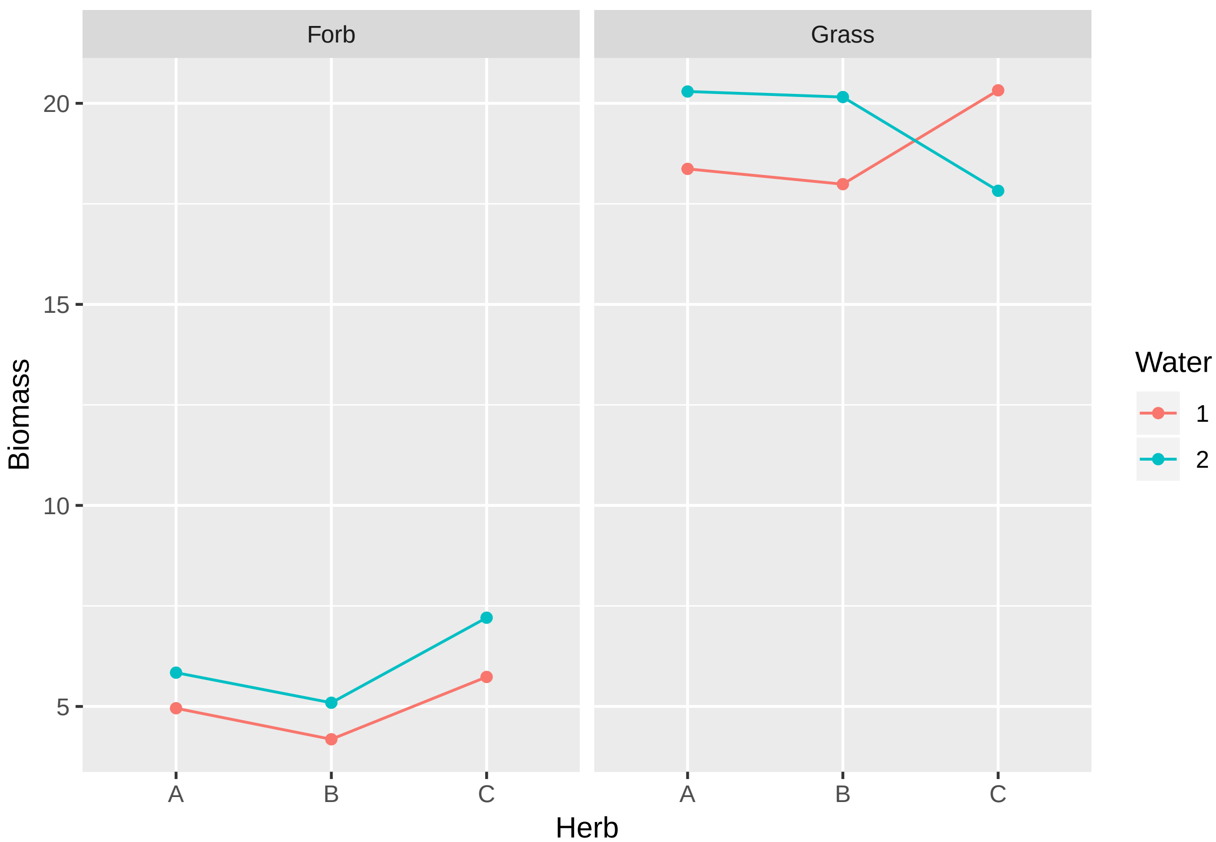
HW8 KEY

40 points total, 2 points per problem part unless otherwise noted.

```
library(dplyr)
library(ggplot2)
library(car)
library(emmeans)
InData <- read.csv("C:/hess/STAT512/HW_2019/HW8/Biomass.csv")
#str(InData)
InData$Water <- as.factor(InData$Water)
```

