

STAT 510 HW #3

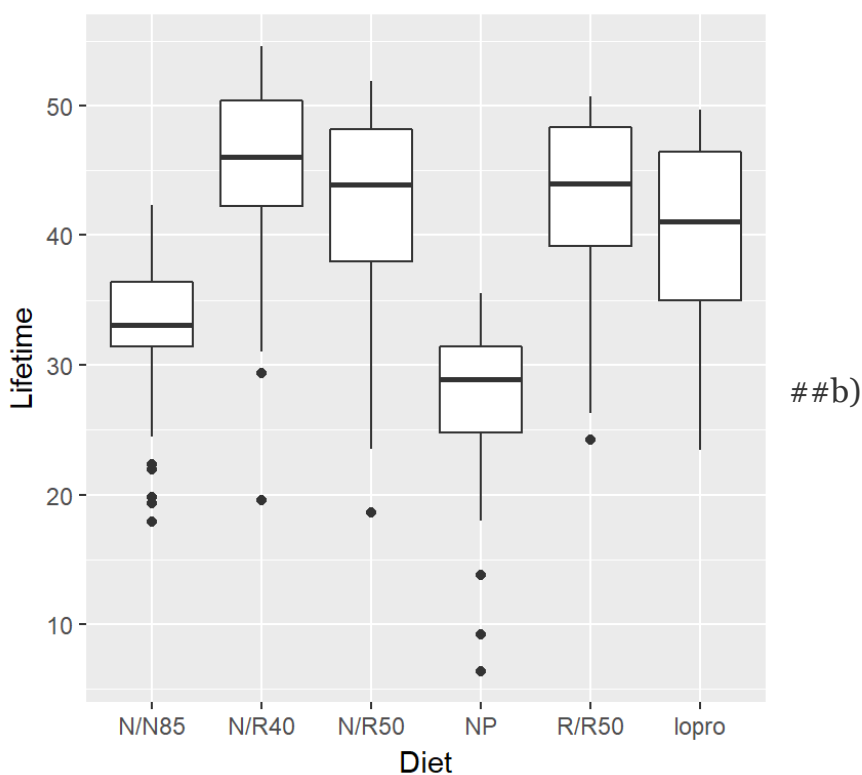
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1)

a)

```
df <- case0501
g <- ggplot(data = df, aes(x = Diet, y = Lifetime))
g + geom_boxplot()
```



```
mod <- lm(Lifetime~0+Diet, data = df)
anva <- anova(mod)
anva
```

```
## Analysis of Variance Table
##
## Response: Lifetime
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Diet         6 538055    89676  2010.7 < 2.2e-16 ***
## Residuals   343  15297         45
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova$`Sum Sq`[2]
```

```
## [1] 15297.42
```

```
#alternative using matrices
lenx <- length(df$Diet)
diets <- arrange(df, Diet)
Ident <- diag(lenx)
X <- model.matrix(~0+factor(diets$Diet))
Px <- X%*%ginv(t(X)%*%X)%*%t(X)
y <- diets$Lifetime
sse <- t(y)%*%(Ident-Px)%*%y
sse
```

```
##           [,1]
## [1,] 15297.42
```

c)

```
#Using ANOVA Table
anova
```

```
## Analysis of Variance Table
##
## Response: Lifetime
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Diet         6 538055    89676 2010.7 < 2.2e-16 ***
## Residuals  343  15297         45
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova$`Mean Sq`[2]
```

```
## [1] 44.59888
```

```
#using matrices
sig2hat <- sse/(lenx - 6)
sig2hat
```

```
##           [,1]
## [1,] 44.59888
```

d)

```
#using lm
dietsn <- diets
#recode
dietsn$Diet[dietsn$Diet=="N/R50"] <- "lopro"
#lm
mod.red <- lm(Lifetime~0+Diet, data = dietsn)
anva.red <- anova(mod.red)
anva.red
```

```
## Analysis of Variance Table
##
## Response: Lifetime
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Diet         5 537841  107568  2385.6 < 2.2e-16 ***
## Residuals  344  15511         45
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anva.red$`Sum Sq`[2]
```

```
## [1] 15510.92
```

```
#using matrices
Xo <- model.matrix(~0+factor(dietsn$Diet))
Po <- Xo%*%ginv(t(Xo)%*%Xo)%*%t(Xo)
y <- diets$Lifetime
sse.red <- t(y)%*%(Ident-Po)%*%y
sse.red
```

```
##           [,1]
## [1,] 15510.92
```

e)

```
#using anova()
anova(mod.red, mod)$F[2]
```

```
## [1] 4.787275
```

```
#using matrices
Fstat <- ((sse.red - sse)/(anva.red$Df[2]-anva$Df[2])) / (sse/anva$Df[2])
Fstat
```

```
##           [,1]
## [1,] 4.787275
```

```
#and a p-value as well
pf(Fstat, df1 = (anva.red$Df[2]-anva$Df[2]), df2 = (anva$Df[2]), lower.tail = F)
```

```
##           [,1]
## [1,] 0.02934503
```

f)

The F-statistic can be used to test whether there is a *significant difference in mean lifetimes* of the two groups of mice that were fed reduced calorie diets only after weaning but not before (groups N/R50 and N/R50 loopro). The test would help determine whether there was an effect of the low protein diet when mice were fed reduced calorie diets only after weaning. ##g) Our β matrix is just a vector of group means,

$$\beta = \begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \\ \mu_4 \\ \mu_5 \\ \mu_6 \end{bmatrix}$$

Where each μ_i is the group mean for each treatment group listed in the order of the statement. We want to test whether group 3 has the same treatment mean as group 5, or that $\mu_3 - \mu_5 = 0$. Then

$$\mathbf{C} = \begin{bmatrix} 0 & 0 & 1 & 0 & -1 & 0 \end{bmatrix}$$

and $\mathbf{d} = 0$

Then our F-statistic should be the same as before, and now using the matrix method on slide 20, we get

```

C = t(c(0,0,1,0,0,-1)) #I sorted the data so C is different than specified above
q = 1
d = 0
y <- diets$Lifetime
X <- model.matrix(~0+factor(diets$Diet))
betahat = ginv(t(X)%*%X)%*%t(X)%*%y
Fc = (t((C%*%betahat))%*%solve(C%*%(ginv(t(X)%*%X))%*%t(C))%*%(C%*%betahat) / 1) / (sig2hat)
Fc

```

```

##           [,1]
## [1,] 4.787275

```

2)

Let

$$\mathbf{A} = \begin{bmatrix} -1 & 1 \\ 1 & 1 \end{bmatrix}$$

and let

$$\mathbf{G} = \begin{bmatrix} -1/2 & -1 \\ 1 & -1/2 \end{bmatrix}$$

Simple matrix multiplication will show that $\mathbf{AGA} = \mathbf{A}$, thus by definition \mathbf{G} is a generalized inverse of \mathbf{A} . But \mathbf{A} is symmetric (off-diagonal elements are the same), and \mathbf{G} is clearly not symmetric as $-1 \neq 1$, so generalized inverses of symmetric matrices need not be symmetric.

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