Chapter 6 Exercise

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```
\#\#Section 6.5 and Excercise 6.4
```

```
data("PlantGrowth")
PlantGrowth
##
      weight group
## 1
        4.17
             ctrl
## 2
        5.58 ctrl
## 3
       5.18 ctrl
## 4
       6.11 ctrl
## 5
        4.50 ctrl
## 6
        4.61 ctrl
## 7
       5.17
             ctrl
## 8
       4.53 ctrl
## 9
       5.33 ctrl
## 10
       5.14 ctrl
## 11
       4.81 trt1
## 12
        4.17 trt1
        4.41 trt1
## 13
## 14
        3.59 trt1
       5.87
## 15
             trt1
## 16
       3.83 trt1
## 17
        6.03 trt1
## 18
        4.89 trt1
## 19
        4.32 trt1
## 20
        4.69 trt1
## 21
        6.31 trt2
## 22
        5.12 trt2
## 23
       5.54 trt2
## 24
       5.50 trt2
## 25
       5.37 trt2
## 26
       5.29 trt2
## 27
        4.92 trt2
## 28
        6.15 trt2
## 29
        5.80 trt2
## 30
       5.26 trt2
PlantGrowth %>%
   mutate(group = fct_recode(group,
                            Control = "ctrl",
                            `Treatment 1` = "trt1",
                            `Treatment 2` = "trt2")) %>%
  ggplot(aes(x = group, y = weight)) +
  geom_beeswarm() +
```

```
labs(x = "")
```

```
6.0 -

5.5 -

5.0 -

4.5 -

4.0 -

3.5 -

Control Treatment 1 Treatment 2
```

```
PlantGrowth %>%
  filter(group %in% c("ctrl", "trt2")) %>%
    t.test(weight ~ group, data = .)
##
   Welch Two Sample t-test
##
## data: weight by group
## 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 in group ctrl mean in group trt2
##
                5.032
                                    5.526
library("broom")
PlantGrowth %>%
  filter(group %in% c("ctrl", "trt2")) %>%
  t.test(weight ~ group, data = .) %>%
    tidy()
## # A tibble: 1 x 10
     estimate estimate1 estimate2 statistic p.value parameter conf.low conf.high
##
        <dbl>
                  <dbl>
                            <dbl>
                                       <dbl>
                                               <dbl>
                                                         <dbl>
                                                                   <dbl>
                                                                             <dbl>
       -0.494
                   5.03
                             5.53
                                       -2.13 0.0479
                                                          16.8
                                                                  -0.983 -0.00513
## # ... with 2 more variables: method <chr>, alternative <chr>
When data is duplicated we get much smaller p-value due to increased sample size:
PlantGrowth %>%
  bind_rows(PlantGrowth) %>% # Add the duplicate of the dataset
  filter(group %in% c("ctrl", "trt2")) %>%
  t.test(weight ~ group, data = .) %>%
  tidy()
## # A tibble: 1 x 10
##
     estimate estimate1 estimate2 statistic p.value parameter conf.low conf.high
##
        <dbl>
                                                                   <dbl>
                  <dbl>
                             <dbl>
                                       <dbl>
                                               <dbl>
                                                         <dbl>
                                                                             <dbl>
     -0.494
                   5.03
                              5.53
                                       -3.10 0.00377
                                                          35.4
                                                                  -0.817
                                                                            -0.171
## # ... with 2 more variables: method <chr>, alternative <chr>
```

Resample only half the data:

```
PlantGrowth %>%
  sample_frac(size = 0.5) %>%
  bind_rows(., .) %>%
  filter(group %in% c("ctrl", "trt2")) %>%
  t.test(weight ~ group, data = .) %>%
 tidy()
## # A tibble: 1 x 10
   estimate estimate1 estimate2 statistic p.value parameter conf.low conf.high
##
        <dbl>
                  <dbl>
                            <dbl>
                                       <dbl>
                                               <dbl>
                                                         <dbl>
                                                                  <dbl>
                                                                             <dbl>
## 1 0.0382
                   5.21
                             5.17
                                       0.246
                                               0.809
                                                                 -0.289
                                                                             0.366
                                                          17.4
## # ... with 2 more variables: method <chr>, alternative <chr>
Resample half the data and add random noise:
pg1 <- PlantGrowth %>%
  sample_frac(size = 0.5)
pg2 <- pg1 %>%
  mutate(noise = rnorm(15, mean = 0, sd = 0.2),
         weight = weight + noise) %>%
  select(-noise)
pg1 %>%
  bind rows(pg2) %>%
  filter(group %in% c("ctrl", "trt2")) %>%
  t.test(weight ~ group, data = .) %>%
 tidy()
## # A tibble: 1 x 10
     estimate estimate1 estimate2 statistic p.value parameter conf.low conf.high
        <dbl>
                  <dbl>
                            <dbl>
                                       <dbl>
                                               <dbl>
                                                         <dbl>
                                                                  <dbl>
                                                                             <dbl>
##
                             5.35
## 1
       -0.404
                   4.95
                                       -1.61
                                               0.129
                                                          14.1
                                                                 -0.940
                                                                            0.132
## # ... with 2 more variables: method <chr>, alternative <chr>
```