512 Project Part II

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# 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)   
  
  
# 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)  
  
  
# 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

1. 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.

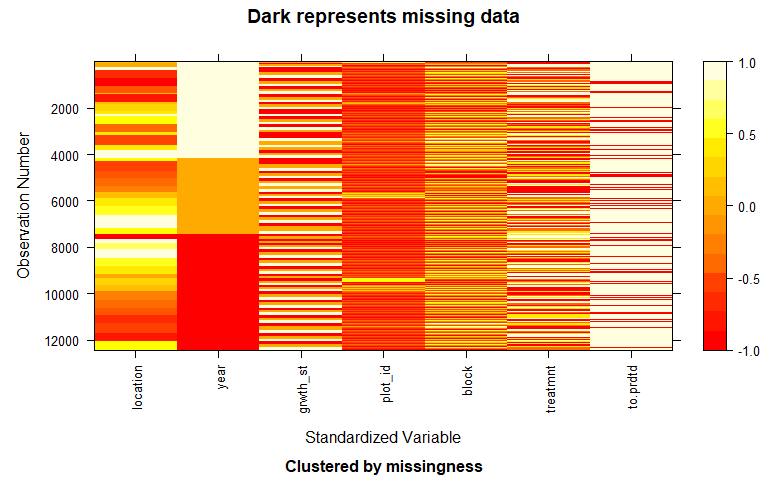
**Study design:**  **Treatments** = 4; No cover crop, early-terminated cover crop, late-terminated cover crop, planting green **Plots** = 20; 5 blocks composed of 4 plots each = 20 plots / study site / year **Years** = 3 (2021,2022,2023) **Locations** = This project comprises 16 states. Not all states collected sentinel prey data every year. 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.

1. Make a missing\_data.frame plot of your data set and explain any missing values indicated:

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

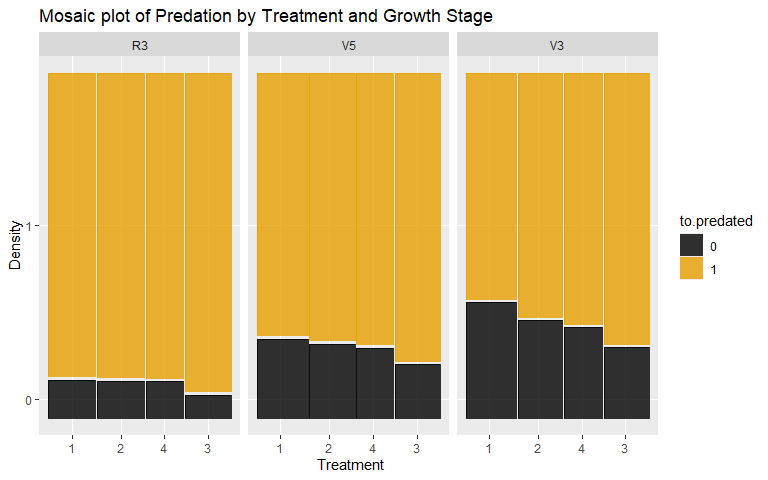


1. Discuss any other use in classes or theses for the data - either that you have used it for or are currently working on for future submissions.

**I am working on this for a publication. There is no published paper yet. None of the code from that is used here. This analysis is for all of the states combined, but in the future, I plan to run each state individually with their three years of data. I suspect results to differ based on some regional grouping (e.g., growing degree days, growth region, etc.), but am yet to decide what I will use. For now, I am mainly interested in the treatment and growth stage effects on the whole data set.**

1. 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.

sent %>%   
 ggplot() +  
 geom\_mosaic(aes(x = product(treatment), fill = to.predated))+  
 facet\_wrap(~growth\_stage)+  
 scale\_fill\_colorblind()+  
 labs(title = 'Mosaic plot of Predation by Treatment and Growth Stage',  
 y = 'Density',  
 x = ' Treatment')



1. 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: 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

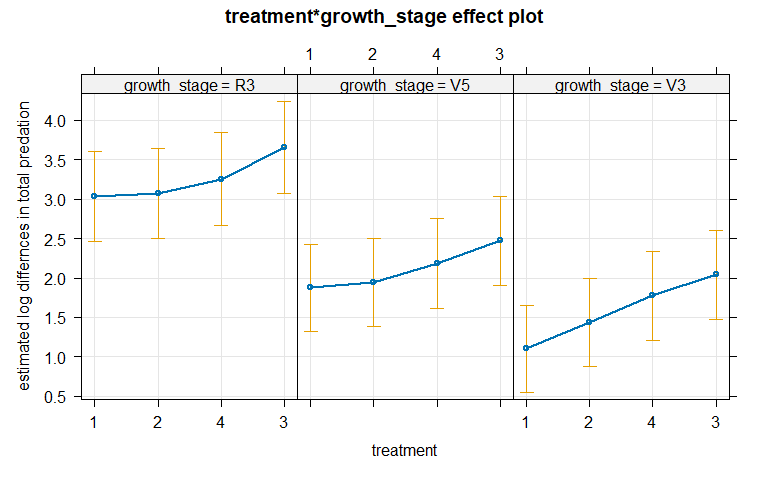
m2 <- glmer(to.predated ~ treatment\*growth\_stage + (1|year/location/block/plot\_id) , family = binomial, data = sent)  
summary(m2)

