# Homework 5

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# 7/10/2021

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## Questions for this Week

The homework for week five is exercises 6 through 10 on pages 86 and 87.

# Question 6

The PlantGrowth data set contains three different groups, with each representing various plant food diets (you may need to type data(PlantGrowth) to activate it). The group labeled "ctrl" is the control group, while "trt1" and "trt2" are different types of experimental treatment.

As a reminder, this subsetting statement accesses the weight data for the control group: PlantGrowth\$weight[PlantGrowth\$gand this subsetting statement accesses the weight data for treatment group 1: PlantGrowth\$weight[PlantGrowth\$group=="t

#### Plant Growth T-Test

Run a t-test to compare the means of the control group ("ctrl") and treatment group 1 ("trt1") in the PlantGrowth data.

```
data(PlantGrowth)

dfCtrl <- PlantGrowth$weight[PlantGrowth$group=="ctrl"]

dfTrt1 <- PlantGrowth$weight[PlantGrowth$group=="trt1"]

# CT Test
t.test(dfCtrl,dfTrt1)</pre>
```

```
##
## Welch Two Sample t-test
##
## data: dfCtrl and dfTrt1
## t = 1.1913, df = 16.524, p-value = 0.2504
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.2875162 1.0295162
## sample estimates:
## mean of x mean of y
## 5.032 4.661
```

#### T-Test Results

Report the observed value of t, the degrees of freedom, and the p-value associated with the observed value.

- t = 1.1913
- degrees of freedom = 16.524
- p-value = 0.25

## Hypothesis testing

Assuming an alpha threshold of .05, decide whether you should reject the null hypothesis or fail to reject the null hypothesis.

- Comparing the Control and Treatment 1, I would reject the null hypothesis as the p-values are less than the alpha at 0.05.
- In addition due to the alpha crossing 0 I would reject the null hpyothesis.

#### Confidence Interval

In addition, report the upper and lower bound of the confidence interval.

Upper Bound: -0.2875162Lower bound: 1.0295162Mean Difference: 0.371

## Question 7

### **BEST** Compare

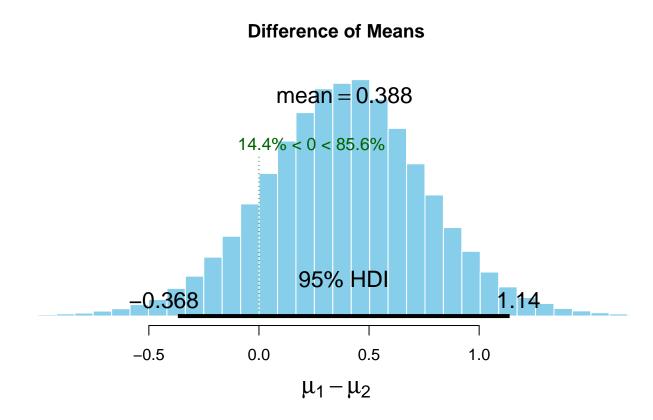
Install and library() the BEST package. Note that you may need to install a program called JAGS onto your computer before you try to install the BEST package inside of R. Use BESTmcmc() to compare the PlantGrowth control group ("ctrl") to treatment group 1 ("trtl").

```
# install.packages("rjags")
# install.packages("BEST")
library(BEST)
## Loading required package: HDInterval
BEST Output <- BESTmcmc(dfCtrl,dfTrt1)</pre>
## Waiting for parallel processing to complete...
## done.
BEST_Output
## MCMC fit results for BEST analysis:
## 100002 simulations saved.
##
                          median HDIlo
                                          HDIup Rhat n.eff
                       sd
                           5.0283 4.5772
## mu1
           5.0281
                  0.2260
                                          5.476
                                                    1 57121
           4.6399 0.3059
                          4.6366 4.0413
                                          5.262
                                                    1 55525
## mu2
          34.2152 29.2575 25.7591 1.1812 92.728
                                                    1 21491
          0.6619 0.2049 0.6228 0.3456
                                                    1 24568
## sigma2 0.8948 0.2770 0.8436 0.4647
                                         1.466
                                                    1 26950
## 'HDIlo' and 'HDIup' are the limits of a 95% HDI credible interval.
## 'Rhat' is the potential scale reduction factor (at convergence, Rhat=1).
## 'n.eff' is a crude measure of effective sample size.
```

#### Plot BEST

Plot the result and document the boundary values that BESTmcmc() calculated for the HDI.

plot(BEST\_Output)



### **Brief Definition**

Write a brief definition of the meaning of the HDI and interpret the results from this comparison. - HDI: Also known as High Density Interval, which means that the difference in the population mean between the two groups falls between the upper and lower bound of the HDI. - Interpreting the Results: There is a 95% chance that the population mean difference of 0.383 for the control and test food diet falls within -0.367 and 1.13. Unlike the t.test ran above, the MCMC gives a clearer understanding of the true interval of the population mean. Where if we were to run the test 100 times the population mean will fall within the 95% of the intervals. - In addition about 85% of the food diet estimates are higher than 0. Meaning that typically the diet in group 1 is more effective in increasing the weight of plant.

# Question 8

Compare and contrast the results of Exercise 6 and Exercise 7. You have three types of evidence: the results of the null hypothesis test, the confidence interval, and the HDI from the BESTmcmc() procedure. Each one adds something, in turn, to the understanding of the difference between groups. Explain what information each test provides about the comparison of the control group ("ctrl") and the treatment group 1 ("trtl").

