ES 193DS Homework 3

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Preparations

Reading in packages

```
# general use
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.0     v tibble    3.2.1
v lubridate 1.9.3     v tidyr     1.3.1
v purrr     1.0.2
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becor
```

```
library(readxl)
library(here)
```

```
here() starts at /Users/ellastookey/Desktop/ENVS-193DS/git/stookey-ella_homework-03
```

```
library(janitor)
```

```
Attaching package: 'janitor'

The following objects are masked from 'package:stats':

    chisq.test, fisher.test
```

```
# visualizing pairs
library(GGally)
```

```
Registered S3 method overwritten by 'GGally':
  method from
  +.gg   ggplot2
```

```
# model selection
library(MuMIn)

# model predictions
library(ggeffects)

# model tables
library(gtsummary)
library(flextable)
```

```
Attaching package: 'flextable'

The following objects are masked from 'package:gtsummary':

    as_flextable, continuous_summary

The following object is masked from 'package:purrr':

    compose
```

```
library(modelsummary)
```

```
`modelsummary` 2.0.0 now uses `tinytable` as its default table-drawing
  backend. Learn more at: https://vincentarelbundock.github.io/tinytable/
```

```
Revert to `kableExtra` for one session:

  options(modelsummary_factory_default = 'kableExtra')
  options(modelsummary_factory_latex = 'kableExtra')
  options(modelsummary_factory_html = 'kableExtra')

Silence this message forever:

  config_modelsummary(startup_message = FALSE)
```

```
drought_exp <- read_xlsx(path = here("data",
                                     "Valliere_etal_EcoApps_Data.xlsx"),
                         sheet = "First Harvest")

# quick look at data
str(drought_exp)
```

```
tibble [70 x 13] (S3: tbl_df/tbl/data.frame)
 $ Species            : chr [1:70] "ENCCAL" "ENCCAL" "ENCCAL" "ENCCAL" ...
 $ Water              : chr [1:70] "WW" "WW" "WW" "WW" ...
 $ Rep #              : num [1:70] 1 2 3 4 5 1 2 3 4 5 ...
 $ Height (cm)        : num [1:70] 5.8 4.9 8.4 6.5 7.1 3.2 4.4 4.2 4.5 3.9 ...
 $ Leaf #             : num [1:70] 11 8 11 12 10 7 7 10 8 6 ...
 $ Leaf dry weight (g): num [1:70] 0.0294 0.0185 0.0177 0.0178 0.0164 0.017 0.0193 0.0153 0.0
 $ Leaf area (cm2)    : num [1:70] 5.01 3.98 3.69 3.84 3.63 3.06 3.1 2.94 2.73 2.61 ...
 $ SLA                : num [1:70] 170 215 209 216 222 ...
 $ Total LA           : num [1:70] 55.1 31.8 40.6 46.1 36.3 ...
 $ Shoot (g)          : num [1:70] 0.253 0.164 0.241 0.213 0.232 ...
 $ Root (g)           : num [1:70] 0.202 0.165 0.209 0.146 0.12 ...
 $ Total (g)          : num [1:70] 0.455 0.329 0.45 0.359 0.352 ...
 $ R:S                : num [1:70] 0.8 1 0.9 0.7 0.5 0.8 1.2 3.1 0.9 1.2 ...
```

```
class(drought_exp)
```

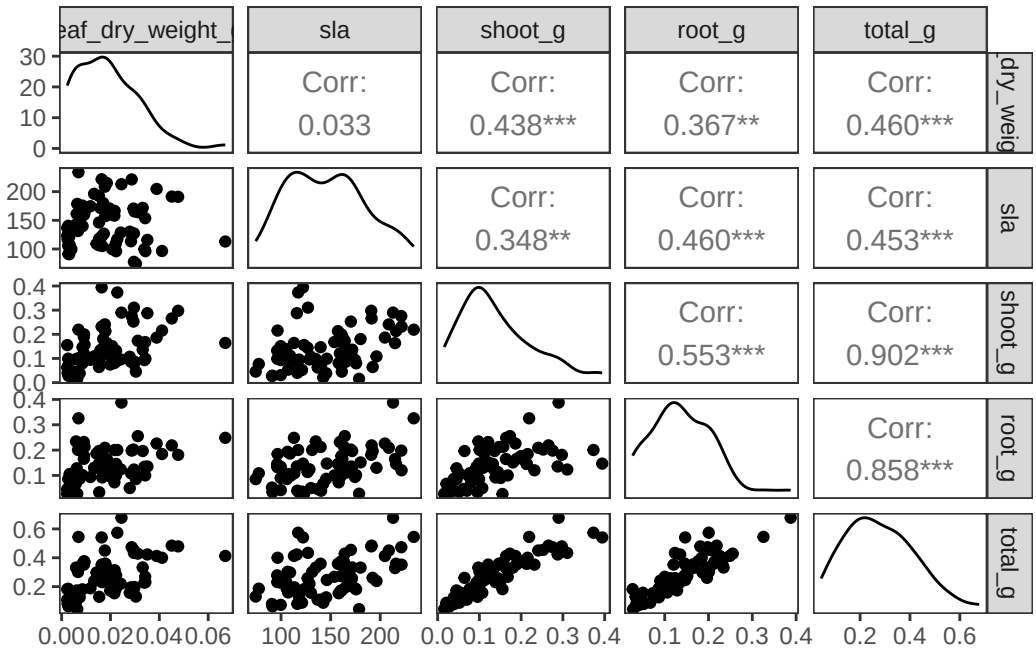
```
[1] "tbl_df"     "tbl"        "data.frame"
```

