microstegium_elymus_model_parameters_experiment

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Contents

1 Set-up

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

# load libraries
library(tidyverse)
```

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.

```
A_germ_dat <- read_csv("../../big-oaks-field-experiment-2018-2019/microstegium-bipolaris/intermediate-da
    mutate(mv_germ_planted_cor_jul = ifelse(mv_germ_planted_cor_jul > 200,
        200, mv_germ_planted_cor_jul), prop_germ = mv_germ_planted_cor_jul/200)
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   site = col_character(),
##   flag_color = col_character(),
##   litter = col_character(),
##   litter_density = col_character(),
##   litter_microbes = col_character(),
##   seeds_added = col_character(),
##   justification = col_character()
## )
```

```
## See spec(...) for full column specifications.
```

```
g.A_parms <- filter(A_germ_dat, litter_density == "none") %>% summarise(g.A = mean_cl_boot(prop_germ)$y
    g.A_low = mean_cl_boot(prop_germ)$ymin, g.A_hi = mean_cl_boot(prop_germ)$ymax)
```

```
g.A_parms$g.A
```

```
## [1] 0.54625
```

```
# Stats: need to constrain the values to 0 to 1 (manually constrained
# to 0 in mv_germination_disease_analysis_2018_litter_exp.R and 1
# above) and incorporate uncertainty in the background germination into
# the estimate.
```

2.3 reduced annual germination due to litter

Same experiment as above except also using plots with litter added

```r
# subset data
A_litter_dat <- filter(A_germ_dat, litter %in% c("sterilized", "none"))

# fit non-linear curve
beta.A_mod <- nls(prop_germ ~ germ0 / (1 + beta * litter_weight.g),
                  start = list(germ0 = g.A_parms$g.A, beta = 1),
                  data = A_litter_dat)
summary(beta.A_mod)
```

```
##
## Formula: prop_germ ~ germ0/(1 + beta * litter_weight.g)
##
## Parameters:
##        Estimate Std. Error t value Pr(>|t|)
## germ0 0.491956   0.135826   3.622  0.00277 **
## beta  0.004884   0.005610   0.871  0.39863
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2937 on 14 degrees of freedom
##
## Number of iterations to convergence: 11
## Achieved convergence tolerance: 9.877e-06
```

```r
# look at fit
litter_germ_df <- tibble(litter_weight.g = seq(0, 200, length.out = 100))
litter_germ_df$prop_germ <- predict(beta.A_mod, newdata = litter_germ_df)
ggplot(A_litter_dat, aes(x = litter_weight.g, y = prop_germ)) +
  geom_point(size = 2) +
  geom_line(data = litter_germ_df)
```
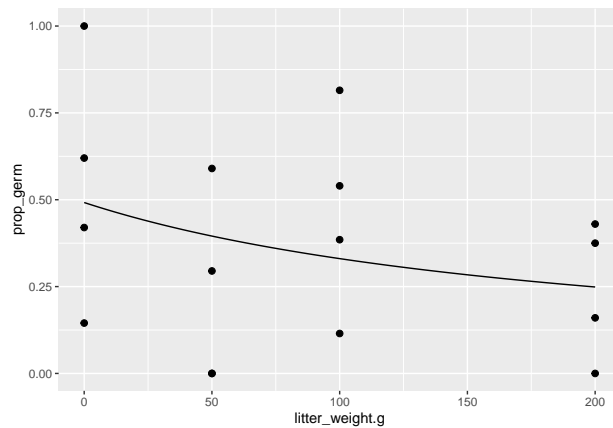


```r
# save baseline germination and beta
(g.A <- coef(beta.A_mod)[1])
```

```
##     germ0
## 0.4919557
```

```r
(beta.A <- coef(beta.A_mod)[2])
```

```
##        beta
## 0.004884462
```

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.

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

```
## Parsed with column specification:
## cols(
##   process_date = col_character(),
##   site = col_character(),
##   plot = col_double(),
##   treatment = col_character(),
##   sp = col_character(),
##   plant = col_double(),
##   flowers = col_double(),
##   stem_seed_weight.g = col_double(),
##   biomass_weight.g = col_double(),
##   flag = col_character(),
##   background = col_character(),
##   background_sp = col_character(),
##   background_density = col_double(),
##   density_level = col_character(),
##   seeds_per_flower = col_double(),
##   background_density_tot = col_double(),
##   flower_seeds = col_double()
## )
```

```
# choose the low density treatment because no neighbors is a really low
# biomass (update when data collection is complete)
v.A_parms <- A_bio_dat %>% filter(treatment == "fungicide" & density_level ==
    "low") %>% summarise(v.A = mean_cl_boot(biomass_weight.g)$y, v.A_low = mean_cl_boot(biomass_weight.g
    v.A_hi = mean_cl_boot(biomass_weight.g)$ymax)
```

```
v.A_parms$v.A
```

```
## [1] 29.879
```

2.6 reduction in annual growth due to intraspecific competition

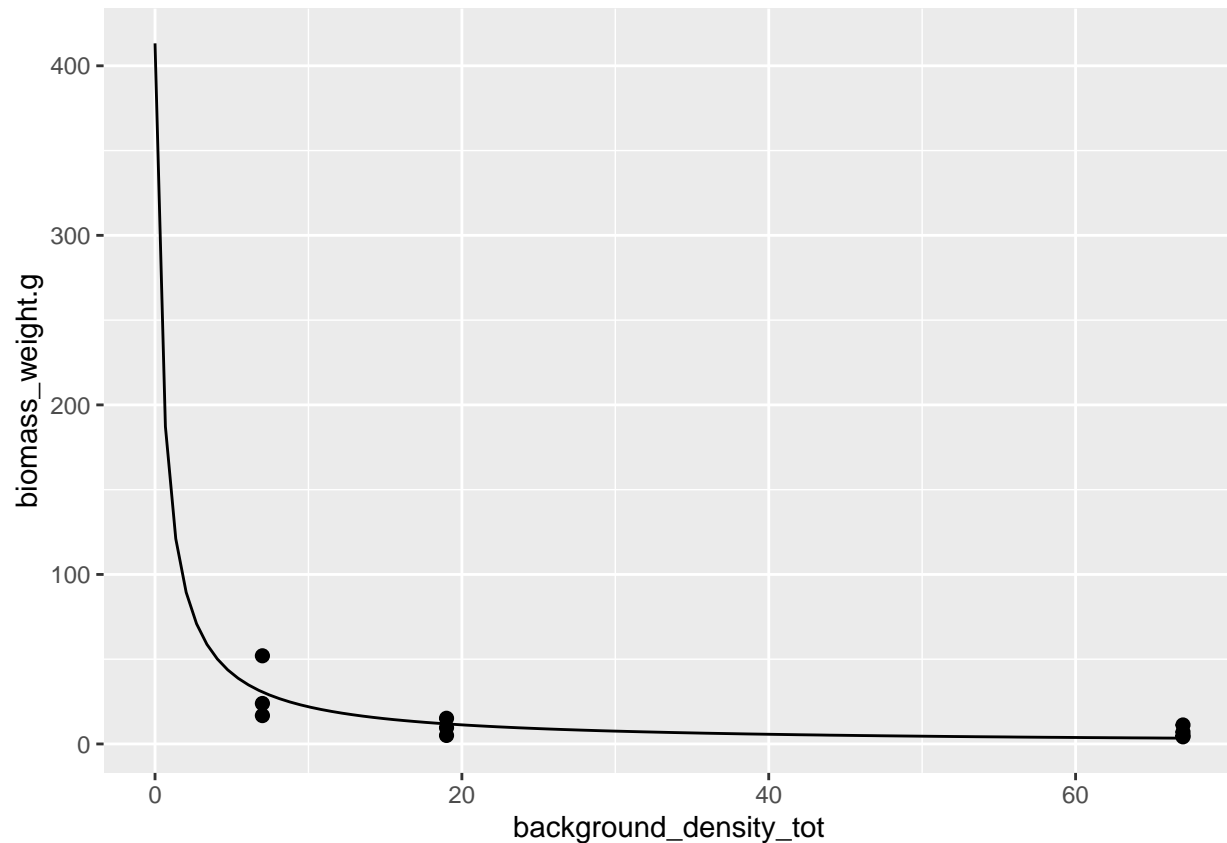Same as above, but with higher density treatments.

