512 Project Part I

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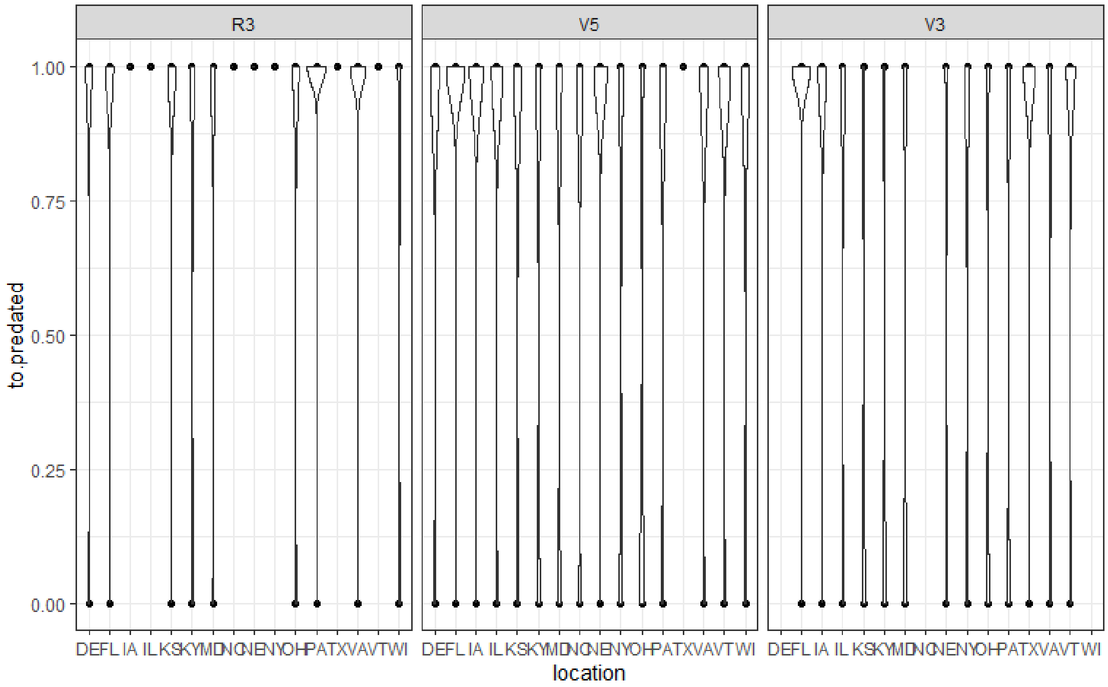
Due Sept 27

Part I (512 only, project proposal, 25 pts):

1) Read in your data set and run dim on it:

```
set.seed(654321)
s21 <- read_csv('data/2021 Sentinel Prey Assessment.csv')
s22 <- read_csv("data/PSA_CE2_SentinelPrey.csv")
s23 <- read_csv('data/PSA_Sent.prey.2023.csv')

# I need to get total predation into a column as a binary. 1 = predation, 0 =
not

# 2021 cleaning
s21

## # A tibble: 5,281 × 17
##    location date    n.weather d.weather growth_stage plot_id rep.block
treatment
##    <chr>    <chr>       <dbl> <chr>     <chr>          <dbl>     <dbl>
<dbl>
##  1 PA       6/16/2…      15.3 18.44     V3               101         1
1
##  2 PA       6/16/2…      15.3 18.44     V3               101         1
1
##  3 PA       6/16/2…      15.3 18.44     V3               101         1
1
##  4 PA       6/16/2…      15.3 18.44     V3               101         1
1
##  5 PA       6/16/2…      15.3 18.44     V3               101         1
1
##  6 PA       6/16/2…      15.3 18.44     V3               101         1
1
##  7 PA       6/16/2…      15.3 18.44     V3               102         1
3
##  8 PA       6/16/2…      15.3 18.44     V3               102         1
3
##  9 PA       6/16/2…      15.3 18.44     V3               102         1
3
## 10 PA       6/16/2…      15.3 18.44     V3               102         1
3
## # ℹ 5,271 more rows
## # ℹ 9 more variables: row <dbl>, sample <dbl>, n.absent <chr>, n.partial
```

```
<chr>,
## #   n.predated <chr>, d.absent <chr>, d.partial <chr>, d.predated <chr>,
## #   to.predated <chr>

clean21 <- s21 %>%
  mutate(year = '2021') %>%
  dplyr::select(location, year, growth_stage, plot_id, rep.block, treatment,
to.predated) %>%
  mutate(to.predated = as.double(to.predated)) %>%
  dplyr::rename(block = rep.block) %>%
  group_by(location, year, growth_stage, plot_id, block, treatment) %>%
  # dplyr::summarise(total = sum(to.predated)) %>%
  na.omit() %>%
  mutate(treatment = case_when(
    treatment == '33' ~ '3',
    .default = as.factor(treatment))) %>%
  dplyr::filter(treatment != '6',
                treatment != '7',
                treatment != '8') %>%
  mutate_at(vars(1:6), as.factor)

ggplot(clean21, aes(x = location, y = to.predated))+
  geom_point()+
  geom_violin()+
  facet_wrap(~growth_stage)
```



```
# 2022 cleaning
s22
```

```
## # A tibble: 3,246 × 19
##    location date      am.weather pm.weather growth_stage plotid block
treatment
##    <chr>    <chr>          <dbl> <chr>      <chr>         <dbl> <dbl>
<dbl>
##  1 PA       6/22/2022       22.7 26.1       V3              101     1
1
##  2 PA       6/22/2022       22.7 26.1       V3              101     1
1
##  3 PA       6/22/2022       22.7 26.1       V3              101     1
1
##  4 PA       6/22/2022       22.7 26.1       V3              101     1
1
##  5 PA       6/22/2022       22.7 26.1       V3              101     1
1
##  6 PA       6/22/2022       22.7 26.1       V3              101     1
1
##  7 PA       6/22/2022       22.7 26.1       V3              102     1
3
##  8 PA       6/22/2022       22.7 26.1       V3              102     1
3
##  9 PA       6/22/2022       22.7 26.1       V3              102     1
3
## 10 PA       6/22/2022       22.7 26.1       V3              102     1
3
## # ℹ 3,236 more rows
## # ℹ 11 more variables: row <dbl>, sample <dbl>, am.absent <chr>,
## #   am.partial <chr>, am.predators <chr>, pm.absent <chr>, pm.partial
<chr>,
## #   pm.predators <chr>, to.predated <dbl>, n.predated <dbl>, d.predated
<dbl>
```

```
unique(s22$treatment)
```