Cleaning

```r
# cleaning
drought_exp_clean <- drought_exp %>%
  clean_names() %>% # nicer column names
  mutate(species_name = case_when( # adding column with species scientific names
    species == "ENCCAL" ~ "Encelia californica", # bush sunflower
    species == "ESCCAL" ~ "Eschscholzia californica", # California poppy
    species == "PENCEN" ~ "Penstemon centranthifolius", # Scarlet bugler
    species == "GRICAM" ~ "Grindelia camporum", # great valley gumweed
    species == "SALLEU" ~ "Salvia leucophylla", # Purple sage
    species == "STIPUL" ~ "Nasella pulchra", # Purple needlegrass
    species == "LOTSCO" ~ "Acmispon glaber" # deerweed
  )) %>%
  relocate(species_name, .after = species) %>% # moving species_name column after species
  mutate(water_treatment = case_when( # adding column with full treatment names
    water == "WW" ~ "Well watered",
    water == "DS" ~ "Drought stressed"
  )) %>%
  relocate(water_treatment, .after = water) # moving water_treatment column after water
```

correlations

```r
ggpairs(drought_exp_clean, # data frame
        columns = c("leaf_dry_weight_g", # columns to visualize
                    "sla",
                    "shoot_g",
                    "root_g",
                    "total_g"),
        upper = list(method = "pearson")) + # calculating Pearson correlation coefficient
  theme_bw() + # cleaner theme
  theme(panel.grid = element_blank()) # getting rid of gridlines
```




```
# bottom left scatterplots of listed variables -- Leaf dry weight on x axis, y axis is total
# diagnol shows ?
# upper right shows Pearson's correlation -- positively correlated
```

Problem 1. Multiple linear regression: model selection and construction

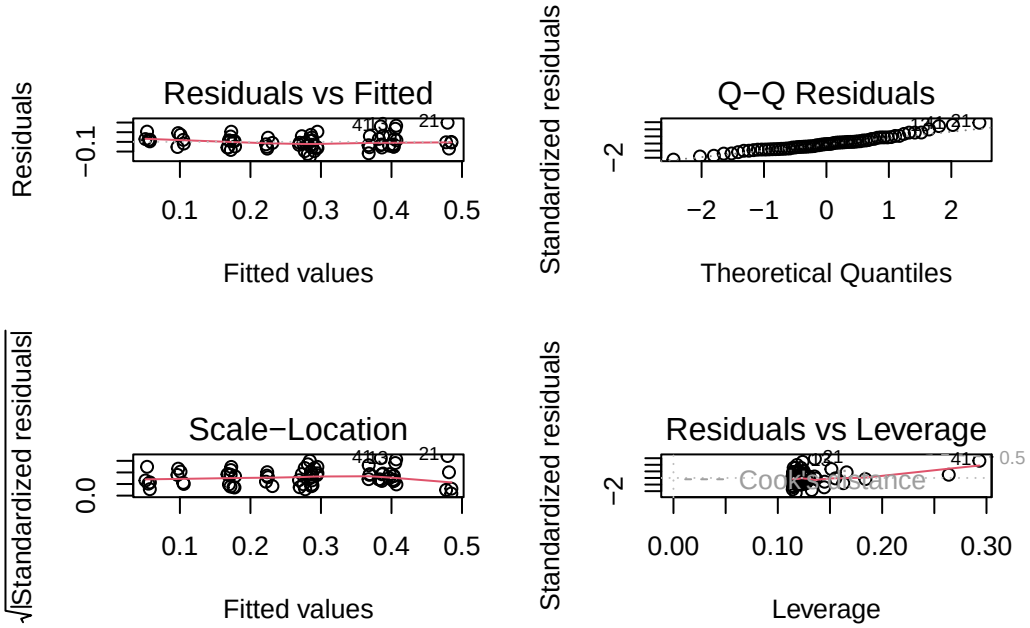
Part a

0. Null model

```
model0 <- lm(total_g ~ 1, # formula
             data = drought_exp_clean) # data frame
```

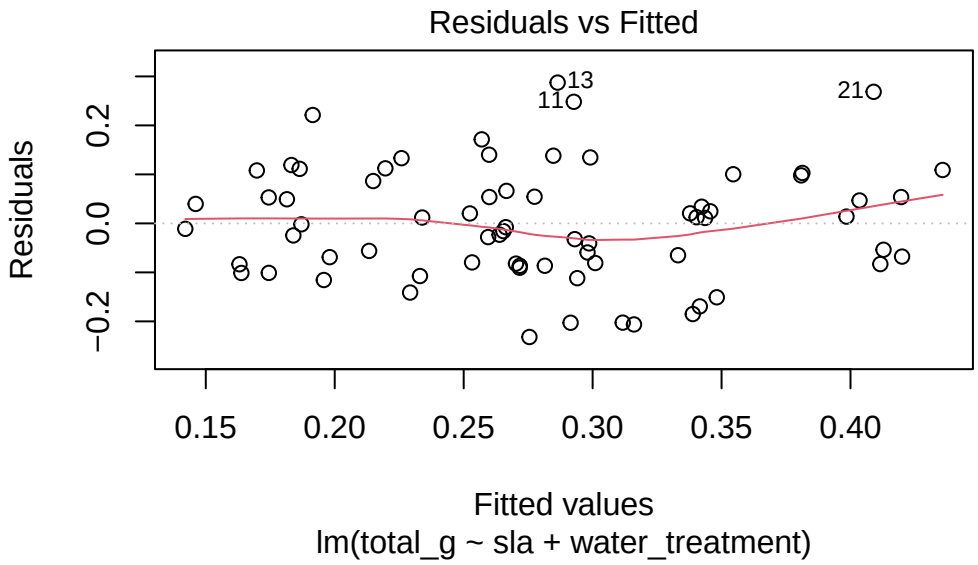
1. total biomass as a function of SLA, water treatment, and species