```r
# subset data
A_alphaAA_dat <- filter(A_bio_dat, treatment == "fungicide" & density_level !=
    "none" & background == "Mv seedling")

# fit non-linear curve
alpha.AA_mod <- nls(biomass_weight.g ~ bio0/(1 + beta * background_density_tot),
    start = list(bio0 = v.A_parms$v.A, beta = 1), data = A_alphaAA_dat)
summary(alpha.AA_mod)
```

```
##
## Formula: biomass_weight.g ~ bio0/(1 + beta * background_density_tot)
##
## Parameters:
##       Estimate Std. Error t value Pr(>|t|)
## bio0   413.254   4093.627   0.101    0.922
## beta     1.783     18.940   0.094    0.927
##
## Residual standard error: 10.21 on 8 degrees of freedom
##
## Number of iterations to convergence: 8
## Achieved convergence tolerance: 9.376e-06
##    (26 observations deleted due to missingness)
```

```r
# look at fit
alpha_AA_df <- tibble(background_density_tot = seq(0, 67, length.out = 100))
alpha_AA_df$biomass_weight.g <- predict(alpha.AA_mod, newdata = alpha_AA_df)
ggplot(A_alphaAA_dat, aes(x = background_density_tot, y = biomass_weight.g)) +
    geom_point(size = 2) + geom_line(data = alpha_AA_df)
```

```
## Warning: Removed 26 rows containing missing values (geom_point).
```

```
# save coefficients
(v.A <- coef(alpha.AA_mod)[1])
```

```
##      bio0
## 413.2539
```

```
# this intercept seems very high compared to observed values
(alpha.AA <- coef(alpha.AA_mod)[2])
```

```
##     beta
## 1.783412
```

```
# Stats: may need to do an Alee-effect type model if no neighbors is
# really low after all data are collected
```

2.7 reduction in annual growth due to interspecific seedling competition

Same as above, but with perennial seedling density treatments.
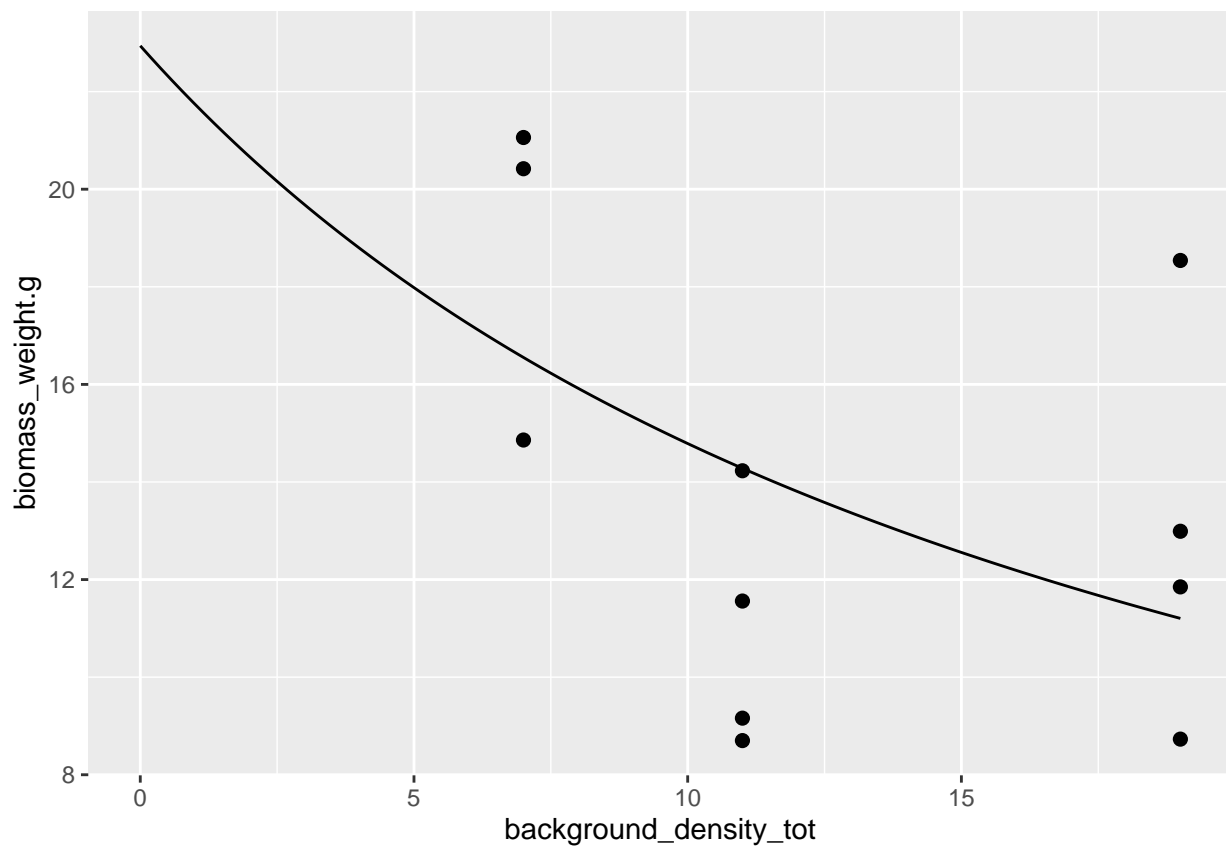
```
# subset data
A_alphaAS_dat <- filter(A_bio_dat, treatment == "fungicide" & density_level !=
    "none" & background == "Ev seedling")

# fit non-linear curve
alpha.AS_mod <- nls(biomass_weight.g ~ bio0/(1 + beta * background_density_tot),
    start = list(bio0 = v.A_parms$v.A, beta = 1), data = A_alphaAS_dat)
summary(alpha.AS_mod)
```

```
## 
## Formula: biomass_weight.g ~ bio0/(1 + beta * background_density_tot)
## 
## Parameters:
##      Estimate Std. Error t value Pr(>|t|)
## bio0 22.93952    9.12736   2.513   0.0331 *
## beta  0.05513    0.05750   0.959   0.3627
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.3 on 9 degrees of freedom
## 
## Number of iterations to convergence: 11
## Achieved convergence tolerance: 7.58e-06
##    (25 observations deleted due to missingness)
```

```r
# look at fit
alpha_AS_df <- tibble(background_density_tot = seq(0, 19, length.out = 100))
alpha_AS_df$biomass_weight.g <- predict(alpha.AS_mod, newdata = alpha_AS_df)
ggplot(A_alphaAS_dat, aes(x = background_density_tot, y = biomass_weight.g)) +
    geom_point(size = 2) + geom_line(data = alpha_AS_df)
```

```
## Warning: Removed 25 rows containing missing values (geom_point).
```



```r
# save coefficient
(alpha.AS <- coef(alpha.AS_mod)[2])
```

```
##       beta
```

```
## 0.05512826
```
```
# Stats: need to update with all data
```

2.8 reduction in annual growth due to interspecific adult competition

Same as above, but with perennial adult density treatments.

