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]))
```

The above code produces two paired samples ▾ of size $n =$ 30 where the differences between the samples are from a normal ▾ distribution with mean of zero and standard deviation of 3.5 ▾ . Thus, the true average difference between sample1 and sample2 is 0 , i.e., $H_0 : \mu_d = 0$

Suppose we just had theData 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:

```
myTest <- t.test(values ~ group, data = theData, paired = TRUE, mu = 0) ▾
observedTestStat <- myTest$ statistic ▾

N <- 2000
permutedTestStats <-  rep(NA, N)
for  (i in 1:N ) {
  permutedData <- sample(x=c(1,-1), size=30, replace=TRUE) ▾
  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)
~~~~

~~~
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]))


# Perform the permutation test:
myTest <-  ...
observedTestStat <- myTest$...


N <- 2000
permutedTestStats <-  rep(NA, N)
for  (i in 1:N ) {
  permutedData <- ...
  permutedTest <- ...
  permutedTestStats[i]  <-  permutedTest$...
}
hist(permutedTestStats)
abline(v=observedTestStat)
sum(permutedTestStats >= observedTestStat)/N
sum(permutedTestStats <= observedTestStat)/N
```
~~~

observedTestStat = -0.5384 (Round to 4 decimal places.)

"Greater than" p-value = 0.69 (Round to 2 decimal places.)

"Less than" p-value = 0.31 (Round to 2 decimal places.)

"Two-sided" p-value = 0.62 (Round to 2 decimal places.)