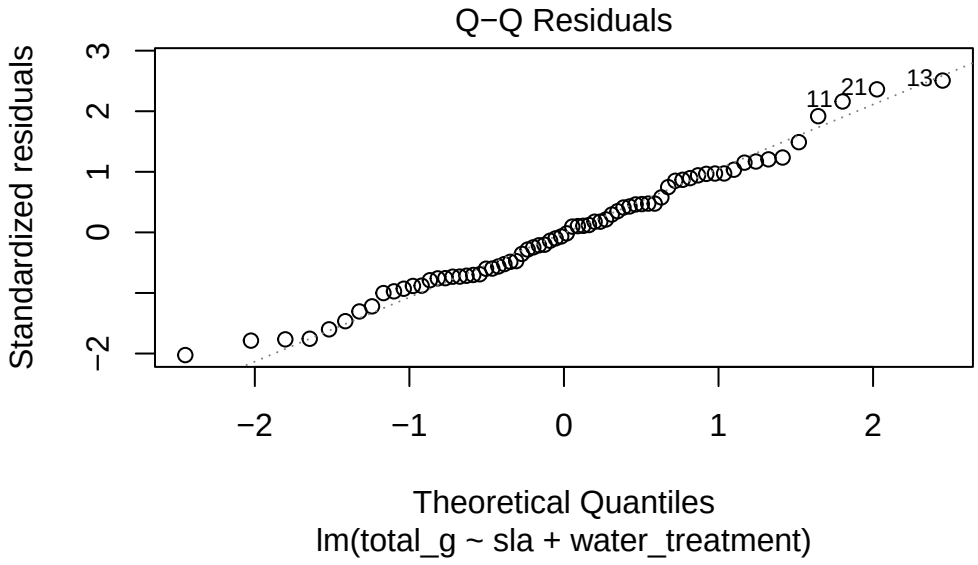
```
# saturated model
model1 <- lm(total_g ~ sla + water_treatment + species_name,
             data = drought_exp_clean)

par(mfrow = c(2, 2))
plot(model1)
```

