Managing pests by increasing predators, and improving agroecosystem quality through late termination of cover crops

Introduction

With growing popularity of delaying cover-crop termination and planting green, there is a need to understand effects of delayed cover-crop termination on pest control in no-till agronomic systems. In this report, I quantify in no-till corn systems in 16 locations (Delaware, Florida, Iowa, Illinois, Kansas, Kentucky, Maryland, North Carolina, Nebraska, New York, Ohio, Pennsylvania, Texas, Virginia, Virginia Tech, and Wisconsin) effects of differential timing of termination of a cereal-rye (*Secale cereal* L.) cover crop on pest and predator communities. With this framework, I ask the question: How do sentinel prey rates change among treatments and growth stages, and is there an interaction between the two? I hypothesized that by increasing overall cover-crop biomass (ecosystem complexity) and using IPM (i.e., avoiding preventative insecticides), I would record higher levels of predation.

Study design

In a three-year field experiment (2021-2023) across sixteen collaborating locations (typically a University) at their respective research stations, we established a single-factor experiment, arranged in a randomized complete block design with four cover crop treatment levels and five-six replicates. Plots were 12 x 15 m with 16 crop rows at 30 inch spacing. Cover-crop treatments varied by the timing of termination of a cereal-rye cover crop and included 1) a no cover-crop control (Referred to here as 'No CC') and cover-crop terminations of: 2) 14-28 days pre-planting (DPP; referred to here as 'early terminated'), 3) 3-7 DPP ('late terminated'), and 4) 1-3 days after planting (DAP; 'planting green') of the cash crop. Cover crops were terminated using glyphosate (1.27 kg ae ha^{-1}) and ammonium sulfate (2.5% v/v) using water as a carrier at 140 L ha^{-1}. Based on abiotic conditions, planting dates of cover and cash crops, and termination dates varied annually among locations. We established a 3-m border of cover crop around the experiment and 9 m alleys between blocks. The border and the alleys follow the planting-green schedule for termination and cash-crop planting (Fig. 1).

To assess the influence of the timing of cover-crop termination on predation by generalist invertebrate predators, I conducted sentinel prey assays with waxworms (*Galleria mellonella*; Timberline Fisheries, Marion, IL) in corn across growth stages (Lundgren e al. 2006; Busch et al. 2020). We pinned waxworms through their terminal segment into balls of modelling clay, which we laid on the soil surface. We deployed six waxworms per plot in vertebrate exclusion cages made from hardware cloth (4-mm mesh) and capped with a plastic lid that allows for free passage of predatory invertebrate species. We deployed three waxworms per row at ~8:00 in two rows of each plot (between rows 6 and 7 and 11 and 12, approximately 4, 8, and 12 m from the western edge of each plot; total of 6 cages per plot). We checked on caterpillars at ~20:00 and again the next day at ~8:00, recording presence/absence and noting any predators (e.g., wolf spider, carabid beetle, ant, etc.) that were present. Missing waxworms were not replaced with living ones.

Statistical Procedures

I conducted all statistical analyses in R (version 4.4.1). On several occasions observations were missing due to trap disturbances in the field. These were recorded as 'NA' and removed during the wrangling process. Summary statistics for predation at the treatment and growth stage levels are in Table 1. This table was created using the Mosaic package (Pruim et al., 2017). The estimated mean probabilities for growth stages V3 and V5 were similar, at 0.72 and 0.79, respectively. The estimated mean probability for growth R3 was higher than both V3 and V5 at 0.9. The number of observations per growth stage varied slightly, $n_{V3} = 3902$, $n_{V5} = 4196$, and $n_{R3} = 4334$, respectively. While this is unbalanced, there are many observations within each growth stage. At the treatment level, the estimated mean probabilities for No CC, early-termination, late termination, and planting green are relatively similar, 0.77, 0.8, 0.81, and 0.86, respectively. Sample sizes varied, $n_{Trt1} = 3439$, $n_{Trt2} = 3203$, $n_{Trt3} = 2605$, and $n_{Trt4} = 3185$, respectively. Again, while unbalanced, there are many observations within each treatment.

The response variable was the binomial of predation with 1 referring to predation (success) and 0 referring to no predation (failure). The fixed effects terms for this model were treatment, growth stage,

and their interaction. To account for the repeated measure structure of sampling six traps from the same plot, I developed a nested random effects term with plot within block within location within year (Fig. 2). Figure 2 was created using the DiagrammeRsvg package (Iannone, 2016). The final data frame size used in the model(s) had 12432 observations of plot:(block:(location:year)), 744 observations of block:(location:year), 39 observations of location:year, and 3 observations of year.

A density plot to visualize the data before modeling was also created using the Mosaic package (Fig. 3, Pruim et al., 2017). This was done to ensure no instances of 100% success (predation) or failure (no predation). To analyze effects of timing of cover-crop termination, I ran a generalized linear mixed-effect model (GLMM) on sentinel prey (binomial) data. Model refinement was done using a Type-II Wald-X^2 test with P-values, derived from the car package (Weisberg, 2019). All models were followed by effects plots (effects package) on both the response and link scale and pairwise Tukey-comparisons using the emmeans package (Fox and Hong, 2009; Lenth, 2024). R-squared values were derived from the performance package (Lüdecke et al., 2021).

To answer the question of interest, it was necessary to determine if the interaction between treatment and growth stage was needed in the model. After an initial model, I conducted a Type-II Wald-X^2 test, and using the P-values, interpreted the effect of the interaction term ($X^2(6) = 8.25$, *P-value* = 0.22). With this initial model, I can conclude that there is weak evidence against the null hypothesis of no interaction between treatment and growth stage on total predation, after controlling for plot nested in block nested in location nested in year, and will remove it from the model.

Results

The final theoretical model was: $\pi\,(Predation|Treatment, GrowthStage) \sim \beta_0 + \beta_1 I_{Treatment=2i} + \beta_2 I_{Treatment=4i} + \beta_3 I_{Treatment=3i} + \beta_4 I_{GrowthStage=V5i} + \beta_5 I_{GrowthStage=V3i} + Year_i + Location_i + Block_i + Plot_i + Error_i$

where treatment was a four-level categorical variable represented by the indicator variables $I_{Treatment=2}$ (which takes on a value of 1 if the treatment is 2, and 0 if not), $I_{Treatment=3}$ (which takes on a value of 1 if the treatment is 3, and 0 if not), $I_{Treatment=4}$ (which takes on a value of 1 if the treatment is 4, and 0 if not), and growth stage was a three-level categorical variable represented by indicator variables $I_{GrowthStage=V3}$ (which takes on a value of 1 if the growth stage is V3, and 0 if not), and $I_{GrowthStage=V5}$ (which takes on a value of 1 if the growth stage is V5, and 0 if not). This means that the first treatment level (No CC) and the third growth stage (R3) are treated as references.

A Type-II Wald-X^2 test was generated to assess the model. Accounting for growth stage, year, location, block, and plot, there is very strong evidence against the null hypothesis of no differences among treatment ($X^2(3) = 60.988$, *P-value* < 0.0001), so we would conclude that there is some difference in the estimated log differences of total predation across treatments. Accounting for treatment, year, location, block, and plot, there is very strong evidence against the null hypothesis of no differences among growth stages ($X^2(2) = 528.43$, *P-value* < 0.0001), so we would conclude that there is some difference in the estimated log differences of total predation across growth stages. The model has a conditional R-squared of 0.528 and a marginal R-squared of 0.083. This means that the random effects explain 52.8% of the variation on total predation and treatment and growth stage explain 8.3% of the variation on total predation. After we account for treatment and growth stage, the estimated correlation (ICC) at the plot level was 0.236. This indicates a low correlation between two observations once we account for systematic changes across plots. To visualize the effects of treatment and growth stage on the log-link and response scale, effects plots are displayed in Figure 4. In Figure 4, panel *a* is on the log-link scale and panel *b* is on the response scale. Figures 5 and 6 display the raw data estimated probabilities with compact-letter display derived from the post-hoc emmeans Tukey-comparisons on the response scale.

For two otherwise similar plots that differ by treatment, there is an estimated probability of 0.88 of predation in the No CC-treatment (95% CI: 0.787 to 0.935), an estimated probability of 0.895 of

predation for the early-terminated treatment (95% CI: 0.812 to 0.944), an estimated probability of 0.918 of predation for the late-terminated treatment (95% CI: 0.849 to 0.957), and an estimated probability of 0.938 of predation for the planting-green treatment (95% CI: 0.884 to 0.968), controlling for growth stage, year, location, block, and plot. For two otherwise similar plots that differ by growth stage, there is an estimated probability of 0.828 of predation for growth stage V3 (95% CI: 0.717 to 0.902), an estimated probability of 0.893 of predation on growth stage V5 (95% CI: 0.814 to 0.941), and an estimated probability of 0.963 of predation for growth stage R3 (95% CI: 0.931 to 0.980), controlling for growth stage, year, location, block, and plot..

