

Homework #5

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1. Tip Percentage and Gender

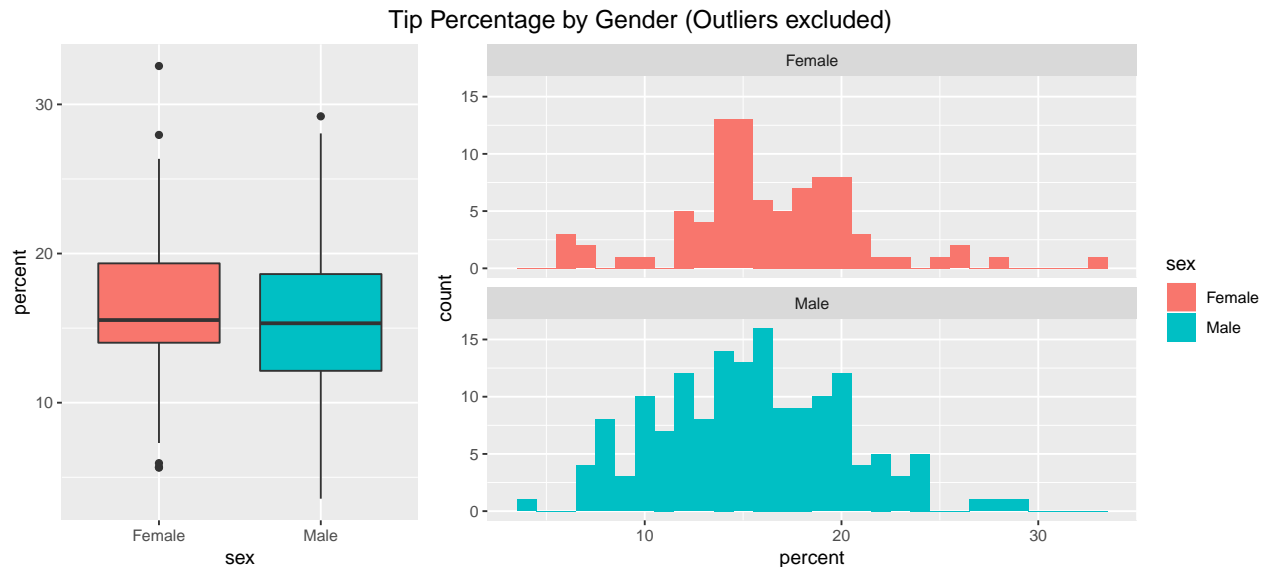
Student t-test

```
hist_full <- ggplot(tips, aes(x = percent, fill = sex)) +  
  geom_histogram(bins = 30) +  
  facet_wrap(~sex, ncol = 1)  
  
bplot_full <- ggplot(tips, aes(x = sex, y = percent, fill = sex)) +  
  geom_boxplot(show.legend = FALSE)  
  
grid.arrange(bplot_full, hist_full,  
  ncol = 2,  
  widths = c(1, 2),  
  top = textGrob("Tip Percentage by Gender",  
    gp=gpar(fontsize=14,font=1),just=c("center")))
```



```
full_test <- t.test(percent ~ sex, data = tips)  
  
hist_sans <- ggplot(tips_sans_outliers, aes(x = percent, fill = sex)) +  
  geom_histogram(bins = 30) +  
  facet_wrap(~sex, ncol = 1)  
  
bplot_sans <- ggplot(tips_sans_outliers, aes(x = sex, y = percent, fill = sex)) +  
  geom_boxplot(show.legend = FALSE)  
  
grid.arrange(bplot_sans, hist_sans,  
  ncol = 2,  
  widths = c(1, 2),
```

```
top = textGrob("Tip Percentage by Gender (Outliers excluded)",
  gp=gpar(fontsize=14,font=1),just=c("center"))
```



```
sans_test <- t.test(percent ~ sex, data = tips_sans_outliers)
```

Put both tests in the same graph

```
knitr::kable(
  bind_rows(tidy(full_test) %>%
    mutate(desc="With Outliers"),
    tidy(sans_test) %>%
    mutate(desc="Without Outliers")
  ) %>%
  select(desc, estimate1, estimate2, p.value, conf.low, conf.high) %>%
  mutate(estimate=estimate1 - estimate2),
  digits = 4,
  col.names = c("", "Mean Female %", "Mean Male %", "P-Value", "C.I - Lower", "C.I - Upper", "Estimate")
  align = 'l')
```

	Mean Female %	Mean Male %	P-Value	C.I - Lower	C.I - Upper	Estimate
With Outliers	16.6491	15.7651	0.2542	-0.6404	2.4084	0.8840
Without Outliers	16.3582	15.4108	0.1336	-0.2934	2.1882	0.9474

The p-values produced by the full and sans outliers datasets are 0.2542 and 0.1336 respectively. The difference between these p-values is 0.1206.