```
# subset data
A_alphaAP_dat <- filter(A_bio_dat, treatment == "fungicide" & density_level !=
    "none" & background == "Ev adult")

# fit non-linear curve
alpha.AP_mod <- nls(biomass_weight.g ~ bio0/(1 + beta * background_density_tot),
    start = list(bio0 = v.A_parms$v.A, beta = 1), data = A_alphaAP_dat)
summary(alpha.AP_mod)
```

```
##
## Formula: biomass_weight.g ~ bio0/(1 + beta * background_density_tot)
##
## Parameters:
##      Estimate Std. Error t value Pr(>|t|)
## bio0 23.83019    7.10172   3.356   0.0100 **
## beta -0.06663    0.01684  -3.955   0.0042 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.85 on 8 degrees of freedom
##
## Number of iterations to convergence: 10
## Achieved convergence tolerance: 2.558e-06
##    (26 observations deleted due to missingness)
```
```
# look at fit
alpha_AP_df <- tibble(background_density_tot = seq(0, 9, length.out = 100))
alpha_AP_df$biomass_weight.g <- predict(alpha.AP_mod, newdata = alpha_AP_df)
ggplot(A_alphaAP_dat, aes(x = background_density_tot, y = biomass_weight.g)) +
    geom_point(size = 2) + geom_line(data = alpha_AP_df)
```

```
## Warning: Removed 26 rows containing missing values (geom_point).
```
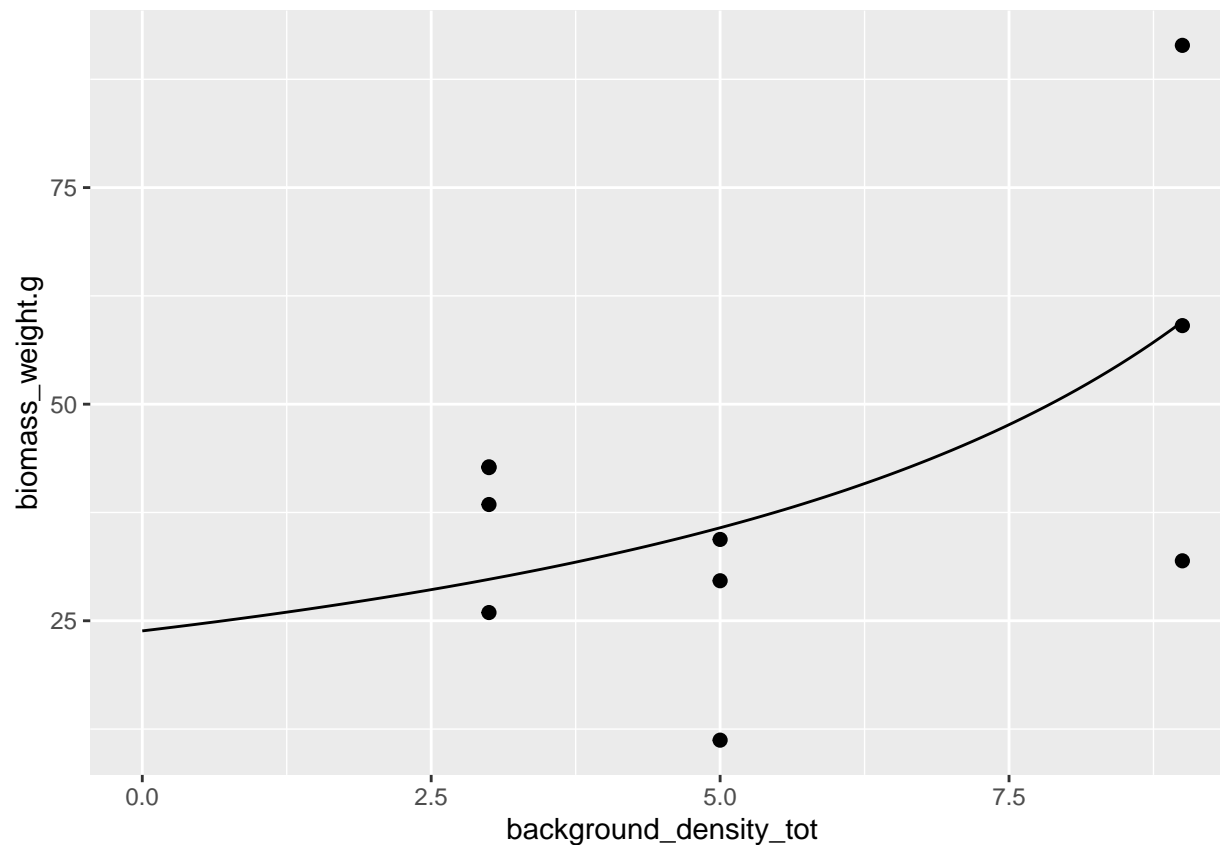
```
# save coefficient
(alpha.AP <- coef(alpha.AP_mod)[2])
```

```
##       beta
## -0.0666274
```

```
# suggests facilitation, use 0 until we have more data
alpha.AP <- 0
# Stats: need to update with all data
```

2.9 conversion from annual biomass to seed production

```
# round seed count
A_seed_dat <- A_bio_dat %>% filter(treatment == "fungicide")

# fit regression
y.A_mod <- lm(flower_seeds ~ 0 + biomass_weight.g, data = A_seed_dat)
summary(y.A_mod)
```

```
##
## Call:
## lm(formula = flower_seeds ~ 0 + biomass_weight.g, data = A_seed_dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -575.26 -209.89  -66.65  -13.46 1250.65
```

```
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## biomass_weight.g   26.092      1.833   14.23   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 299 on 38 degrees of freedom
##   (105 observations deleted due to missingness)
## Multiple R-squared:  0.8421, Adjusted R-squared:  0.8379
## F-statistic: 202.6 on 1 and 38 DF,  p-value: < 2.2e-16
```

```r
# extract coefficient for estimate
(y.A0 <- coef(y.A_mod)[1])
```

```
## biomass_weight.g
##         26.09224
```

```r
# see effect on highest observed biomass
y.A0 * max(A_seed_dat$biomass_weight.g, na.rm = T)
```