Scope of Inference

The locations chosen for this experiment were not randomly selected (Universities volunteered to join the project), and thus the results would not generalize beyond the locations present. Additionally, the results only apply to the years 2021-2023 in a corn monoculture following a cereal-rye cover crop. Data were collected at three, non-random time points throughout the season, and we cannot generalize beyond those time points. And so, we cannot infer results on other locations that do not fall within this range of years, crop, nor sampling time points. In-field location of plots, however, was randomly assigned and thus we can infer on these respected locations the effects of treatment on predation. Furthermore, we can make causal inference on predation levels at the treatment level. Keeping these limitations in mind, the study showed that by delaying cover-crop termination, there was an increase in predation. Additionally, as the season persisted (V3-V5-R3), there was an increase in predation. Based on Figure 5 we see treatment impacts total predation that with delayed cover-crop termination there is an increase in the estimated proportion of predation. Based on Figure 6 we see growth stage impacts total predation that as the season persists (V3-V5-R3), there is an increase in the estimated proportion of predation.
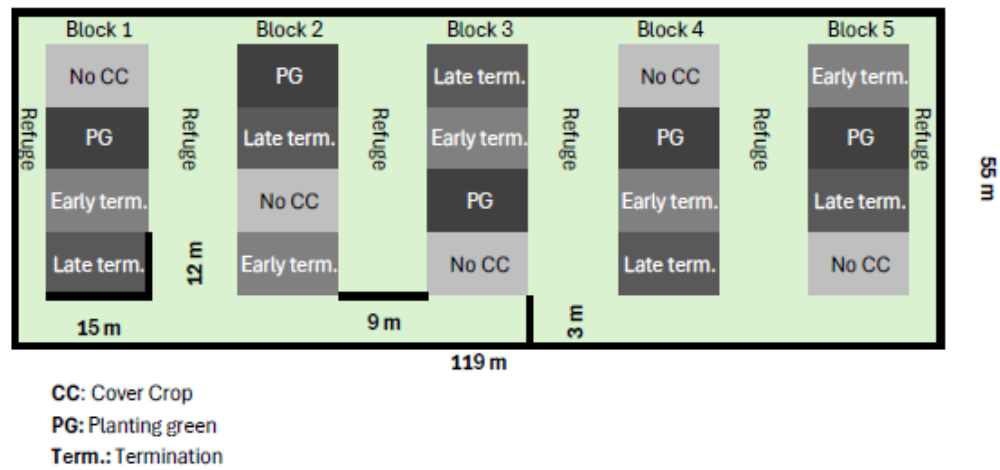
Figures

Figure 1. Example schematic diagram of the design showing treatments, blocks, and buffer areas. The treatment layouts may differ by location and year of the experiment. (Early: 14-28 DPP; Late: 3-7 DPP; Green: 1-3 DAP)
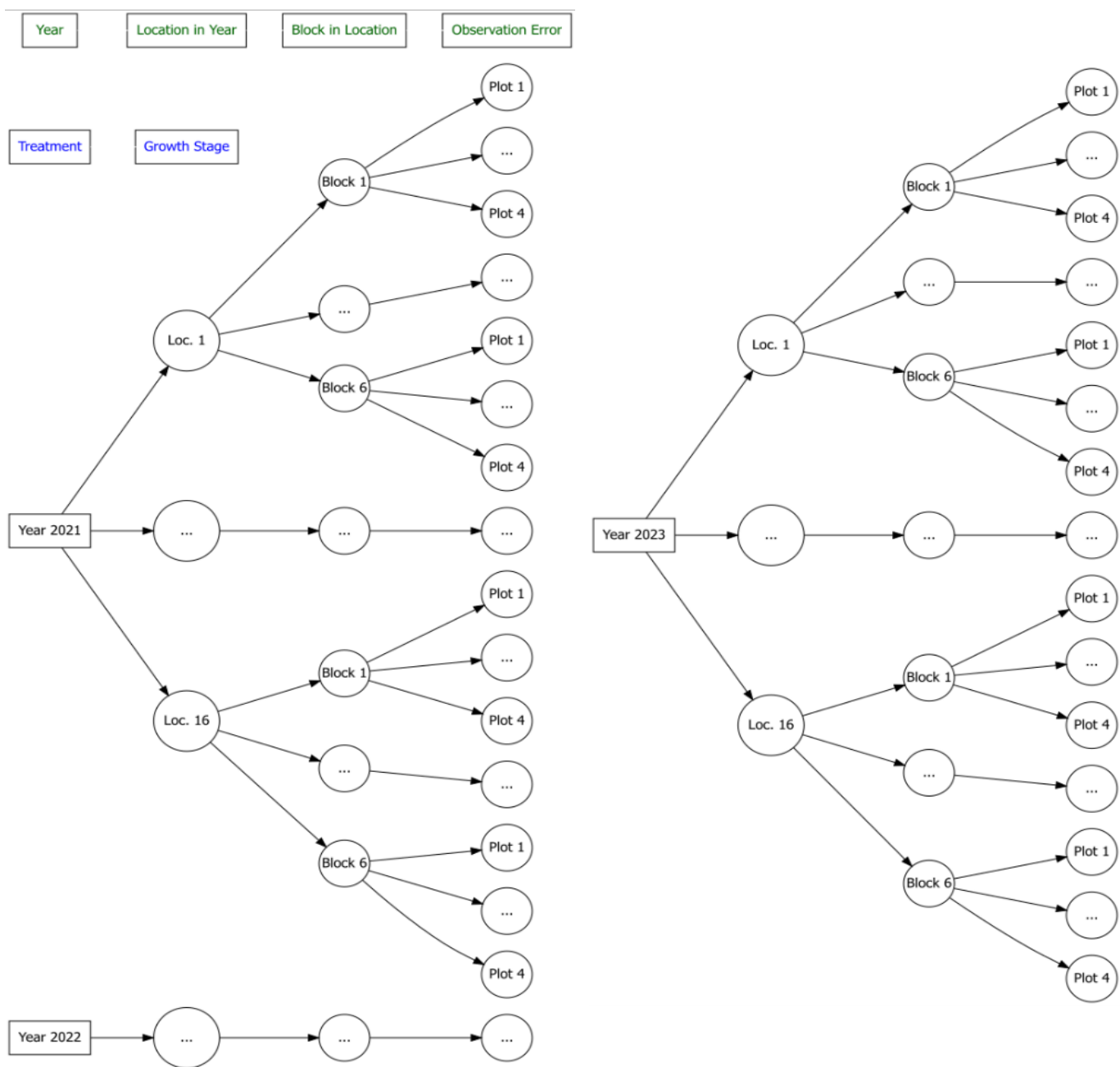
Figure 2: Mapped out random effects hierarchy. This figure displays the nested structure for the plot within block within location within year design.

Figure 3: Density plot of the raw response variable across the treatment and growth stage predictors. Yellow represents a success (predation) and black represents a failure (no predation).
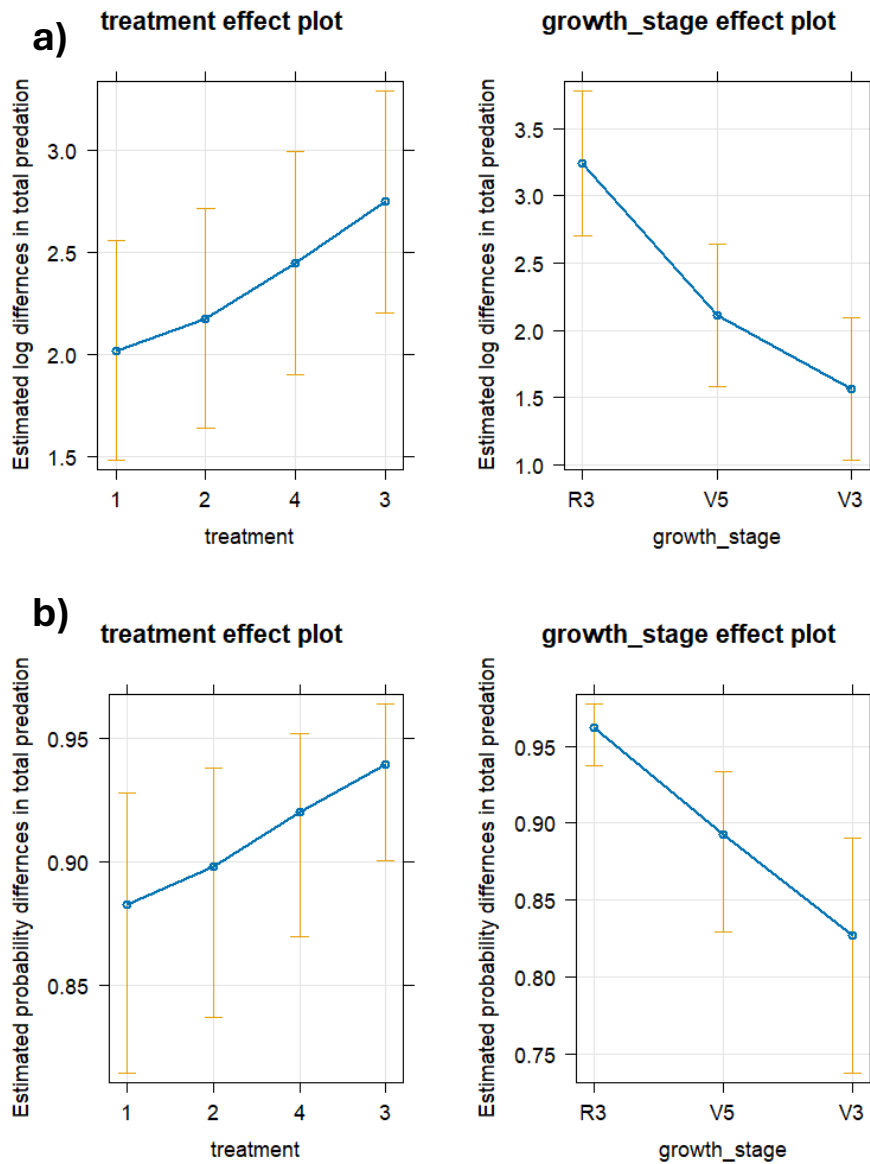
Figure 4: a) Effects plots of the estimated log differences in predation among treatments and growth stages. **b)** Effects plots of the estimated probability differences in predation among treatments and growth stages.
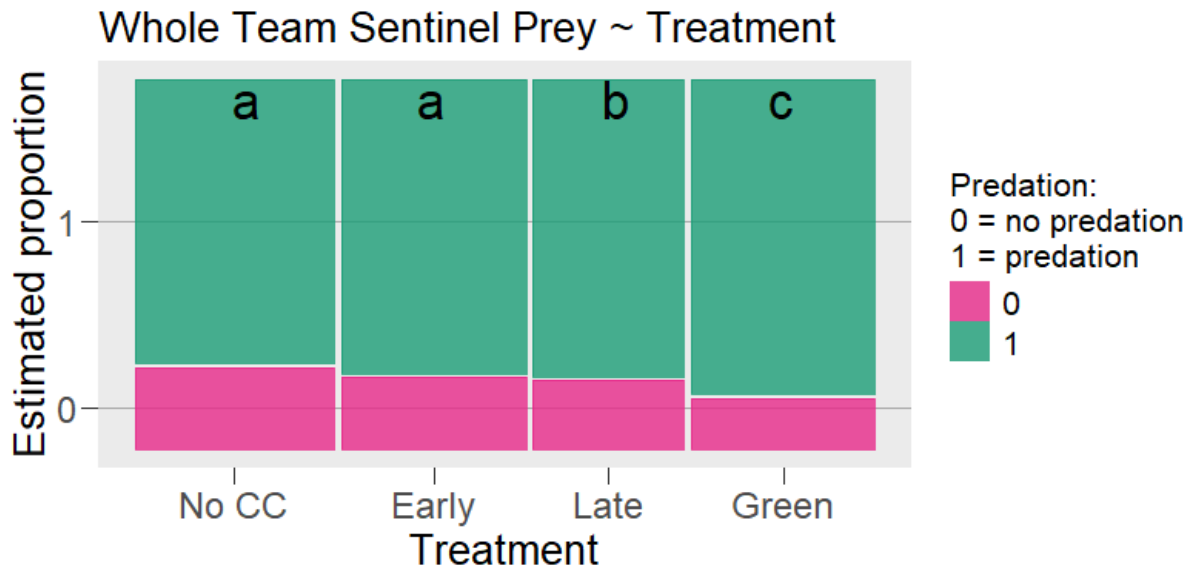
Whole Team Sentinel Prey ~ Treatment