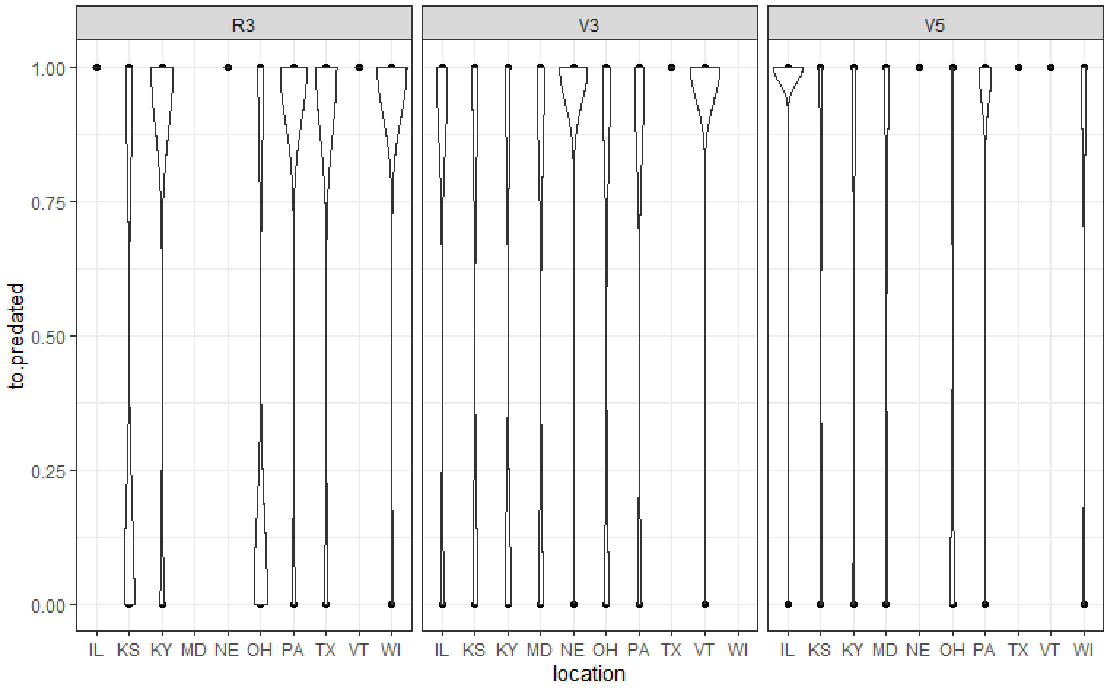
```
## [1] 1 3 2 4
```

```
unique(s22$growth_stage)
```