Wilcoxon Rank Sum

```
wilcox_test(percent~sex, data=tips, distribution="exact")
```

```
##
## Exact Wilcoxon-Mann-Whitney Test
##
## data: percent by sex (Female, Male)
## Z = 1.495, p-value = 0.1352
## alternative hypothesis: true mu is not equal to 0
```

```
wilcox_test(percent~sex, data=tips_sans_outliers, distribution="exact")
```

```
##
## Exact Wilcoxon-Mann-Whitney Test
##
## data: percent by sex (Female, Male)
## Z = 1.4485, p-value = 0.1479
## alternative hypothesis: true mu is not equal to 0
```

The p-values produced by the full and sans outliers datasets are 0.1332 and 0.1479 respectively. The difference between these p-values is 0.0147.

The p-value difference produced by the Wilcoxon Rank Sum Test are significantly smaller than the p-value difference produced by the t-test. This suggests that the Wilcoxon Rank Sum Test is more robust to outliers than the t-test.

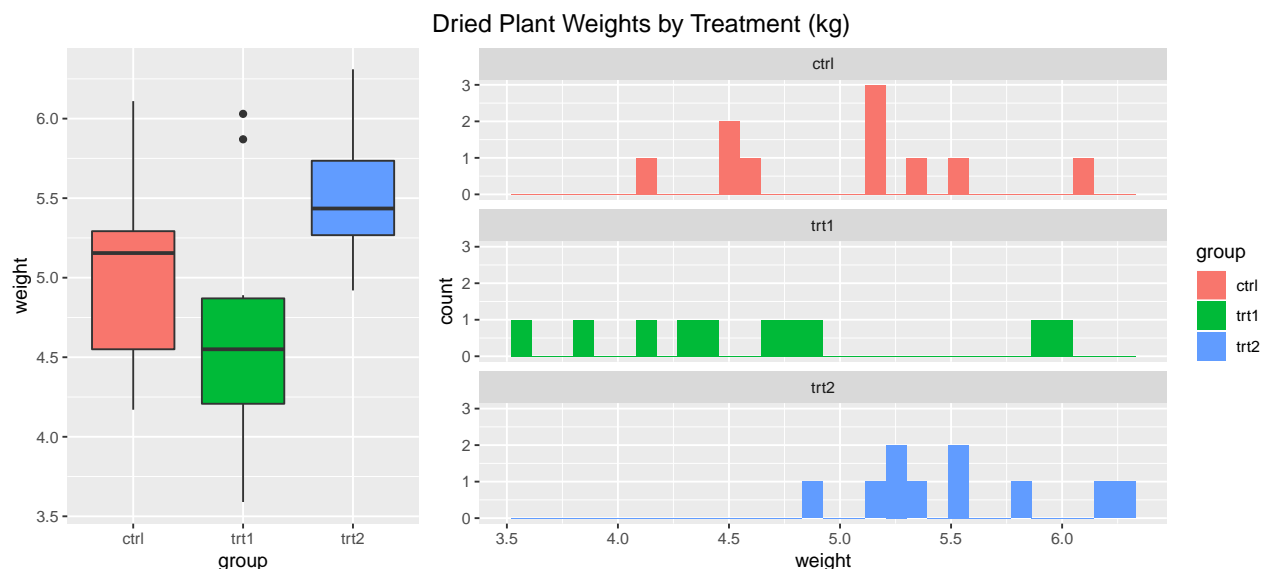
2. Plant Growth

```
plant_bplot <- ggplot(PlantGrowth, aes(x = group, y = weight, fill = group)) +
  geom_boxplot(show.legend = FALSE)

plant_hist <- ggplot(PlantGrowth, aes(x = weight, fill = group)) +
  geom_histogram() +
  facet_wrap(~group, ncol = 1)

grid.arrange(plant_bplot, plant_hist,
  ncol = 2,
  widths = c(1, 2),
  top = textGrob("Dried Plant Weights by Treatment (kg)",
    gp=gpar(fontsize=14,font=1),just=c("center")))
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
knitr::kable(
  PlantGrowth %>%
```

```

group_by(group) %>%
  summarise_all(funs(mean, sd, length, min, "25%"=quantile(weight, 0.25), median, "75%"=quantile(weight, 0.75),
  digits = 4,
  col.names = c("Treatment Group", "Mean", "Std. Dev", "Sample Size", "Min", "Q1", "Median", "Q3", "Max"),
  align = 'l'
)