Figure 5:
Total predation binary where 1 = predation and 0 = no predation.
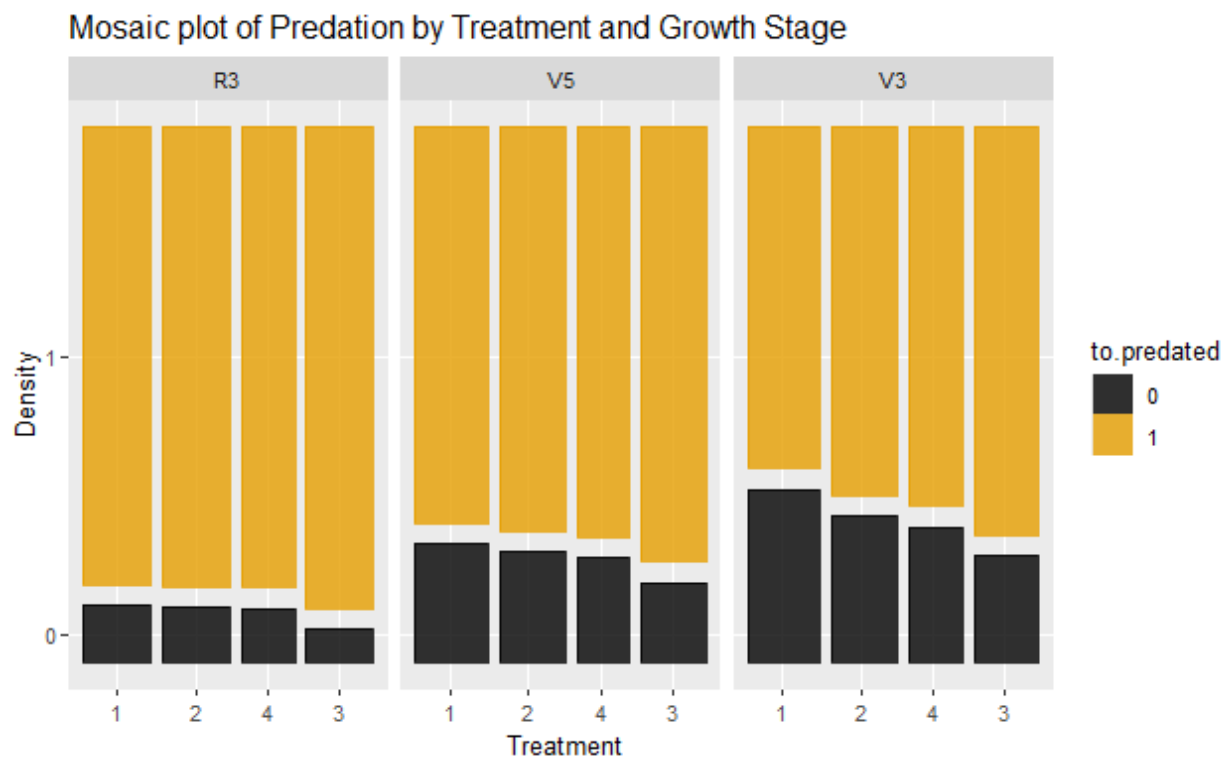Predation levels differed between the no-cover and late-terminated treatment
and the no-cover and planting-green treatment (p < 0.05).
Compact letter display denotes differences among treatments.

Whole Team Sentinel Prey ~ Growth Stage

Figure 6:
Total predation binary where 1 = predation and 0 = no predation.
Predation levels differed among all growth stages (p < 0.05), where R3 was the highest,
followed by V5, and then V3. Growth stages are ordered in reverse-chronological order.
Compact letter display denotes differences among growth stages

Tables

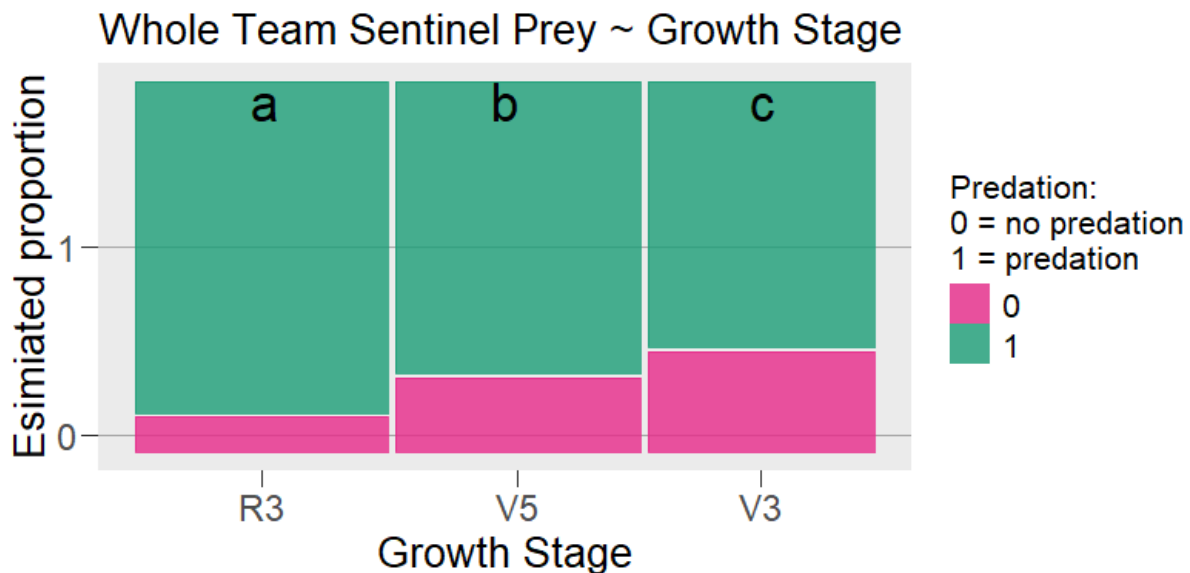| Treatment	Growth stage	Probability	Standard Dev.	n
No CC	V3	0.66	0.47	1098
Early terminated	V3	0.72	0.45	986
Late terminated	V3	0.74	0.44	836
Planting green	V3	0.79	0.41	982
All treatments	**V3**	**0.72**	**0.45**	**3902**
No CC	V5	0.77	0.42	1195
Early terminated	V5	0.78	0.41	1068
Late terminated	V5	0.79	0.4	871
Planting green	V5	0.84	0.36	1062
All treatments	**V5**	**0.79**	**0.4**	**4196**
No CC	R3	0.89	0.32	1146
Early terminated	R3	0.89	0.31	1149
Late terminated	R3	0.89	0.31	898
Planting green	R3	0.93	0.25	1141
All treatments	**R3**	**0.9**	**0.3**	**4334**
No CC	-	0.77	0.42	3439
Early terminated	-	0.8	0.4	3203
Late terminated	-	0.81	0.4	2605
Planting green	-	0.86	0.35	3185

Table 1: Breakdown of mean, standard deviation, and sample size for each treatment and growth stage pair. The response is on a binomial scale (1 = predation/ success, 0 = failure/ no predation). Data derived from the Mosaic package. Growth stages are order chronologically (V3, V5, R3).