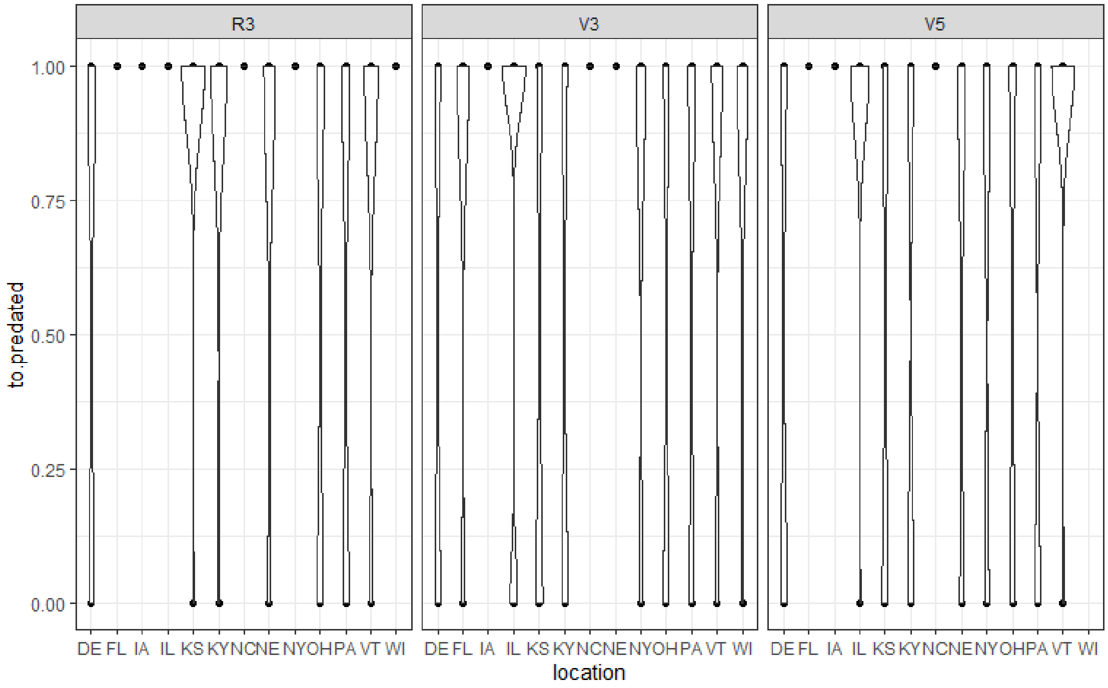
```
## [1] "V3" "V5" "R3" "R2"
```

```
clean22 <- s22 %>%
  mutate(year = '2022') %>%
  dplyr::select(location, year, growth_stage, plotid, block, treatment,
to.predated) %>%
  dplyr::rename(plot_id = plotid) %>%
  mutate(growth_stage = case_when(growth_stage == 'R2' ~ 'R3',
                                  .default = as.character(growth_stage))) %>%
  dplyr::group_by(location, year, growth_stage, plot_id, block, treatment)
%>%
  # dplyr::summarise(total = sum(to.predated)) %>%
  mutate_at(vars(1:6), as.factor)
```

```
ggplot(clean22, aes(x = location, y = to.predated))+
  geom_point()+
  geom_violin()+
  facet_wrap(~growth_stage)
```



```
# 2023 cleaning

clean23 <- s23 %>%
  mutate(year = '2023') %>%
  relocate(am.partial, am.absent, pm.partial, pm.absent) %>%
  mutate_at(vars(1:4), as.double) %>%
  mutate(to.predated = if_else(am.partial | am.absent | pm.partial |
pm.absent == 1, 1, 0)) %>%
  relocate(to.predated)%>%
  mutate(growth_stage = case_when((location == 'NC' & date == '7/20/2023') ~
'R3',
                                  .default = as.character(growth_stage))) %>%
  dplyr::select(location, year, growth_stage, plotid, block, treatmetn,
to.predated) %>%
  dplyr::rename(plot_id = plotid,
         treatment = treatmetn) %>%
  distinct() %>%
  group_by(location, year, growth_stage, plot_id, block, treatment) %>%
  na.omit() %>%
  filter(treatment != 5) %>%
  mutate_at(vars(1:6),as.factor)

ggplot(clean23, aes(x = location, y = to.predated))+
  geom_point()+
  geom_violin()+
  facet_wrap(~growth_stage)
```



```
# and in the darkness, bind them
sent <- rbind(clean21, clean22, clean23)
as_tibble(sent)

## # A tibble: 9,227 × 7
##    location year  growth_stage plot_id block treatment to.predated
##    <fct>    <fct> <fct>        <fct>   <fct> <fct>           <dbl>
##  1 PA       2021  V3           101     1     1                   0
##  2 PA       2021  V3           101     1     1                   0
##  3 PA       2021  V3           101     1     1                   0
##  4 PA       2021  V3           101     1     1                   0
##  5 PA       2021  V3           101     1     1                   0
##  6 PA       2021  V3           101     1     1                   0
##  7 PA       2021  V3           102     1     3                   1
##  8 PA       2021  V3           102     1     3                   1
##  9 PA       2021  V3           102     1     3                   0
## 10 PA       2021  V3           102     1     3                   1
## # ℹ 9,217 more rows

dim(sent)

## [1] 9227    7
```

2) Prepare a short description of your data set (source if published paper exists), especially providing the study design, sample size, and variables of primary interest.