```
## biomass_weight.g
##         2385.353
```

```r
# Stats: need to add in chasmogamous seeds and all of 2018 data
```

2.10   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.

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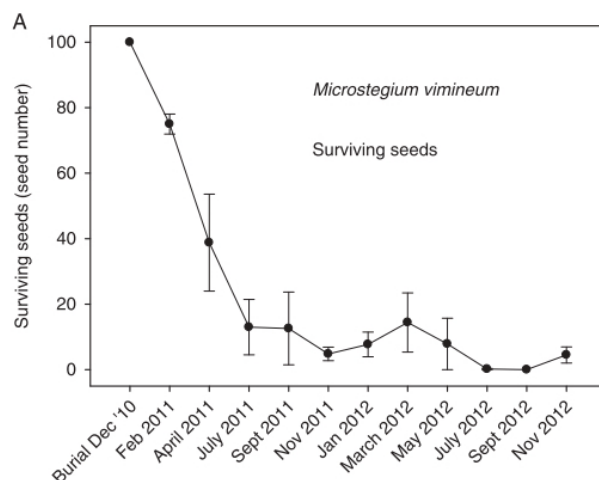


```r
w.A <- 0.4
(y.A <- y.A0 * w.A)
```

```
## biomass_weight.g
```

```
##           10.4369
(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.

```
# 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
```
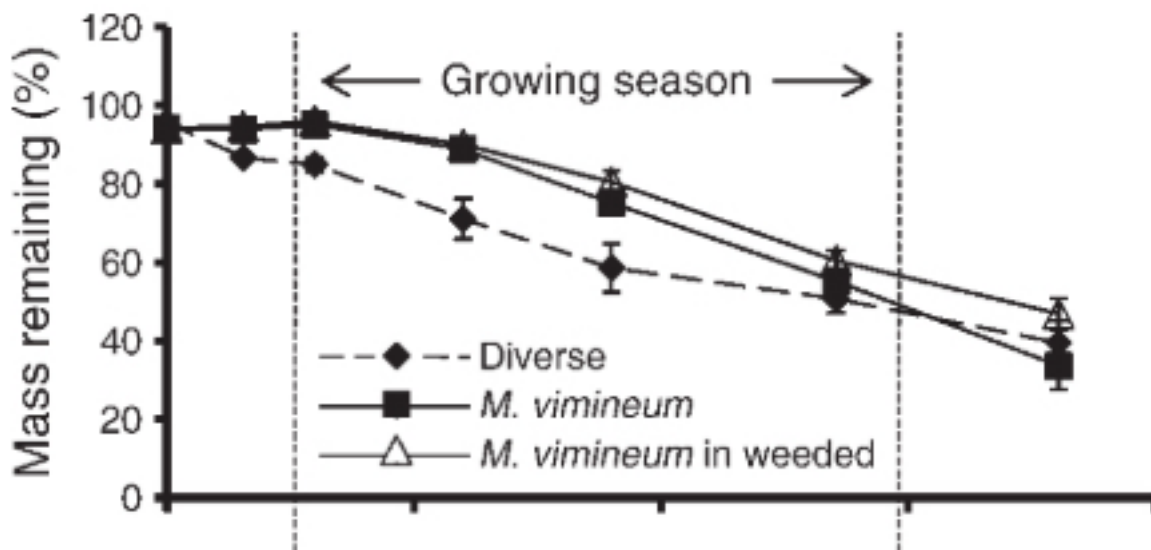
3.3 annual litter decomposition

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. seed production 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 2019 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

```r
# 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
```

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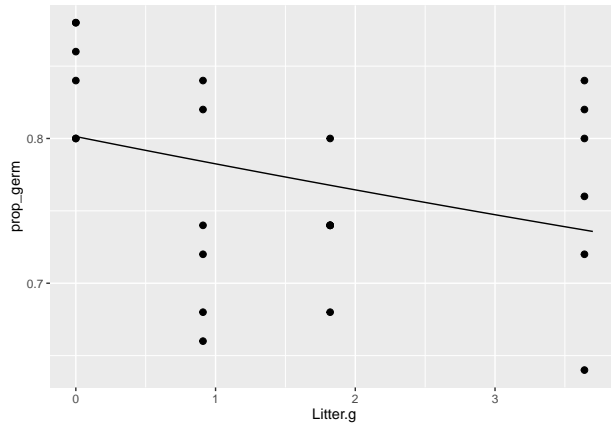
```r
# save beta
(beta.S <- coef(beta.S_mod)[2])
```

```
##       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.

```r
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

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

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

4.6 perennial seed production in the absence of competition

Stevens (1957) harvested one *Elymus virginicus* plant in North Dakota, which was growing with relatively low competition and judged to be of average size. He reported 435 seeds and 14 spikes. We assumed that perennial seedlings produce 1/10th the amount of seeds.

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

```
## Parsed with column specification:
## cols(
##   site = col_character(),
##   plot = col_double(),
##   plant = col_character(),
##   collect_date = col_double(),
##   spikelet_date = col_double(),
##   spikelet_weight.g = col_double(),
##   spikelet_notes = col_character(),
##   treatment = col_character(),
```

```
##    ID = col_character(),
##    age = col_character(),
##    seeds = col_double(),
##    flag = col_character(),
##    background = col_character(),
##    background_sp = col_character(),
##    background_density = col_double(),
##    density_level = col_character(),
##    background_density_tot = col_double()
## )
```

```r
# adult seed production specify background because 0 densities are
# repeated for each type
S_seed_dat_adult <- S_seed_dat %>% filter(age == "adult")
f.P0_parms <- filter(S_seed_dat_adult, background_density == 0 & background ==
    "Ev adult" & treatment == "fungicide") %>% summarise(f.P0 = mean(seeds))
(f.P <- f.P0_parms$f.P0 * w.S)
```

```
## [1] 64.43271
```

```r
# first year seed production
S_seed_dat_seed <- S_seed_dat %>% filter(age == "seedling")
f.10_parms <- filter(S_seed_dat_seed, background_density == 0 & background ==
    "Ev seedling" & treatment == "fungicide") %>% summarise(f.10 = mean(seeds))
(f.P <- f.10_parms$f.10 * w.S)
```

```
## [1] 14.63267
```

```r
# Stats: data needs conversion from this year and to be checked for
# mislabelling
```

4.7 reduction in perennial seed production due to intraspecific competition from the same life stage

