

microstegium_elymus_model_summary

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1 Summary

Simulation of *Microstegium vimineum* and *Elymus virginicus* over time. *M. vimineum* is an invasive annual grass and *E. virginicus* is a native perennial grass. *E. virginicus* grows by itself for 100 years, and then *M. vimineum* is introduced. Disease effects arise 100 years later. Population dynamics are similar in the absence of disease and when both species are susceptible to disease. In both cases, *M. vimineum* reduces the size of the *E. virginicus* population. *M. vimineum* is able to recover population losses due to disease. *E. virginicus* seedlings are impacted more than adults. When only *M. vimineum* is susceptible to disease, its population crashes.

2 Set-up

```
# clear all existing data
rm(list = ls())

# open libraries
library(data.table)
library(plotly)
library(cowplot)
library(popbio)
library(tidyverse)
```

```

# plotting parameters
axisText = 10
axisTitle = 12
legendText = 10
legendTitle = 0
colPal = c("#0072B2", "#56B4E9", "#009E73", "#E69F00")

# import data
params <- read_csv("../data/mv_ev_model_parameters_021320.csv", col_types = cols())

```

3 Parameters

3.1 Formatting:

- subscripts follow “.”
- A = annual plant
- L = annual litter
- P = perennial adult (at least 1 year old)
- S = perennial seedling (germinated that spring)
- Composite parameters are capitalized

3.2 Settings:

```

# simulation time
simtime = 500

# invasion time
invtime = 100

# disease time
distime = invtime + 100

# initial conditions
NO.A = 0 # initial annual population size
NO.S = 1 # initial perennial seedling population size
NO.P = 0 # initial perennial adult population size
LO = 0 # initial annual litter amount
Ni.A = 1 # introduction of annual

```

3.3 Literature:

parameter	symbol	value	units	reference
annual germination without litter	g.A	0.8000	year ⁻¹	Redwood et al. 2018
litter suppression of germination	beta	0.0065	g ⁻¹ year ⁻¹	Foster and Gross 1998
annual seed survival	s.A	0.1300	year ⁻¹	Redwood et al. 2018
annual biomass without competition	v.A	17.4000	g year ⁻¹	Wilson et al. 2015
annual biomass-seed conversion	y.A	86.0000	seeds g ⁻¹ year ⁻¹	Wilson et al. 2015, Redwood et al. 2018

parameter	symbol	value	units	reference
annual litter-biomass conversion	a	0.9500	year ⁻¹	DeMeester and Richter 2010
litter decomposition rate	b	0.6700	year ⁻¹	DeMeester and Richter 2010
perennial germination without litter	g.S	0.8000	year ⁻¹	Garrison and Stier 2010
perennial seed survival	s.S	1.0000	year ⁻¹	Garrison and Stier 2010
adult perennial seed production without competition	f.P	361.0000	seeds year ⁻¹	Stevens 1957, Garrison and Stier 2010
seedling perennial seed production without competition	f.1	36.0000	seeds year ⁻¹	1/10 of f.P
perennial seedling survival	s.1	0.4000	year ⁻¹	Mottl et al. 2006
perennial adult survival	s.P	0.8900	year ⁻¹	Mottl et al. 2006
competitive effect of annual	alpha.A	0.0200	year ⁻¹	average of alpha.iA
competitive effect of perennial seedling	alpha.S	0.0020	year ⁻¹	average of alpha.iS
competitive effect of perennial adult	alpha.P	0.0200	year ⁻¹	average of alpha.iP
reduction in biomass due to disease	dis	0.3500	year ⁻¹	Flory et al. 2011, Stricker et al. 2016

4 Model

4.1 Population equations:

Assume counts are being conducted in the spring

$$N.A[t+1] = s.A * (1-G.A) * N.A[t] + G.A * V.A * y.A * N.A[t]$$

annual seeds = seed bank survival + seed production

$$L[t+1] = a * G.A * V.A * N.A[t] + (1-b) * L[t]$$

annual litter = biomass from previous fall + decomposition

$$N.S[t+1] = s.S * (1-G.S) * N.S[t] + G.S * F.1 * N.S[t] + F.P * N.P[t]$$

perennial seeds = seed bank survival + seedling seed production + adult seed production

$$N.P[t+1] = s.P * N.P[t] + s.1 * G.S * N.S[t]$$

perennial adults = survival + seedling maturation

4.2 Litter suppression of germination

$$G.A = g.A / (1 + \beta * L[t])$$

annual seed germination = germination in the absence of litter / reduction due to litter

$$G.S = g.S / (1 + \beta * L[t])$$

perennial seed germination = germination in the absence of litter / reduction due to litter