Citations

Busch, A. K., Douglas, M. R., Malcolm, G. M., Karsten, H. D., & Tooker, J. F. (2020). A high-diversity/IPM cropping system fosters beneficial arthropod populations, limits invertebrate pests, and produces competitive maize yields. *Agriculture, Ecosystems & Environment*, *292*, 106812. https://doi.org/10.1016/j.agee.2019.106812

Fox J, Weisberg S (2019). _An R Companion to Applied Regression_, Third edition. Sage, Thousand Oaks CA.<https://socialsciences.mcmaster.ca/jfox/Books/Companion/>.

Iannone R (2016). _DiagrammeRsvg: Export DiagrammeR Graphviz Graphs as SVG_. R package version 0.1, <https://CRAN.R-project.org/package=DiagrammeRsvg>.

John Fox and Sanford Weisberg (2019). An R Companion to Applied Regression, 3rd Edition. Thousand Oaks, CA https://socialsciences.mcmaster.ca/jfox/Books/Companion/index.html

John Fox, Jangman Hong (2009). Effect Displays in R for Multinomial and Proportional-Odds Logit Models: Extensions to the effects Package. Journal of Statistical Software, 32(1), 1-24. doi 10.18637/jss.v032.i01

Lenth R (2024). _emmeans: Estimated Marginal Means, aka Least-Squares Means_. R package version 1.10.4, commit 52c445c77326050a97e70999b376424266495419, <https://github.com/rvlenth/emmeans>.

Lüdecke et al., (2021). performance: An R Package for Assessment, Comparison and Testing of Statistical Models. Journal of Open Source Software, 6(60), 3139. https://doi.org/10.21105/joss.03139

Lundgren, J. G., Shaw, J. T., Zaborski, E. R., & Eastman, C. E. (2006). The influence of organic transition systems on beneficial ground-dwelling arthropods and predation of insects and weed seeds. *Renewable Agriculture and Food Systems*, *21*(4), 227–237. https://doi.org/10.1079/RAF2006152

R. Pruim, D. T. Kaplan and N. J. Horton. The mosaic Package: Helping Students to 'Think with Data' Using R (2017). The R Journal, 9(1):77-102.

Final project

Jared Adam

12/6/2024

Packages

Data import and wrangling

```r
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)


# 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>
```

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

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

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

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

```r
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)


# 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) %>%
  group_by(location, year, growth_stage, plot_id, block, treatment) %>%
  na.omit() %>%
  filter(treatment != 5) %>%
  mutate_at(vars(1:6),as.factor)
```

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

## # A tibble: 12,432 × 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 12,422 more rows

dim(sent)

## [1] 12432      7

unique(sent$location)

##  [1] PA FL IL IA KS KY MD NE NY NC OH TX VT VA WI DE
## Levels: DE FL IA IL KS KY MD NC NE NY OH PA TX VA VT WI
```

Experimental design

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; 5-6 blocks (location dependent) 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. Each site year was in a different field. **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 a binomial of 6 traps/ counts per plot. Pseudoreplication is account for in the random term. **Explanatory** = Crop growth stage (timing, three levels) and treatment (four levels). I am not interested in the fixed

effects of location. **Random effects** = Plot in block in location, in year. I want to account for pseduoreplication and all of the site/year combinations.

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.

Locating missing values

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


Dark represents missing data
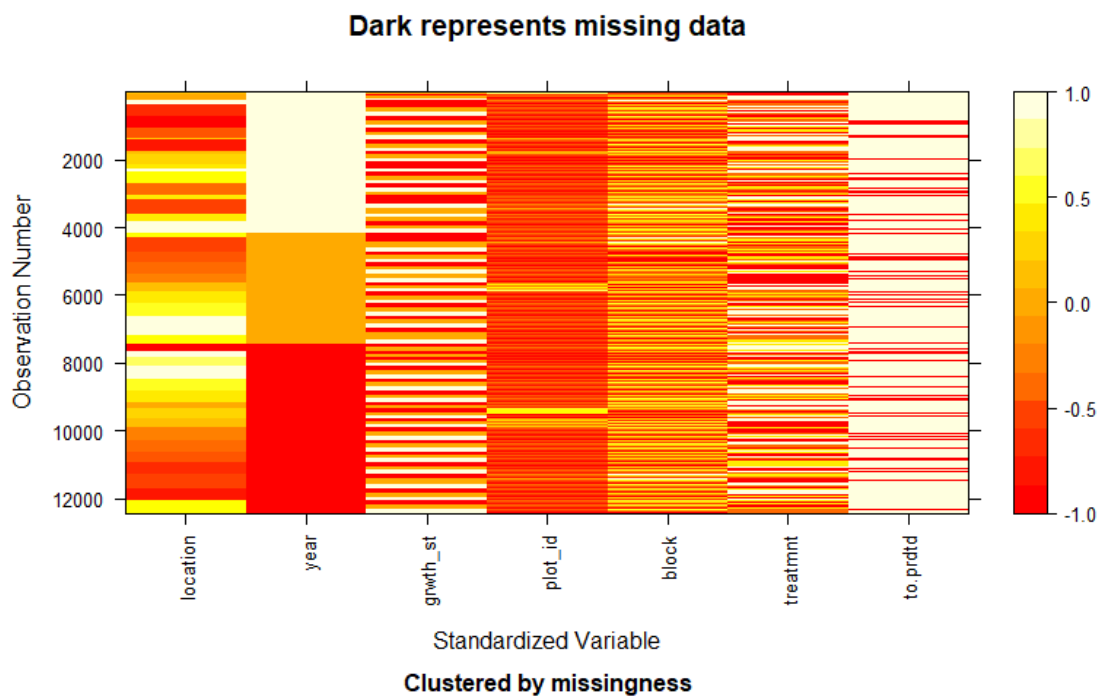
Preliminary data display

```
sent %>%
  ggplot() +
  geom_mosaic(aes(x = product(treatment), fill = to.predated), offset =
0.04)+
  facet_wrap(~growth_stage)+
  scale_fill_colorblind()+
  labs(title = 'Mosaic plot of Predation by Treatment and Growth Stage',
       y = 'Density',
       x = ' Treatment')
```

Mosaic plot of Predation by Treatment and Growth Stage
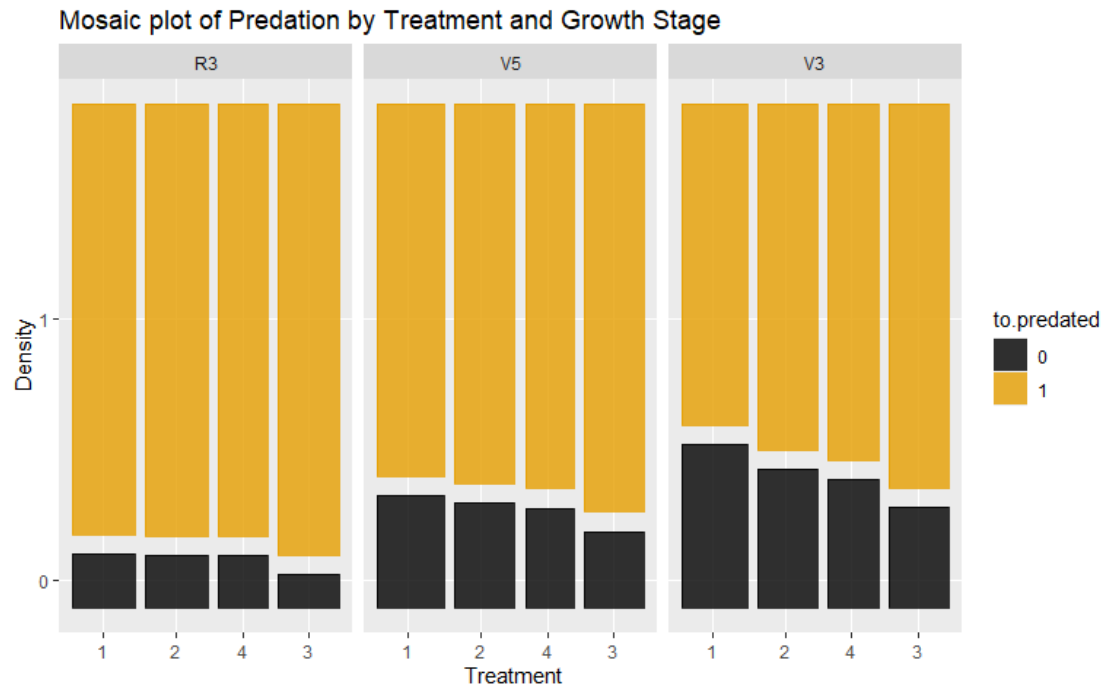
Modeling

Theoretical model:

${Predation|Treatment,GrowthStage} \sim \beta_0 + \beta_1 I_{Treatment = 2}_i + \beta_2 I_{Treatment = 4}_i + \beta_3 I_{Treatment = 3}_i + \beta_4 I_{GrowthStage = V5}_i + \beta_5 I_{GrowthStage = V3}_i + Year_i + Location_i + Block_i + Plot_i + Error_i$

Add the appropriate stuff below

$\pi\{Predation|Treatment, GrowthStage} \sim \beta_0 + \beta_1 I_{Treatment = 2} + \beta_2 I_{Treatment = 4} + \beta_3 I_{Treatment = 3} + \beta_4 I_{GrowthStage = V5} + \beta_5 I_{GrowthStage = V3}$

Initial model