If there is random sampling, note the population sampled from. If there is random assignment, note how and for which variable(s).

Data: Sentinel Prey assessment of arthropod-predator activity in corn fields.

These data come from the Precision Sustainable Agriculture effort through the USDA. I am the lead on the entomology component of this project and responsible for analyzing this three year data set which spans multiple states. This effort began during my Master's degree, but I only analyzed Pennsylvania data for my thesis.

Study design: Treatments = 4; No cover crop, early-terminated cover crop, late-terminated cover crop, planting green

Plots = 20; 5 blocks composed of 4 plots each = 20 plots / study site / year **Years** = 3 (2021,2022,2023)

Locations = This project comprises 16 states. Not all states collected sentinel prey data every year.

Effort = Data were collected at three corn growth stages / year (V3,V5,R3).

Sample = 6 sentinel prey traps were placed in each plot = 120 samples collected / growth stage. Total sample effort per state per season = 360 samples.

Variables: Response = Total level of predation. This is transformed into a proportion over a constant total. Binomial response

Explanatory = Crop growth stage (timing, three levels) and treatment (four levels).

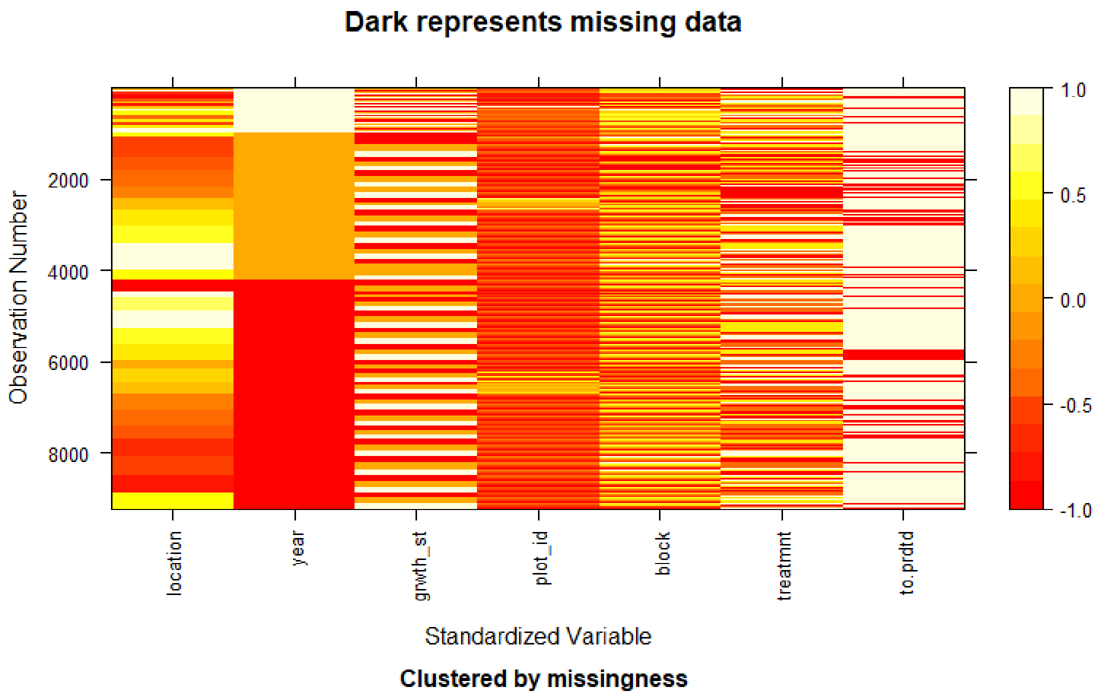
Random effects = Year, location, block, and plot. I am unsure how to use location. I am not interested in seeing how each state differs in the analysis because that is *not* a research question. I plan to go through and conduct each state's own analysis later.

Repeated measure = I visit the same trap three times throughout the year. This feels like a term I should identify. If I were to choose, I would select *growth stage*.

Plots were randomly assigned to each block. Field sites were as random as they could be at each respective research station. Sentinel prey traps were placed between pre-determined rows and at specific length intervals within each plot to maintain consistency.

