Analysis

Untitled

```
beers <- c("Sierra(Pale_ale)", "Coors(Generic)", "Guinness(Dark)", "Pliny(IPA)")
Nolan <- c(NA, 6, 5.5, 3)
Jon <- c(5.5, 6, 3.5, NA)
Benni <- c(7, NA, 4, 8.5)
Zach <- c(2.5, 6.5, NA, 2)

raw_data <- data.frame(beers, Nolan, Jon, Benni, Zach)

pivoted_raw_data <- pivot_longer(raw_data,
                         cols=-beers,
                         names_to = "names",
                         values_to = "rating")

cleaned_data <- pivoted_raw_data %>%
  drop_na(rating)

cleaned_data
```

```
# A tibble: 12 x 3
   beers            names rating
   <chr>            <chr>  <dbl>
 1 Sierra(Pale_ale) Jon      5.5
 2 Sierra(Pale_ale) Benni    7
 3 Sierra(Pale_ale) Zach     2.5
 4 Coors(Generic)   Nolan    6
 5 Coors(Generic)   Jon      6
 6 Coors(Generic)   Zach     6.5
 7 Guinness(Dark)   Nolan    5.5
 8 Guinness(Dark)   Jon      3.5
 9 Guinness(Dark)   Benni    4
10 Pliny(IPA)       Nolan    3
```

```
11 Pliny(IPA)       Benni    8.5
12 Pliny(IPA)       Zach     2
```

```
model <- lm(rating~names+beers,
            data = cleaned_data)
resid <- residuals(model)
```

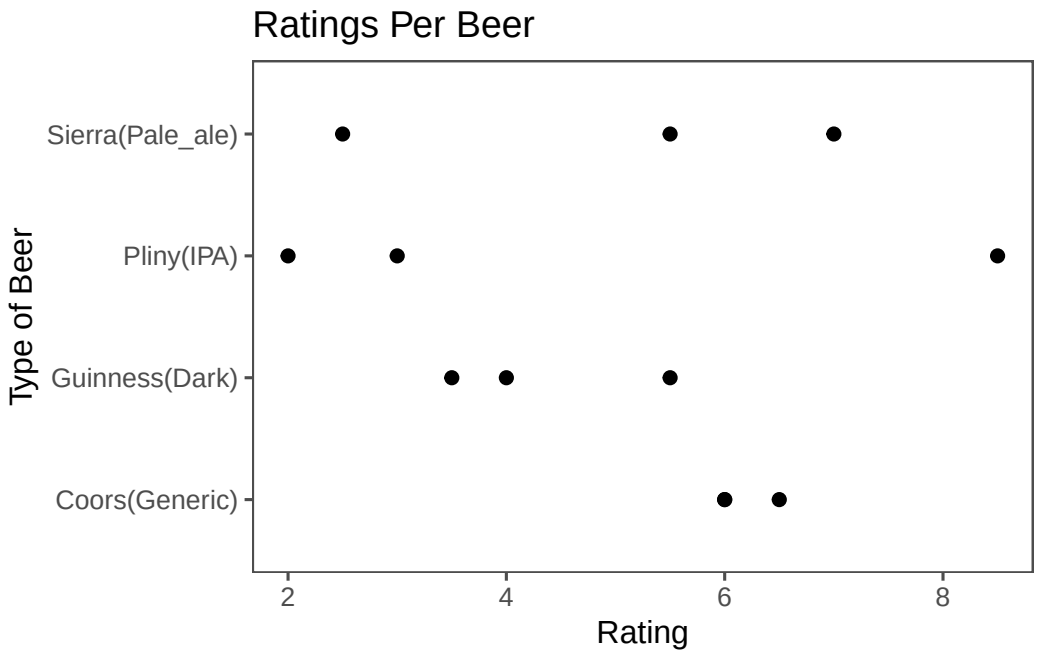
```
anova(model)
```

```
Analysis of Variance Table

Response: rating
          Df Sum Sq Mean Sq F value Pr(>F)
names      3 12.167  4.0556  1.1972 0.4002
beers      3 14.396  4.7986  1.4166 0.3415
Residuals  5 16.938  3.3875
```