```
sent

## # A tibble: 12,432 × 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 12,422 more rows

m2 <- glmer(to.predated ~ treatment*growth_stage +
(1|year/location/block/plot_id) , family = binomial, data = sent)
summary(m2)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## to.predated ~ treatment * growth_stage + (1 | year/location/block/plot_id)
##    Data: sent
##
##      AIC      BIC    logLik deviance df.resid
##   9135.0   9253.8  -4551.5   9103.0    12416
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -11.4203   0.0801   0.2125   0.4224   2.9757
##
## Random effects:
##  Groups                          Name        Variance  Std.Dev.
##  plot_id:(block:(location:year)) (Intercept) 2.611e-01 0.511004
##  block:(location:year)           (Intercept) 1.701e-01 0.412483
##  location:year                   (Intercept) 2.689e+00 1.639802
##  year                            (Intercept) 1.545e-05 0.003931
## Number of obs: 12432, 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)                3.03307    0.29061  10.437  < 2e-16
## treatment2                 0.03549    0.16020   0.222 0.824674
## treatment4                 0.22142    0.17252   1.283 0.199352
## treatment3                 0.62055    0.17515   3.543 0.000396
## growth_stageV5            -1.15589    0.13170  -8.776  < 2e-16
## growth_stageV3            -1.92785    0.13398 -14.389  < 2e-16
## treatment2:growth_stageV5  0.03110    0.18796   0.165 0.868581
## treatment4:growth_stageV5  0.08776    0.20154   0.435 0.663242
## treatment3:growth_stageV5 -0.02574    0.20392  -0.126 0.899541
## treatment2:growth_stageV3  0.29511    0.18920   1.560 0.118818
## treatment4:growth_stageV3  0.44923    0.20103   2.235 0.025439
## treatment3:growth_stageV3  0.31249    0.20397   1.532 0.125508
##
## Correlation of Fixed Effects:
```

```
##              (Intr) trtmn2 trtmn4 trtmn3 grw_V5 grw_V3 t2:_V5 t4:_V5 t3:_V5
## treatment2   -0.272
## treatment4   -0.248  0.458
## treatment3   -0.246  0.453  0.421
## grwth_stgV5  -0.293  0.511  0.472  0.466
## grwth_stgV3  -0.300  0.511  0.474  0.464  0.647
## trtmnt2:_V5   0.199 -0.724 -0.332 -0.327 -0.693 -0.446
## trtmnt4:_V5   0.185 -0.334 -0.719 -0.305 -0.646 -0.415  0.453
## trtmnt3:_V5   0.184 -0.330 -0.306 -0.744 -0.639 -0.412  0.448  0.417
## trtmnt2:_V3   0.203 -0.727 -0.334 -0.330 -0.451 -0.692  0.622  0.294  0.290
## trtmnt4:_V3   0.192 -0.339 -0.728 -0.310 -0.424 -0.655  0.297  0.623  0.273
## trtmnt3:_V3   0.191 -0.335 -0.309 -0.747 -0.420 -0.645  0.292  0.272  0.645
##              t2:_V3 t4:_V3
## treatment2
## treatment4
## treatment3
## grwth_stgV5
## grwth_stgV3
## trtmnt2:_V5
## trtmnt4:_V5
## trtmnt3:_V5
## trtmnt2:_V3
## trtmnt4:_V3   0.459
## trtmnt3:_V3   0.454  0.427
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.0296809 (tol = 0.002,
component 1)

Anova(m2)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: to.predated
##                          Chisq Df Pr(>Chisq)
## treatment              60.9286  3   3.722e-13
## growth_stage          526.0579  2  < 2.2e-16
## treatment:growth_stage  8.2544  6       0.22

plot(allEffects(m2), type = 'link',ylab = 'estimated log differnces in total
predation', grid = T)
```

treatment*growth_stage effect plot

growth_stage = R3   growth_stage = V5   growth_stage = V3

estimated log differnces in total predation
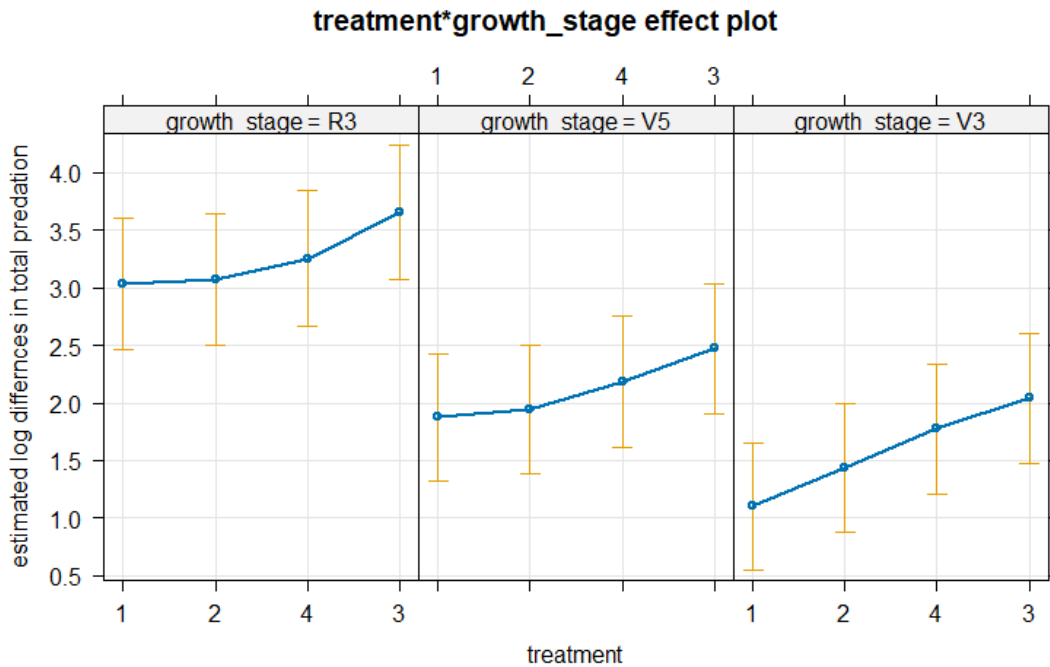
treatment

```r
plot(allEffects(m2), type = 'response', xlim = c(0,1),ylab = 'estimated
probability differnces in total predation', grid = T)
```

treatment*growth_stage effect plot

growth_stage = R3   growth_stage = V5   growth_stage = V3

estimated probability differnces in total predation
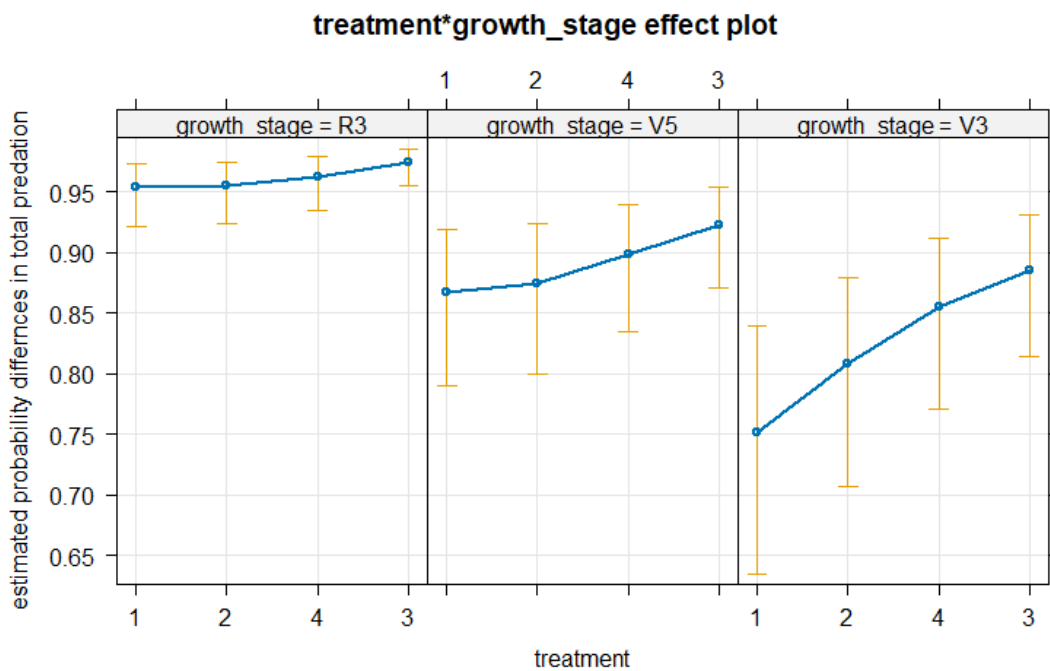
treatment

* There is weak evidence against the null of no interaction between treatment and growth stage Chi squared(6) = 8.25, p = 0.22, after controlling for the random effect of plot nested in block nested in location nested in year, and will remove the interaction term from the model.

Model refinement