## 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)

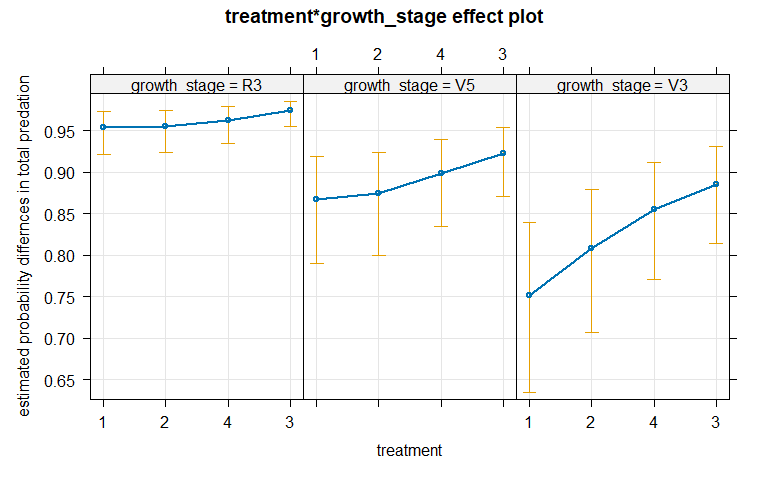
Anova(m2)

## 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)



plot(allEffects(m2), type = 'response', ylab = 'estimated probability differnces in total predation', grid = T)

 \* 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**

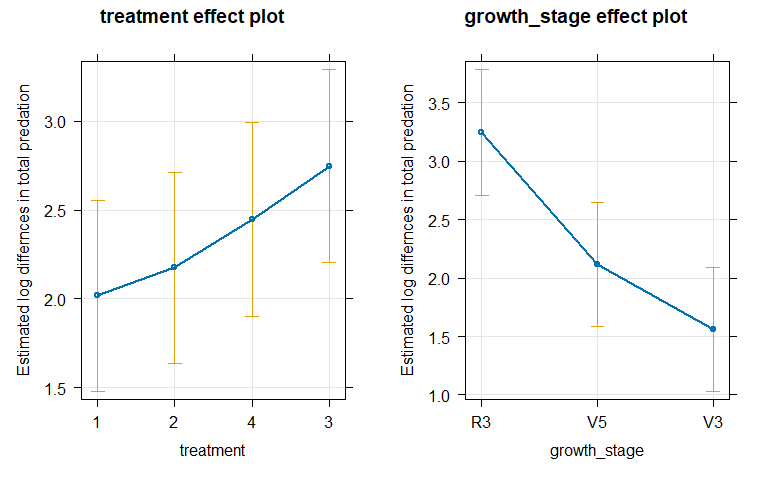
m3 <- glmer(to.predated ~ treatment+growth\_stage + (1|year/location/block/plot\_id) , family = binomial, data = sent)  
summary(m3)

## 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)

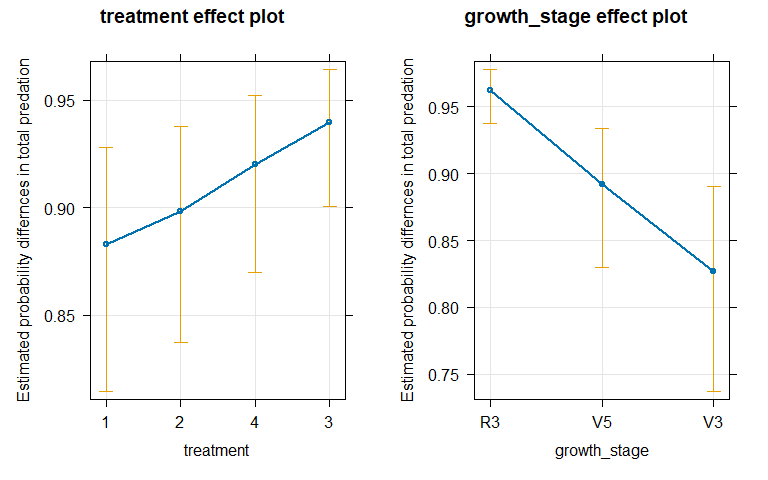
Anova(m3)

## 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

plot(allEffects(m3), type = 'link',ylab = 'Estimated log differnces in total predation', grid = T)



plot(allEffects(m3), type = 'response', ylab = 'Estimated probability differnces in total predation', grid = T)



