

IST 777

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Homework #5

6. Run t-test to compare means of the control group and treatment group 1.

```
> t.test(PlantGrowth$weight[PlantGrowth$group ==  
"ctrl"], PlantGrowth$weight[PlantGrowth$group == "trt1"] )
```

Welch Two Sample t-test

```
data: PlantGrowth$weight[PlantGrowth$group == "ctrl"] and  
PlantGrowth$weight[PlantGrowth$group == "trt1"]  
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
```

The observed value of t is 1.1913

The degrees of freedom is 16.524

The p value associated with the observed value is 0.2504

Given the p value of 0.2504 is significantly higher than the alpha threshold of .05 we would fail to reject the null hypothesis.

We constructed a 95% confidence interval around the mean difference between the control and treatment group 1 with an lower bound confidence interval of -0.2875162 and an upper bound confidence interval of 1.0295162. Note that this confidence interval may or may not contain the true population value.

7. Load BEST package
> library(BEST)

Compare PlantGrowth control group to treatment group 1 (Using BEST)

```
> besttrt1 <- BESTmcmc(PlantGrowth$weight[PlantGrowth$group ==  
"ctrl"], PlantGrowth$weight[PlantGrowth$group == "trt1"])
```

Waiting for parallel processing to complete...done.

```
> besttrt1
```

MCMC fit results for BEST analysis:

100002 simulations saved.

	mean	sd	median	HDIlo	HDIup	Rhat	n.eff
mu1	5.0261	0.2250	5.0254	4.5847	5.480	1.000	56058
mu2	4.6420	0.3068	4.6396	4.0413	5.268	1.000	52883
nu	34.3118	29.8371	25.6451	1.0934	93.485	1.000	20337
sigma1	0.6613	0.2049	0.6229	0.3500	1.072	1.002	26206
sigma2	0.8990	0.2818	0.8475	0.4559	1.464	1.000	25056

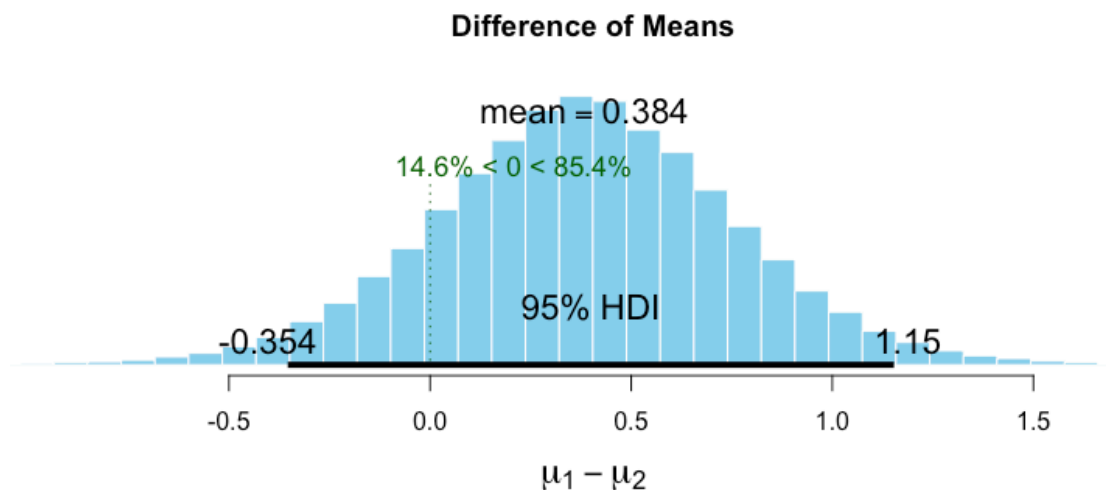
'HDIlo' and 'HDIup' are the limits of a 95% HDI credible interval.

'Rhat' is the potential scale reduction factor (at convergence, Rhat=1).

'n.eff' is a crude measure of effective sample size.

Plot result

```
> plot(besttrt1)
```



The boundary values for HDI are between -0.362 and 1.14.

The HDI stands for High Density Interval and would look similar to a confidence interval; however, it looks at the most frequent means using Bayesian statistics of the two different means. The results from this HDI shows that 95% of sample means that were run were between that HDI interval with the midpoint of the interval at 0.383.

- Between the T-test and BEST, there are major differences when analyzing the way at arriving to an interval. The information the t-test displays such as t-value, degrees of freedom, and p-value should aid in the significance of the values, but, according to the ASA it is not proof. The BEST information provided are the mean, median, standard deviation, values for control and test group 1. Additionally, BEST provides HDI low and high values provides a range which result in a difference of means HDI interval and can be used without caveats of uncertainty.

9. Use all methods from previous Exercises and apply to treatment group 2

T-test

```
> t.test(PlantGrowth$weight[PlantGrowth$group ==  
"ctrl"], PlantGrowth$weight[PlantGrowth$group == "trt2"] )
```

Welch Two Sample t-test

```
data: PlantGrowth$weight[PlantGrowth$group == "ctrl"] and  
PlantGrowth$weight[PlantGrowth$group == "trt2"]  
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
```

The observed value of t is -2.134

The degrees of freedom is 16.786

The p value associated with the observed value is 0.0479

Given the p value of 0.0479 is significantly higher than the alpha threshold of .05 we would reject the null hypothesis.

We constructed a 95% confidence interval around the mean difference between the control and treatment group 1 with an lower bound confidence interval of -0.98287213 and an upper bound confidence interval of -0.00512787. Note that this confidence interval may or may not contain the true population value.

Compare PlantGrowth control group to treatment group 2 (Using BEST)

```
> besttrt2 <- BESTmcmc(PlantGrowth$weight[PlantGrowth$group ==  
"ctrl"], PlantGrowth$weight[PlantGrowth$group == "trt2"])  
Waiting for parallel processing to complete...done.  
> besttrt2
```

MCMC fit results for BEST analysis:

100002 simulations saved.

	mean	sd	median	HDIlo	HDIup	Rhat	n.eff
mu1	5.0289	0.2276	5.0271	4.5854	5.4916	1	50670
mu2	5.5151	0.1726	5.5127	5.1738	5.8642	1	53559
nu	34.7154	29.8667	25.9370	1.3431	94.7085	1	20469
sigma1	0.6635	0.2055	0.6241	0.3434	1.0715	1	24723
sigma2	0.5018	0.1569	0.4721	0.2583	0.8179	1	25371

'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 result

```
> plot(besttrt2)
```

The boundary values for HDI are between -1.05 and 0.0734.

10. Consider given t-test and run

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

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 = -6.1358, df = 199991, p-value = 8.49e-10

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-0.13764697 -0.07099858

sample estimates:

mean of x mean of y

17.10851 17.21283

The observed value of t is -4.0506

The degrees of freedom is 2e+05

The p value associated with the observed value is 5.111e-05

Given the p value of 5.111e-05 is significantly higher than the alpha threshold of .05 we would reject the null hypothesis.

We constructed a 95% confidence interval around the mean difference between the control and treatment group 1 with an lower bound confidence interval of -0.10209787 and an upper bound confidence interval of -0.03551178. Note that this confidence interval may or may not contain the true population value.

The implications of using the NHST on very large datasets is a rejection of the null hypothesis due to a really low p value, a large degree of freedom, and a tight confidence interval ranging less than 0.07.

All this change is accounted just from a 0.1 difference in the mean after running 100,000 observations.