

microstegium_elymus_model_parameters_experiment

Amy Kendig

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1 Set-up

```
# clear
rm(list=ls())

# load libraries
library(tidyverse)
```

```
library(brms)
library(glmmTMB)
```

2 Annual plant parameters

2.1 events

1. seeds germinate or don't
 - a. germination depends on the amount of litter
2. seeds that don't germinate (i.e., dormant) must survive to the next spring (1 year)
3. germinants grow and produce more seeds
 - a. growth depends on competition
4. newly produced seeds must survive to the next spring (overwinter)

2.2 annual germination in the absence of litter

Microstegium vimineum germination from 200 planted seeds and an estimated number of background seeds based on a neighboring subplot in plots with litter removed. Methods: field_litter_experiment_2018.docx.

```
# import model
load("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/output/mv_germination_litter_model.Rsave")
load("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/output/mv_germination_all_data_model.Rsave")

# extract fixed effects
A_germ_est <- fixef(mv_germ_litter_mod) %>%
  as_tibble() %>%
  mutate(param = c("max_germ_autoclaved", "max_germ_live", "alpha_autoclaved", "alpha_live"))

# check
A_germ_est

## # A tibble: 4 x 5
##   Estimate Est.Error    Q2.5   Q97.5 param
##   <dbl>     <dbl>    <dbl>   <dbl> <chr>
## 1  113.      34.8   42.6    180. max_germ_autoclaved
## 2  120.      50.3   15.4    196. max_germ_live
## 3   1.24     1.80  0.00374  6.37 alpha_autoclaved
## 4   1.03     1.66  0.00470  5.86 alpha_live

# germination with(out) autoclaved litter is lower than with(out) live litter (net benefit of live litter)
# use the live litter values

# germination of seeds from fungicide-treated and control plots
summary(mv_germ_mod)

## Family: binomial
## Links: mu = logit
## Formula: germination_final | trials(seeds) ~ fungicide + (1 | site/plot)
## Data: dat_treat (Number of observations: 184)
```

```
## Samples: 3 chains, each with iter = 6000; warmup = 1000; thin = 1;
##       total post-warmup samples = 15000
##
## Group-Level Effects:
## ~site (Number of levels: 5)
##       Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.21    0.20    0.01    0.73 1.00    2866    5644
##
## ~site:plot (Number of levels: 41)
##       Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.37    0.06    0.27    0.51 1.00    5650    8580
##
## Population-Level Effects:
##       Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      1.38    0.18    1.05    1.77 1.00    6808    5604
## fungicide     -0.11    0.07   -0.24    0.02 1.00   25632   11635
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).

# negative effect of fungicide

# select the no-litter values
g.A_parms <- filter(A_germ_est, parm == "max_germ_live") %>%
  mutate(Estimate = Estimate / 200,
         Q2.5 = Q2.5 / 200,
         Q97.5 = Q97.5 / 200)

# check
g.A_parms$Estimate

## [1] 0.6017131
```

2.3 reduced annual germination due to litter

Same experiment as above except also using plots with litter added

```
# select the no-litter values
beta.A_parms <- filter(A_germ_est, parm == "alpha_live")

beta.A_parms$Estimate

## [1] 1.027311
```

2.4 survival of dormant annual seeds

We used the survival data collected by Redwood et al. (2018) in November 2011 (buried for one year). Some of these seeds would have germinated had they been exposed to a germination test earlier in the year. Scroll down to seed viability for final survival value.

```
# load extracted figure data
rw18_2a <- read_csv("../data/Redwood_2018_Fig2A.csv")

## Parsed with column specification:
```

```
## cols(
##   month = col_character(),
##   surv = col_double()
## )

# select month
(s.A0 <- filter(rw18_2a, month == "Nov 11") %>%
  select(surv) %>%
  round(digits = 1) / 100)

##   surv
## 1 0.05
```

2.5 survival of annual seedlings

Survival is not clearly affected by density, so the raw data mean is used.

```
summer_surv <- read_csv("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/intermediate-")

## Parsed with column specification:
## cols(
##   site = col_character(),
##   plot = col_double(),
##   treatment = col_character(),
##   ID = col_character(),
##   focal = col_double(),
##   plant_type = col_character(),
##   survival = col_double(),
##   flag = col_character(),
##   background = col_character(),
##   background_sp = col_character(),
##   background_density = col_double(),
##   density_level = col_character()
## )

(h.A <- summer_surv %>%
  filter(plant_type == "Mv seedling" & treatment == "fungicide") %>%
  summarise(h.A = mean(survival)))

## # A tibble: 1 x 1
##       h.A
##   <dbl>
## 1 0.983
```