Same as above, but with higher density treatments.

```r
# subset data
P_alphaPP_dat <- filter(S_seed_dat_adult, treatment == "fungicide" & background ==
    "Ev adult")
S_alphaSS_dat <- filter(S_seed_dat_seed, treatment == "fungicide" & background ==
    "Ev seedling")

# fit non-linear curve
alphaPP_mod <- nls(seeds ~ seed0/(1 + beta * background_density_tot), start = list(seed0 = f.P0_parms$f
    beta = 1), data = P_alphaPP_dat)
summary(alphaPP_mod)
```

```
##
## Formula: seeds ~ seed0/(1 + beta * background_density_tot)
##
## Parameters:
##        Estimate Std. Error t value Pr(>|t|)
## seed0 74.17197   24.01352   3.089  0.00414 **
## beta   0.02814    0.07989   0.352  0.72701
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 60.86 on 32 degrees of freedom
##
## Number of iterations to convergence: 10
## Achieved convergence tolerance: 3.745e-06
```

```
alphaSS_mod <- nls(seeds ~ seed0/(1 + beta * background_density_tot), start = list(seed0 = f.10_parms$f
    beta = 1), data = S_alphaSS_dat)
summary(alphaSS_mod)
```

```
##
## Formula: seeds ~ seed0/(1 + beta * background_density_tot)
##
## Parameters:
##        Estimate Std. Error t value Pr(>|t|)
## seed0 14.44800    3.97524   3.635 0.000863 ***
## beta  -0.00167    0.02165  -0.077 0.938969
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.91 on 36 degrees of freedom
##
## Number of iterations to convergence: 8
## Achieved convergence tolerance: 2.997e-06
```

```
# look at fit
alphaPP_df <- tibble(background_density_tot = seq(0, 9, length.out = 100))
alphaPP_df$seeds <- predict(alphaPP_mod, newdata = alphaPP_df)
ggplot(P_alphaPP_dat, aes(x = background_density_tot, y = seeds)) + geom_point(size = 2) +
    geom_line(data = alphaPP_df)
```
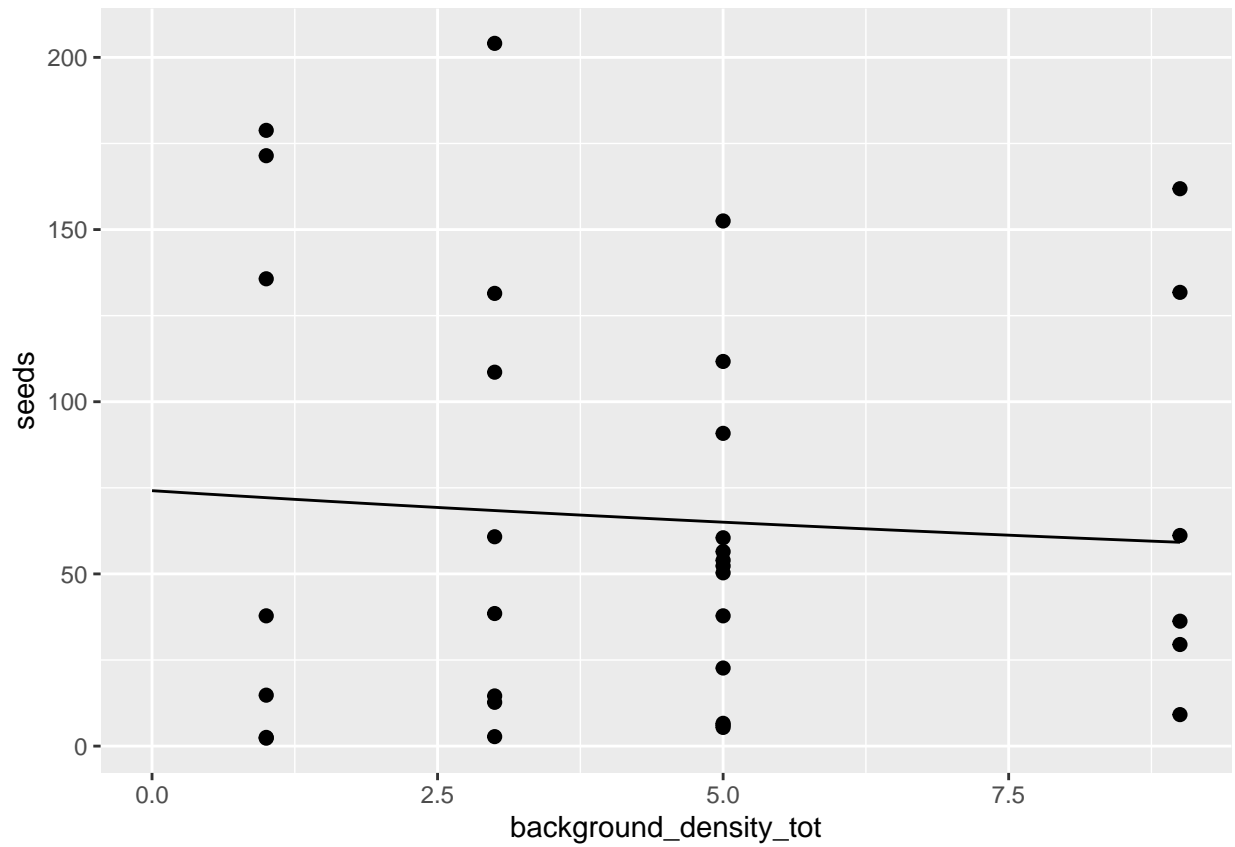
```
alphaSS_df <- tibble(background_density_tot = seq(0, 19, length.out = 100))
alphaSS_df$seeds <- predict(alphaSS_mod, newdata = alphaSS_df)
ggplot(S_alphaSS_dat, aes(x = background_density_tot, y = seeds)) + geom_point(size = 2) +
    geom_line(data = alphaSS_df)
```
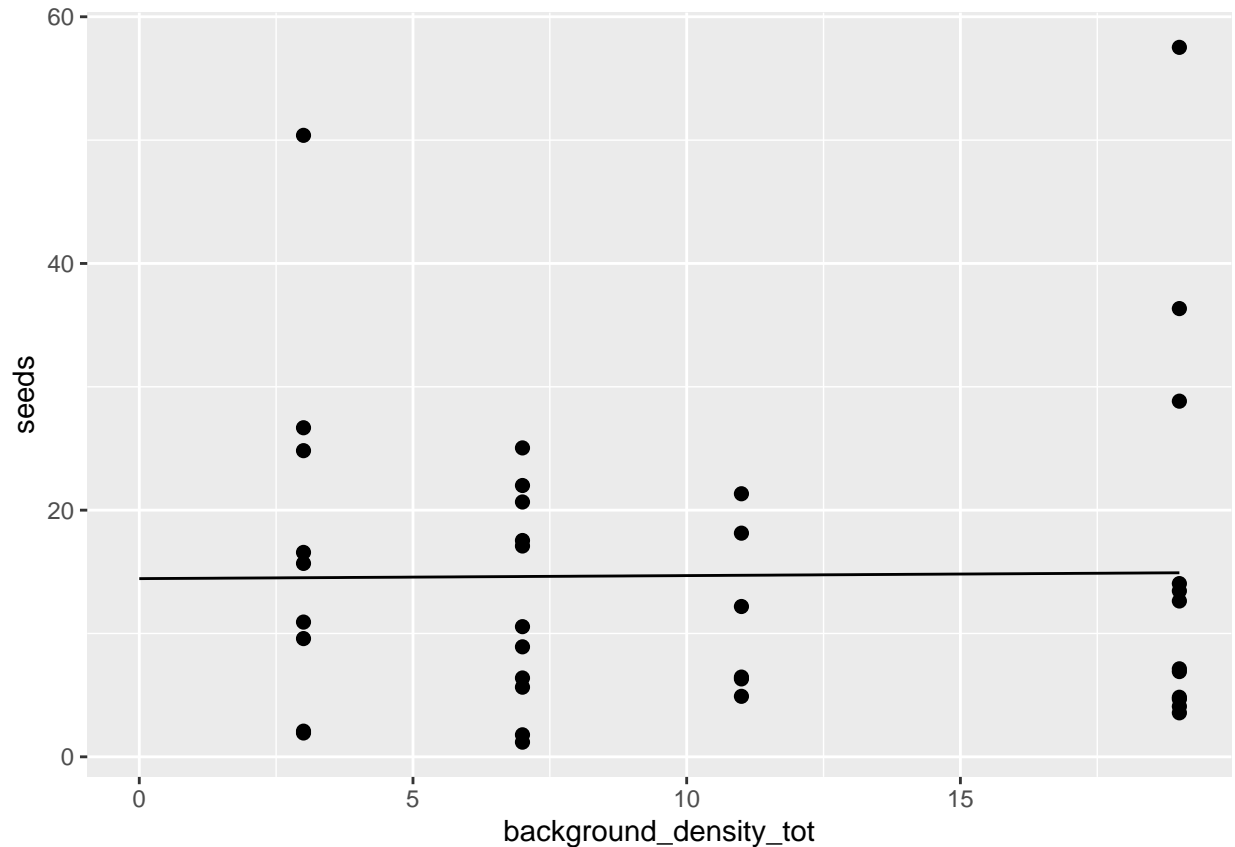
```
# save coefficients
(alpha.PP <- coef(alphaPP_mod)[2])
```

```
##       beta
## 0.02813529
```

```
(alpha.SS <- coef(alphaSS_mod)[2])
```

```
##           beta
## -0.001669568
```

```
# change to zero for now
alpha.SS <- 0
```