```

Treatment Group	Mean	Std. Dev	Sample Size	Min	Q1	Median	Q3	Max
ctrl	5.032	0.5831	10	4.17	4.5500	5.155	5.2925	6.11
trt1	4.661	0.7937	10	3.59	4.2075	4.550	4.8700	6.03
trt2	5.526	0.4426	10	4.92	5.2675	5.435	5.7350	6.31

```

# Calculate pooled standard deviation, and RSS for full and reduced models

```

```

sums <- PlantGrowth %>%
  group_by(group) %>%
  summarise_all(funs(
    avg=mean,
    stdev=sd,
    n=n(),
    ss.full = (weight - avg)^2 %>% sum,
    ss.reduced = (weight - mean(PlantGrowth$weight))^2 %>%
      sum)
  ) %>%
  mutate(
    pool.stdev = sqrt(sum((n - 1) * stdev^2) / sum(n - 1)),
    rss.full = sum(ss.full),
    rss.reduced = sum(ss.reduced)
  )

kable(sums,
  digits = 4)

```

group	avg	stdev	n	ss.full	ss.reduced	pool.stdev	rss.full	rss.reduced
ctrl	5.032	0.5831	10	3.0600	3.0768	0.6234	10.4921	14.2584
trt1	4.661	0.7937	10	5.6693	7.3667	0.6234	10.4921	14.2584
trt2	5.526	0.4426	10	1.7628	3.8149	0.6234	10.4921	14.2584

```

# Confirm that RSS for full and reduced models were calculate correctly

```

```

kable(sums %>%
  select(rss.full, pool.stdev, rss.reduced, n) %>%
  distinct %>%
  mutate(
    rss.full.conf = (n*3 - 3) * pool.stdev^2,
    rss.reduced.conf = (n*3 - 1) * sd(PlantGrowth$weight)^2,
    rss.full.equal = assertthat::are_equal(rss.full, rss.full.conf),
    rss.reduced.equal = assertthat::are_equal(rss.reduced, rss.reduced.conf)),
  digits = 4
)

```

rss.full	pool.stdev	rss.reduced	n	rss.full.conf	rss.reduced.conf	rss.full.equal	rss.reduced.equal
10.4921	0.6234	14.2584	10	10.4921	14.2584	TRUE	TRUE

ANOVA Table

	Sum of Squares	df	MSS	F-value	p-value
Full	3.7663	2	1.8832	4.8461	0.0159
Reduced	10.4921	27	0.3886		
Total	14.2584	29			

There is moderate evidence that the average weight between each group in the study is different (extra sum of squares F-test on 27 and 2 degrees of freedom. p-value = 0.0159)

```
results <- t.test(weight~group, data = PlantGrowth[PlantGrowth$group != "trt2",])
```

```
kable(
  tidy(results) %>%
    select(estimate1, estimate2, p.value, conf.low, conf.high) %>%
    mutate(estimate=estimate1 - estimate2),
  digits = 4,
  col.names = c("Mean Weight Control", "Mean Weight Treatment 1", "P-Value", "C.I - Lower", "C.I - Upper", "Estimate"),
  align = 'l')
```

Mean Weight Control	Mean Weight Treatment 1	P-Value	C.I - Lower	C.I - Upper	Estimate
5.032	4.661	0.2504	-0.2875	1.0295	0.371

With 95% confidence, the average weight difference between the control group and treatment group 1 is between -0.288 and 1.03 kg; thus there is no evidence to suggest that the average weights differ between the control and treatment group 1 (two-tail t-test. p-value = 0.2504).