2.6 growth of annual in the absence of competition

We oven-dried and weighed individual *M. vimineum* at the end of the growing season in 2019. Methods: field_density_experiment_2018_2019.docx

```
# import model
load("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/output/mv_biomass_combined_backg")

# extract fixed effects
A_bio_est <- fixef(mv_bio_mod) %>%
  as_tibble() %>%
```

```

mutate(parm = c("max_bio_fungicide", "max_bio_water", "alpha_EvA_fungicide", "alpha_EvA_water", "alpha_EvS_fungicide", "alpha_EvS_water", "alpha_MvS_fungicide", "alpha_MvS_water"),
       treatment = rep(c("fungicide", "water"), 4),
       parm_type = c(rep("max_bio", 2), rep("alpha", 6)))

# conversion to account for direct (negative) fungicide effects
# fungicide_effects_greenhouse_2019.R
mv_fung_bio_conv <- 23.80 / 21.05

# select intercept with disease suppression
v.A_parms <- filter(A_bio_est, treatment == "fungicide" & parm_type == "max_bio") %>%
  mutate(Estimate = Estimate * mv_fung_bio_conv,
         Q2.5 = Q2.5 * mv_fung_bio_conv,
         Q97.5 = Q97.5 * mv_fung_bio_conv)

# check
v.A_parms$Estimate

## [1] 42.23043

```

2.7 reduction in annual growth due to competition

```

# subset data
A_alpha_dat <- filter(A_bio_est, treatment == "fungicide" & parm_type == "alpha")

# print values
A_alpha_dat %>%
  select(parm, Estimate)

## # A tibble: 3 x 2
##   parm                Estimate
##   <chr>                <dbl>
## 1 alpha_EvA_fungicide    0.126
## 2 alpha_EvS_fungicide    0.188
## 3 alpha_MvS_fungicide    0.190

```

2.8 conversion from annual biomass to seed production

```

# import model
load("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/output/mv_seeds_per_biomass_model.R")

# look at coefficients
summary(mv_seed_bio_mod)

## Family: gaussian (identity)
## Formula: seeds ~ yearf * fungicide * biomass_weight.g + (1 | site)
## Data: dat
##
##      AIC      BIC  logLik deviance df.resid
## 4966.1  5003.6 -2473.1  4946.1      303
##
## Random effects:
##

```

```

## Conditional model:
##   Groups   Name      Variance Std.Dev.
##   site     (Intercept) 22019   148.4
##   Residual              418108  646.6
## Number of obs: 313, groups: site, 4
##
## Dispersion estimate for gaussian family (sigma^2): 4.18e+05
##
## Conditional model:
##                                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)                        1740.685    272.588   6.386 1.71e-10
## yearfYear 2                       -1984.794    285.807  -6.945 3.80e-12
## fungicide                          149.993    388.925   0.386  0.700
## biomass_weight.g                   10.264     14.960   0.686  0.493
## yearfYear 2:fungicide              -218.742    415.275  -0.527  0.598
## yearfYear 2:biomass_weight.g        74.136     16.222   4.570 4.87e-06
## fungicide:biomass_weight.g          4.905      23.030   0.213  0.831
## yearfYear 2:fungicide:biomass_weight.g -12.440     24.175  -0.515  0.607
##
## (Intercept)                        ***
## yearfYear 2                        ***
## fungicide
## biomass_weight.g
## yearfYear 2:fungicide
## yearfYear 2:biomass_weight.g        ***
## fungicide:biomass_weight.g
## yearfYear 2:fungicide:biomass_weight.g
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# manually add up relevant coefficients (biomass, year2:biomass, fungicide:biomass, year2:fungicide:biomass)
(y.A0 <- 10.264 + 74.136 + 4.905 - 12.440)

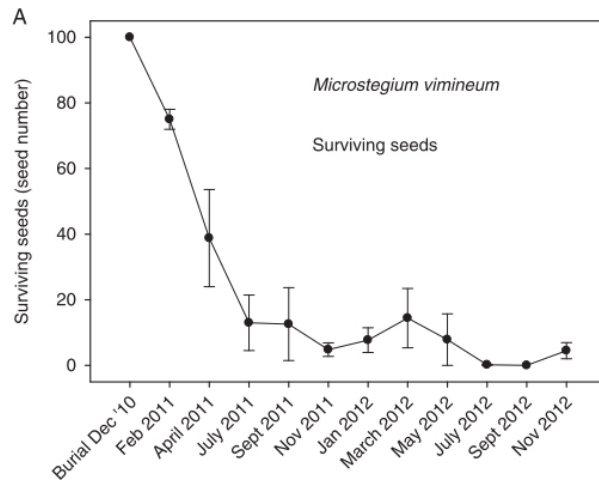
## [1] 76.865

