

Assignment3

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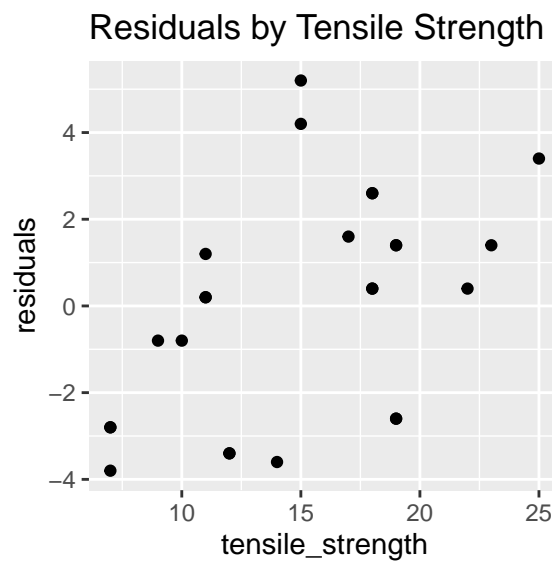
2/11/2020

```
library(tidyverse)
```

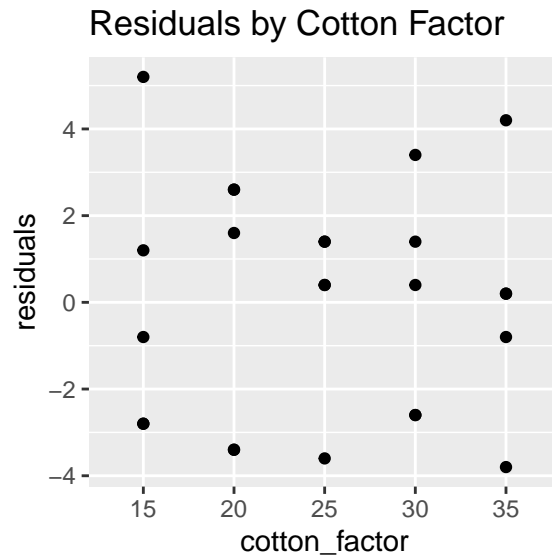
1)

C) Analyze the residuals from this experiment and comment on model adequacy. Use R.

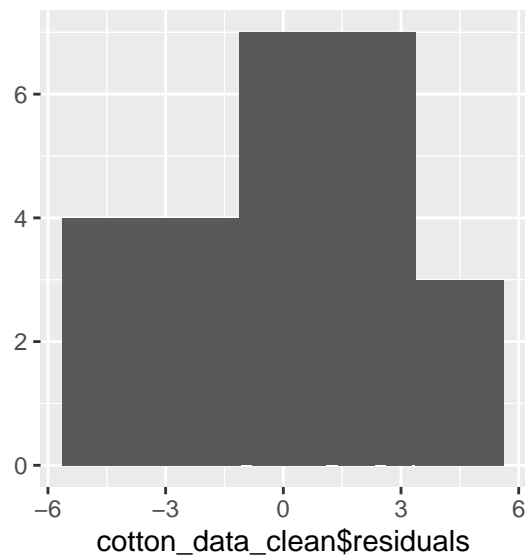
```
cotton_data <- tibble(  
  cotton_factor = gl(n = 5, k = 5, label = c("15", "20", "25", "30", "35")),  
  tensile_strength = c(7, 7, 15, 11, 9, 12, 17, 12, 18, 18, 14, 19, 19, 18, 18, 19, 25, 22, 19, 23, 7,  
  cotton_anova <- aov(tensile_strength ~ cotton_factor, data = cotton_data)  
  
cotton_data_clean <- cotton_data %>%  
  mutate(residuals = cotton_anova$residuals)  
  
ggplot(data = cotton_data_clean, aes(x = tensile_strength, y = residuals)) +  
  geom_point() +  
  labs(title = "Residuals by Tensile Strength")
```



```
ggplot(data = cotton_data_clean, aes(x = cotton_factor, y = residuals)) +  
  geom_point() +  
  labs(title = "Residuals by Cotton Factor")
```



```
qplot(cotton_data_clean$residuals) +
  stat_bin(bins = 5)
```



Overall, the residuals for problem 1, look fine. There's a random spattering around each of the cotton factors and the histogram of the residuals looks fine.

