Homework 3

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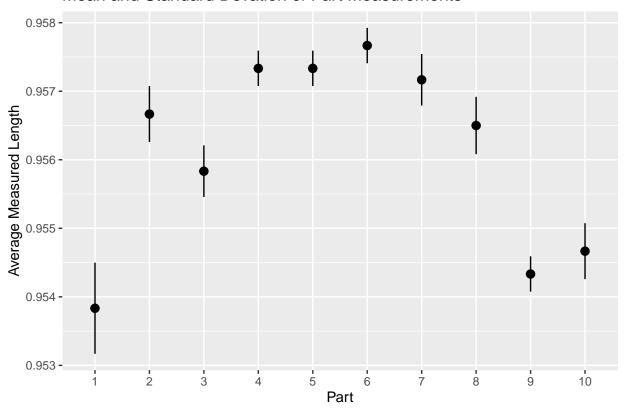
Part A

```
# Read in the data
url <- "https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/ThicknessGauge.dat"</pre>
thickness_gauge <- read.table(url, header = F, skip = 2, fill = T, stringsAsFactors = F)</pre>
# Note: the first row of ThicknessGauge.dat was removed manually.
# For each operator, two columns correspond to the measurements taken by that operator. This column nam
names(thickness_gauge) <- c("Part", "1_1", "1_2", "2_1", "2_2", "3_1", "3_2")
# Reshape the data
reshaped_thickness_gauge <- pivot_longer(thickness_gauge, cols = 2:7, names_to = "measurement", values_
# From the value in each measurement column, can get the Operator used to take the measurement, as well
reshaped_thickness_gauge$Operator <- as.numeric(substring(reshaped_thickness_gauge$measurement, 1, 1))
reshaped_thickness_gauge$trial <- as.numeric(substring(reshaped_thickness_gauge$measurement, 3, 3))
# Get rid of measurement column as it is no longer necessary
reshaped_thickness_gauge <- reshaped_thickness_gauge %>%
  select(Part, Operator, trial, length)
reshaped_thickness_gauge
## # A tibble: 60 x 4
       Part Operator trial length
##
               <dbl> <dbl> <dbl>
##
      <int>
##
                        1 0.953
   1
         1
                   1
## 2
                         2 0.952
          1
                   1
                        1 0.954
## 3
          1
                   2
## 4
                  2
                         2 0.954
         1
## 5
         1
                  3
                        1 0.954
                         2 0.956
## 6
                  3
         1
## 7
         2
                   1
                        1 0.956
## 8
         2
                  1
                        2 0.956
## 9
         2
                   2
                        1 0.956
## 10
                         2 0.957
## # i 50 more rows
# Data summary: for each part, would like the mean of all of the measurements taken from it.
thickness_summary <- reshaped_thickness_gauge %>%
  group_by(Part) %>%
  summarise(avg_meas_length = mean(length), meas_sd = sd(length))
thickness_summary
## # A tibble: 10 x 3
```

Part avg_meas_length meas_sd

```
##
      <int>
                       <dbl>
                                <dbl>
##
    1
                      0.954 0.00133
          1
                      0.957 0.000816
##
    2
          2
##
    3
          3
                      0.956 0.000753
##
    4
          4
                      0.957 0.000516
    5
                      0.957 0.000516
##
          5
                      0.958 0.000516
##
    6
          6
##
    7
          7
                      0.957 0.000753
##
    8
          8
                      0.956 0.000837
    9
          9
                      0.954 0.000516
##
## 10
         10
                      0.955 0.000816
thickness_summary$thickness_LB = thickness_summary$avg_meas_length - thickness_summary$meas_sd/2
thickness_summary$thickness_UB = thickness_summary$avg_meas_length + thickness_summary$meas_sd/2
ggplot(data = thickness_summary) + geom_pointrange(aes(x = as.factor(Part), y = avg_meas_length, ymin =
  labs(title = "Mean and Standard Devation of Part Measurements", x = "Part", y = "Average Measured Length
```