```

2.9 annual seed viability

Using Fig. 2A from Redwood et al. (2018), 40% of the seeds survive from December to April. Survival is the sum of germinated and viable non-germinated seeds. This parameter would only be applied to newly produced seeds (i.e., multiply y.A by w.A). Note that empirical values for seed bank survival include both viability and longer term survival. We divide by viability to get the new survival value because these will be effectively multiplied again in the model.

```
include_graphics("../data/lit_figures/Redwood_2018_Fig2A.jpg")
```



```
w.A <- 0.4
(y.A <- y.A0 * w.A)
```

```
## [1] 30.746
```

```
(s.A <- s.A0 / w.A)
```

```
##      surv
## 1 0.125
```

3 Annual litter parameters

3.1 events

1. newly formed biomass loses water and slightly decomposes over the winter
2. litter decomposes each year

3.2 conversion from annual biomass to litter

We measured biomass from the same area in the same plots with adjacent samples in October 2018 and April 2019. Note: source code needs to be located, but I'm fairly confident this value is correct.

```
# import data
A_lit_dat <- read_csv("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/intermediate-da

## Parsed with column specification:
## cols(
##   .default = col_double(),
##   entry = col_character(),
##   sample_ID = col_character(),
##   site = col_character(),
##   treatment = col_character(),
##   processing_notes = col_character(),
##   flag = col_character(),
##   background = col_character(),
##   background_sp = col_character(),
```

```
## density_level = col_character()
## )

## See spec(...) for full column specifications.
# take average of litter/biomass measurements
(a <- A_lit_dat %>%
  filter(treatment == "fungicide") %>%
  summarise(a = mean(litter_conversion, na.rm = T)))

## # A tibble: 1 x 1
##       a
##   <dbl>
## 1  1.30

# a gain in biomass does not make sense
a <- 1
```