2)

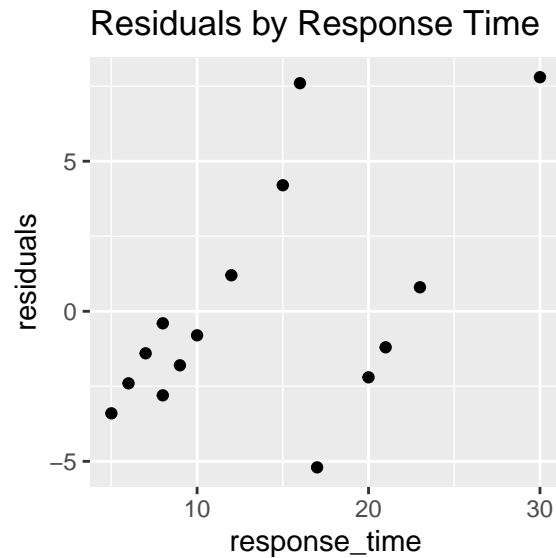
C) Analyze the residuals from this experiment and comment on model adequacy. Use R.

```
circuit_data <- tibble(
  circuit_type = gl(n = 3, k = 5, labels = c("1", "2", "3")),
  response_time = c(9, 12, 10, 8, 15, 20, 21, 23, 17, 30, 6, 5, 8, 16, 7)
)

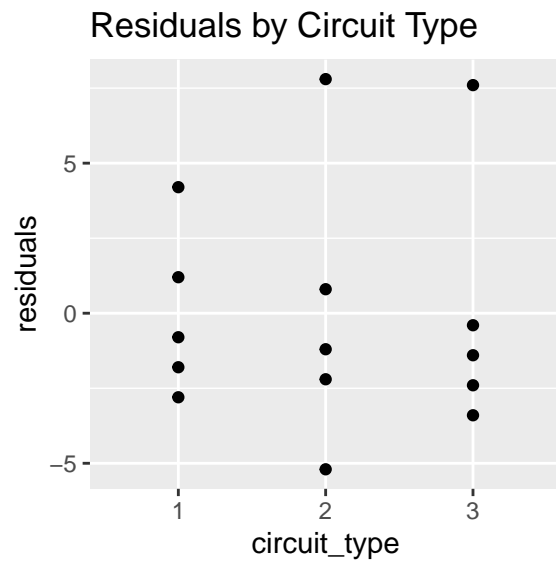
circuit_anova <- aov(response_time ~ circuit_type, data = circuit_data)

circuit_data_clean <- circuit_data %>%
  mutate(residuals = circuit_anova$residuals)
```

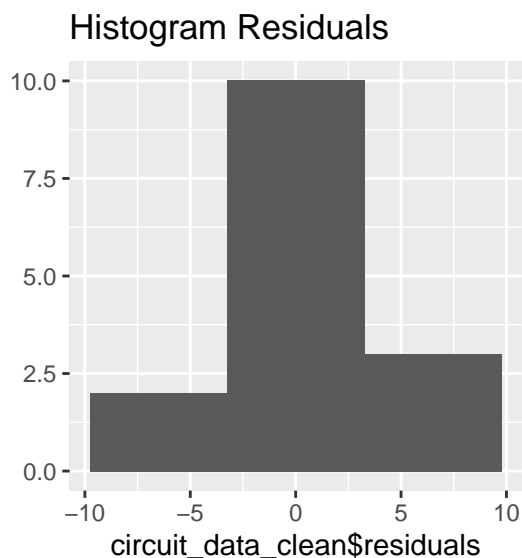
```
ggplot(data = circuit_data_clean, aes(x = response_time, y = residuals)) +
  geom_point() +
  labs(title = "Residuals by Response Time")
```



```
ggplot(data = circuit_data_clean, aes(x = circuit_type, y = residuals)) +
  geom_point() +
  labs(title = "Residuals by Circuit Type")
```



```
qplot(circuit_data_clean$residuals) +
  stat_bin(bins = 3) +
  labs(title = "Histogram Residuals")
```



Overall, the residuals for problem 1, look fine. There's a random spattering around each of the circuit type and the histogram of the residuals looks fine.