```
m3 <- glmer(to.predated ~ treatment+growth_stage +
(1|year/location/block/plot_id) , family = binomial, data = sent)
summary(m3)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## to.predated ~ treatment + growth_stage + (1 | year/location/block/plot_id)
##     Data: sent
##
##      AIC      BIC   logLik deviance df.resid
##   9131.1   9205.4  -4555.5   9111.1    12422
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -11.4488   0.0811   0.2124   0.4229   2.9455
##
## Random effects:
##  Groups                          Name        Variance  Std.Dev.
##  plot_id:(block:(location:year)) (Intercept) 2.600e-01 0.50988
##  block:(location:year)           (Intercept) 1.700e-01 0.41236
##  location:year                   (Intercept) 2.672e+00 1.63473
##  year                            (Intercept) 5.569e-06 0.00236
## Number of obs: 12432, 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)     2.92687    0.27926  10.481  < 2e-16
## treatment2      0.15828    0.09462   1.673   0.0944
## treatment4      0.42821    0.10271   4.169 3.06e-05
## treatment3      0.72957    0.09942   7.338 2.16e-13
## growth_stageV5 -1.13027    0.07256 -15.578  < 2e-16
## growth_stageV3 -1.68191    0.07334 -22.932  < 2e-16
##
## Correlation of Fixed Effects:
##            (Intr) trtmn2 trtmn4 trtmn3 grw_V5
## treatment2 -0.161
## treatment4 -0.138  0.451
## treatment3 -0.141  0.468  0.436
## grwth_stgV5 -0.172 -0.003 -0.015 -0.026
## grwth_stgV3 -0.176 -0.007 -0.024 -0.041  0.625
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.0104819 (tol = 0.002,
component 1)

Anova(m3)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: to.predated
##                 Chisq Df Pr(>Chisq)
## treatment       60.988  3  3.615e-13
## growth_stage   528.427  2  < 2.2e-16
```
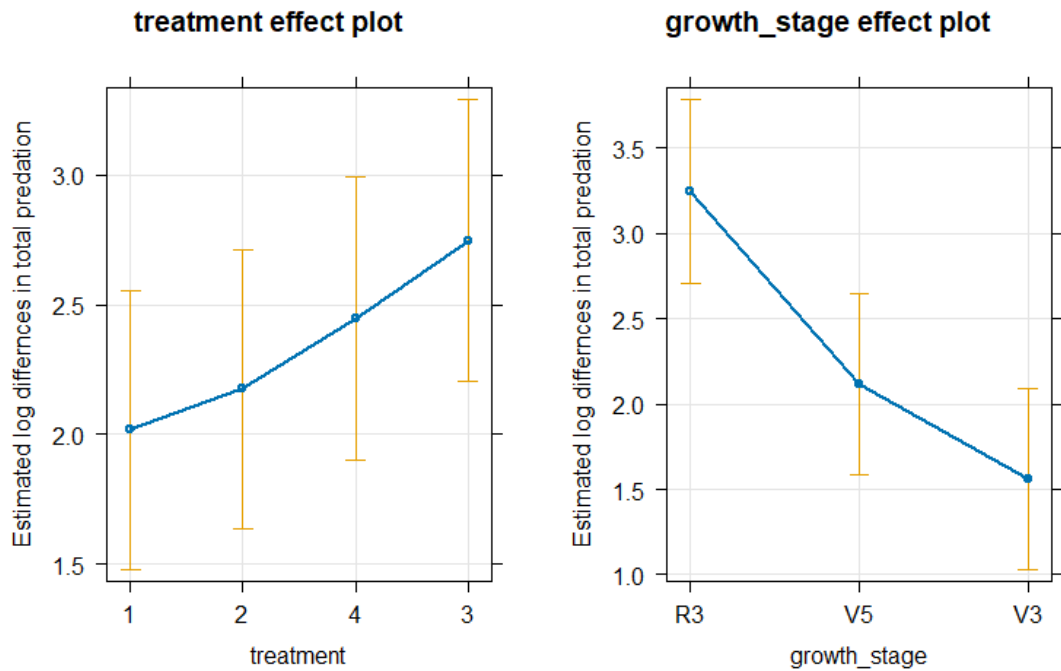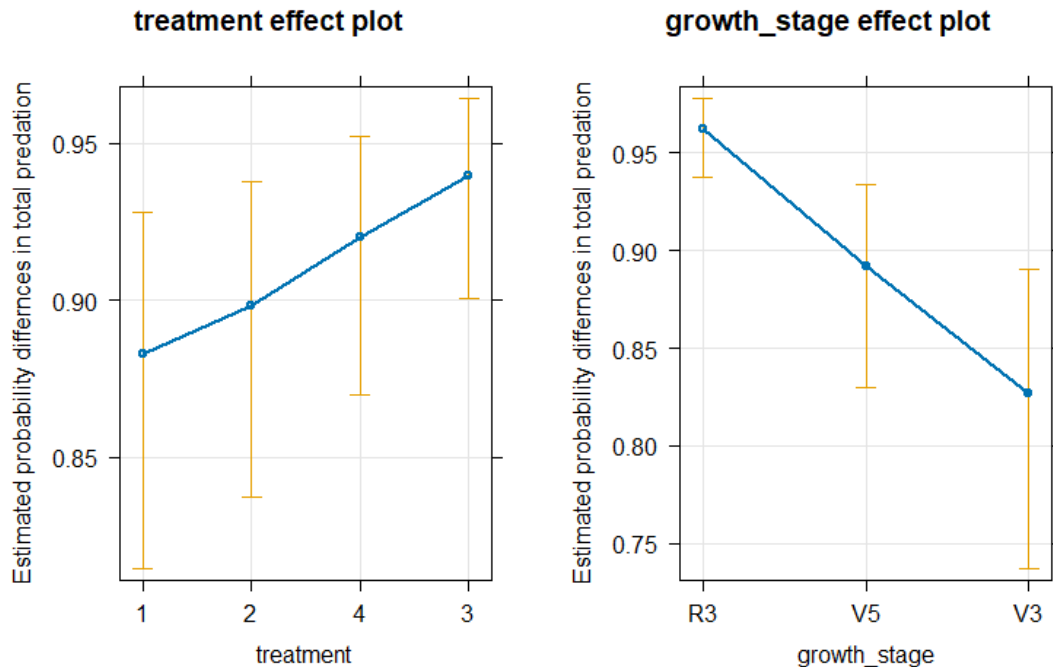
```r
plot(allEffects(m3), type = 'link', ylab = 'Estimated log differnces in total
predation', grid = T)
```



```r
plot(allEffects(m3), type = 'response', xlim = c(0,1),ylab = 'Estimated
probability differnces in total predation', grid = T)
```

treatment effect plot   **growth_stage effect plot**


```
cld(emmeans(m3, ~treatment, adjust = 'tukey', type = 'response'), Letters =
letters)

##  treatment  prob      SE  df asymp.LCL asymp.UCL .group
##  1          0.880 0.0290 Inf     0.787     0.935  a
##  2          0.895 0.0257 Inf     0.812     0.944  a
##  4          0.918 0.0209 Inf     0.849     0.957   b
##  3          0.938 0.0161 Inf     0.884     0.968    c
##
## Results are averaged over the levels of: growth_stage
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 4 estimates
## Intervals are back-transformed from the logit scale
## P value adjustment: tukey method for comparing a family of 4 estimates
## Tests are performed on the log odds ratio scale
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
cld(emmeans(m3, ~growth_stage, adjust = 'tukey', type = 'response'), Letters
= letters)

##  growth_stage  prob       SE  df asymp.LCL asymp.UCL .group
##  V3            0.828 0.03850 Inf     0.717     0.902  a
##  V5            0.893 0.02584 Inf     0.814     0.941   b
##  R3            0.963 0.00981 Inf     0.931     0.980    c
##
## Results are averaged over the levels of: treatment
```

```
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 3 estimates
## Intervals are back-transformed from the logit scale
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log odds ratio scale
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##        then we cannot show them to be different.
##        But we also did not show them to be the same.
```

R squared and ICC

r.squaredGLMM(m3)

```
##                     R2m        R2c
## theoretical 0.08286345 0.527981
## delta       0.05596765 0.356609
```

library(performance)
r2(m3)

```
## # R2 for Mixed Models
##
##   Conditional R2: 0.528
##      Marginal R2: 0.083
```

summary(m3)

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## to.predated ~ treatment + growth_stage + (1 | year/location/block/plot_id)
##    Data: sent
##
##      AIC      BIC   logLik deviance df.resid
##   9131.1   9205.4  -4555.5   9111.1    12422
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -11.4488   0.0811   0.2124   0.4229   2.9455
##
## Random effects:
##  Groups                         Name        Variance  Std.Dev.
##  plot_id:(block:(location:year)) (Intercept) 2.600e-01 0.50988
##  block:(location:year)          (Intercept) 1.700e-01 0.41236
##  location:year                  (Intercept) 2.672e+00 1.63473
##  year                           (Intercept) 5.569e-06 0.00236
## Number of obs: 12432, 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)    2.92687    0.27926  10.481  < 2e-16
## treatment2     0.15828    0.09462   1.673   0.0944
## treatment4     0.42821    0.10271   4.169 3.06e-05
## treatment3     0.72957    0.09942   7.338 2.16e-13
## growth_stageV5 -1.13027   0.07256 -15.578  < 2e-16
## growth_stageV3 -1.68191   0.07334 -22.932  < 2e-16
##
## Correlation of Fixed Effects:
##            (Intr) trtmn2 trtmn4 trtmn3 grw_V5
## treatment2  -0.161
## treatment4  -0.138  0.451
## treatment3  -0.141  0.468  0.436
## grwth_stgV5 -0.172 -0.003 -0.015 -0.026
## grwth_stgV3 -0.176 -0.007 -0.024 -0.041  0.625
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.0104819 (tol = 0.002,
component 1)
```

```r
# for plot
(2.600e-01) / (2.600e-01 + 1.700e-01 + .672e+00 + 5.569e-06)
```

```
## [1] 0.2359335
```

The ICC for plot id is 0.236.