1. Summary Graph (**4pts**)

```
SumStats <- summarize(group_by(InData, Type, Herb, Water),
                      n = n(),
                      Biomass = mean(Biomass),
                      sd = sd(Biomass))
#SumStats
qplot(x = Herb, y = Biomass, colour = Water, group = Water, data = SumStats) +
  geom_line() +
  facet_grid(. ~ Type)
```



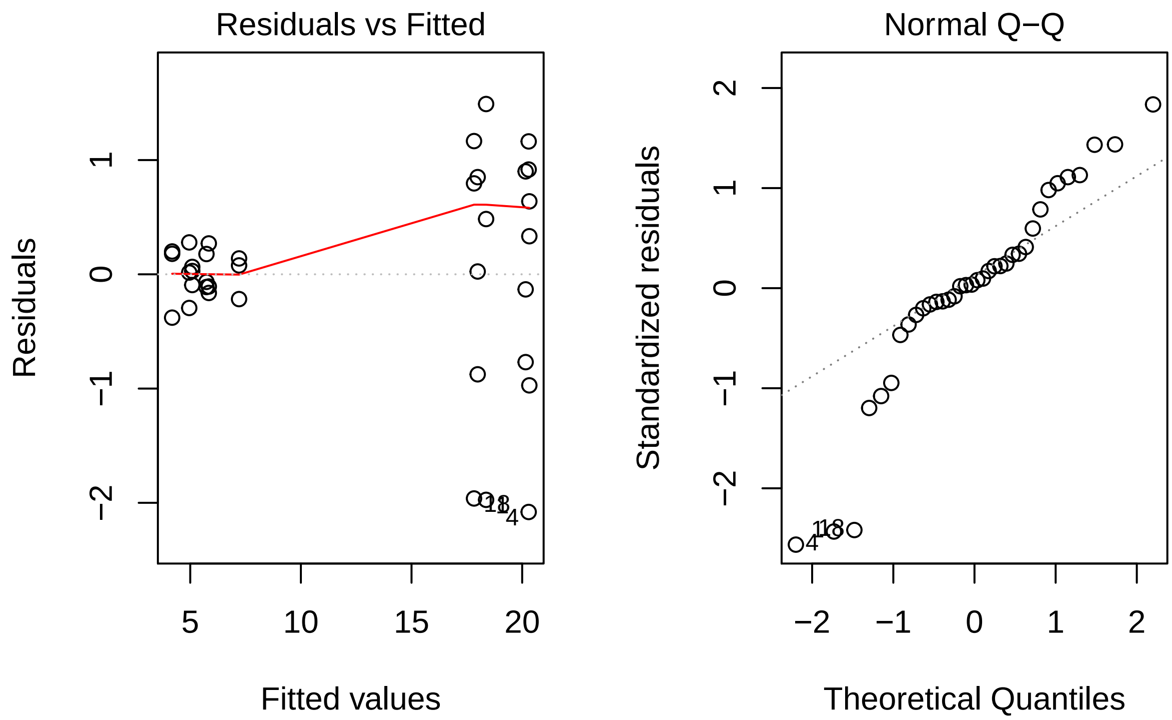
2. Three-way ANOVA table

```r
options(contrasts=c("contr.sum","contr.poly"))
Model1 <- lm(Biomass ~ Type*Herb*Water, data = InData)
Anova(Model1, type = 3)
```

```
## Anova Table (Type III tests)
##
## Response: Biomass
##                  Sum Sq Df   F value    Pr(>F)
## (Intercept)      5473.8  1 5539.1323 < 2.2e-16 ***
## Type             1678.7  1 1698.7721 < 2.2e-16 ***
## Herb                5.1  2    2.5644  0.097872 .
## Water               5.9  1    5.9711  0.022271 *
## Type:Herb           5.4  2    2.7185  0.086259 .
## Type:Water          0.7  1    0.7092  0.408021
## Herb:Water          7.9  2    3.9973  0.031742 *
## Type:Herb:Water    13.1  2    6.6440  0.005055 **
## Residuals          23.7 24
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3. Three-way Diagnostic plots
   Note: Diagnostic plots not required for full credit, but shown here for completeness.
   Based on the plot of Resids vs Fitted, there is strong evidence of unequal variance.
   (Based on the QQplot, there is also some evidence against normality. But this is actually driven by the unequal variance.)