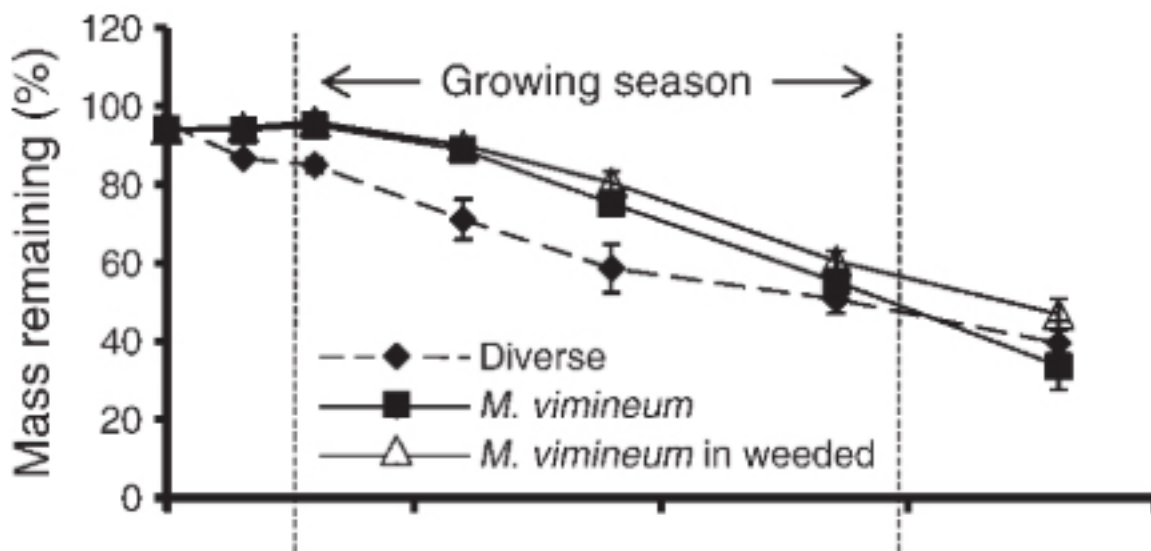
3.3 annual litter decomposition

We used the mass remaining in the litter bags from DeMeester and Richter (2010) after one year in the field.

```
# import data
dr10_3 <- read_csv("../data/DeMeester_2010_Fig3.csv")

## Parsed with column specification:
## cols(
##   days = col_double(),
##   mass.prop = col_double()
## )

# figure
include_graphics("../data/lit_figures/DeMeester_2010_Fig3.jpg")
```



```
# extract parameters
(b <- 1 - filter(dr10_3, days == max(dr10_3$days)) %>% select(mass.prop)/100)

## mass.prop
```



```
## 1      0.67
```

4 Perennial plant parameters

4.1 events

1. seeds germinate or don't
 - a. germination depends on the amount of litter
2. seeds that don't germinate (i.e., dormant) must survive to the next spring (1 year)
3. germinants grow and produce more seeds
 - a. growth depends on competition
4. newly produced seeds must survive to the next spring (overwinter)
5. seedlings that survive to the next spring become adults (1 year)
6. adults also produce seeds, which depends on competition

4.2 perennial germination in the absence of litter

Elymus virginicus germination from 50 planted seeds in field plots with litter removed and in greenhouse pots. Methods: field_litter_experiment_2019.docx, REU 2018 manuscript.

```
# import data
S_field_germ_dat <- read_csv("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/data/botl

## Parsed with column specification:
## cols(
##   date = col_double(),
##   site = col_character(),
##   flag_color = col_character(),
##   treatment = col_character(),
##   block = col_double(),
##   ev_germ = col_double(),
##   ev_infec = col_double(),
##   mv_germ = col_double(),
##   mv_infec = col_double()
## )
S_house_germ_dat <- read_csv("../microstegium-litter-reu/output/ev_establishment_data.csv")

## Parsed with column specification:
## cols(
##   .default = col_double(),
##   Treatment = col_character(),
##   SpPresent = col_character(),
##   Notes = col_character(),
##   Date3 = col_date(format = ""),
##   Shade = col_character(),
##   Litter = col_character(),
##   TrtID = col_character(),
```

```
## Litter.present = col_character(),
## `TrtID != "Mv.Med.yes.3"` = col_logical()
## )

## See spec(...) for full column specifications.
# estimate from field
g.S_field <- filter(S_field_germ_dat, treatment == "removal") %>%
  mutate(prop_germ = ev_germ/50) %>%
  summarise(g.S = mean_cl_boot(prop_germ)$y,
            g.S_low = mean_cl_boot(prop_germ)$ymin,
            g.S_hi = mean_cl_boot(prop_germ)$ymax)

# estimate from greenhouse
g.S_house <- filter(S_house_germ_dat, Litter == "None" & SpPresent == "Ev") %>%
  mutate(prop_germ = NewGermEv/50) %>%
  summarise(g.S = mean_cl_boot(prop_germ)$y,
            g.S_low = mean_cl_boot(prop_germ)$ymin,
            g.S_hi = mean_cl_boot(prop_germ)$ymax)

g.S_field$g.S

## [1] 0.035
g.S_house$g.S

## [1] 0.8433333
(g.S <- mean(c(g.S_field$g.S, g.S_house$g.S)))

## [1] 0.4391667
```