3)

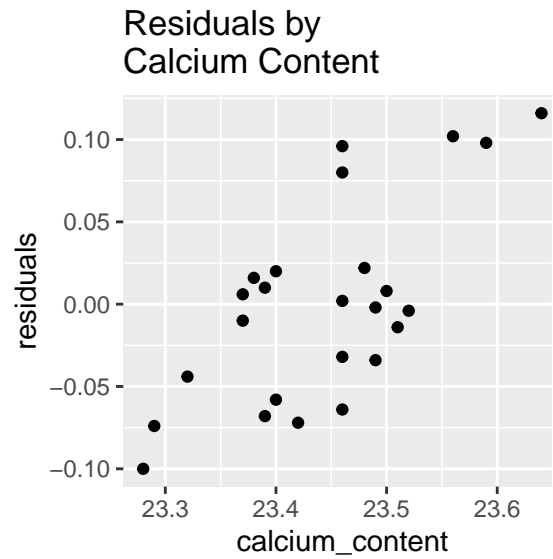
E) Analyze the residuals from this experiment and comment on model adequacy. Use R.

```
calcium_data <- tibble(
  batch_number = gl(n = 5, k = 5, labels = c("batch_1", "batch_2", "batch_3",
                                              "batch_4", "batch_5")),
  calcium_content = c(23.46, 23.48, 23.56, 23.39, 23.40, 23.59, 23.46, 23.42, 23.49, 23.50, 23.51, 23.6)
)

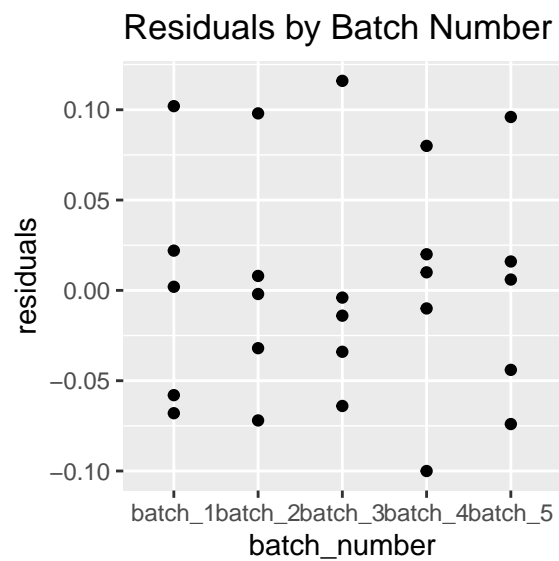
calcium_anova <- aov(calcium_content ~ batch_number, data = calcium_data)

calcium_data_clean <- calcium_data %>%
  mutate(residuals = calcium_anova$residuals)

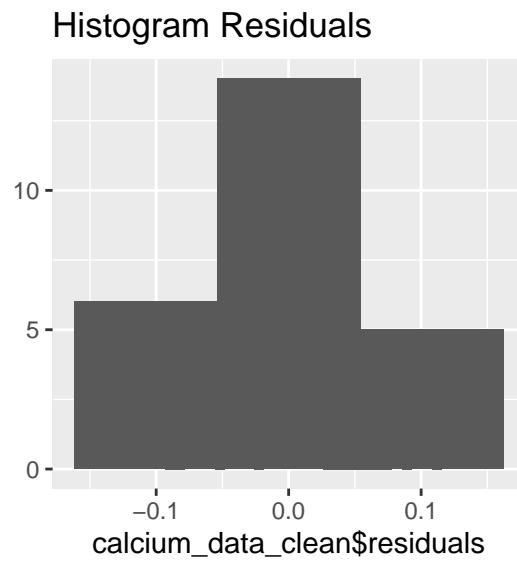
ggplot(data = calcium_data_clean, aes(x = calcium_content, y = residuals)) +
  geom_point() +
  labs(title = "Residuals by \nCalcium Content")
```



```
ggplot(data = calcium_data_clean, aes(x = batch_number, y = residuals)) +  
  geom_point() +  
  labs(title = "Residuals by Batch Number")
```



```
qplot(calcium_data_clean$residuals) +  
  stat_bin(bins = 3) +  
  labs(title = "Histogram Residuals")
```



These residuals are the best out of the three problems. Their spattering by batch number and nice histogram make for an awesome model and we could proceed to post-hoc testing bearing a check on the p-value.