Mean and Standard Devation of Part Measurements

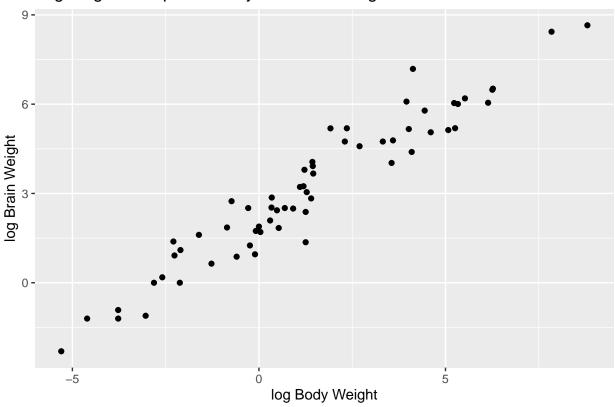


Part B

```
# Read in the data
url <- "https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/BrainandBodyWeight.dat"
brain_body_wt <- read.table(url, header = F, skip = 1, fill = T, stringsAsFactors = F)
# Name the columns appropriately.
names(brain_body_wt) <- c("BodyWt1", "BrainWt1", "BodyWt2", "BrainWt2", "BodyWt3", "BrainWt3")</pre>
```

```
# Reshape the data
body_wt <- pivot_longer(brain_body_wt, cols = c(1,3,5), values_to = "BodyWt")</pre>
brain_wt <- pivot_longer(brain_body_wt, cols = c(2,4,6), values_to = "BrainWt")</pre>
reshaped_brain_body_wt <- data.frame(BodyWt = body_wt$BodyWt, BrainWt = brain_wt$BrainWt) %>%
  filter(!is.na(BodyWt) & !is.na(BrainWt))
# Summary table: mean and sd of the brain and body weights of the subjects.
reshaped_brain_body_wt %>%
  summarise(body_wt_mean = mean(BodyWt), body_wt_sd = sd(BodyWt),
            brain_wt_mean = mean(BrainWt), brain_wt_sd = sd(BrainWt))
     body_wt_mean body_wt_sd brain_wt_mean brain_wt_sd
## 1
           198.79
                     899.158
                                  283.1344
                                               930.2789
ggplot(data = reshaped_brain_body_wt) +
  geom_point(aes(x = log(BodyWt), y = log(BrainWt))) +
 labs(title = "Log-Log Scatterplot of Body and Brain Weight", x = "log Body Weight", y = "log Brain We
```

