

# Exercise 9

*Your Name*

*06 Sep 2016*

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

```
chr8Genes <- genes[genes$Chromosome=="chr8",]
head(chr8Genes)
```

##	probe	HUGO.gene.symbol	Chromosome	Start
##	Contig29827_RC	Contig29827_RC	FUT10	chr8 33228344
##	NM_003046	NM_003046	SLC7A2	chr8 17396286
##	Contig55940_RC	Contig55940_RC	CYHR1	chr8 145675315
##	NM_004133	NM_004133	HNF4G	chr8 76452203
##	NM_004374	NM_004374	COX6C	chr8 100890223
##	AF052142	AF052142	NCALD	chr8 102698770

```
chr8GenesOrd <- chr8Genes[order(chr8Genes$Start),]
head(chr8GenesOrd)
```

##	probe	HUGO.gene.symbol	Chromosome	Start
##	NM_004745	NM_004745	DLGAP2	chr8 1449569
##	NM_018941	NM_018941	CLN8	chr8 1711870
##	AL117604	AL117604	DLC1	chr8 12940872
##	NM_003046	NM_003046	SLC7A2	chr8 17396286
##	Contig58301_RC	Contig58301_RC	SLC7A2	chr8 17396286
##	NM_000662	NM_000662	NAT1	chr8 18067618

```
chr8Expression <- evals[match(chr8GenesOrd$probe, rownames(evals)),]
```

- Create a for loop to perform to test if the expression level of each gene on chromosome 8 is significantly different between ER positive and negative samples

```
ngenes <- nrow(chr8Expression)
pvals <- NULL
for(i in 1:ngenes) {
  tmp <- t.test(as.numeric(chr8Expression[i,]) ~ subjects$er)
  pvals[i] <- tmp$p.value
}
pvals
```

```
## [1] 5.464153e-03 2.408701e-01 5.842811e-05 6.611391e-05 2.590922e-57
## [6] 2.564435e-69 9.382548e-01 7.555477e-01 7.955434e-01 2.088048e-01
## [11] 2.695280e-01 5.440249e-01 3.764754e-02 2.297528e-37 2.077849e-04
## [16] 2.188104e-03 1.340043e-12 2.169950e-08
```

```
table(pvals < 0.05)
```

```
##  
## FALSE  TRUE  
##      7    11
```

```
sum(pvals < 0.05)
```

```
## [1] 11
```