4.3 reduced perennial germination due to litter

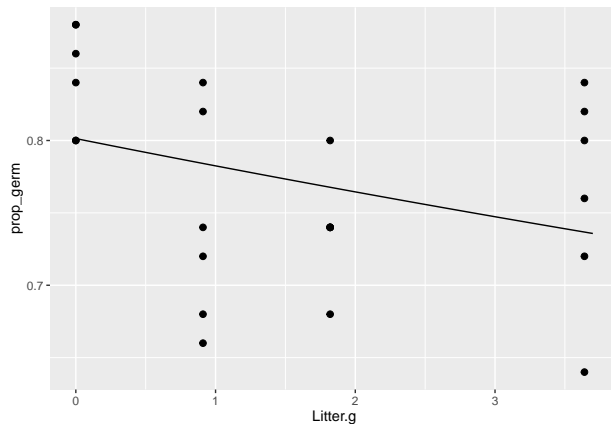
Same experiment as above except also using plots with litter added

```
# subset data
S_litter_dat <- filter(S_house_germ_dat, SpPresent == "Ev") %>%
  mutate(prop_germ = NewGermEv/50)

# fit non-linear curve
beta.S_mod <- nls(prop_germ ~ germ0 / (1 + beta * Litter.g),
                  start = list(germ0 = g.S_house$g.S, beta = 1),
                  data = S_litter_dat)
summary(beta.S_mod)

##
## Formula: prop_germ ~ germ0/(1 + beta * Litter.g)
##
## Parameters:
##      Estimate Std. Error t value Pr(>|t|)
## germ0  0.80132    0.02165  37.009  <2e-16 ***
## beta   0.02408    0.01445   1.667    0.11
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06661 on 22 degrees of freedom
```

```
##
## Number of iterations to convergence: 7
## Achieved convergence tolerance: 2.194e-06
# look at fit
litter_S_germ_df <- tibble(Litter.g = seq(0, 3.7, length.out = 100))
litter_S_germ_df$prop_germ <- predict(beta.S_mod, newdata = litter_S_germ_df)
ggplot(S_litter_dat, aes(x = Litter.g, y = prop_germ)) +
  geom_point(size = 2) +
  geom_line(data = litter_S_germ_df)
```



```
# save beta
(beta.S <- coef(beta.S_mod)[2])
```

```
##      beta
## 0.0240785
```

4.4 survival of dormant perennial seeds

Garrison and Stier (2010) reported that 9% of seeds were viable (all germinated) after buried for one year.

```
s.S0 <- 0.09
```

4.5 perennial seed viability

Garrison and Stier (2010) reported that 83% of seeds were viable at the beginning of the study

```
w.S <- 0.83
(s.S <- s.S0/w.S)
```

```
## [1] 0.1084337
```

4.6 growth of perennial in the absence of competition

We oven-dried and weighed individual *E. virginicus* at the end of the growing season in 2019. Methods: field_density_experiment_2018_2019.docx

```
# import models
load("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/output/ev_seedling_biomass_combined")
load("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/output/ev_adult_biomass_combined")
```

```

# extract fixed effects
S_bio_est <- fixef(eps_bio_mod) %>%
  as_tibble() %>%
  mutate(parm = c("max_bio_fungicide", "max_bio_water", "alpha_EvA_fungicide", "alpha_EvA_water", "alpha_EvS_fungicide", "alpha_EvS_water", "alpha_MvS_fungicide", "alpha_MvS_water"),
         treatment = rep(c("fungicide", "water"), 4),
         parm_type = c(rep("max_bio", 2), rep("alpha", 6)))

P_bio_est <- fixef(eps_bio_mod) %>%
  as_tibble() %>%
  mutate(parm = c("max_bio_fungicide", "max_bio_water", "alpha_EvA_fungicide", "alpha_EvA_water", "alpha_EvS_fungicide", "alpha_EvS_water", "alpha_MvS_fungicide", "alpha_MvS_water"),
         treatment = rep(c("fungicide", "water"), 4),
         parm_type = c(rep("max_bio", 2), rep("alpha", 6)))

# account for direct (positive) effects of fungicide on seedling growth
# fungicide_effects_greenhouse_2019.R
ev_fung_bio_conv <- 13.39 / 13.84

# select intercept with disease suppression
v.S_parms <- filter(S_bio_est, treatment == "fungicide" & parm_type == "max_bio") %>%
  mutate(Estimate = Estimate * ev_fung_bio_conv,
         Q2.5 = Q2.5 * ev_fung_bio_conv,
         Q97.5 = Q97.5 * ev_fung_bio_conv)
v.P_parms <- filter(P_bio_est, treatment == "fungicide" & parm_type == "max_bio")

# check
v.S_parms$Estimate

## [1] 1.997563
v.P_parms$Estimate

## [1] 8.476641