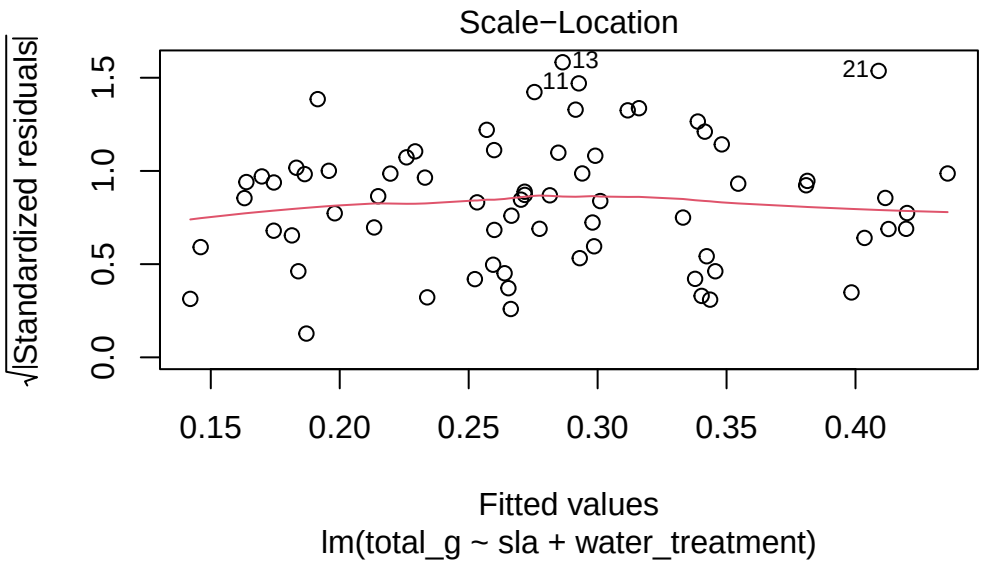


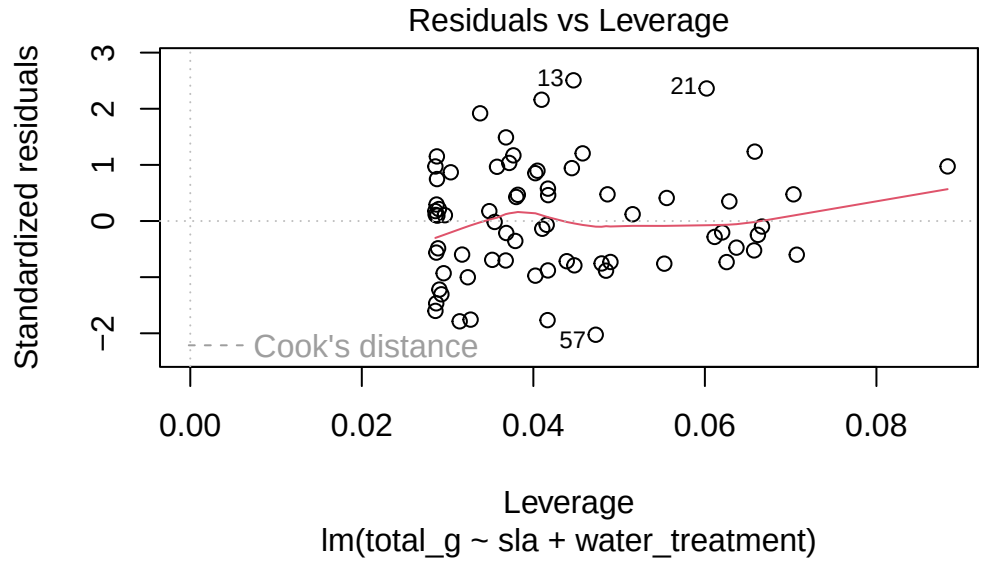
2. total biomass as a function of SLA and water treatment

```
model2 <- lm(total_g ~ sla + water_treatment,
             data = drought_exp_clean)

plot(model2)
```


Residuals vs Fitted
Residuals
−0.2
0.0
0.2
13
11
21
0.15
0.20
0.25
0.30
0.35
0.40
Fitted values
lm(total_g ~ sla + water_treatment)

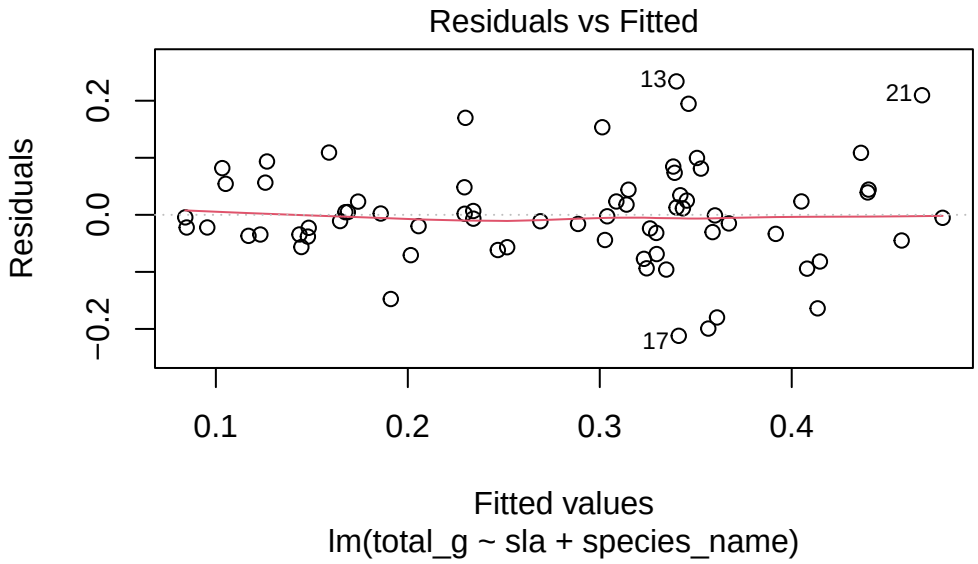

Q−Q Residuals
Standardized residuals
−2
0
1
2
3
11
21
13
−2
−1
0
1
2
Theoretical Quantiles
lm(total_g ~ sla + water_treatment)

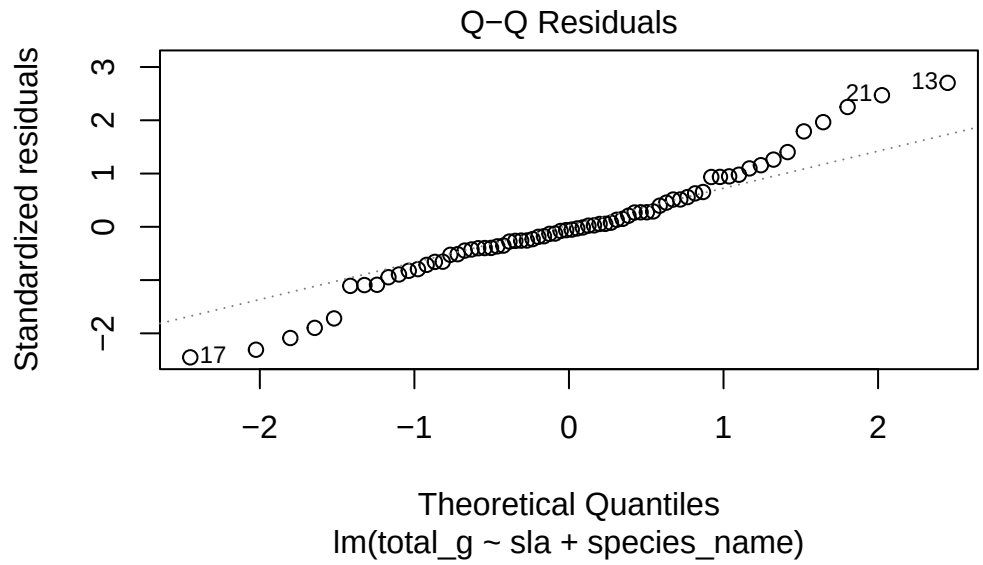

Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
13
11
21
0.15
0.20
0.25
0.30
0.35
0.40
Fitted values
lm(total_g ~ sla + water_treatment)