```r
par(mfrow=c(1,2))
plot(Model1, which = c(1:2))
```



4. Three-way emmeans

```
emout1 <- emmeans(Model1, pairwise ~ Water|Herb*Type)
emout1$contrasts
```

```
## Herb = A, Type = Forb:
##  contrast estimate    SE df t.ratio p.value
##  1 - 2      -0.885 0.812 24 -1.090  0.2865
##
## Herb = B, Type = Forb:
##  contrast estimate    SE df t.ratio p.value
##  1 - 2      -0.908 0.812 24 -1.119  0.2741
##
## Herb = C, Type = Forb:
##  contrast estimate    SE df t.ratio p.value
##  1 - 2      -1.473 0.812 24 -1.815  0.0821
##
## Herb = A, Type = Grass:
##  contrast estimate    SE df t.ratio p.value
##  1 - 2      -1.924 0.812 24 -2.371  0.0261
##
## Herb = B, Type = Grass:
##  contrast estimate    SE df t.ratio p.value
##  1 - 2      -2.167 0.812 24 -2.669  0.0134
##
## Herb = C, Type = Grass:
##  contrast estimate    SE df t.ratio p.value
```

```
##  1 - 2       2.499 0.812 24  3.079  0.0051
```

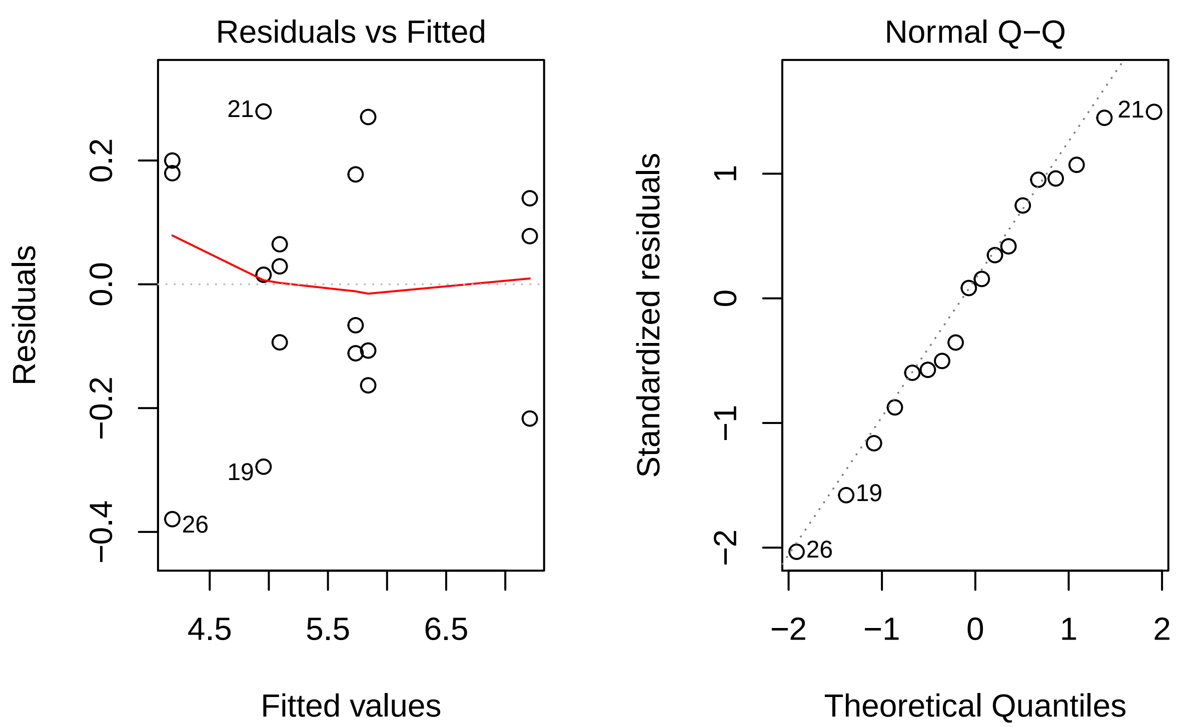
5. FORB Two-way ANOVA table

