
Solutions - functions

A.

```
geneExpression<-read.table("expression.txt",skip=3,header =T)

paste("s",1:9,sep="")

colnames(geneExpression)<-paste("s",1:9,sep="")

rowMeans(geneExpression)

apply(geneExpression,1,min)

apply(geneExpression,1,max)

colMeans(geneExpression)

kind<-factor(rep(c("before","after","control"),each=3))

tapply(geneExpression$s1,kind,mean) )

#If you tried to do it this way:
tapply(geneExpression[1,],kind,mean)
#It didn't work. Why? check the class of geneExpression[1,]
#geneExpression[1,] is a data frame. We need to convert it to a numeric vector.

tapply(as.numeric(geneExpression[1,]),kind,mean)

apply(geneExpression,1,function(x){tapply(x,kind,mean)})
```

B.

```
Trial<-data.frame(PatientAge=sample(2:8,44,replace=TRUE), TesterName=rep(c("Koval","Schmidt"),
data(bacteria, package="MASS")

bacteria[bacteria$week==11,]

bacteriaTrial<-cbind(bacteria[bacteria$week==11,],Trial)

tapply(bacteriaTrial$PatientAge,bacteriaTrial$shilo,mean)

tapply(bacteriaTrial$PatientAge,bacteriaTrial$Tester,range)

tapply(bacteriaTrial$PatientAge,bacteriaTrial$strt,median)

write.table(bacteriaTrial,quote=F,file="bacteriaTrial.txt")
```

Appendix

----- How I constructed geneExpression

```
geneExpression <- data.frame ( t( sapply(1:30, function(x) rnorm(9, runif(1)*10, runif(1)))))

names (geneExpression) <- paste ( rep ("Sample",9), 1:9, sep="")

add <- cbind(sample(c(-1,1),30,replace=T)*t(sapply(sample(seq(0,3,by=0.2),30,replace=T),function(x){x*
x*c(1,1.1,0.8)})),
sample(c(-1,1),30,replace=T)*t(sapply(sample(seq(0,3,by=0.2),30,replace=T),function(x){x*
```

```
sample(c(-1,1),30,replace=T)*t(sapply(sample(seq(0,3,by=0.2),30,replace=T),function(x){x*  
geneExpression<-abs(geneExpression+add)
```
