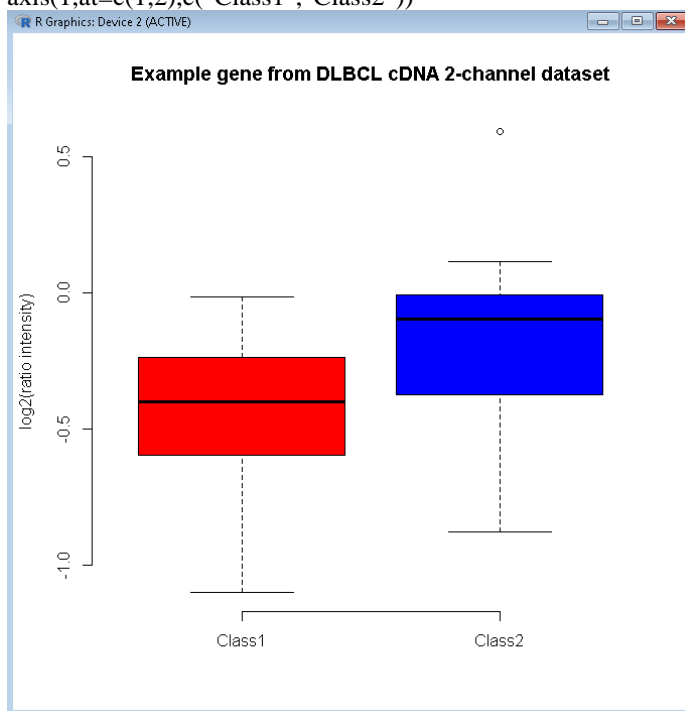


```

1.
2. data <- read.table("eisen.txt",header=T, na.strings="NA", blank.lines.skip=F, row.names=1)
3. classes <- read.table("eisenClasses.txt", header=T)
4. cl <- as.character(classes[,2])
   dat <- data[,cl]
   gc <- cl[1:19]
   act <- cl[20:39]

5. x <- as.numeric(dat[3000,gc])
   y <- as.numeric(dat[3000,act])
   x <- x[!is.na(x)]
   y <- y[!is.na(y)]
   boxplot(x,y,col=c("red","blue"),main="Example gene from DLBCL cDNA 2-channel
dataset",axes=F,ylab="log2(ratio intensity)")
   axis(2)
   axis(1,at=c(1,2),c("Class1","Class2"))

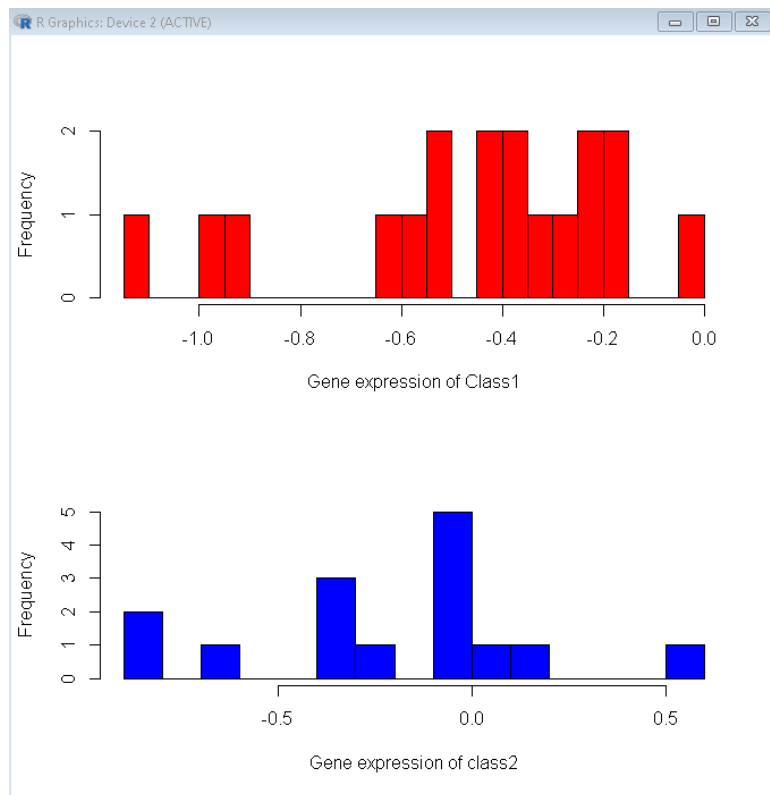
```



```

par(mfrow=c(2,1))
hist(x,n=20, col="red", border="black", main="", xlab="Gene expression of Class1")
hist(y,n=20, col="blue", border="black", main="", xlab="Gene expression of class2")