Final plots

```r
sent %>%
  ggplot()+
  geom_mosaic(aes(x = product(treatment), fill = to.predated))+
  scale_fill_manual(values = c("#E7298A","#1B9E77"))+
  scale_x_productlist(labels=c("No CC", "Early", "Late", "Green"))+
  labs(title = 'Whole Team Sentinel Prey ~ Treatment',
       x = 'Treatment',
       y = 'Estimated proportion',
       caption = 'Figure 5:\nTotal predation binary where 1 = predation and 0
= no predation.\nPredation levels differed between the no-cover and late-
terminated treatment\nand the no-cover and planting-green treatment (p <
0.05).\nCompact letter display denotes differences among treatments.')+
  guides(fill = guide_legend(title = 'Predation:\n0 = no predation\n1 =
predation'))+
  theme(legend.title = element_text(size = 14),
        legend.text = element_text(size = 14),
        axis.text.x = element_text(size=16),
        axis.text.y = element_text(size = 16),
        axis.title = element_text(size = 18),
        plot.title = element_text(size = 18),
        plot.subtitle = element_text(size = 12),
```

```
      panel.grid.major.y = element_line(color = "darkgrey"),
      panel.grid.major.x = element_blank(),
      panel.grid.minor = element_blank(),
      strip.text = element_text(size = 12),
      plot.caption = element_text(hjust = 0, size = 12, color = "grey25"),
      axis.ticks.length=unit(.25, "cm"))+
  annotate('text', x = 0.15, y = 0.95, label = 'a', size = 8)+
  annotate('text', x = .4, y = 0.95, label = 'a', size = 8)+
  annotate('text', x = .65, y = 0.95, label = 'b', size = 8)+
  annotate('text', x = .875, y = 0.95, label = 'c', size = 8)
```

Figure 5:
Total predation binary where 1 = predation and 0 = no predation.
Predation levels differed between the no-cover and late-terminated treatment
and the no-cover and planting-green treatment (p < 0.05).
Compact letter display denotes differences among treatments.

```
sent %>%
  ggplot()+
  geom_mosaic(aes(x = product(growth_stage), fill = to.predated))+
  scale_fill_manual(values = c("#E7298A","#1B9E77"))+
  labs(title = 'Whole Team Sentinel Prey ~ Growth Stage',
       x = 'Growth Stage',
       y = 'Esimiated proportion',
       caption = 'Figure 6:\nTotal predation binary where 1 = predation and 0
= no predation.\nPredation levels differed among all growth stages (p <
0.05), where R3 was the highest,\nfollowed by V5, and then V3. Growth stages
are ordered in reverse-chronological order.\nCompact letter display denotes
differences among growth stages')+
  guides(fill = guide_legend(title = 'Predation:\n0 = no predation\n1 =
predation'))+
  theme(legend.title = element_text(size = 14),
        legend.text = element_text(size = 14),
        axis.text.x = element_text(size=16),
        axis.text.y = element_text(size = 16),
```

```
        axis.title = element_text(size = 18),
        plot.title = element_text(size = 18),
        plot.subtitle = element_text(size = 12),
        panel.grid.major.y = element_line(color = "darkgrey"),
        panel.grid.major.x = element_blank(),
        panel.grid.minor = element_blank(),
        strip.text = element_text(size = 12),
        plot.caption = element_text(hjust = 0, size = 12, color = "grey25"),
        axis.ticks.length=unit(.25, "cm"))+
  annotate('text', x = 0.175, y = 0.95, label = 'a', size = 8)+
  annotate('text', x = .5, y = 0.95, label = 'b', size = 8)+
  annotate('text', x = .85, y = 0.95, label = 'c', size = 8)
```
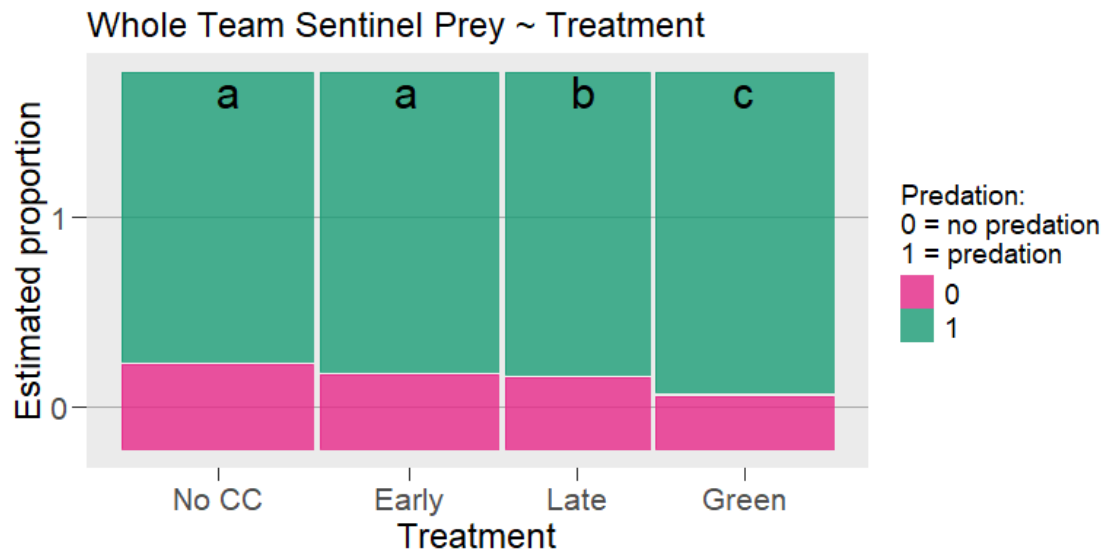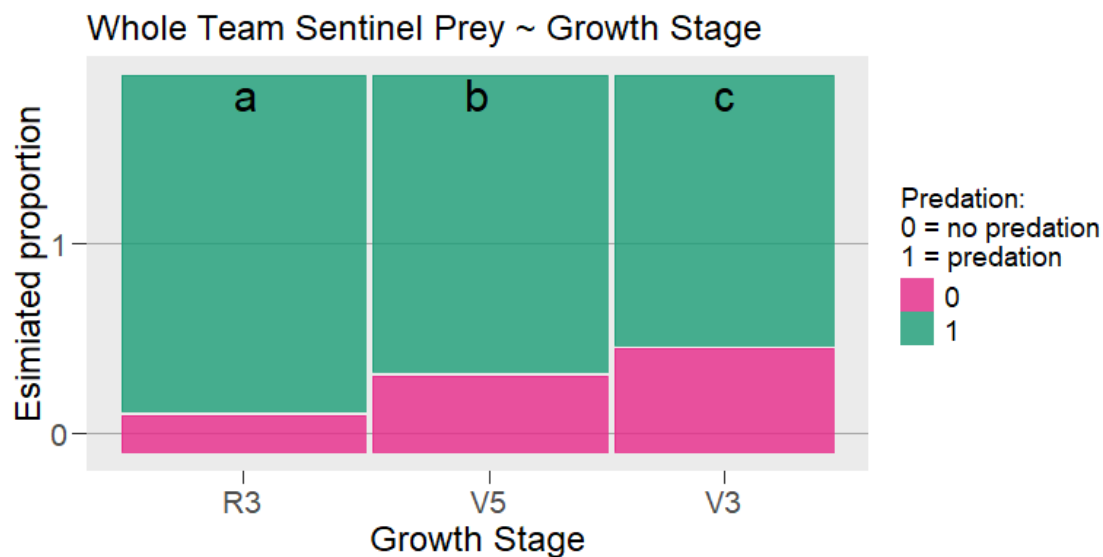

Figure 6:
Total predation binary where 1 = predation and 0 = no predation.
Predation levels differed among all growth stages (p < 0.05), where R3 was the highest,
followed by V5, and then V3. Growth stages are ordered in reverse-chronological order.
Compact letter display denotes differences among growth stages

Table 1

```
# table as a proportion
sent %>%
  group_by(location, treatment, growth_stage) %>%
  summary()

##      location        year       growth_stage     plot_id         block      treatment
## IL      :1296   2021:5004   R3:4334      203     : 608    1:2681    1:3439
## OH      :1173   2022:3246   V5:4196      103     : 607    2:2491    2:3203
## VT      :1080   2023:4182   V3:3902      303     : 607    3:2493    4:2605
## PA      :1074                            401     : 603    4:2514    3:3185
## KY      :1054                            102     : 591    5:1969
## KS      : 848                            202     : 589    6: 284
## (Other):5907                             (Other):8827
```

```
##    to.predated
##  Min.   :0.0000
##  1st Qu.:1.0000
##  Median :1.0000
##  Mean   :0.8103
##  3rd Qu.:1.0000
##  Max.   :1.0000
##
```

```r
sent %>%
  group_by(growth_stage) %>%
  summary()
```

```
##      location       year      growth_stage    plot_id       block      treatment
##  IL     :1296   2021:5004   R3:4334      203    : 608   1:2681    1:3439
##  OH     :1173   2022:3246   V5:4196      103    : 607   2:2491    2:3203
##  VT     :1080   2023:4182   V3:3902      303    : 607   3:2493    4:2605
##  PA     :1074                            401    : 603   4:2514    3:3185
##  KY     :1054                            102    : 591   5:1969
##  KS     : 848                            202    : 589   6: 284
##  (Other):5907                            (Other):8827
##    to.predated
##  Min.   :0.0000
##  1st Qu.:1.0000
##  Median :1.0000
##  Mean   :0.8103
##  3rd Qu.:1.0000
##  Max.   :1.0000
##
```

```r
tally(to.predated ~ treatment + growth_stage, data = sent)
```

```
## , , growth_stage = R3
##
##            treatment
## to.predated    1    2    4    3
##           0  128  125   96   77
##           1 1018 1024  802 1064
##
## , , growth_stage = V5
##
##            treatment
## to.predated    1    2    4    3
##           0  277  232  179  167
##           1  918  836  692  895
##
## , , growth_stage = V3
##
##            treatment
## to.predated    1    2    4    3
```

```
##           0  371  281  221  204
##           1  727  705  615  778
```

```
datasummary_balance( ~ to.predated,data = sent)
```