3) Make a `missing_data.frame` plot of your data set and explain any missing values indicated:

```r
library(mi)
# make an object of the missing df and then present the image
tdf <- missing_data.frame(data.frame(sent))
image(tdf)
```

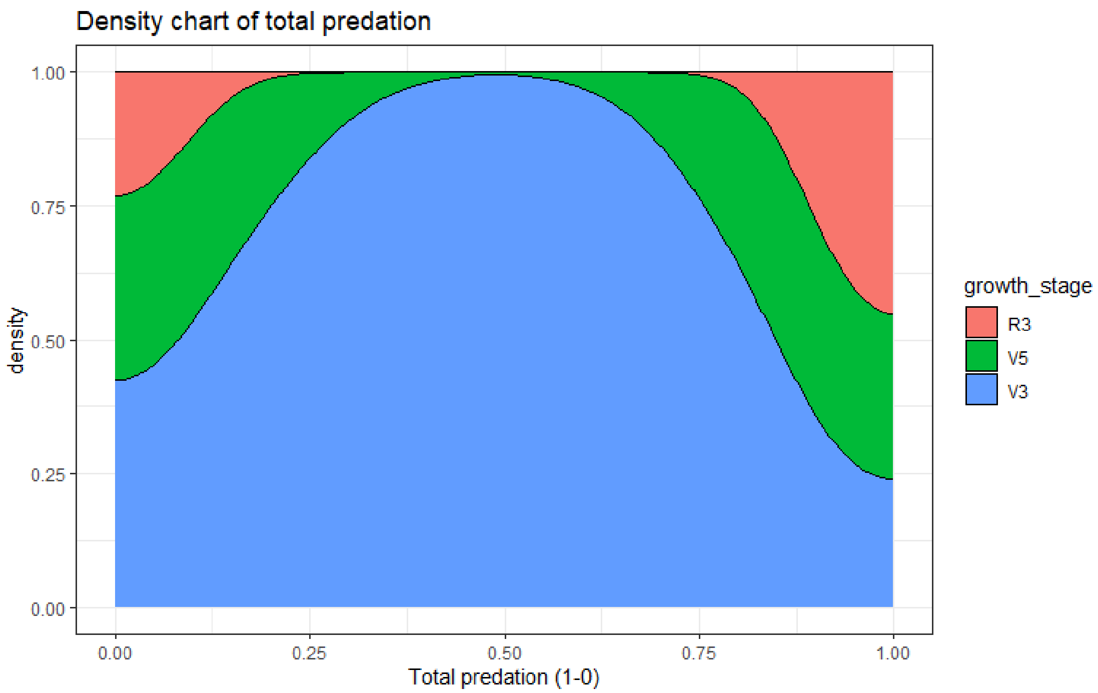


4) Discuss any other use in classes or theses for the data - either that you have used it for or are currently working on for future submissions.

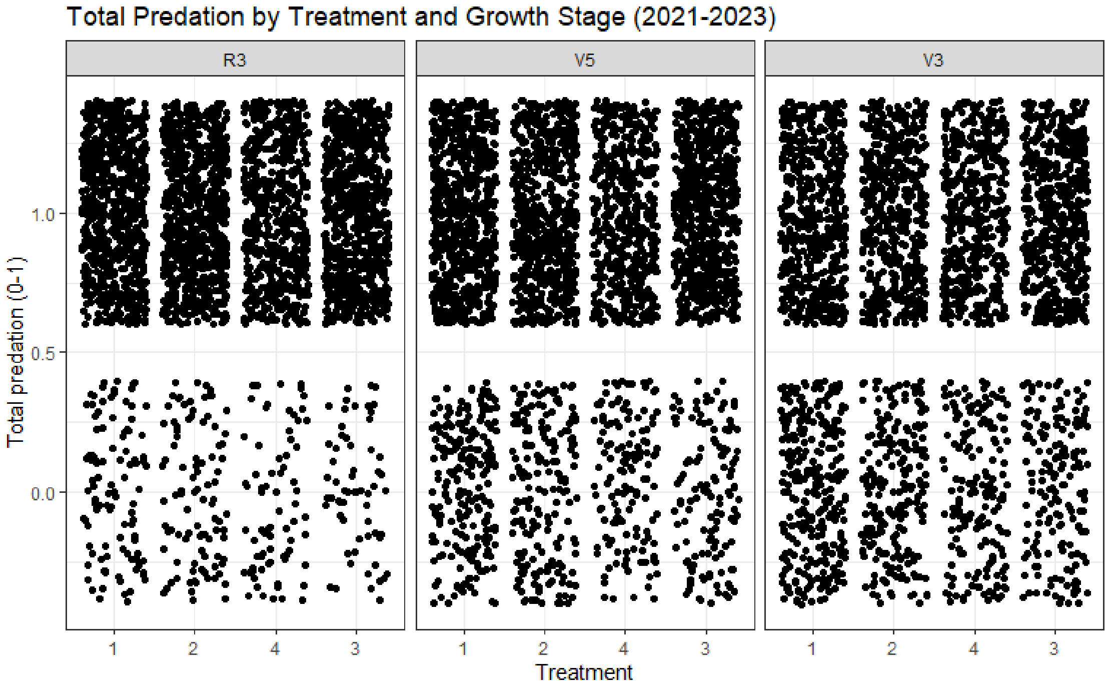
I am working on this for a publication. The Pennsylvania-exclusive data were analyzed for me master's thesis and Pennsylvania publication. The larger, whole-project data set is for our national publication.

