

# Exercise 8

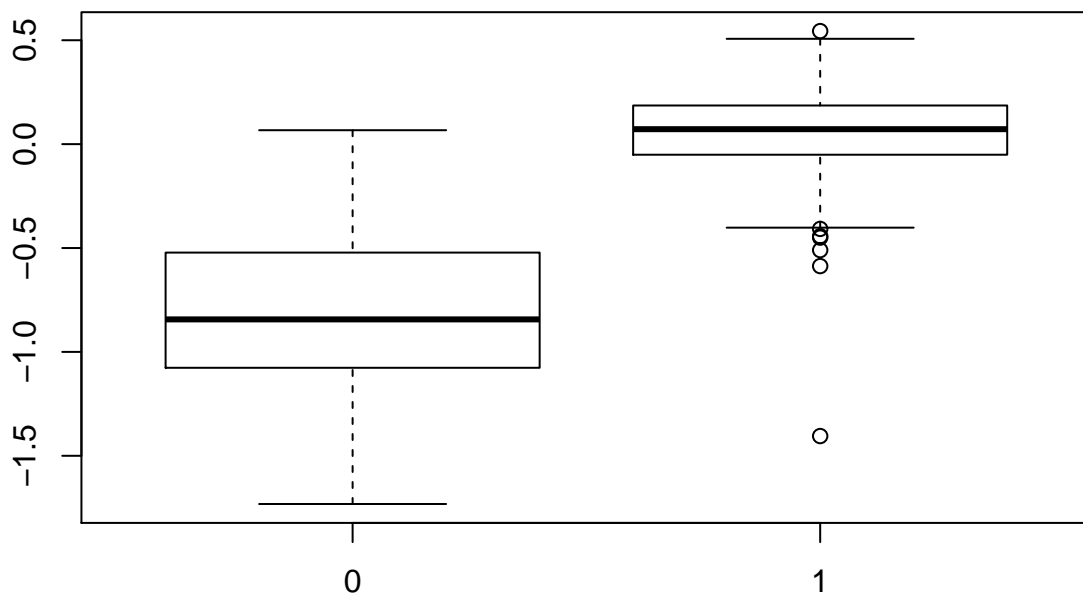
*Your Name*

*Last modified: 22 Dec 2016*

```
genes <- read.delim("gene.description.txt")
subjects <- read.delim("cancer.patients.txt")
evals <- read.delim("gene.expression.txt",stringsAsFactors = FALSE)
```

```
ind <- match("GATA3", genes[,2])
probe <- genes[ind,1]
genevals <- evals[match(probe,rownames(evals)),]
```

```
boxplot(as.numeric(genevals)~factor(subjects$er))
```



```
t.test(as.numeric(genevals)~factor(subjects$er))
```

```
##
##  Welch Two Sample t-test
##
## data:  as.numeric(genevals) by factor(subjects$er)
## t = -19.204, df = 106.52, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.9439213 -0.7672735
```

```
## sample estimates:  
## mean in group 0 mean in group 1  
##      -0.79421591      0.06138153
```