4.8 reduction in perennial seed production due to intraspecific competition from the other life stage

Same as above, but with higher density treatments.

```
# subset data
P_alphaPS_dat <- filter(S_seed_dat_adult, treatment == "fungicide" & background ==
    "Ev seedling")
S_alphaSP_dat <- filter(S_seed_dat_seed, treatment == "fungicide" & background ==
    "Ev adult")

# fit non-linear curve
alphaPS_mod <- nls(seeds ~ seed0/(1 + beta * background_density_tot), start = list(seed0 = f.P0_parms$f
```

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```
    beta = 1), data = P_alphaPS_dat)
summary(alphaPS_mod)
```

```
##
## Formula: seeds ~ seed0/(1 + beta * background_density_tot)
##
## Parameters:
##       Estimate Std. Error t value Pr(>|t|)
## seed0 136.3892    87.9174   1.551    0.132
## beta    0.2350     0.2735   0.859    0.397
##
## Residual standard error: 47.7 on 29 degrees of freedom
##
## Number of iterations to convergence: 6
## Achieved convergence tolerance: 6.051e-06
```

```
alphaSP_mod <- nls(seeds ~ seed0/(1 + beta * background_density_tot), start = list(seed0 = f.10_parms$f
    beta = 1), data = S_alphaSP_dat)
summary(alphaSP_mod)
```

```
##
## Formula: seeds ~ seed0/(1 + beta * background_density_tot)
##
## Parameters:
##       Estimate Std. Error t value Pr(>|t|)
## seed0  19.7660     5.1369   3.848 0.000327 ***
## beta    0.1210     0.1016   1.191 0.239197
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.35 on 52 degrees of freedom
##
## Number of iterations to convergence: 7
## Achieved convergence tolerance: 1.076e-06
```

```
# look at fit
alphaPS_df <- tibble(background_density_tot = seq(0, 19, length.out = 100))
alphaPS_df$seeds <- predict(alphaPS_mod, newdata = alphaPS_df)
ggplot(P_alphaPS_dat, aes(x = background_density_tot, y = seeds)) + geom_point(size = 2) +
    geom_line(data = alphaPS_df)
```
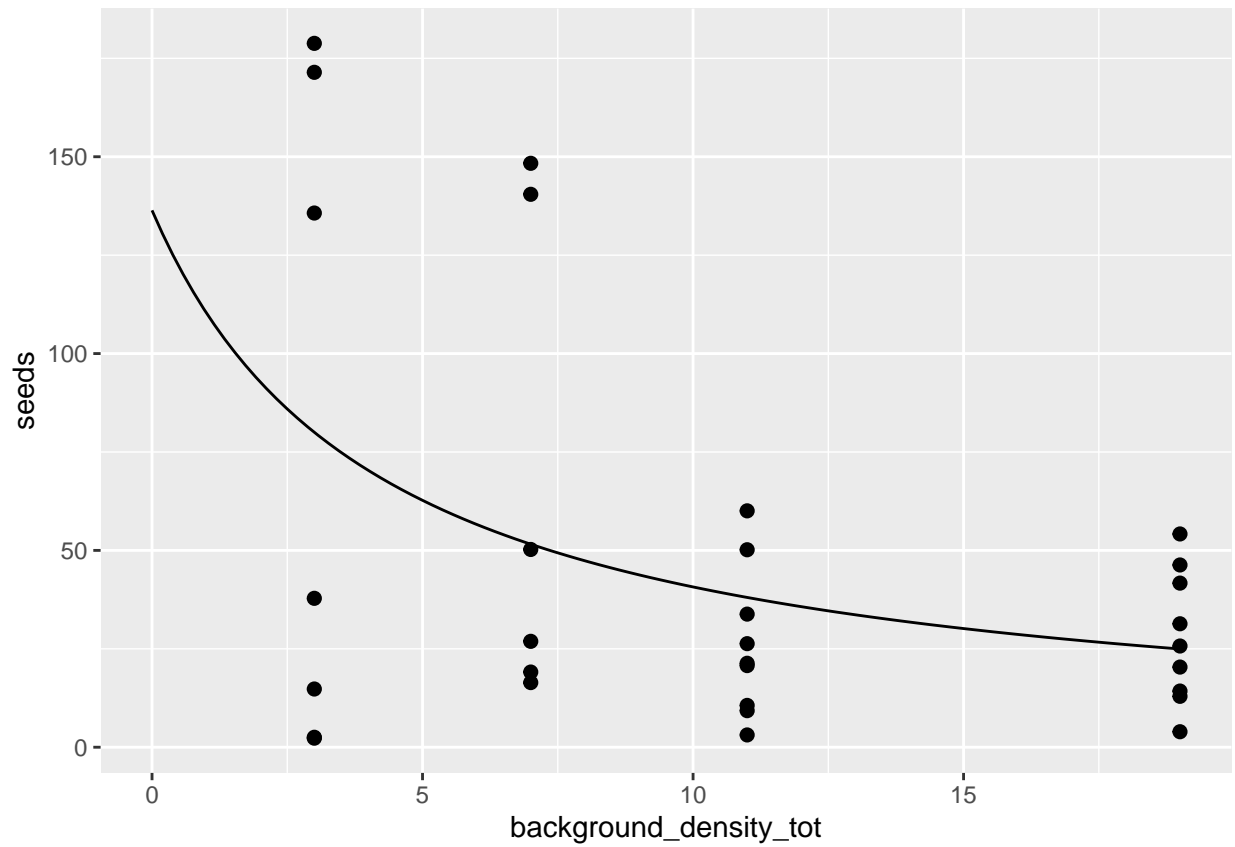
```r
alphaSP_df <- tibble(background_density_tot = seq(0, 9, length.out = 100))
alphaSP_df$seeds <- predict(alphaSP_mod, newdata = alphaSP_df)
ggplot(S_alphaSP_dat, aes(x = background_density_tot, y = seeds)) + geom_point(size = 2) +
    geom_line(data = alphaSP_df)
```
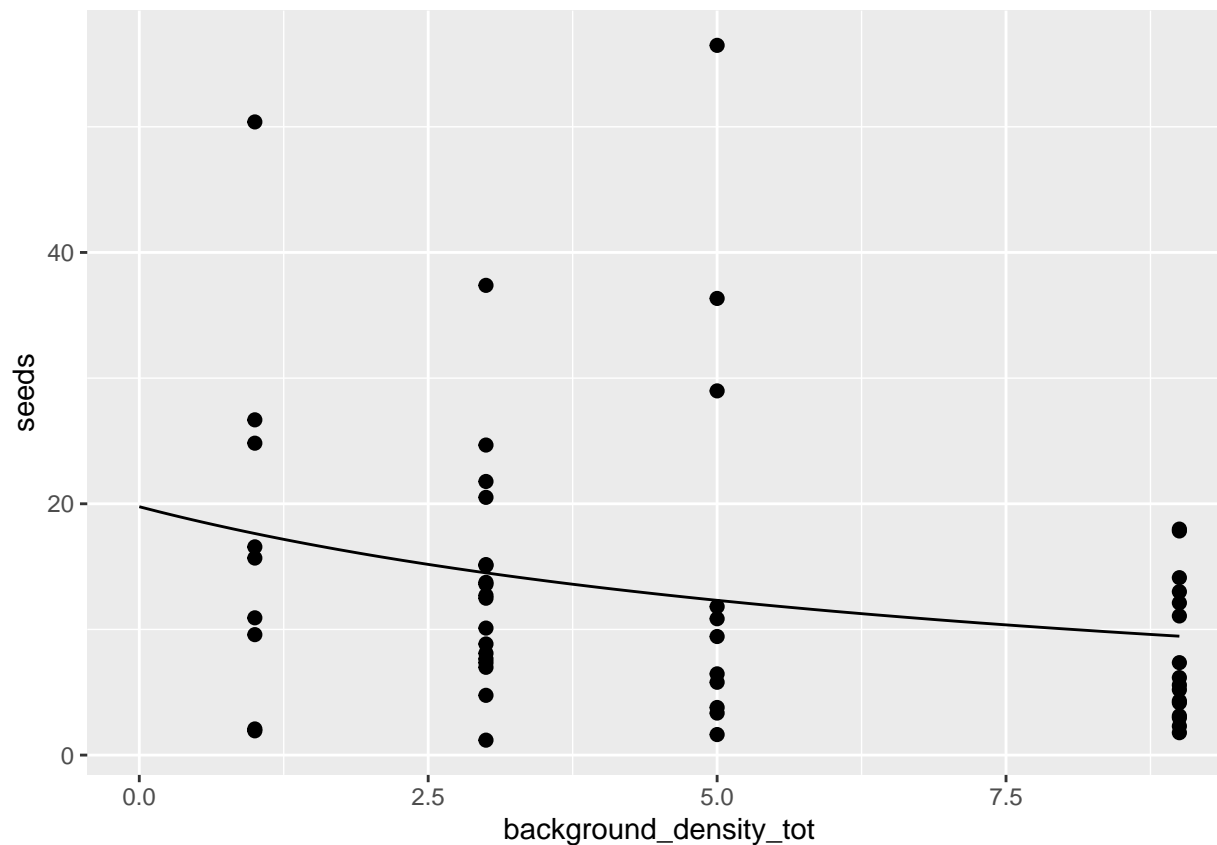
```
# save coefficients
(alpha.PS <- coef(alphaPS_mod)[2])
```