5) Provide at least one display of the data, focusing on the response of interest versus a predictor. If you have multiple predictors, try to plot the response versus those too.

```r
ggplot(sent, aes(x = to.predated, fill = growth_stage))+
  geom_density(position = 'fill')+
  labs(title = 'Density chart of total predation',
       x = 'Total predation (1-0)')
```



```
ggplot(sent, aes(x = treatment, y = to.predated))+
  geom_point()+
  facet_wrap(~growth_stage)+
  geom_jitter()+
  labs(title = 'Total Predation by Treatment and Growth Stage (2021-2023)',
       x = 'Treatment',
       y = 'Total predation (0-1)')
```

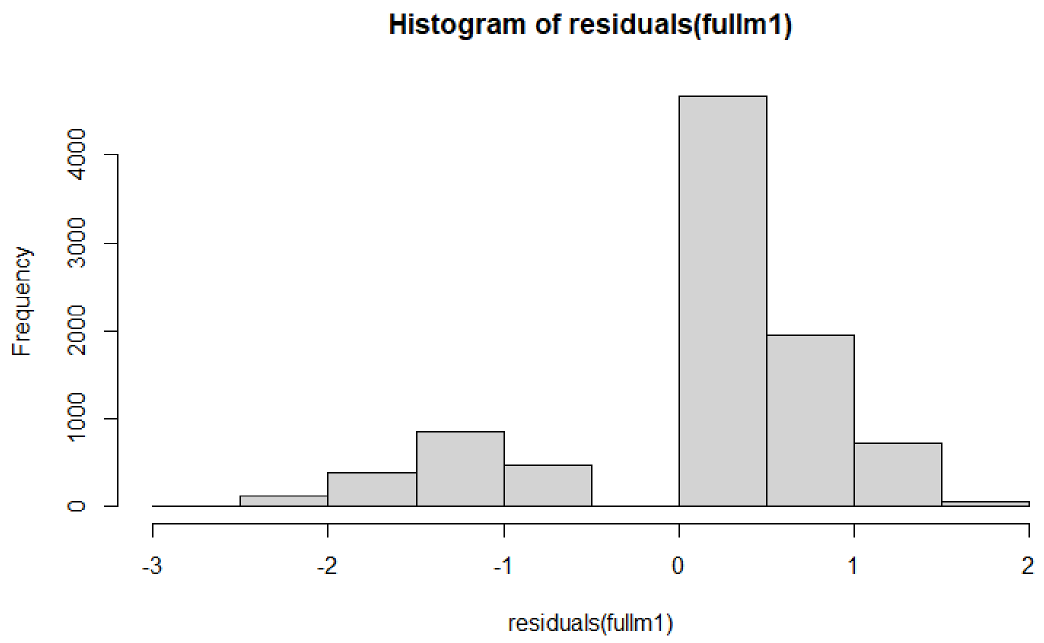


6) Provide an initial model you hope to fit (does not need to be fit). If you fit a model, add a model summary and effects plot.