Log-Log Scatterplot of Body and Brain Weight

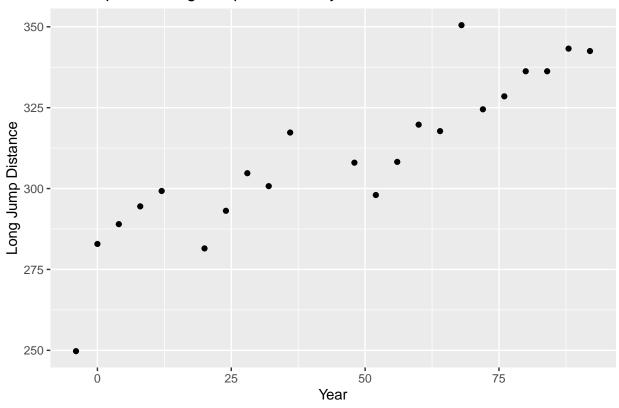


Part C

```
# Read in the data
url = "https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LongJumpData.dat"
long_jump <- fread(url, fill = TRUE, skip = 1)
# Reshape the data
years <- long_jump[,c(1,3,5,7)]
distances <- long_jump[,c(2,4,6,8)]
years_long <- pivot_longer(years, cols = 1:4, values_to = "Year")</pre>
```

```
distances_long <- pivot_longer(distances, cols = 1:4, values_to = "Distance")</pre>
reshaped_long_jump <- data.frame(Year = years_long$Year, Distance = distances_long$Distance) %>%
  filter(!is.na(Year) & !is.na(Distance))
reshaped_long_jump <- reshaped_long_jump[order(reshaped_long_jump$Year),]
reshaped_long_jump
##
      Year Distance
## 1
        -4
            249.75
## 5
         0
            282.88
## 9
         4
            289.00
## 13
        8
           294.50
## 17
           299.25
        12
## 20
           281.50
        20
## 2
       24 293.13
## 6
        28 304.75
## 10
       32 300.75
## 14
        36
            317.31
## 18
       48 308.00
## 21
       52 298.00
## 3
           308.25
       56
## 7
       60
            319.75
## 11
       64 317.75
## 15
           350.50
       68
## 19
       72
           324.50
## 22
       76
            328.50
## 4
       80
           336.25
## 8
       84
           336.25
## 12
       88
           343.25
## 16
            342.50
       92
# Summary table: the mean and sd of the long jump distances
reshaped_long_jump %>%
  summarise(distance_mean = mean(Distance), distance_sd = sd(Distance))
##
     distance_mean distance_sd
## 1
          310.2873
                     24.36121
ggplot(data = reshaped_long_jump) +
  geom_point(aes(x = Year, y = Distance)) +
  labs(title = "Scatterplot of Long Jump Distance by Year", x = "Year", y = "Long Jump Distance")
```

Scatterplot of Long Jump Distance by Year



Part D

```
# Read in the data
url = "https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/tomato.dat"
lines <- gsub(",", " ", readLines(url)[-2:-1])
text = lines[1]
for(i in 2:length(lines)){
  text <- paste(text, lines[i], sep = "\n")</pre>
}
tomato <- fread(text)</pre>
# Reshape the data
names(tomato) <- c("Variety", "1_1", "1_2", "1_3",</pre>
                               "2_1", "2_2", "2_3",
                               "3_1", "3_2", "3_3")
reshaped_tomato <- pivot_longer(tomato, cols = 2:10, names_to = "measurement", values_to = "Yield") %>%
  mutate(Depth = as.numeric(substring(measurement, 1, 1))*10000,
         trial = as.numeric(substring(measurement, 3, 3))) %>%
  select(Variety, Depth, trial, Yield)
reshaped_tomato
# Summary Table: the mean yield of each variety of tomato at each depth
reshaped_tomato %>%
  group_by(Variety, Depth) %>%
  summarise(mean_meas_yield = mean(Yield))
```

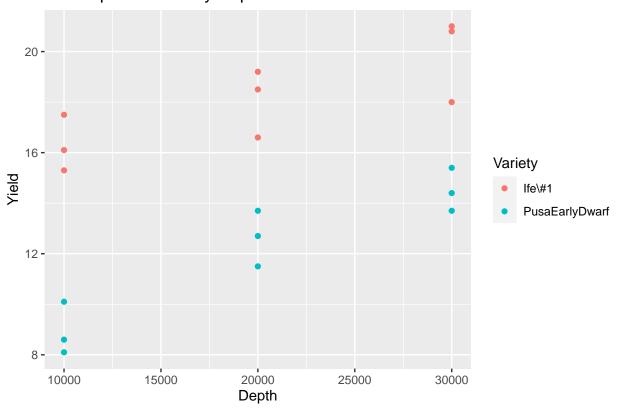
```
## `summarise()` has grouped output by 'Variety'. You can override using the
## `.groups` argument.

# Unfortunately summarise gives unwanted console output here.

ggplot(data = reshaped_tomato) +
    geom_point(aes(x = Depth, y = Yield, color = Variety)) +
```

labs(title = "Scatterplot of Yield by Depth", x = "Depth", y = "Yield")

Scatterplot of Yield by Depth



Part E

```
group_by(Age, Treatment) %>%
summarise(mean_larvae = mean(larvae))
```

`summarise()` has grouped output by 'Age'. You can override using the `.groups` ## argument.

```
ggplot(data = reshaped_larvae) +
  geom_boxplot(aes(x = as.factor(Treatment), y = larvae, color = as.factor(Age))) +
  labs(title = "Boxplots of Larvae Count by Treatment", x = "Treatment", y = "Larvae Count", color = "Age")
```

Boxplots of Larvae Count by Treatment

