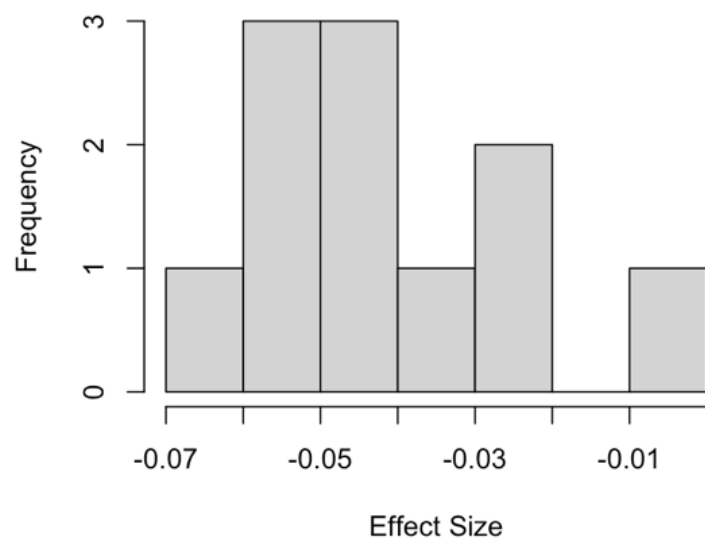
Histogram of Effect Sizes for AML Patients


```
#D
top_3_indices <- order(effect_size_b, decreasing = TRUE)[1:3]
top_3_gene_names <- golub.gnames[top_3_indices, 2]
cat("Top 3 largest effect sizes:\n", effect_size_b[top_3_indices], "\n")
cat("Corresponding gene names:\n", top_3_gene_names, "\n")
```

Top 3 largest effect sizes:
 -0.0024024 -0.02142832 -0.02593292

Corresponding gene names:
AFFX-HUMRGE/M10098_5_at (endogenous control)
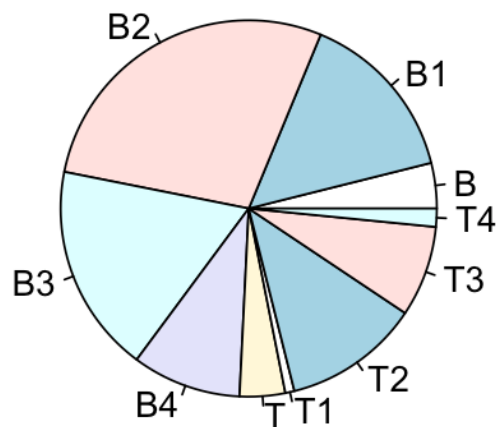AFFX-HUMGAPDH/M33197_5_at (endogenous control)
AFFX-HUMISGF3A/M97935_3_at (endogenous control)

```
rm(list=ls())
#2
library(ALL)
data(ALL)
#A
table_data <- table(ALL$BT)
print(table_data)
```
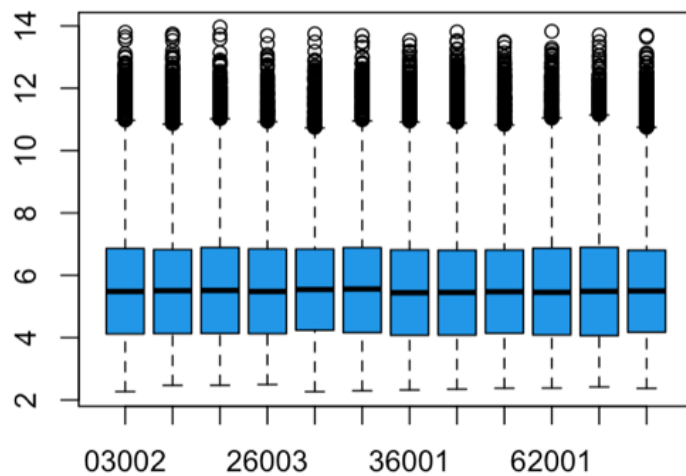
```
pie(table_data, labels = names(table_data), main = "Leukemia Patients
Disease Type/Stage")
```

Leukemia Patients Disease Type/Stage


```
#B
B4exp<-exprs(ALL[,ALL$BT=="B4"])
boxplot(B4exp, col = 12, main = "Gene Expressions for Patients in
Disease Stage B4")
```

Gene Expressions for Patients in Disease Stage


```
#C
patient_mean <- apply(B4exp, 2, mean)
print(patient_mean)
```

03002   24019   24022   26003   28003   28019   36001   43007   43012
5.633270 5.622644 5.658085 5.626134 5.664679 5.656176 5.612269 5.606912
5.608924
  62001   62002   62003
5.624548 5.635707 5.630090

```
rm(list=ls())
#3
library(MASS)
data(cats)
#A
male_cats <- sum(cats$Sex == "M" & cats$Bwt > 3)
cat("Number of male cats weighing more than 3 kg:", male_cats, "\n")
```

Number of male cats weighing more than 3 kg: 36

#B

```
female_cats <- subset(cats, Sex == "F", select = c(Bwt, Hwt))
write.csv(female_cats, file = "CatsF.csv", row.names = FALSE)
cat("Data for female cats saved to CatsF.csv\n")
```

#C

```
plot(cats$Hwt, cats$Bwt, col = ifelse(cats$Sex == "M", "purple", "red"),
pch = ifelse(cats$Sex == "M",18, 8),
    xlab = "Heart weight (g)", ylab = "Body weight (kg)")

legend("topleft",c("Male", "Female"), col = c("purple", "red"), pch =
c(18, 8))
```