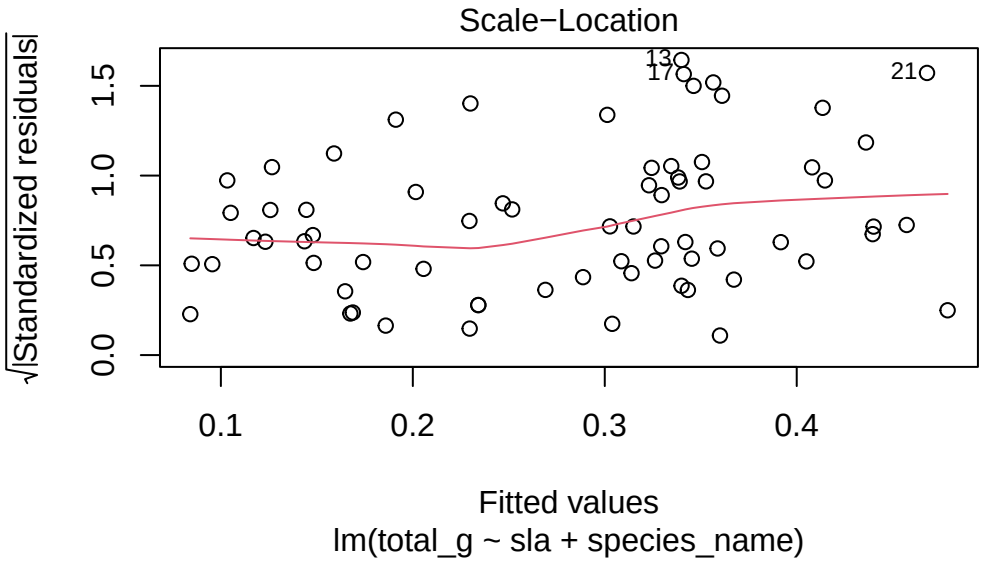

Residuals vs Leverage
Standardized residuals
−2
0
1
2
3
13
21
57
Cook's distance
0.00
0.02
0.04
0.06
0.08
Leverage
lm(total_g ~ sla + water_treatment)

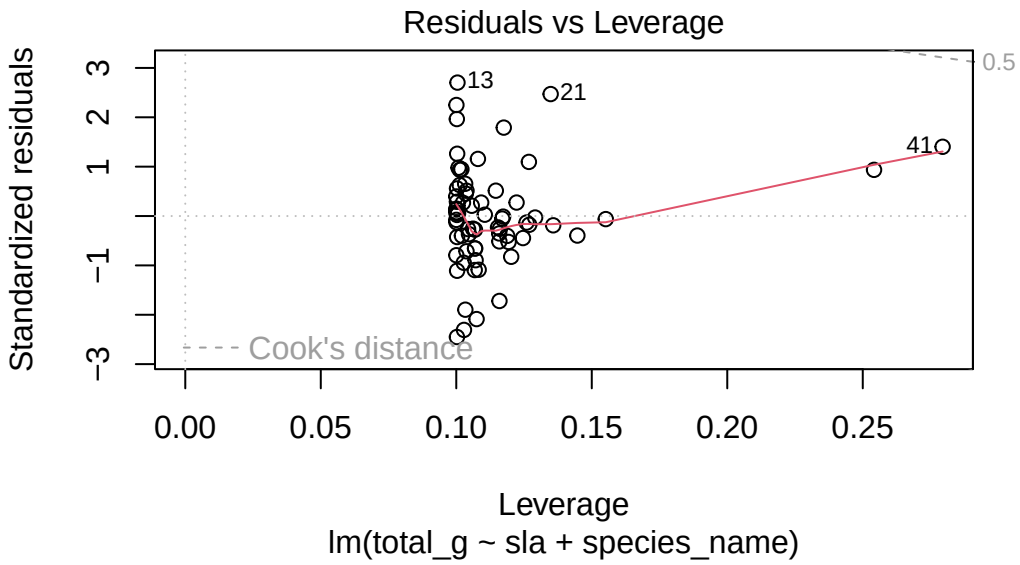
3. total biomass as a function of SLA and species

```
model3 <- lm(total_g ~ sla + species_name,
             data = drought_exp_clean)

plot(model3)
```