```
##      beta
## 0.2349613
```

```
(alpha.SP <- coef(alphaSP_mod)[2])
```

```
##     beta
## 0.120978
```

4.9 reduction in perennial seed production due to interspecific competition

Same as above, but with higher annual density treatments.

```
# subset data
P_alphaPA_dat <- filter(S_seed_dat_adult, treatment == "fungicide" & background ==
    "Mv seedling")
S_alphaSA_dat <- filter(S_seed_dat_seed, treatment == "fungicide" & background ==
    "Mv seedling")

# fit non-linear curve
alphaPA_mod <- nls(seeds ~ seed0/(1 + beta * background_density_tot), start = list(seed0 = f.P0_parms$f
    beta = 1), data = P_alphaPA_dat)
summary(alphaPA_mod)
```

```
##
```

```
## Formula: seeds ~ seed0/(1 + beta * background_density_tot)
##
## Parameters:
##       Estimate Std. Error t value Pr(>|t|)
## seed0 90.86739   32.80453    2.77  0.00871 **
## beta   0.06772    0.06839    0.99  0.32849
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 52.21 on 37 degrees of freedom
##
## Number of iterations to convergence: 8
## Achieved convergence tolerance: 2.732e-06
```

```r
alphaSA_mod <- nls(seeds ~ seed0/(1 + beta * background_density_tot), start = list(seed0 = f.10_parms$f
    beta = 1), data = S_alphaSA_dat)
summary(alphaSA_mod)
```

```
##
## Formula: seeds ~ seed0/(1 + beta * background_density_tot)
##
## Parameters:
##       Estimate Std. Error t value Pr(>|t|)
## seed0 18.63508    3.94282   4.726 1.68e-05 ***
## beta   0.02824    0.02183   1.294    0.201
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.6 on 54 degrees of freedom
##
## Number of iterations to convergence: 10
## Achieved convergence tolerance: 2.615e-06
```