```



```
6. > nx <- length(x)
> ny <- length(y)
> pool.var <- (((nx-1)*var(x)) + ((ny-1)*var(y)))/(nx+ny-2)
dif.1.5fold <- log2(1.5)/sqrt(pool.var)
sample <- pwr.t.test(d=dif.1.5fold,sig.level=.01,power=0.8,type="two.sample")
```

```
Two-sample t test power calculation
```

```
      n = 9.721124
      d = 1.715853
sig.level = 0.01
power = 0.8
alternative = two.sided
```

NOTE: n is number in *each* group

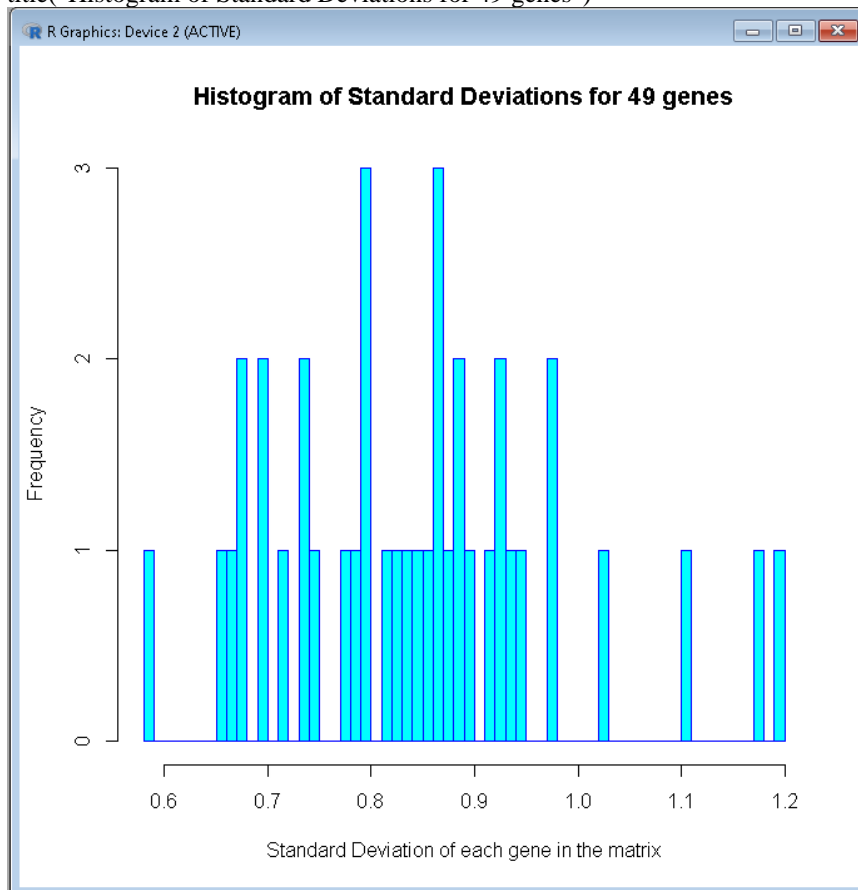
```
7. dif <- abs(mean(x)-mean(y))/sqrt(pool.var)
Sample2 <- pwr.t.test(d=dif,sig.level=.01,power=0.8,type="two.sample")
```

```
Two-sample t test power calculation
```

```
      n = 45.60501
      d = 0.7292759
sig.level = 0.01
power = 0.8
alternative = two.sided
```

NOTE: n is number in *each* group

```
8. sapply(dat,sd,na.rm=T)\
hist(sapply(dat,sd,na.rm=T),n=49, col="cyan", border="blue", main="", xlab="Standard Deviation of each gene in
the matrix")
title("Histogram of Standard Deviations for 49 genes")
```



```
9.
sd2<-sapply(dat,sd,na.rm=T)
ssize.plot(all.size, lwd=2, col="magenta", xlim=c(1,39))
xmax <- par("usr")[2]-1;
ymin <- par("usr")[3] + 0.05
legend(x=xmax, y=ymin, legend= strsplit( paste("fold change=",fold.change,",", "alpha=", sig.level, ",",
"power=",power,",", "# genes=", length(sd2), sep="), ", " )[[1]], xjust=1, yjust=0, cex=1.0)
title("Sample Size to Detect 2-Fold Change")
```

Sample Size to Detect 2-Fold Change