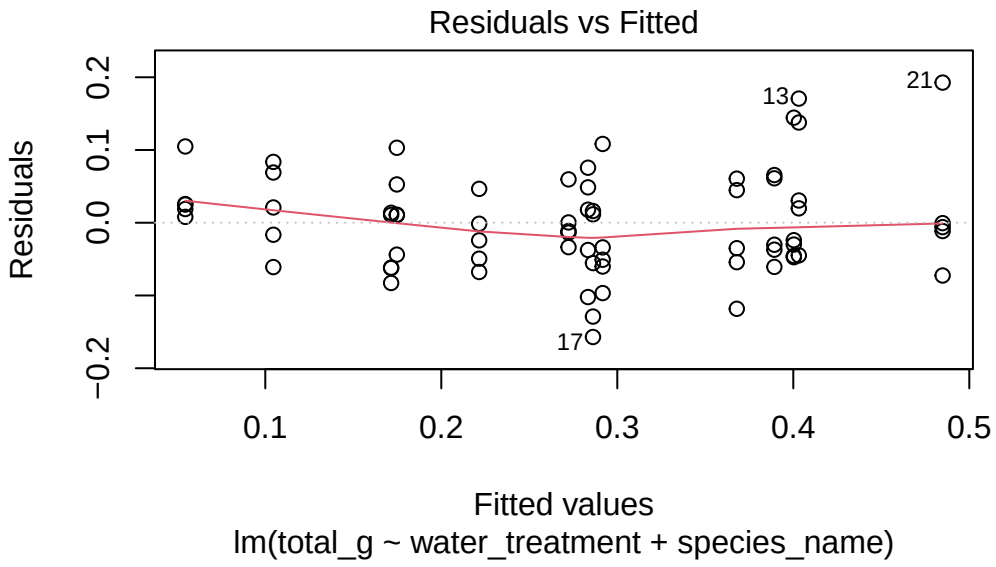

Q−Q Residuals
Standardized residuals
−2
0
1
2
3
17
21
13
−2
−1
0
1
2
Theoretical Quantiles
lm(total_g ~ sla + species_name)

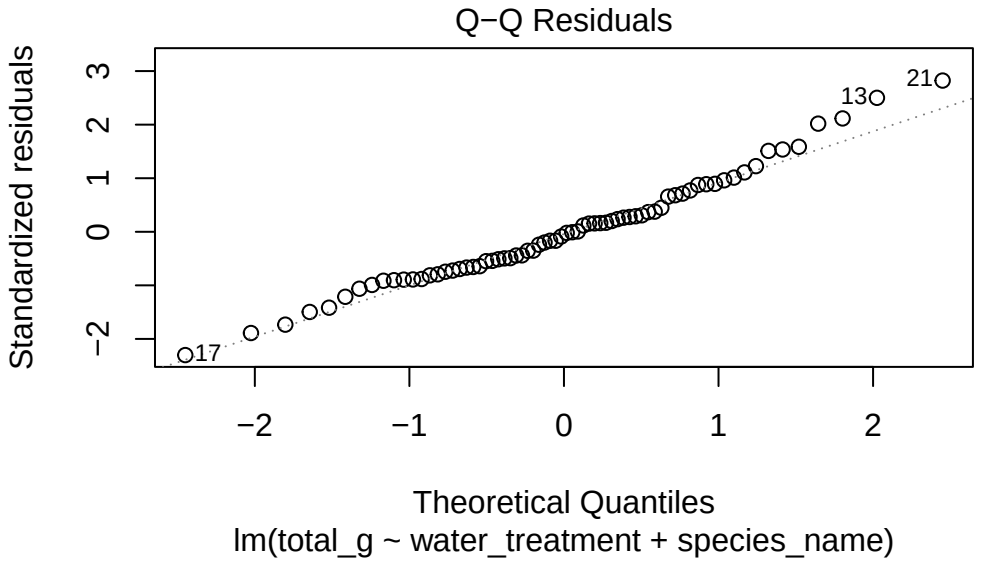

Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
13
17
21
0.1
0.2
0.3
0.4
Fitted values
lm(total_g ~ sla + species_name)