```r
# look at fit
alphaPA_df <- tibble(background_density_tot = seq(0, 67, length.out = 100))
alphaPA_df$seeds <- predict(alphaPA_mod, newdata = alphaPA_df)
ggplot(P_alphaPA_dat, aes(x = background_density_tot, y = seeds)) + geom_point(size = 2) +
    geom_line(data = alphaPA_df)
```
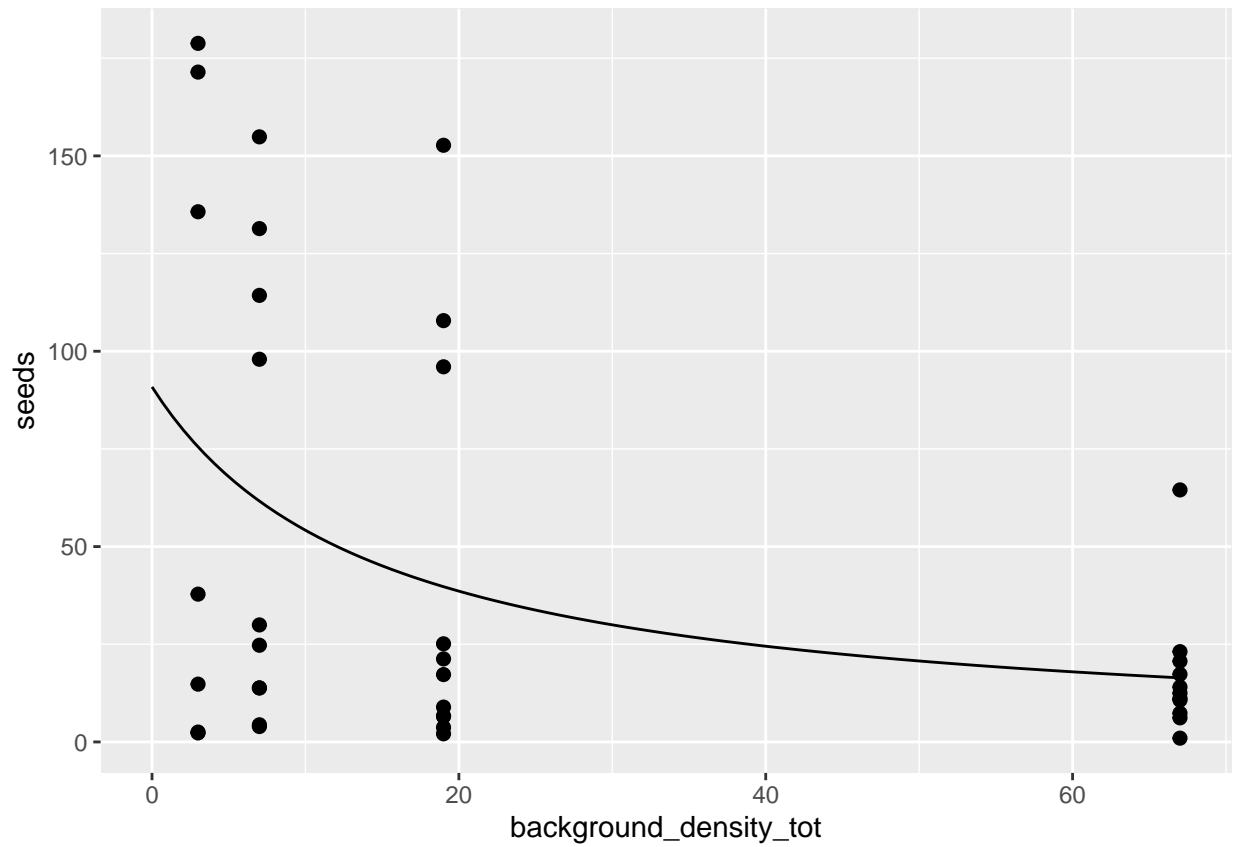
```
alphaSA_df <- tibble(background_density_tot = seq(0, 67, length.out = 100))
alphaSA_df$seeds <- predict(alphaSA_mod, newdata = alphaSA_df)
ggplot(S_alphaSA_dat, aes(x = background_density_tot, y = seeds)) + geom_point(size = 2) +
    geom_line(data = alphaSA_df)
```
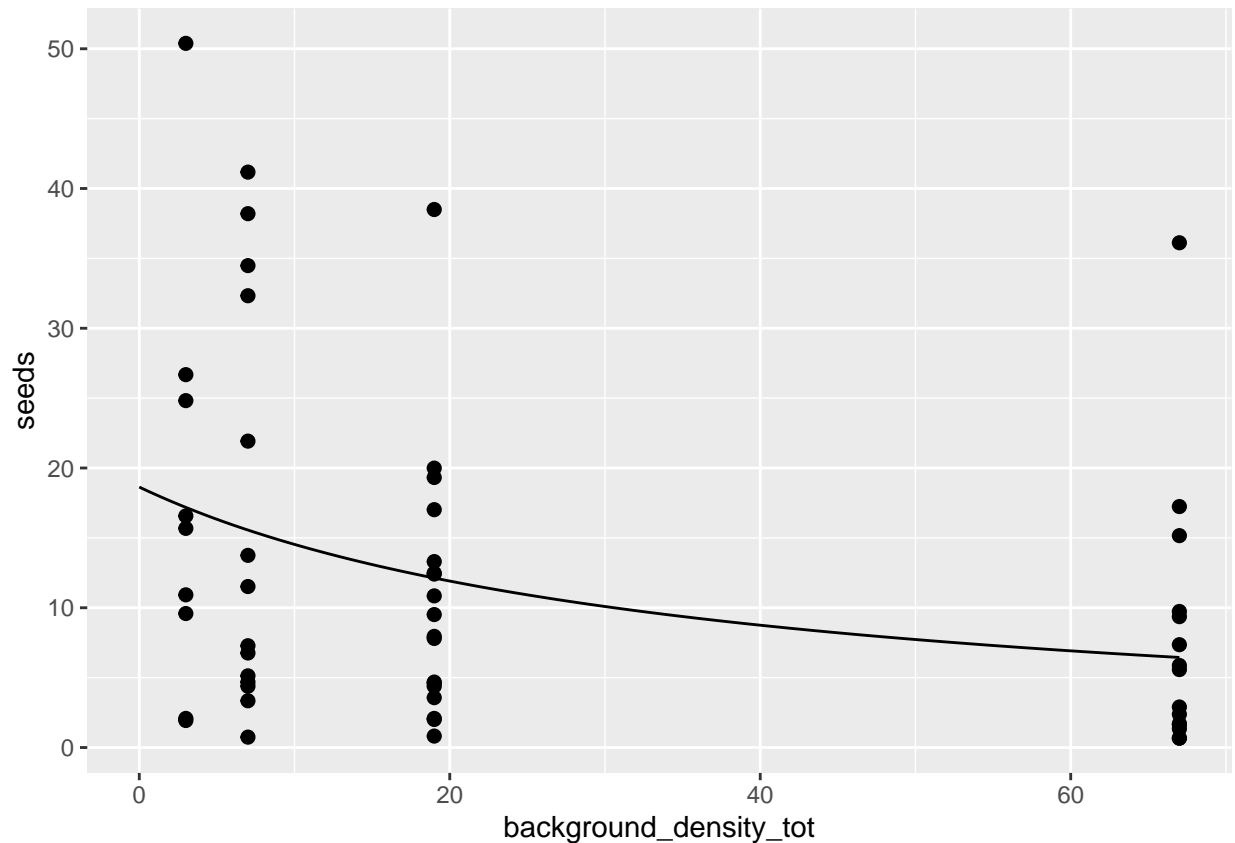
```
# save coefficients
(alpha.PA <- coef(alphaPA_mod)[2])
```

```
##       beta
## 0.06772412
```

```
(alpha.SA <- coef(alphaSA_mod)[2])
```

```
##       beta
## 0.02823642
```

4.10   seedling and adult survival in the absence of competition

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

```
## 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(),
##   survival_seeds = col_double(),
```

```
##    month = col_character(),
##    survival = col_double(),
##    field_notes = col_character()
## )
```

```
# join with plot data (need to edit experiment code to add this in)
S_surv_dat2 <- A_bio_dat %>% select(site, plot, treatment, background,
    background_sp, background_density, density_level, background_density_tot) %>%
    right_join(S_surv_dat)
```

```
## Joining, by = c("site", "plot", "treatment")
```

```
# seedling survival
s.1_parms <- S_surv_dat2 %>% filter(month == "April" & age == "seedling" &
    density_level == "none" & background == "Ev adult" & treatment == "fungicide") %>%
    summarise(s.1 = mean_cl_boot(survival)$y, s.1_low = mean_cl_boot(survival)$ymin,
        s.1_hi = mean_cl_boot(survival)$ymax)

# adult survival
s.P_parms <- S_surv_dat2 %>% filter(month == "April" & age == "adult" &
    density_level == "none" & background == "Ev adult" & treatment == "fungicide") %>%
    summarise(s.P = mean_cl_boot(survival)$y, s.P_low = mean_cl_boot(survival)$ymin,
        s.P_hi = mean_cl_boot(survival)$ymax)

(s.1 <- s.1_parms$s.1)
```

```
## [1] 0.25
```

```
(s.P <- s.P_parms$s.P)
```

```
## [1] 0.75
```

```
# Stats: used old code from 2018 - need to update with 2019 summer
# survival data
```