Modeling

```r
# create model
mod_full <- aov(Glucose ~ Gender + NutritionBar*Minutes + Error(Participant), data = nb)
tab_full <- summary(mod_full)
kable(tab_full$`Error: Participant`[[1]], caption = "Error: Participant")
```

Error: Participant

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Gender	1	110.2500	110.25000	2.189084	0.1772572
NutritionBar	2	1405.8139	702.90694	13.956662	0.0024623
Residuals	8	402.9083	50.36354	NA	NA

```r
kable(tab_full$`Error: Within`[[1]], caption = "Error: Within")
```

Error: Within

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Minutes	2	696.2222	348.11111	23.675063	0.0000091
NutritionBar:Minutes	4	397.7778	99.44444	6.763224	0.0016612
Residuals	18	264.6667	14.70370	NA	NA

```
# reduce model
mod_red <- aov(Glucose ~ NutritionBar*Minutes + Error(Participant), data = nb)
tab_red <- summary(mod_red)
kable(tab_red$`Error: Participant`[[1]], caption = "Error: Participant")
```

Error: Participant

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
NutritionBar	2	1503.3889	751.69444	16.27893	0.0010237
Residuals	9	415.5833	46.17593	NA	NA

```
kable(tab_red$`Error: Within`[[1]], caption = "Error: Within")
```

Error: Within

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Minutes	2	696.2222	348.11111	23.675063	0.0000091
NutritionBar:Minutes	4	397.7778	99.44444	6.763224	0.0016612
Residuals	18	264.6667	14.70370	NA	NA

```
# create model/objects for residual plots
mod_plot <- lmer(Glucose ~ NutritionBar*Minutes + (1 | NutritionBar:Participant), data = nb)
mod_resid <- resid(mod_plot)
mod_fitted <- fitted(mod_plot)
nb1 <- nb %>% 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`.
```
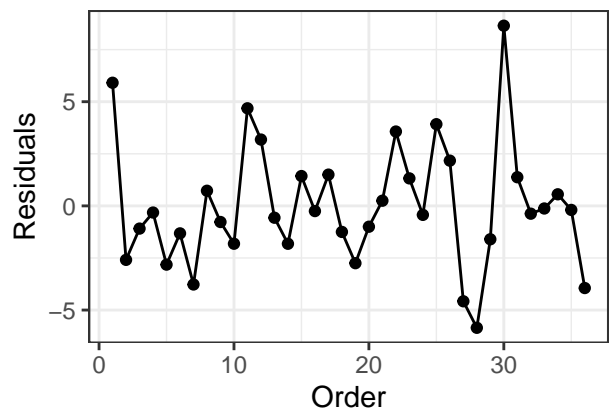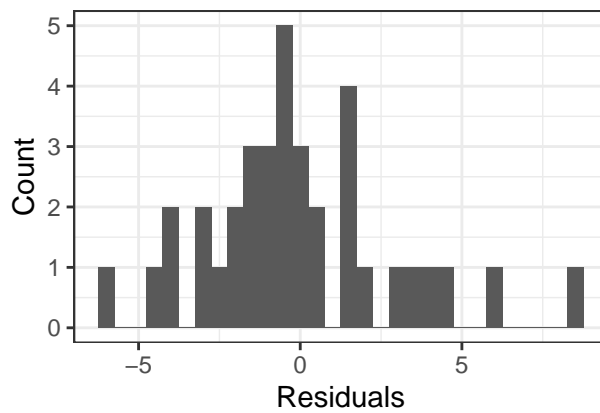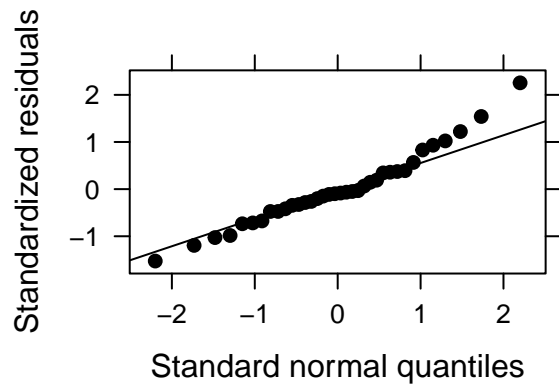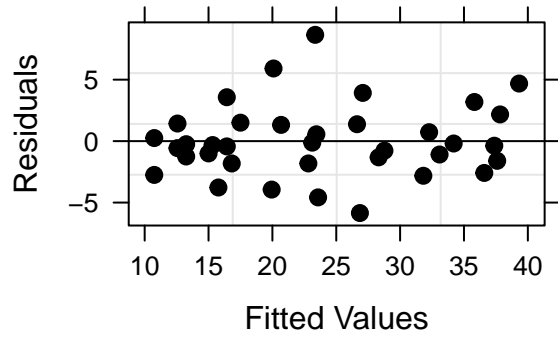
```
# residual checks
# resid_test <- nb$Glucose - mod_fitted
# round(mod_resid, 3) == round(resid_test, 3)
```