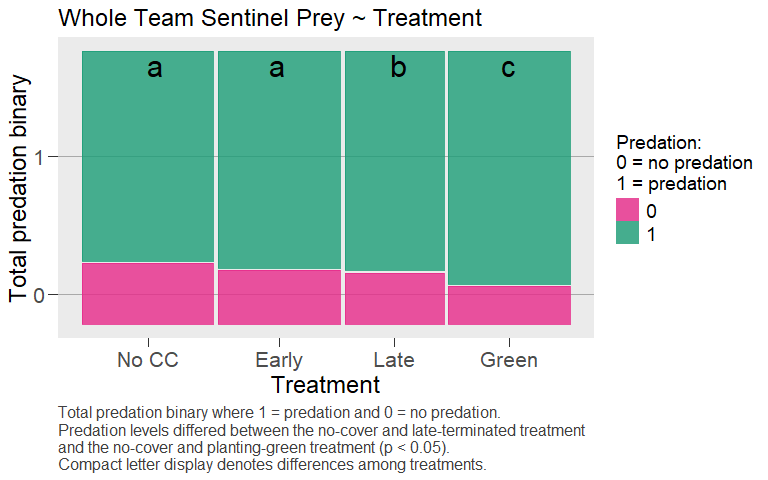
cld(emmeans(m3, ~treatment), Letters = letters)

## treatment emmean SE df asymp.LCL asymp.UCL .group  
## 1 1.99 0.274 Inf 1.45 2.53 a   
## 2 2.15 0.275 Inf 1.61 2.69 a   
## 4 2.42 0.279 Inf 1.87 2.96 b   
## 3 2.72 0.277 Inf 2.18 3.26 c   
##   
## Results are averaged over the levels of: growth\_stage   
## Results are given on the logit (not the response) scale.   
## Confidence level used: 0.95   
## Results are given on the log odds ratio (not the response) scale.   
## P value adjustment: tukey method for comparing a family of 4 estimates   
## 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.

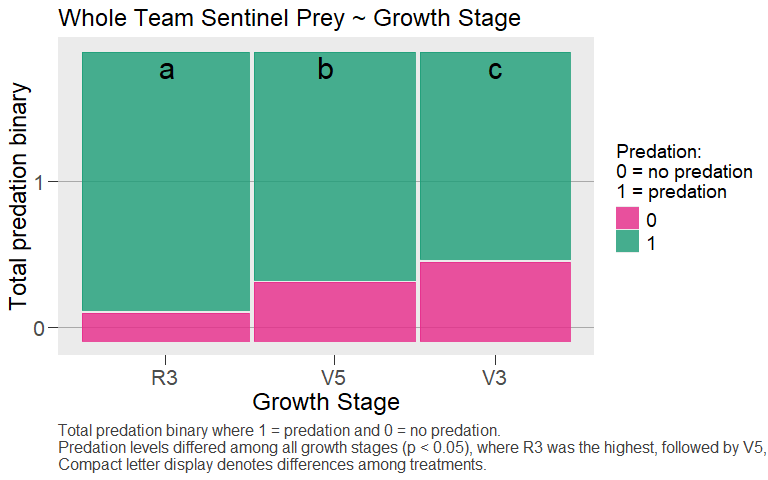
cld(emmeans(m3, ~growth\_stage), Letters = letters)

## growth\_stage emmean SE df asymp.LCL asymp.UCL .group  
## V3 1.57 0.271 Inf 1.04 2.10 a   
## V5 2.13 0.271 Inf 1.59 2.66 b   
## R3 3.26 0.275 Inf 2.72 3.79 c   
##   
## Results are averaged over the levels of: treatment   
## Results are given on the logit (not the response) scale.   
## Confidence level used: 0.95   
## Results are given on the log odds ratio (not the response) scale.   
## P value adjustment: tukey method for comparing a family of 3 estimates   
## 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.

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 = 'Total predation binary',  
 caption = 'Total 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)



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 = 'Total predation binary',  
 caption = 'Total predation binary where 1 = predation and 0 = no predation.\nPredation levels differed among all growth stages (p < 0.05), where R3 was the highest, followed by V5, and then V3.\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 = 0.175, 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)

 \* I plan to make additional plots with the proportion of predation.

* Used <https://haleyjeppson.github.io/ggmosaic/reference/geom_mosaic.html> for the scale\_x\_productlist function.

**How to I reorder my x axis? I was not able to find the syntax online. I tried limits, but it seems limits in the scale\_x\_productlist does not work like it does in scale\_x\_discrete. I would like it to do V3, V5, R3. I tried functions from the forcats package, but it seems ggmosaic is overriding those or is not compatible with them in the same line.**

1. 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   
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   
##

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   
##

tally(treatment ~ growth\_stage, data = sent)

## growth\_stage  
## treatment R3 V5 V3  
## 1 1146 1195 1098  
## 2 1149 1068 986  
## 4 898 871 836  
## 3 1141 1062 982

1. Research question:

How do sentinel prey rates (1,0) change among treatments and growth stages and is there an interaction between treatment and growth stage?

1. SOI

G: 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 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.

C: The treatments and the trap location were randomly assigned in the field and thus, we can make causal inference on the predation levels within different treatments and parts of the field.