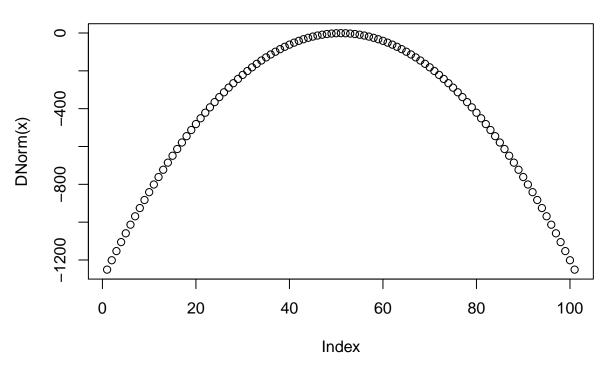
Homework 11

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Writing functions for equations

```
library(ggplot2)
library(TeachingDemos)
char2seed("Cruel April")
# function: DNorm
# DNorm dist
\# input: x is the vector of quantiles, m = vector of means, sd = vector of standard deviations
# output: S is a vector of species richness values
DNorm <- function(x=-50:50, m=0, sd=1){
 dNorm <- dnorm(x, mean=m,sd=sd,log = TRUE)</pre>
return(dNorm)
head(DNorm())
## [1] -1250.919 -1201.419 -1152.919 -1105.419 -1058.919 -1013.419
# function: DNormPlot
# plot DNorm distribution
# input:
# output: smoothed curve with parameters in graph
#-----
DNormPlot <- function(x=-50:50,m=0,sd=1) {
 plot(DNorm(x),main = "log { Normal density }")
 return()
}
DNormPlot()
```

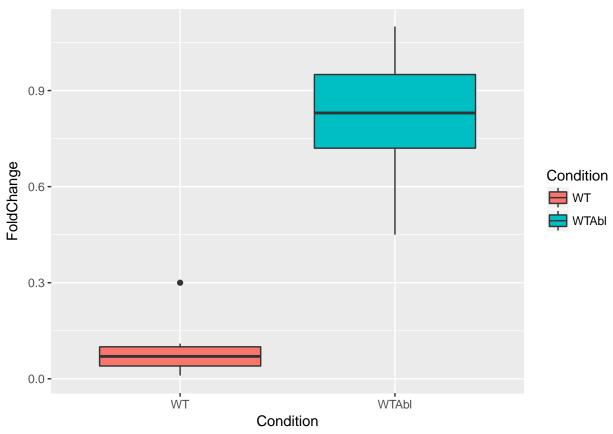
log { Normal density }



NULL

Randomization test

```
# Function: readData
# read in data frame
# input: file name (or nothing for the demo)
# output: 3-column data frame of observed data (ID, xVar, yVar)
readData <- function(z=NULL) {</pre>
 if(is.null(z)){
   d <- read.table(file="testData.csv",header=TRUE,sep=",")</pre>
 }
 return(d)
# Function: plotData
# ggplot graph
# input: list of observed metric
# output: ggplot graph
plotData <- function(z=NULL) {</pre>
 if(is.null(z)){
   d <- read.table(file="testData.csv",header=TRUE,sep=",")</pre>
```



```
. <- aov(FoldChange~Condition,data=d)
 . <- summary(.)[[1]][["Pr(>F)"]][[1]]
 pVal <- .
 return(pVal)
getMetric()
## [1] 1.522155e-08
# Function: shuffleData
# randomize data for variance analysis
# input: 2-column data frame (xVar, yVar)
# output: 2-column data frame (xVar, yVar)
shuffleData <- function(z=NULL) {</pre>
 if(is.null(z)){
  z <- read.table(file="testData.csv",header=TRUE,sep=",")</pre>
  z[,2] \leftarrow sample(z[,2])
 return(z)
}
shuffleData()
    Condition FoldChange
##
## 1
       WT
                1.10
## 2
         WT
                0.83
         WT
## 3
                0.01
## 4
        WT
               0.95
## 5
        WT
               0.87
         WT
               0.06
## 6
## 7
        WT
               0.69
## 8
        WT
               0.76
## 9
         WT
               0.72
## 10
      WTAbl
               0.09
## 11
               0.30
      WTAbl
## 12
      WTAbl
               0.45
## 13
      WTAbl
               0.02
## 14
       WTAbl
                0.07
## 15
      WTAbl
               0.10
                0.04
## 16
      WTAbl
## 17
       WTAbl
                 0.11
## 18
       WTAbl
                 0.98
# Function: getPVal
# calculate p-value for observed, simulated data
# input: list of observed metric and vector of simulated metric
# output: lower, upper tail probability vector
```

```
getPVal <- function(z=NULL) {</pre>
 if(is.null(z)){
   z <- list(x0bs=runif(1),xSim=runif(1000))</pre>
 pLower <- mean(z[[2]]<=z[[1]]) # mean of the second element (vector), when it's less than or equal to
 pUpper \leftarrow mean(z[[2]])=z[[1]])
 return(c(pL=pLower,pU=pUpper))
getPVal()
## pL pU
## 0.054 0.946
# Function: plotRanTest
# ggplot graph
# input: list of observed metric and vector of simulated metric
# output: ggplot graph
plotRanTest <- function(z=NULL) {</pre>
 if(is.null(z)){
   z <- list(x0bs=runif(1),xSim=runif(1000))</pre>
 dF <- data.frame(ID=seq_along(z[[2]]),</pre>
                xSim=z[[2]])
 p1 <- ggplot(data=dF,mapping=aes(x=xSim))</pre>
 p1 + geom_histogram(mapping=aes(fill=I("goldenrod"),color=I("black"))) + geom_vline(aes(xintercept=z[
 return(print(p1))
# Main body of the code
nSim <- 1000 # number of simulations
xSim <- rep(NA,nSim)
d <- readData()</pre>
x0bs <- getMetric(d)</pre>
x0bs
## [1] 1.522155e-08
for(i in seq_len(nSim)){
 xSim[i] <- getMetricRandom()</pre>
}
```

```
slopes <- list(x0bs,xSim)
getPVal(slopes)</pre>
```

pL pU ## 0 1