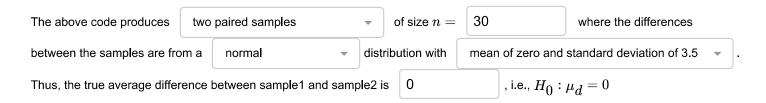
Run the following codes in R.

```
set.seed(121) \\ sample1 <- rnorm(30, 185, 8) \\ sample2 <- sample1 - rnorm(30, 0, 3.5) \\ theData <- data.frame(values = c(sample1, sample2), group = rep(c(1,2), each=30), id = rep(c(1:30), times=2)) \\ View(theData) \\ with(theData, hist(values[group==1] - values[group==2])) \\
```



Suppose we just had the Data dataset without knowledge of the population this data came from. The permutation test of the stated null hypothesis would then be coded in R as:

```
t.test(values ~ group, data = theData, paired = TRUE, mu = 0)
myTest <-
observedTestStat <- myTest$
                                statistic
N \le 2000
permutedTestStats <- rep(NA, N)
for (i in 1:N) {
                      sample(x=c(1,-1), size=30, replace=TRUE)
  permutedData <-
  permutedTest <-
                     with(theData, t.test(permutedData*(values[group==1] - values[group==2]), mu = 0))
  permutedTestStats[i] <- permutedTest$
                                            statistic
}
hist(permutedTestStats)
abline(v=observedTestStat)
sum(permutedTestStats >= observedTestStat)/N
sum(permutedTestStats <= observedTestStat)/N
```

Run the above code in R by copying and pasting the code below into a new R Chunk in your ClassNotes.Rmd file. Then type in the correct answers from above by hand into the places with "..." in the code below.

IMPORTANT: to match the answer key for the questions below, your R-Chunk you add to your ClassNotes.Rmd file will need to use set.seed() as follows. This ensures everyone gets the same "random" data each time.

```
"``{r, eval=FALSE}
# Create the data:
set.seed(121)
sample1 <- rnorm(30, 185, 8)
sample2 <- sample1 - rnorm(30, 0, 3.5)
```

```
the Data <- data.frame(values = c(sample1, sample2), group = rep(c(1,2), each=30), id = rep(c(1:30), times=2))
View(theData)
with(theData, hist(values[group==1] - values[group==2]))
# Perform the permutation test:
myTest <- ...
observedTestStat <- myTest$...
N <- 2000
permutedTestStats <- rep(NA, N)
for (i in 1:N)
 permutedData <- ...
 permutedTest <- ...
  permutedTestStats[i] <- permutedTest$...</pre>
hist(permutedTestStats)
abline(v=observedTestStat)
sum(permutedTestStats >= observedTestStat)/N
sum(permutedTestStats <= observedTestStat)/N</pre>
observedTestStat =
                      -0.5384
                                         (Round to 4 decimal places.)
                           0.69
"Greater than" p-value =
                                              (Round to 2 decimal places.)
"Less than" p-value =
                        0.31
                                           (Round to 2 decimal places.)
                        0.62
"Two-sided" p-value =
                                           (Round to 2 decimal places.)
```