```

4.7 reduction in perennial seedling growth due to competition

```

# subset data
S_alpha_dat <- filter(S_bio_est, treatment == "fungicide" & parm_type == "alpha")

# print values
S_alpha_dat %>%
  select(parm, Estimate)

## # A tibble: 3 x 2
##   parm                Estimate
##   <chr>              <dbl>
## 1 alpha_EvA_fungicide 0.0467
## 2 alpha_EvS_fungicide 0.00681
## 3 alpha_MvS_fungicide 0.0145

```

4.8 reduction in perennial seedling growth due to competition

```
# subset data
P_alpha_dat <- filter(P_bio_est, treatment == "fungicide" & parm_type == "alpha")

# print values
P_alpha_dat %>%
  select(parm, Estimate)

## # A tibble: 3 x 2
##   parm                Estimate
##   <chr>                <dbl>
## 1 alpha_EvA_fungicide  0.0692
## 2 alpha_EvS_fungicide  0.177
## 3 alpha_MvS_fungicide  0.0653
```

4.9 conversion from perennial biomass to seed production

```
# import model
load("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/output/ev_seeds_per_biomass_model.R")

# look at coefficients
summary(ev_seed_bio_mod)

## Family: gaussian ( identity )
## Formula: seeds ~ age * fungicide * biomass_weight.g + (1 | site)
## Data: dat
##
##      AIC      BIC  logLik deviance df.resid
## 2993.0  3030.6 -1486.5  2973.0      309
##
## Random effects:
##
## Conditional model:
## Groups   Name                Variance Std.Dev.
## site     (Intercept)  45.88      6.773
## Residual                    637.73   25.253
## Number of obs: 319, groups: site, 4
##
## Dispersion estimate for gaussian family (sigma^2): 638
##
## Conditional model:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -15.8525     7.5221  -2.107  0.03508 *
## ageseedling    19.0575     7.7738   2.452  0.01423 *
## fungicide     -18.9954     9.0977  -2.088  0.03680 *
## biomass_weight.g  18.6107     0.9348  19.910 < 2e-16 ***
## ageseedling:fungicide  14.8740    10.8237   1.374  0.16938
## ageseedling:biomass_weight.g -12.2603     2.4212  -5.064 4.11e-07 ***
## fungicide:biomass_weight.g   3.6171     1.1824   3.059  0.00222 **
## ageseedling:fungicide:biomass_weight.g -2.3515     3.1313  -0.751  0.45267
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

# manually add up relevant coefficients (biomass, age:biomass, fungicide:biomass, age:fungicide:biomass)
(y.S0 <- 18.6107 - 12.2603 + 3.6171 - 2.3515)

## [1] 7.616

(y.P0 <- 18.6107 + 3.6171)

## [1] 22.2278
# multiply by viability
(y.S <- y.S0 * w.S)

## [1] 6.32128
(y.P <- y.P0 * w.S)

## [1] 18.44907

```

4.10 seedling and adult survival

Winter survival only includes those that survived the summer. Summer and winter survival are multiplied for a full year of survival.

```

winter_surv <- read_csv("../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/intermediate-

## Parsed with column specification:
## cols(
##   site = col_character(),
##   plot = col_double(),
##   treatment = col_character(),
##   sp = col_character(),
##   age = col_character(),
##   ID = col_character(),
##   focal = col_double(),
##   plant_type = col_character(),
##   Treatment = col_character(),
##   fungicide = col_double(),
##   survival = col_double()
## )

(h.S <- summer_surv %>%
  filter(plant_type == "Ev seedling" & treatment == "fungicide") %>%
  summarise(summer = mean(survival)) %>%
  merge(winter_surv %>%
    filter(plant_type == "Ev seedling" & treatment == "fungicide") %>%
    summarise(winter = mean(survival)), all = T) %>%
  mutate(yearly = summer * winter))

##   summer   winter   yearly
## 1 0.984375 0.9230769 0.9086538

(h.P <- summer_surv %>%
  filter(plant_type == "Ev adult" & treatment == "fungicide") %>%
  summarise(summer = mean(survival)) %>%
  merge(winter_surv %>%
    filter(plant_type == "Ev adult" & treatment == "fungicide") %>%

```

```
      summarise(winter = mean(survival)), all = T) %>%  
mutate(yearly = summer * winter))
```

```
##      summer    winter    yearly  
## 1 0.9519231 0.9756098 0.9287054
```