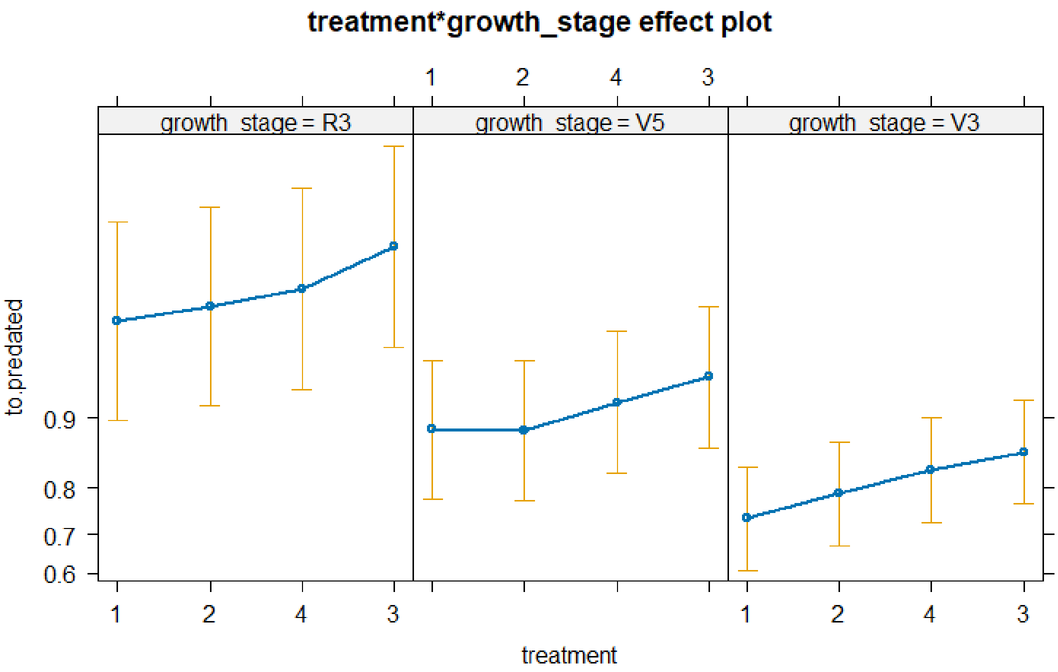
```
sent

## # A tibble: 9,227 × 7
## # Groups:   location, year, growth_stage, plot_id, block, treatment
[2,091]
##    location year  growth_stage plot_id block treatment to.predated
##    <fct>    <fct> <fct>        <fct>   <fct> <fct>           <dbl>
##  1 PA       2021  V3           101     1     1                   0
##  2 PA       2021  V3           101     1     1                   0
##  3 PA       2021  V3           101     1     1                   0
##  4 PA       2021  V3           101     1     1                   0
##  5 PA       2021  V3           101     1     1                   0
##  6 PA       2021  V3           101     1     1                   0
##  7 PA       2021  V3           102     1     3                   1
##  8 PA       2021  V3           102     1     3                   1
##  9 PA       2021  V3           102     1     3                   0
## 10 PA       2021  V3           102     1     3                   1
## # ℹ 9,217 more rows

nullm1 <- glmer(to.predated ~  (growth_stage|year/location/block/plot_id),
family = binomial, data = sent)


fullm1 <- glmer(to.predated ~ treatment*growth_stage +
(growth_stage|year/location/block/plot_id), family = binomial, data = sent)
summary(fullm1)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## to.predated ~ treatment * growth_stage + (growth_stage |
year/location/block/plot_id)
##    Data: sent
##
##      AIC      BIC   logLik deviance df.resid
##   6811.8   7068.5  -3369.9   6739.8     9191
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -6.6897  0.0490  0.1914  0.4187  2.3997
##
## Random effects:
##  Groups                            Name           Variance Std.Dev. Corr
##  plot_id:(block:(location:year)) (Intercept)    0.27964  0.5288
##                                    growth_stageV5 0.36146  0.6012   -0.72
##                                    growth_stageV3 0.53538  0.7317   -0.71
1.00
```

```
##  block:(location:year)          (Intercept)    0.10357  0.3218
##                                 growth_stageV5 0.02733  0.1653    0.99
##                                 growth_stageV3 0.02714  0.1647   -0.63 -
0.73
##  location:year                  (Intercept)    6.10710  2.4713
##                                 growth_stageV5 2.88527  1.6986   -0.61
##                                 growth_stageV3 4.69651  2.1671   -0.81
0.82
##  year                           (Intercept)    0.31795  0.5639
##                                 growth_stageV5 0.80014  0.8945   -1.00
##                                 growth_stageV3 0.61540  0.7845   -1.00
1.00
## Number of obs: 9227, groups:
## plot_id:(block:(location:year)), 744; block:(location:year), 191;
location:year, 39; year, 3
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                3.30346    0.58113   5.685 1.31e-08
## treatment2                 0.17282    0.20454   0.845 0.398164
## treatment4                 0.36630    0.22329   1.640 0.100916
## treatment3                 0.86350    0.22294   3.873 0.000107
## growth_stageV5            -1.24603    0.66472  -1.875 0.060861
## growth_stageV3            -2.27113    0.64784  -3.506 0.000455
## treatment2:growth_stageV5 -0.18140    0.25131  -0.722 0.470411
## treatment4:growth_stageV5 -0.05476    0.27467  -0.199 0.841964
## treatment3:growth_stageV5 -0.25759    0.27106  -0.950 0.341952
## treatment2:growth_stageV3  0.11873    0.25261   0.470 0.638340
## treatment4:growth_stageV3  0.19620    0.27264   0.720 0.471767
## treatment3:growth_stageV3 -0.09241    0.27018  -0.342 0.732318
##
## Correlation of Fixed Effects:
##             (Intr) trtmn2 trtmn4 trtmn3 grw_V5 grw_V3 t2:_V5 t4:_V5 t3:_V5
## treatment2  -0.165
## treatment4  -0.143  0.443
## treatment3  -0.139  0.449  0.413
## grwth_stgV5 -0.794  0.142  0.123  0.119
## grwth_stgV3 -0.886  0.148  0.127  0.124  0.904
## trtmnt2:_V5  0.135 -0.799 -0.355 -0.358 -0.183 -0.130
## trtmnt4:_V5  0.116 -0.354 -0.798 -0.329 -0.158 -0.111  0.447
## trtmnt3:_V5  0.114 -0.362 -0.335 -0.809 -0.157 -0.111  0.456  0.422
## trtmnt2:_V3  0.133 -0.809 -0.358 -0.364 -0.124 -0.182  0.694  0.307  0.315
## trtmnt4:_V3  0.116 -0.362 -0.818 -0.337 -0.108 -0.159  0.312  0.701  0.293
## trtmnt3:_V3  0.114 -0.368 -0.341 -0.821 -0.106 -0.157  0.315  0.292  0.707
##             t2:_V3 t4:_V3
## treatment2
## treatment4
## treatment3
## grwth_stgV5
## grwth_stgV3
## trtmnt2:_V5
## trtmnt4:_V5
## trtmnt3:_V5
## trtmnt2:_V3
## trtmnt4:_V3  0.449
## trtmnt3:_V3  0.456  0.428
## optimizer (Nelder_Mead) convergence code: 4 (failure to converge in 10000
evaluations)
## Model failed to converge with max|grad| = 0.139343 (tol = 0.002, component
1)
## failure to converge in 10000 evaluations
```

```
hist(residuals(fullm1))
```



```
plot(allEffects(fullm1))
```



```
# F test
Anova(fullm1)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: to.predated
##                          Chisq Df Pr(>Chisq)
## treatment              54.7613  3  7.720e-12
## growth_stage           19.7806  2  5.066e-05
## treatment:growth_stage  3.5339  6     0.7395

# Likelihood test
anova(nullm1, fullm1)

## Data: sent
## Models:
## nullm1: to.predated ~ (growth_stage | year/location/block/plot_id)
## fullm1: to.predated ~ treatment * growth_stage + (growth_stage |
year/location/block/plot_id)
##        npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## nullm1   25 6854.2 7032.4 -3402.1   6804.2
## fullm1   36 6811.8 7068.5 -3369.9   6739.8 64.35 11  1.428e-09
```

