

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("micedata.csv", header=T, sep=",")
> attach(mice)
> dim(mice)
> 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!
# (because (a) we might not have equal sample sizes, and (b)
# our columns should be our variables... one response, one treatment)

> boxplot(LIFETIME ~ DIET, ylab="lifetime (months)")
> boxplot(LIFETIME ~ DIET2, ylab="lifetime (months)")

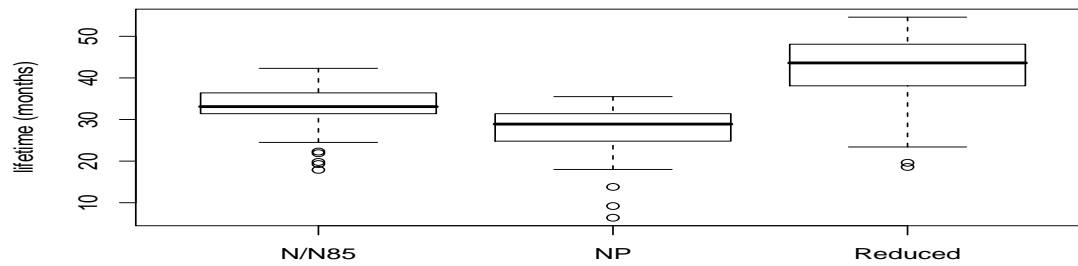
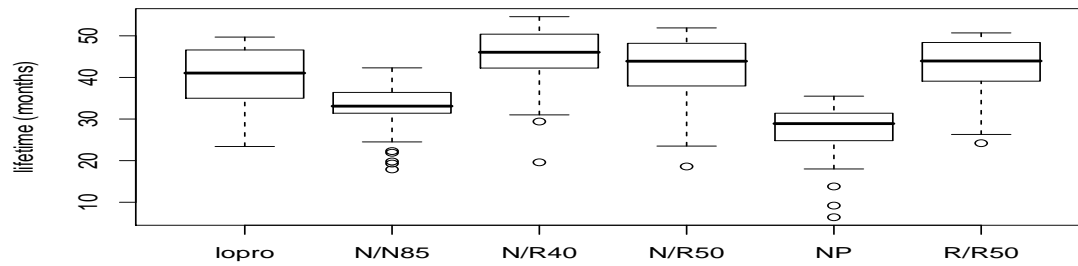
> mice1.aov <- aov(LIFETIME ~ DIET)
> mice2.aov <- aov(LIFETIME ~ DIET2)

> anova(mice1.aov)
Analysis of Variance Table

Response: LIFETIME
      Df Sum Sq Mean Sq F value    Pr(>F)
DIET    5 12733.9   2546.8   57.104 < 2.2e-16 ***
Residuals 343 15297.4     44.6

> anova(mice2.aov)
Analysis of Variance Table

Response: LIFETIME
      Df Sum Sq Mean Sq F value    Pr(>F)
DIET2   2 11868.5   5934.3  127.04 < 2.2e-16 ***
Residuals 346 16162.8     46.7
```



```
> tapply(LIFETIME, DIET, mean)
  lopro  N/N85  N/R40  N/R50    NP  R/R50
39.68571 32.69123 45.11667 42.29718 27.40204 42.88571
```

```
> tapply(LIFETIME, DIET, sd)
  lopro  N/N85  N/R40  N/R50    NP  R/R50
6.991695 5.125297 6.703406 7.768195 6.133701 6.683152
```

```
> table(DIET)
lopro N/N85 N/R40 N/R50    NP R/R50
  56    57    60    71    49    56
```

```
> tapply(LIFETIME, DIET2, mean)
  N/N85    NP Reduced
32.69123 27.40204 42.52716
```

```
> tapply(LIFETIME, DIET2, sd)
  N/N85    NP Reduced
5.125297 6.133701 7.297096
```

```
> table(DIET2)
  N/N85    NP Reduced
    57    49    243
```