

Modeling

```
# create model
mod_full <- aov(Glucose ~ Gender + NutritionBar*factor(Minutes) + Error(factor(Participant)), data = nb)
summary(mod_full)
```

```
##
## Error: factor(Participant)
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Gender      1  110.3    110.3    2.189 0.17726
## NutritionBar 2 1405.8    702.9   13.957 0.00246 **
## Residuals    8  402.9     50.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Error: Within
##           Df Sum Sq Mean Sq F value    Pr(>F)
## factor(Minutes)      2  696.2    348.1   23.675 9.13e-06 ***
## NutritionBar:factor(Minutes) 4  397.8     99.4    6.763 0.00166 **
## Residuals           18  264.7     14.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# reduce model
mod_red <- aov(Glucose ~ NutritionBar*factor(Minutes) + Error(factor(Participant)), data = nb)
summary(mod_red)
```

```
##
## Error: factor(Participant)
##           Df Sum Sq Mean Sq F value    Pr(>F)
## NutritionBar 2 1503.4    751.7   16.28 0.00102 **
## Residuals    9  415.6     46.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Error: Within
##           Df Sum Sq Mean Sq F value    Pr(>F)
## factor(Minutes)      2  696.2    348.1   23.675 9.13e-06 ***
## NutritionBar:factor(Minutes) 4  397.8     99.4    6.763 0.00166 **
## Residuals           18  264.7     14.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# create model/objects for residual plots
mod_plot <- lmer(Glucose ~ NutritionBar*Minutes + (1 | NutritionBar:Participant), data = nb)
```

```
## boundary (singular) fit: see ?isSingular
```

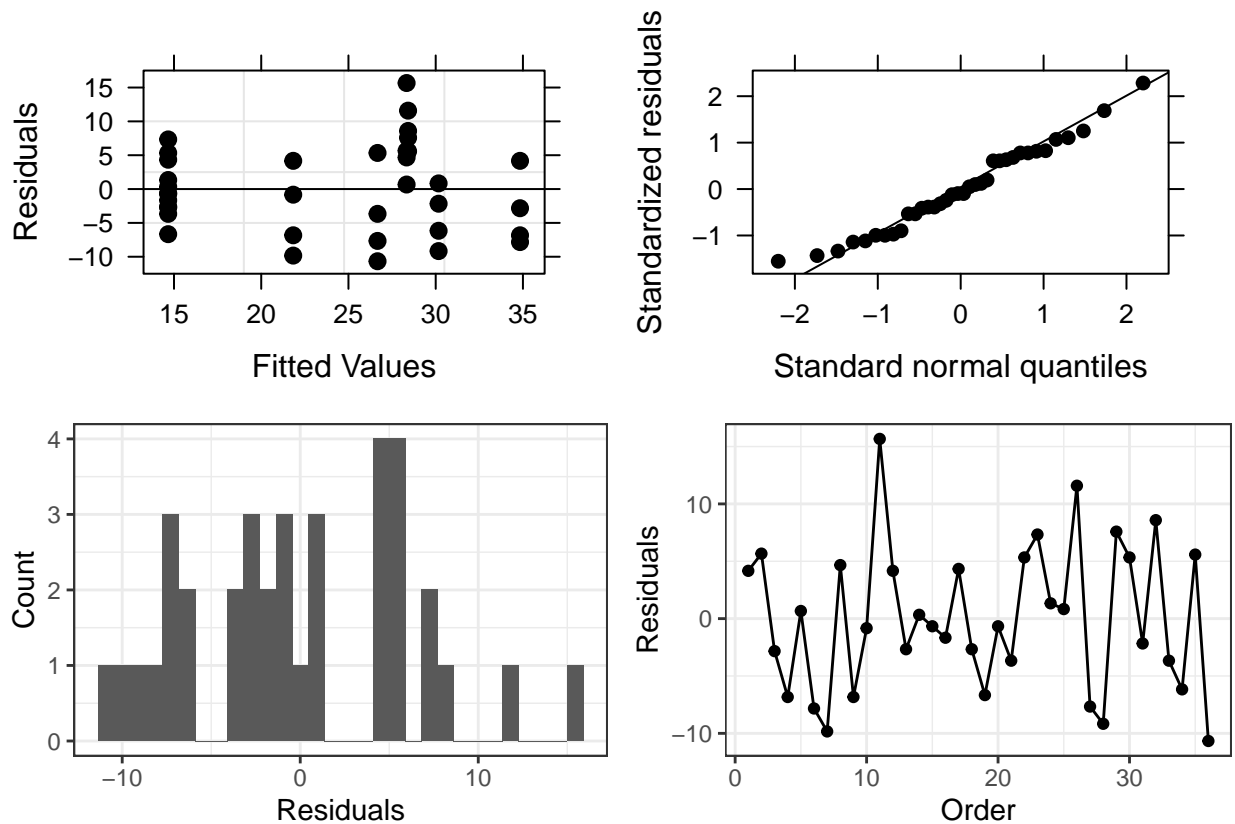
```

mod_resid <- resid(mod_plot)
mod_fitted <- fitted(mod_plot)
nb1 <- nb1 %>% mutate(res = mod_resid,
                      index = 1:n())

# generate plots
r1 <- plot(mod_plot, xlab = "Fitted Values", ylab = "Residuals", pch = 19, col = "black")
r2 <- qqmath(mod_plot, pch = 19, col = "black")
r3 <- ggplot(nb1, aes(res)) +
  geom_histogram() +
  xlab("Residuals") +
  ylab("Count")
r4 <- ggplot(nb1, aes(index, res)) +
  geom_point() +
  geom_line() +
  xlab("Order") +
  ylab("Residuals")
grid.arrange(r1, r2, r3, r4, nrow = 2)

```

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



```

# residual checks
resid_test <- nb$Glucose - mod_fitted
round(mod_resid, 3) == round(resid_test, 3)

```

```

##      1      2      3      4      5      6      7      8      9     10     11     12     13     14     15     16
## TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
##     17     18     19     20     21     22     23     24     25     26     27     28     29     30     31     32
## TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
##     33     34     35     36
## TRUE TRUE TRUE TRUE

```