```r
Model2 <- lm(Biomass ~ Herb*Water, data = InData[InData$Type == "Forb",])
Anova(Model2, type =3)
```

```
## Anova Table (Type III tests)
##
## Response: Biomass
##              Sum Sq Df    F value    Pr(>F)
## (Intercept) 544.92  1 10432.1562 < 2.2e-16 ***
## Herb         10.17  2    97.3895 3.820e-08 ***
## Water         5.33  1   102.1229 3.197e-07 ***
## Herb:Water    0.33  2     3.1846   0.07772 .
## Residuals     0.63 12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

6. FORB diagnostic plots look much better! Some evidence of unequal variance, but not severe.

```r
par(mfrow = c(1,2))
plot(Model2, which = c(1:2))
```



7. FORB emmeans #1 (interaction comparisons)

```r
emout2 <- emmeans(Model2, pairwise ~ pairwise ~ Water|Herb)
emout2$contrasts
```

```
## Herb = A:
```

```
##  contrast estimate    SE df t.ratio p.value
##  1 - 2      -0.885 0.187 12 -4.742  0.0005
##
## Herb = B:
##  contrast estimate    SE df t.ratio p.value
##  1 - 2      -0.908 0.187 12 -4.868  0.0004
##
## Herb = C:
##  contrast estimate    SE df t.ratio p.value
##  1 - 2      -1.473 0.187 12 -7.894  <.0001
```

8. FORB LSD #1 (interaction comparisons)

```
qt(0.975, df = 12)*sqrt(2*(0.63/12)/3)
```

```
## [1] 0.4076186
```

```
qt(0.975, df = 12)*0.187
```

```
## [1] 0.407438
```

9. FORB emmeans #2 (main effect comparison)

```
emout3 <- emmeans(Model2, pairwise ~ Water)
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
emout3$contrasts
```

```
##  contrast estimate    SE df t.ratio p.value
##  1 - 2       -1.09 0.108 12 -10.106 <.0001
##
## Results are averaged over the levels of: Herb
```

10. FORB LSD #2 (main effect comparison)

```
qt(0.975, df = 12)*sqrt(2*(0.63/12)/9)
```

```
## [1] 0.2353387
```

```
qt(0.975, df = 12)*0.108
```

```
## [1] 0.2353118
```

