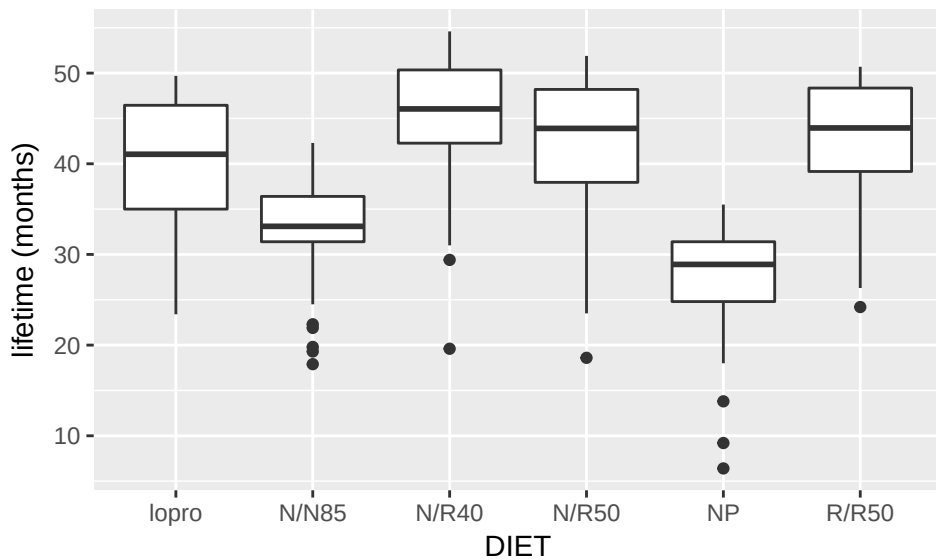
Consider the ANOVA model from the handout on lifetimes of mice on six different diets:

$$\begin{aligned} E[Y_{ij}] &= \mu_i \\ Y_{ij} &= \text{months survived, } LIFETIME \\ i &= \text{index for which diet, } DIET \end{aligned}$$

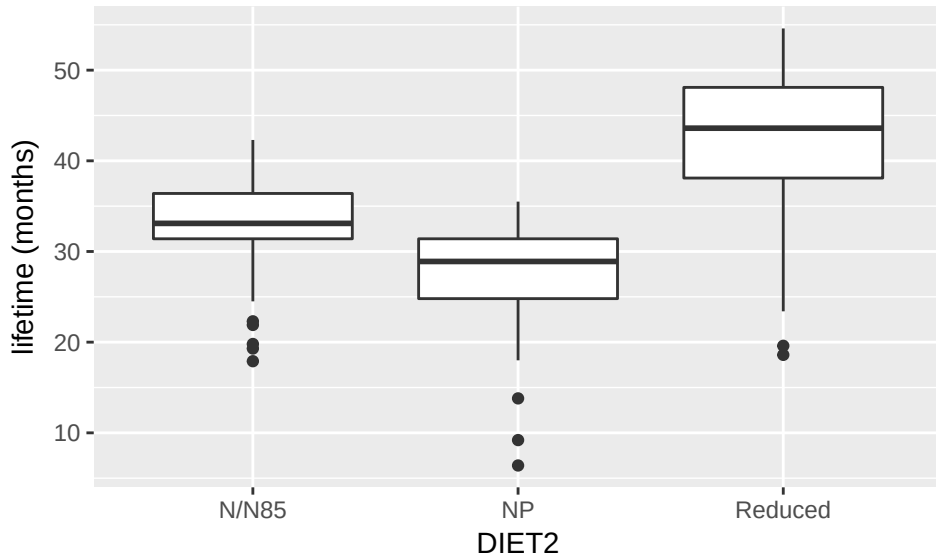
```
mice <- read.table("http://pages.pomona.edu/~jsh04747/courses/math158/micedata.csv",
                   header=T, sep=",")

mice <- mice %>%
  mutate(DIET2 = ifelse(DIET=="NP","NP", ifelse(DIET=="N/N85","N/N85","Reduced")))
```

Note that the mice data is 349 x 2 which is how we want it!

```
ggplot(mice, aes(x=DIET, y=LIFETIME)) + geom_boxplot() +  ylab("lifetime (months)")
```




```
ggplot(mice, aes(x=DIET2, y=LIFETIME)) + geom_boxplot() +  ylab("lifetime (months)")
```




```
mice1.aov <- aov(LIFETIME ~ DIET, data=mice)
mice2.aov <- aov(LIFETIME ~ DIET2, data=mice)
anova(mice1.aov)

## Analysis of Variance Table
##
## Response: LIFETIME
##            Df Sum Sq Mean Sq F value Pr(>F)
## DIET        5  12734    2547    57.1 <2e-16 ***
## Residuals 343  15297      45
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mice2.aov)

## Analysis of Variance Table
##
## Response: LIFETIME
##            Df Sum Sq Mean Sq F value Pr(>F)
## DIET2       2  11869    5934     127 <2e-16 ***
## Residuals 346  16163      47
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mice %>%
  group_by(DIET) %>%
  summarize(mean(LIFETIME), sd(LIFETIME), n())

## # A tibble: 6 x 4
##   DIET  `mean(LIFETIME)` `sd(LIFETIME)` `n()`
##   <fct>            <dbl>          <dbl> <int>
## 1 lopro             39.7           6.99    56
```

```
## 2 N/N85              32.7           5.13    57
## 3 N/R40              45.1           6.70    60
## 4 N/R50              42.3           7.77    71
## 5 NP                 27.4           6.13    49
## 6 R/R50              42.9           6.68    56
```

```
mice %>%
  group_by(DIET2) %>%
  summarize(mean(LIFETIME), sd(LIFETIME), n())
```

```
## # A tibble: 3 x 4
##   DIET2   `mean(LIFETIME)` `sd(LIFETIME)` `n()`
##   <chr>              <dbl>          <dbl> <int>
## 1 N/N85               32.7           5.13    57
## 2 NP                  27.4           6.13    49
## 3 Reduced             42.5           7.30   243
```

To obtain the fitted and residual values...

```
library(broom)

aov(LIFETIME ~ DIET, data=mice) %>% augment() %>%
  select(.fitted, .resid) %>%
  head()
```

```
##   .fitted .resid
## 1    27.4    8.1
## 2    27.4    8.0
## 3    27.4    7.5
## 4    27.4    7.4
## 5    27.4    6.4
## 6    27.4    6.1
```

```
lm(LIFETIME ~ DIET, data=mice) %>% augment() %>%
  select(.fitted, .resid) %>%
  head()
```

```
##   .fitted .resid
## 1    27.4    8.1
## 2    27.4    8.0
## 3    27.4    7.5
## 4    27.4    7.4
## 5    27.4    6.4
## 6    27.4    6.1
```