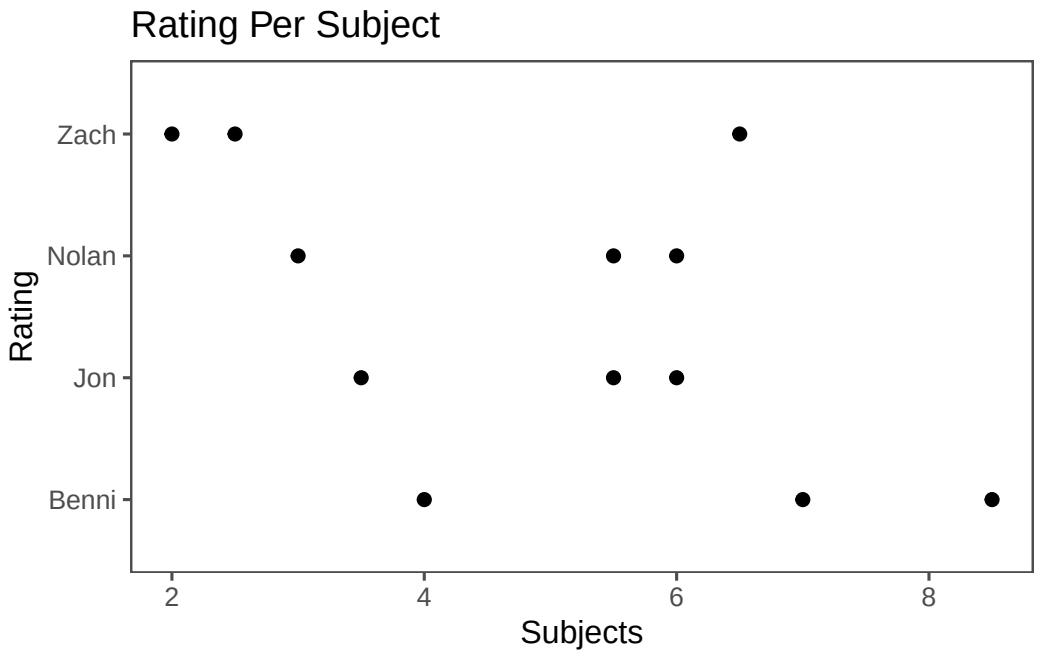
```
shapiro.test(resid)
```

```
    Shapiro-Wilk normality test

data:  resid
W = 0.91467, p-value = 0.2448
```

```
cleaned_data %>%
  ggplot(aes(x = rating,
             y = beers))+
  geom_point(size = 2)+
  theme_few()+
  ggtitle("Ratings Per Beer")+
  ylab("Type of Beer")+
  xlab("Rating")
```




```
cleaned_data %>%
  ggplot(aes(x = rating,
             y = names))+
  geom_point(size = 2)+
  theme_few()+
  ggtitle("Rating Per Subject")+
  xlab("Subjects")+
  ylab("Rating")
```




```
library(lme4)
```

```
Loading required package: Matrix
```

```
Warning: package 'Matrix' was built under R version 4.2.3
```

```

Attaching package: 'Matrix'
```

```
The following objects are masked from 'package:tidyr':

    expand, pack, unpack
```

```
library(lmerTest)
```

```
Warning: package 'lmerTest' was built under R version 4.2.3
```

```

Attaching package: 'lmerTest'
```

```
The following object is masked from 'package:lme4':

    lmer

The following object is masked from 'package:stats':

    step
```

```r
model <- lmer(rating ~ beers + (1 | names), data = cleaned_data)
```

```r
summary(model)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: rating ~ beers + (1 | names)
   Data: cleaned_data

REML criterion at convergence: 38.9

Scaled residuals:
    Min      1Q  Median      3Q     Max
-0.8642 -0.6377 -0.2325  0.4799  1.6111

Random effects:
 Groups   Name        Variance Std.Dev.
 names    (Intercept) 1.279    1.131
 Residual             3.387    1.841
Number of obs: 12, groups:  names, 4

Fixed effects:
                     Estimate Std. Error     df t value Pr(>|t|)
(Intercept)             6.522      1.226  7.764   5.322 0.000783 ***
beersGuinness(Dark)    -2.481      1.549  5.606  -1.602 0.163788
beersPliny(IPA)        -2.053      1.549  5.606  -1.325 0.236464
beersSierra(Pale_ale)  -1.553      1.549  5.606  -1.003 0.357288
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) brG(D) bP(IPA
```

```
brsGnnss(D) -0.632
brsPln(IPA) -0.632  0.500
brsSrr(Pl_) -0.632  0.500  0.500
```

```r
raw_data %>%
  kable(
    caption = "Beer Ratings by Participant",
    col.names = c("Beers", "Nolan", "Jon", "Benni", "Zach"),
    align = "c"
  )
```

Table 1: Beer Ratings by Participant

Beers	Nolan	Jon	Benni	Zach
Sierra(Pale_ale)	NA	5.5	7.0	2.5
Coors(Generic)	6.0	6.0	NA	6.5
Guinness(Dark)	5.5	3.5	4.0	NA
Pliny(IPA)	3.0	NA	8.5	2.0