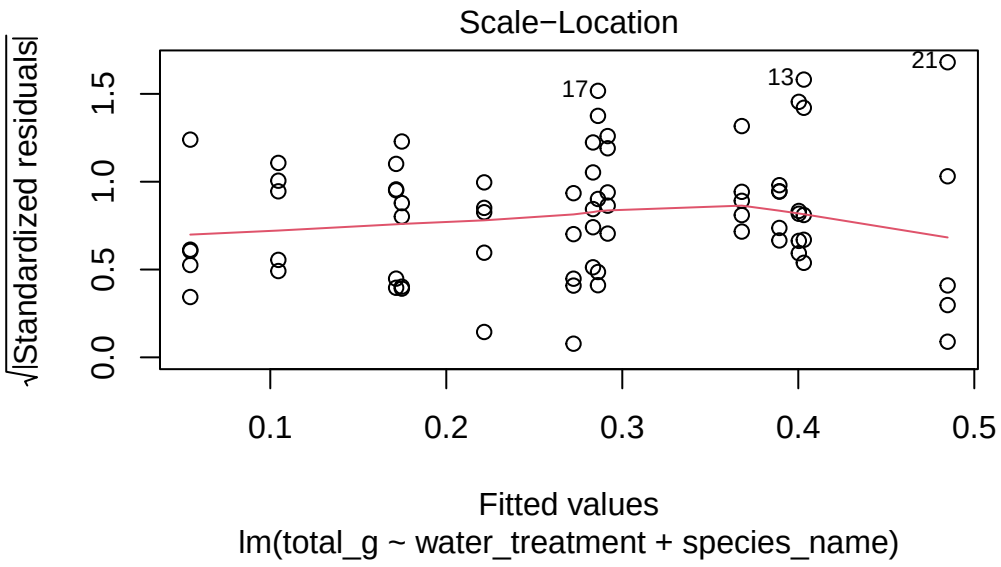


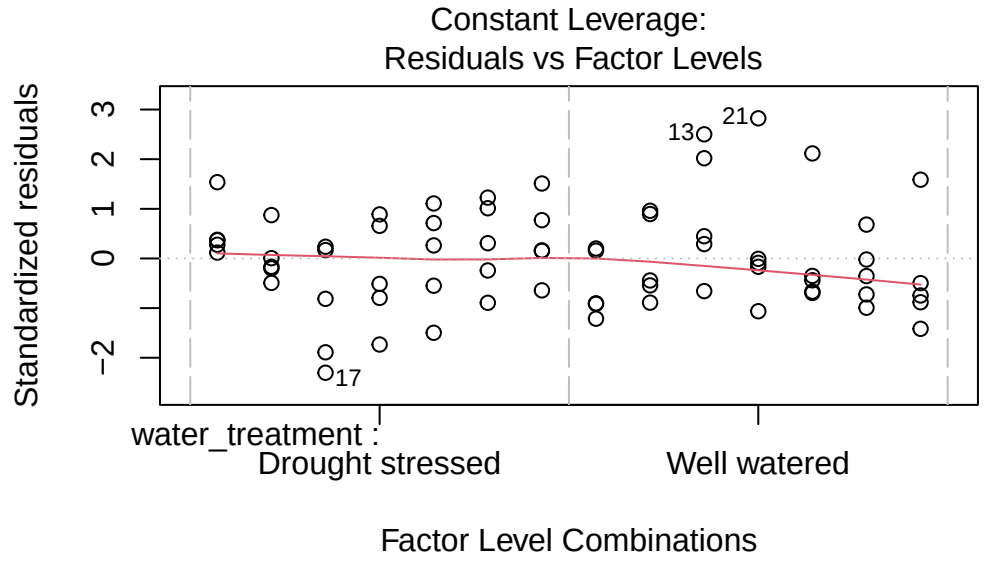
4. total biomass as a function of water treatment and species

```
model4 <- lm(total_g ~ water_treatment + species_name,
             data = drought_exp_clean)

plot(model4)
```


Residuals vs Fitted
Residuals
Fitted values
lm(total_g ~ water_treatment + species_name)
21
13
17


Q−Q Residuals
Standardized residuals
Theoretical Quantiles
lm(total_g ~ water_treatment + species_name)
21
13
17






```
modelselectiontable <- model.sel(model0,
          model1,
          model2,
          model3,
```

```
          model4)
# delta for the best AIC will always be 0
```

Table presentation

```
# one option for a single model
flextable::as_flextable(modelselectiontable)
```

(Intercept)	sla	species_name	water_treatment	df	logLik	AICc
numeric	numeric	factor	factor	integer	numeric	numeric
0.1		+	+	9	88.6	-156.2
0.1	-0.0	+	+	10	88.7	-153.8
-0.0	0.0	+		9	72.5	-124.1
0.0	0.0		+	4	52.2	-95.8
0.3				2	39.6	-75.0
n: 5						

```
# comparing models
modelsummary::modelsummary( # this function takes a list of models
  list(
    "null" = model0, # "model name" = model object
    "model 1" = model1,
    "model 2" = model2,
    "model 3" = model3,
    "model 4" = model4
  )
)
```

	null	model 1	model 2	model 3	model 4
(Intercept)	0.279	0.080	0.047	−0.033	0.055
	(0.017)	(0.056)	(0.054)	(0.067)	(0.025)
sla		0.000	0.001	0.001	
		(0.000)	(0.000)	(0.001)	
water_treatmentWell watered		0.122	0.090		0.117
		(0.020)	(0.029)		(0.017)
species_nameEncelia californica		0.238		0.115	0.218
		(0.051)		(0.059)	(0.032)
species_nameEschscholzia californica		0.234		0.222	0.232
		(0.033)		(0.041)	(0.032)
species_nameGrindelia camporum		0.330		0.226	0.313
		(0.047)		(0.054)	(0.032)
species_nameNasella pulchra		0.241		0.168	0.229
		(0.040)		(0.048)	(0.032)
species_namePenstemon centranthifolius		0.061		−0.006	0.050
		(0.039)		(0.047)	(0.032)
species_nameSalvia leucophylla		0.117		0.139	0.120
		(0.033)		(0.041)	(0.032)
Num.Obs.	70	70	70	70	70
R2	0.000	0.755	0.303	0.610	0.754
R2 Adj.	0.000	0.722	0.282	0.566	0.726
AIC	−75.2	−157.5	−96.4	−127.1	−159.2
BIC	−70.7	−135.0	−87.4	−106.8	−139.0
Log.Lik.	39.580	88.741	52.220	72.538	88.598
RMSE	0.14	0.07	0.11	0.09	0.07