		0		1	
		N	Pct.	N	Pct.
location	DE	193	8.2	405	4.0
	FL	19	0.8	692	6.9
	IA	16	0.7	705	7.0
	IL	95	4.0	1201	11.9
	KS	345	14.6	503	5.0
	KY	373	15.8	681	6.8
	MD	192	8.1	408	4.1
	NC	19	0.8	341	3.4
	NE	65	2.8	706	7.0
	NY	94	4.0	474	4.7
	OH	531	22.5	642	6.4
	PA	240	10.2	834	8.3
	TX	22	0.9	698	6.9
	VA	49	2.1	239	2.4
	VT	38	1.6	1042	10.3
	WI	67	2.8	503	5.0
year	2021	883	37.4	4121	40.9
	2022	676	28.7	2570	25.5
	2023	799	33.9	3383	33.6
growth_stage	R3	426	18.1	3908	38.8
	V5	855	36.3	3341	33.2
	V3	1077	45.7	2825	28.0
plot_id	101	161	6.8	425	4.2
	102	112	4.7	479	4.8
	103	126	5.3	481	4.8
	104	119	5.0	426	4.2
	201	112	4.7	452	4.5
	202	117	5.0	472	4.7
	203	113	4.8	495	4.9
	204	129	5.5	445	4.4
	301	111	4.7	478	4.7

	0		1	
	N	Pct.	N	Pct.
302	112	4.7	455	4.5
303	123	5.2	484	4.8
304	120	5.1	450	4.5
401	130	5.5	473	4.7
402	112	4.7	477	4.7
403	106	4.5	461	4.6
404	101	4.3	473	4.7
501	108	4.6	400	4.0
502	79	3.4	422	4.2
503	82	3.5	442	4.4
504	71	3.0	386	3.8
601	2	0.1	111	1.1
602	1	0.0	75	0.7
603	9	0.4	86	0.9
604	11	0.5	96	1.0
505	5	0.2	22	0.2
506	3	0.1	33	0.3
701	5	0.2	49	0.5
702	2	0.1	34	0.3
706	2	0.1	34	0.3
803	3	0.1	33	0.3
804	7	0.3	25	0.2
805	1	0.0	35	0.3
901	4	0.2	32	0.3
905	6	0.3	27	0.3
906	4	0.2	50	0.5
105	2	0.1	16	0.2
106	11	0.5	7	0.1
205	3	0.1	15	0.1
206	3	0.1	15	0.1
305	4	0.2	14	0.1
306	5	0.2	13	0.1
405	6	0.3	12	0.1
406	4	0.2	13	0.1

		0		1	
		N	Pct.	N	Pct.
	605	0	0.0	30	0.3
	705	2	0.1	33	0.3
	801	3	0.1	32	0.3
	902	1	0.0	17	0.2
	606	0	0.0	9	0.1
	802	4	0.2	13	0.1
	904	1	0.0	17	0.2
block	1	631	26.8	2050	20.3
	2	479	20.3	2012	20.0
	3	468	19.8	2025	20.1
	4	435	18.4	2079	20.6
	5	331	14.0	1638	16.3
	6	14	0.6	270	2.7
treatment	1	776	32.9	2663	26.4
	2	638	27.1	2565	25.5
	4	496	21.0	2109	20.9
	3	448	19.0	2737	27.2

```
# install.packages('openxlsx')
# library(openxlsx)
#
# table <- favstats(to.predated ~ treatment + growth_stage, data = sent)
# write.xlsx(table, 'test.xlsx')
# favstats(to.predated ~ growth_stage, data = sent)
# favstats(to.predated ~ treatment, data = sent)
# citation('mosaic')
```

Study design figure

```
tally(~ year, sent)

## year
## 2021 2022 2023
## 5004 3246 4182

tally(~location, sent)

## location
##   DE   FL   IA   IL   KS   KY   MD   NC   NE   NY   OH   PA   TX   VA   VT
## WI
##  598  711  721 1296  848 1054  600  360  771  568 1173 1074  720  288 1080
## 570
```

```
tally(~block, sent)

## block
##    1    2    3    4    5    6
## 2681 2491 2493 2514 1969  284

tally(~plot_id, sent)

## plot_id
## 101 102 103 104 201 202 203 204 301 302 303 304 401 402 403 404 501 502
503 504
## 586 591 607 545 564 589 608 574 589 567 607 570 603 589 567 574 508 501
524 457
## 601 602 603 604 505 506 701 702 706 803 804 805 901 905 906 105 106 205
206 305
## 113  76  95 107  27  36  54  36  36  36  32  36  36  33  54  18  18  18
18  18
## 306 405 406 605 705 801 902 606 802 904
##  18  18  17  30  35  35  18   9  17  18

names1 <- list("Year 2021", "Year 2022", "Year 2023")
names2 <- list("Loc. 1", "...", "Loc. 16", "...", "Loc. 1", "...", "Loc. 16")
names3 <- list("Block 1", "...", "Block 6")
names4 <- list("Plot 1", "...", "Plot 4")
namesF <- list("Treatment", "Growth Stage")
namesR <- list("Year", "Location in Year", "Block in Location", "Observation
Error")
```

Citations

```
citation('DiagrammeRsvg')

## To cite package 'DiagrammeRsvg' in publications use:
##
##   Iannone R (2016). _DiagrammeRsvg: Export DiagrammeR Graphviz Graphs
##   as SVG_. R package version 0.1,
##   <https://CRAN.R-project.org/package=DiagrammeRsvg>.
##
## A BibTeX entry for LaTeX users is
##
##   @Manual{,
##     title = {DiagrammeRsvg: Export DiagrammeR Graphviz Graphs as SVG},
##     author = {Richard Iannone},
##     year = {2016},
##     note = {R package version 0.1},
##     url = {https://CRAN.R-project.org/package=DiagrammeRsvg},
##   }

citation('car')
```

```
## To cite the car package in publications use:
##
##   Fox J, Weisberg S (2019). _An R Companion to Applied Regression_,
##   Third edition. Sage, Thousand Oaks CA.
##   <https://socialsciences.mcmaster.ca/jfox/Books/Companion/>.
##
## A BibTeX entry for LaTeX users is
##
##   @Book{,
##     title = {An {R} Companion to Applied Regression},
##     edition = {Third},
##     author = {John Fox and Sanford Weisberg},
##     year = {2019},
##     publisher = {Sage},
##     address = {Thousand Oaks {CA}},
##     url = {https://socialsciences.mcmaster.ca/jfox/Books/Companion/},
##   }

citation('effects')

## To cite effects in publications use:
##
##   John Fox and Sanford Weisberg (2019). An R Companion to Applied
##   Regression, 3rd Edition. Thousand Oaks, CA
##   <https://socialsciences.mcmaster.ca/jfox/Books/Companion/index.html>
##
## For predictor effects or partial residuals also cite:
##
##   John Fox, Sanford Weisberg (2018). Visualizing Fit and Lack of Fit in
##   Complex Regression Models with Predictor Effect Plots and Partial
##   Residuals. Journal of Statistical Software, 87(9), 1-27. doi
##   10.18637/jss.v087.i09
##
## For generalized linear models also cite:
##
##   John Fox (2003). Effect Displays in R for Generalised Linear Models.
##   Journal of Statistical Software, 8(15), 1-27. doi
##   10.18637/jss.v008.i15
##
## For usage in multinomial and proportional-odds logit models also cite:
##
##   John Fox, Jangman Hong (2009). Effect Displays in R for Multinomial
##   and Proportional-Odds Logit Models: Extensions to the effects
##   Package. Journal of Statistical Software, 32(1), 1-24. doi
##   10.18637/jss.v032.i01
##
## To see these entries in BibTeX format, use 'print(<citation>,
## bibtex=TRUE)', 'toBibtex(.)', or set
## 'options(citation.bibtex.max=999)'.
```

```r
citation('emmeans')
```

```
## To cite package 'emmeans' in publications use:
##
##   Lenth R (2024). _emmeans: Estimated Marginal Means, aka Least-Squares
##   Means_. R package version 1.10.4, commit
##   52c445c77326050a97e70999b376424266495419,
##   <https://github.com/rvlenth/emmeans>.
##
## A BibTeX entry for LaTeX users is
##
##   @Manual{,
##     title = {emmeans: Estimated Marginal Means, aka Least-Squares Means},
##     author = {Russell V. Lenth},
##     year = {2024},
##     note = {R package version 1.10.4, commit
52c445c77326050a97e70999b376424266495419},
##     url = {https://github.com/rvlenth/emmeans},
##   }
```