- After reviewing the data we really can not tell which one to prefer because the confidence interval crosses 0.
- Interpreting the results we see that the test group was less successful in increasing the plants weight. The test group was 0.371 less than the control group.
- Again due to the population mean bounds or bands of uncertainty in the MCMC crossing 0 we can not tell which one to prefer.
- In exercise 7 group 1's treatment has a little more success than looking at just the confidence interval, but in both cases the treatment produced less weight.
- Therefore we failed to reject the null hypothesis and can suggest that treatment 1 is not better over the control group.

## Question 9

Using the same PlantGrowth data set, compare the "ctrl" group to the "trt2" group. Use all of the methods described earlier (t-test, confidence interval, and Bayesian method) and explain all of the results.

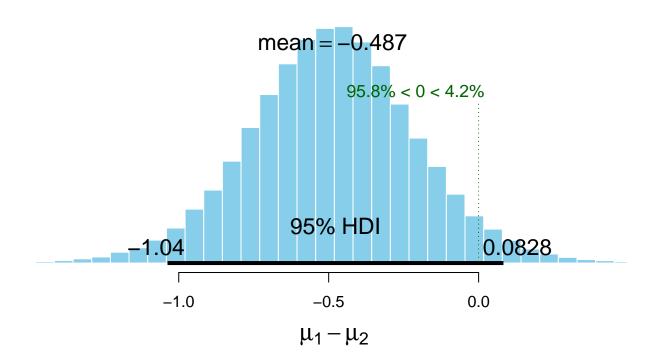
```
dfCtrl <- PlantGrowth$weight[PlantGrowth$group=="ctrl"]</pre>
dfTrt2 <- PlantGrowth$weight[PlantGrowth$group=="trt2"]</pre>
# Control Group
t.test(dfCtrl,dfTrt2)
##
##
   Welch Two Sample t-test
##
## data: dfCtrl and dfTrt2
## t = -2.134, df = 16.786, p-value = 0.0479
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.98287213 -0.00512787
## sample estimates:
## mean of x mean of y
       5.032
##
                 5.526
# MCMC
BEST_Output <- BESTmcmc(dfCtrl,dfTrt2)</pre>
## Waiting for parallel processing to complete...done.
BEST_Output
## MCMC fit results for BEST analysis:
## 100002 simulations saved.
             mean
                       sd median HDIlo
                                           HDIup Rhat n.eff
           5.0266 0.2235 5.0265 4.5854
                                          5.4801 1.000 57173
## mu1
## mu2
           5.5141 0.1715 5.5127 5.1707
                                          5.8512 1.000 55027
          34.4652 29.6308 25.8365 1.3835 93.3195 1.001 20130
## sigma1 0.6597 0.1992 0.6222 0.3441 1.0604 1.000 27822
```

## sigma2 0.5001 0.1545 0.4714 0.2542 0.8107 1.001 26210

```
##
## 'HDIlo' and 'HDIup' are the limits of a 95% HDI credible interval.
## 'Rhat' is the potential scale reduction factor (at convergence, Rhat=1).
## 'n.eff' is a crude measure of effective sample size.
```

plot(BEST\_Output)

# **Difference of Means**



### T-Test

 $\bullet$  The T-Value is -2.134, the degrees of freedom is 16.786, and the p-value is 0.0479 which is less than the alpha.

## Confidence Interval

- $\bullet$  The bounds are -0.9828 and -0.00512
- The bounds also do not cross 0

## **Bayesian Method**

• The bounds for the MCMC are a bit wider, -1.05 and 0.0719.

#### Overall

- Between the 2 results treatment 2 is likely to perform better than the control group.
- The mean difference of treatment 2 at -0.51 lies between -0.9828 and -0.005.

t.test(rnorm(100000, mean=17.1, sd=3.8), rnorm(100000, mean=17.2, sd=3.8))

• This is further confirmed with the population mean difference of -0.48 within the population means bounds of the Bayesian method which is at a 96% likelhood that Treatment 2 is better than the control.

## Question 10

Consider this t-test, which compares two groups of n = 100,000 observations each: t.test(rnorm(100000,mean=17.1,sd=3.8 For each of the groups, the rnorm() command was used to generate a random normal distribution of observations similar to those for the automatic transmission group in the mtcars database (compare the programmed standard deviation for the random normal data to the actual mtcars data). The only difference between the two groups is that in the first rnorm() call, the mean is set to 17.1 mpg and in the second it is set to 17.2 mpg. I think you would agree that this is a negligible difference, if we are discussing fuel economy. Run this line of code and comment on the results of the t-test. What are the implications in terms of using the NHST on very large data sets?

```
##
## Welch Two Sample t-test
```

```
## Welch Two Sample t-test
##
## data: rnorm(1e+05, mean = 17.1, sd = 3.8) and rnorm(1e+05, mean = 17.2, sd = 3.8)
## t = -6.0874, df = 199989, p-value = 1.149e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.13669453 -0.07010962
## sample estimates:
## mean of x mean of y
## 17.08935 17.19275
```

According to the book "once we have more than about n=1,000 observations" we will be statistically significant. Therefore the NHST is insightful in informing the outcome of a piece of analysis. The increase of the MPG mean by 0.1 shows that the mean difference of 0.089 is within the 95% confidence interval. The P-Value is quite low at 0.00001 therefore we would interpret that the change in MPG had a noticeable impact on results. Therefore when running this analysis we see that 100,000 observation is well over 1,000. The effects can be related to the law of large numbers in that the results obtained from a large number of trials should be close to the expected value. In addition to Central Limit Theorem in which distribution will become normal as we sample many times.