Part b

Part c

Model predictions

Note: only plot terms in the model you select - if your doesn't include one of these terms, take it out and adjust the plotting code accordingly!

```
model_preds <- ggpredict(model4,
                         terms = c(
                                   "water_treatment",
                                   "species_name"))

# use View(model_preds) to see the predictions as a data frame
# use model_preds to see the predictions formatted nicely
```

```
# creating new data frame of model predictions for plotting
model_preds_for_plotting <- model_preds %>%
  rename(water_treatment = x, # renaming columns to make this easier to use
         species_name = group)

# use View(model_preds_for_plotting)
# to compare this to the original model_preds data frame

ggplot() +
  # underlying data
  geom_point(data = drought_exp_clean,
             aes(x = water_treatment,
                 y = total_g,
                 color = water_treatment),
             alpha = 0.1) +
  # model prediction 95% CI ribbon
  geom_ribbon(data = model_preds_for_plotting,
              aes(x = water_treatment,
                  y = predicted,
                  ymin = conf.low,
                  ymax = conf.high,
                  fill = water_treatment),
              alpha = 0.2) +
  # model prediction lines
```

```
  geom_line(data = model_preds_for_plotting,
            aes(x = water_treatment,
                y = predicted,
                color = water_treatment)) +
  # cleaner theme
  theme_classic() +
  # creating different panels for species
  facet_wrap(~species_name)
```

```
`geom_line()`: Each group consists of only one observation.
i Do you need to adjust the group aesthetic?
`geom_line()`: Each group consists of only one observation.
i Do you need to adjust the group aesthetic?
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`geom_line()`: Each group consists of only one observation.
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`geom_line()`: Each group consists of only one observation.
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`geom_line()`: Each group consists of only one observation.
i Do you need to adjust the group aesthetic?
```

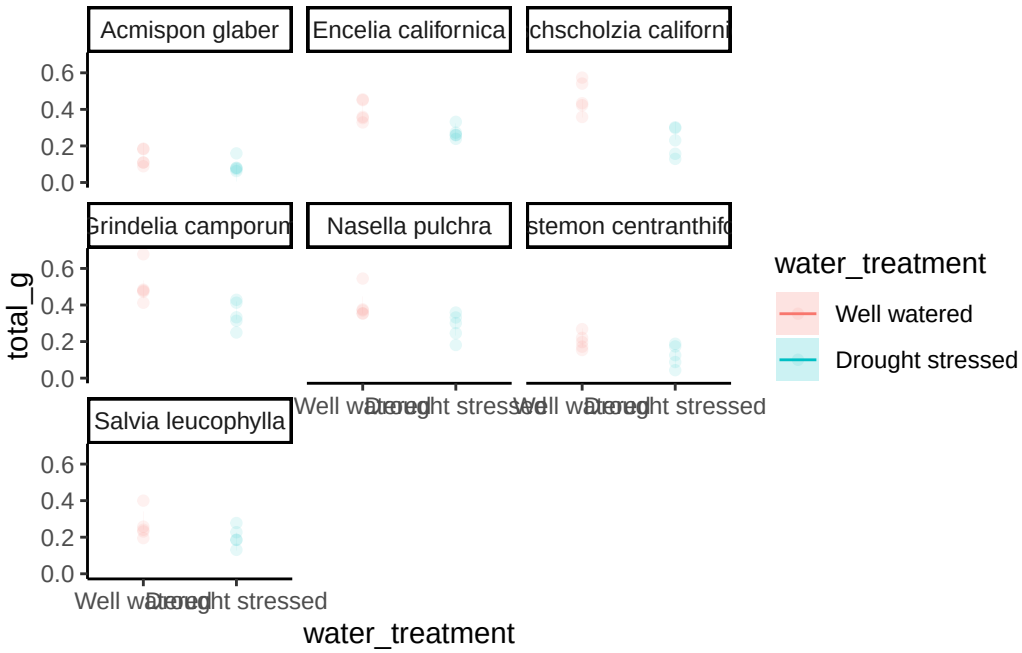

Part d

Part e

Problem 2. Affective visualization

Part a

For my personal data set, where I am examining the distance traveled each day, I could use a bar graph and outline the perimeter of each peak. In doing so, the graph will appear to be "hilly". Since my data is about driving, I will turn this into a scene with a car driving over hills (ie the bar graph).

Part b

Part c

Part d

Problem 3. Statistical critique

Part a

To examine the long-term effects of a wildfire on soil nutrients and makeup, the researchers used a two-way ANOVA test and if significant differences were found ($p < 0.05$), a Tukey HSD post-hoc test was applied. The authors represented these statistical tests in three tables. Table 1 shows the results of the ANOVA test and Tables 2 & 3 show the descriptive statitics for certain nutrients. In addition to the tables, there were two figures. The first was a map that illustrated the study location and areas with varying fire severity. The second figure was an RDA for the relation between factors 1 and 2.

Part b

All three tables were very clear, with descriptive captions and column and row labels. Figure 1 was also simple to understand because it consisted of images and maps for context. However, figure 2 was significantly more confusing to understand because I have never looked at a redundancy analysis (RDA) plot before. There are no units on the x and y axis and at first glance the numbers seem quiet arbitrary. After researching how to read the plot, it made more sense and I could see how the variables' summary statistics (means and standard deviations) were being shown. No model predictions were in the matrix, but rather just the collected data.

Part c

The tables all hold a lot of information and data making them seem a bit visually cluttered. However, this was crucial information for the researchers to show so it was necessary to include it all. SUGGEST HOW TO MAKE IT BETTER? Figure 2, the RDA plot, had a very good data to ink ratio, only consisting of a few lines, two colors, and minimal lettering.

Part d