7) Start to work on a Table 1 that summarizes variables of interest, possibly by groups of interest. At a minimum, summarize the response variable, by a grouping variable if one exists.

```
# table as a proportion
all_locs <- sent %>%
  group_by(location, treatment, growth_stage) %>%
  dplyr::summarise(prop = mean(to.predated),
                   sd = sd(to.predated),
                   n = n(),
                   se = sd/sqrt(n))

by_trt <- sent %>%
  group_by(treatment) %>%
  dplyr::summarise(prop = mean(to.predated),
                   sd = sd(to.predated),
                   n = n(),
                   se = sd/sqrt(n))
by_trt

## # A tibble: 4 × 5
##   treatment  prop    sd     n      se
##   <fct>     <dbl> <dbl> <int>   <dbl>
## 1 1         0.764 0.425  2593 0.00835
## 2 2         0.791 0.407  2353 0.00839
## 3 4         0.803 0.398  1943 0.00902
## 4 3         0.849 0.359  2338 0.00741

by_growth <- sent %>%
  group_by(growth_stage) %>%
  dplyr::summarise(prop = mean(to.predated),
                   sd = sd(to.predated),
                   n = n(),
                   se = sd/sqrt(n))
by_growth

## # A tibble: 3 × 5
##   growth_stage  prop    sd     n      se
##   <fct>        <dbl> <dbl> <int>   <dbl>
## 1 R3           0.894 0.308  3098 0.00554
## 2 V5           0.793 0.405  3248 0.00710
## 3 V3           0.708 0.455  2881 0.00847
```

7a) Comparing my old way of summary stats with yours. Which do I like more?

```r
datasummary(treatment + growth_stage ~ to.predated, data = sent, output =
'markdown')
```

		to.predated
treatment	1	2593.00
	2	2353.00
	4	1943.00
	3	2338.00
growth_stage	R3	3098.00
	V5	3248.00
	V3	2881.00

I do not think this is great for binary data.

8) Provide the names of feedback group members and the date, time, and location of your feedback session interaction.
My group of Eme Morgan, Rennie Winkelman, and Kaelin Smith met before class on 9/25/2024 in the stats classroom to provide initial feedback.

Graded for completion/not but there are points for participation in a feedback session. Note that 412 students get full credit for this.