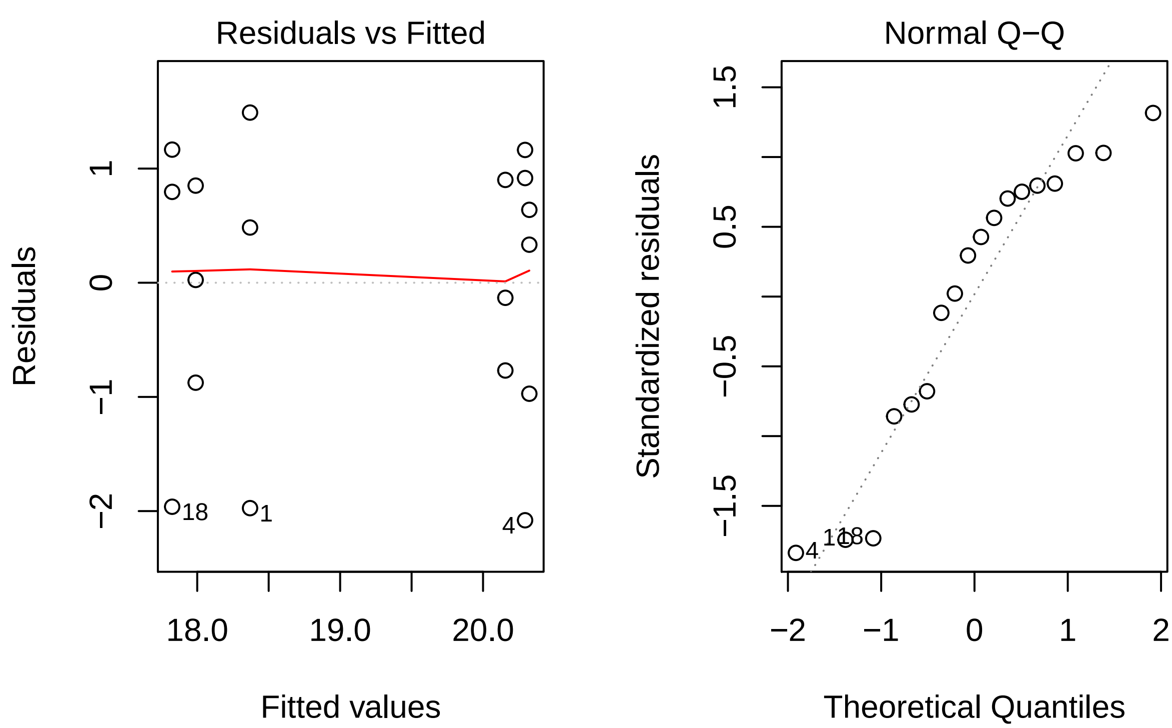
11. The power is higher for the main effect comparison (#10) becuase the LSD (ME) is smaller.
12. GRASS Two-way ANOVA table

```
Model3 <- lm(Biomass ~ Herb*Water, data = InData[InData$Type == "Grass",])
Anova(Model3, type =3)
```

```
## Anova Table (Type III tests)
##
## Response: Biomass
##             Sum Sq Df   F value    Pr(>F)
## (Intercept) 6607.6  1 3433.9972 4.029e-16 ***
## Herb           0.3  2    0.0694    0.9333
## Water          1.3  1    0.6586    0.4329
## Herb:Water    20.7  2    5.3786    0.0215 *
## Residuals     23.1 12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

13. GRASS diagnostic plots look much better! Some evidence of skew (non-normality), but not severe.

```r
par(mfrow = c(1,2))
plot(Model3, which = c(1:2))
```



14. GRASS emmeans (interaction comparisons)

```r
emout4 <- emmeans(Model3, pairwise ~ Water|Herb)
emout4$contrasts
```

```
## Herb = A:
##  contrast estimate   SE df t.ratio p.value
##  1 - 2       -1.92 1.13 12 -1.699  0.1150
##
## Herb = B:
##  contrast estimate   SE df t.ratio p.value
##  1 - 2       -2.17 1.13 12 -1.913  0.0799
##
## Herb = C:
##  contrast estimate   SE df t.ratio p.value
##  1 - 2        2.50 1.13 12  2.207  0.0476
```

15. No, because there is evidence of an interaction between Water and Herb. In particular, the estimated difference in mean response changes sign when comparing across Herb. When there is evidence of an interaction, it does not make sense to look at main effects.

16. (**4pts**) The estimated differences are the SAME.
The SEs are DIFFERENT (Combined SE = 0.812, Forb SE = 0.187, Grass SE = 1.13).
The df is DIFFERENT (combined df = 24, split df = 12).

17. (1) The combined analysis showed strong evidence of unequal variance. The model assumptions are better satisfied using the split analyses. (2) The combined analysis showed evidence of a three-way interaction.

18. (1) When we split the analysis we reduce the df (hence reducing power). (2) When we split the analysis we cannot get direct comparisons of Forb versus Grass.