4.3 Density-dependence on growth and fecundity

$$V.A = v.A / (1 + \alpha.A * G.A * N.A[t] + \alpha.P * N.P[t] + \alpha.S * G.S * N.S[t])$$

annual growth = growth in the absence of competition / (competition from annuals + competition from perennial adults + competition from perennial seedlings)

$$F.1 = f.1 / (1 + \alpha.A * G.A * N.A[t] + \alpha.P * N.P[t] + \alpha.S * G.S * N.S[t])$$

perennial seedling seed production = seed production in the absence of competition / (competition from annuals + competition from perennial adults + competition from perennial seedlings)

$$F.P = f.P / (1 + \alpha.A * G.A * N.A[t] + \alpha.P * N.P[t] + \alpha.S * G.S * N.S[t])$$
 perennial adult seed production = seed production in the absence of competition / (competition from annuals + competition from perennial adults + competition from perennial seedlings)

5 Function

```

simFun = function(params, NO.A, NO.S, NO.P, L0, Ni.A, simtime, invtime,
  distime) {

  # define parameters
  g.A = filter(params, symbol == "g.A")$value
  beta = filter(params, symbol == "beta")$value
  s.A = filter(params, symbol == "s.A")$value
  v.A = filter(params, symbol == "v.A")$value
  y.A = filter(params, symbol == "y.A")$value
  a = filter(params, symbol == "a")$value
  b = filter(params, symbol == "b")$value
  g.S = filter(params, symbol == "g.S")$value
  s.S = filter(params, symbol == "s.S")$value
  f.P = filter(params, symbol == "f.P")$value
  f.1 = filter(params, symbol == "f.1")$value
  s.1 = filter(params, symbol == "s.1")$value
  s.P = filter(params, symbol == "s.P")$value
  alpha.A = filter(params, symbol == "alpha.A")$value
  alpha.S = filter(params, symbol == "alpha.S")$value
  alpha.P = filter(params, symbol == "alpha.P")$value
  dis = filter(params, symbol == "dis")$value

  # initialize populations
  N.A = rep(NA, simtime)
  N.S = rep(NA, simtime)
  N.P = rep(NA, simtime)
  L = rep(NA, simtime)

  N.A[1] = NO.A
  N.S[1] = NO.S
  N.P[1] = NO.P
  L[1] = L0

  # simulate population dynamics
  for (t in 1:(simtime - 1)) {

    # introduce annual at t=100
    N.A[t] = ifelse(NO.A == 0 & t == invtime, Ni.A, N.A[t])

    # calculate parameters to introduce disease at distime
    growth.A = ifelse(t < distime, v.A, dis * g.A)

    # reduce germination due to litter
    G.A = g.A/(1 + beta * L[t])
    G.S = g.S/(1 + beta * L[t])
  }
}

```

```

# reduce fecundity or growth due to competition
V.A = growth.A/(1 + alpha.A * G.A * N.A[t] + alpha.P * N.P[t] +
  alpha.S * G.S * N.S[t])
F.1 = f.1/(1 + alpha.A * G.A * N.A[t] + alpha.P * N.P[t] + alpha.S *
  G.S * N.S[t])
F.P = f.P/(1 + alpha.A * G.A * N.A[t] + alpha.P * N.P[t] + alpha.S *
  G.S * N.S[t])

# population size
N.A[t + 1] = s.A * (1 - G.A) * N.A[t] + G.A * V.A * y.A * N.A[t]
L[t + 1] = a * G.A * V.A * N.A[t] + (1 - b) * L[t]
N.S[t + 1] = s.S * (1 - G.S) * N.S[t] + G.S * F.1 * N.S[t] + F.P *
  N.P[t]
N.P[t + 1] = s.P * N.P[t] + s.1 * G.S * N.S[t]

# correct to prevent negative numbers
N.A[t + 1] = ifelse(N.A[t + 1] < 1, 0, N.A[t + 1])
L[t + 1] = ifelse(L[t + 1] < 1, 0, L[t + 1])
N.S[t + 1] = ifelse(N.S[t + 1] < 1, 0, N.S[t + 1])
N.P[t + 1] = ifelse(N.P[t + 1] < 1, 0, N.P[t + 1])
}

# save data
dfN = data.frame(time = rep(1:simtime, 4), N = c(N.S, N.P, N.A, L),
  species = rep(c("Elymus seedling", "Elymus adult", "Microstegium",
    "Microstegium litter"), each = simtime))

# return
return(dfN)
}

```

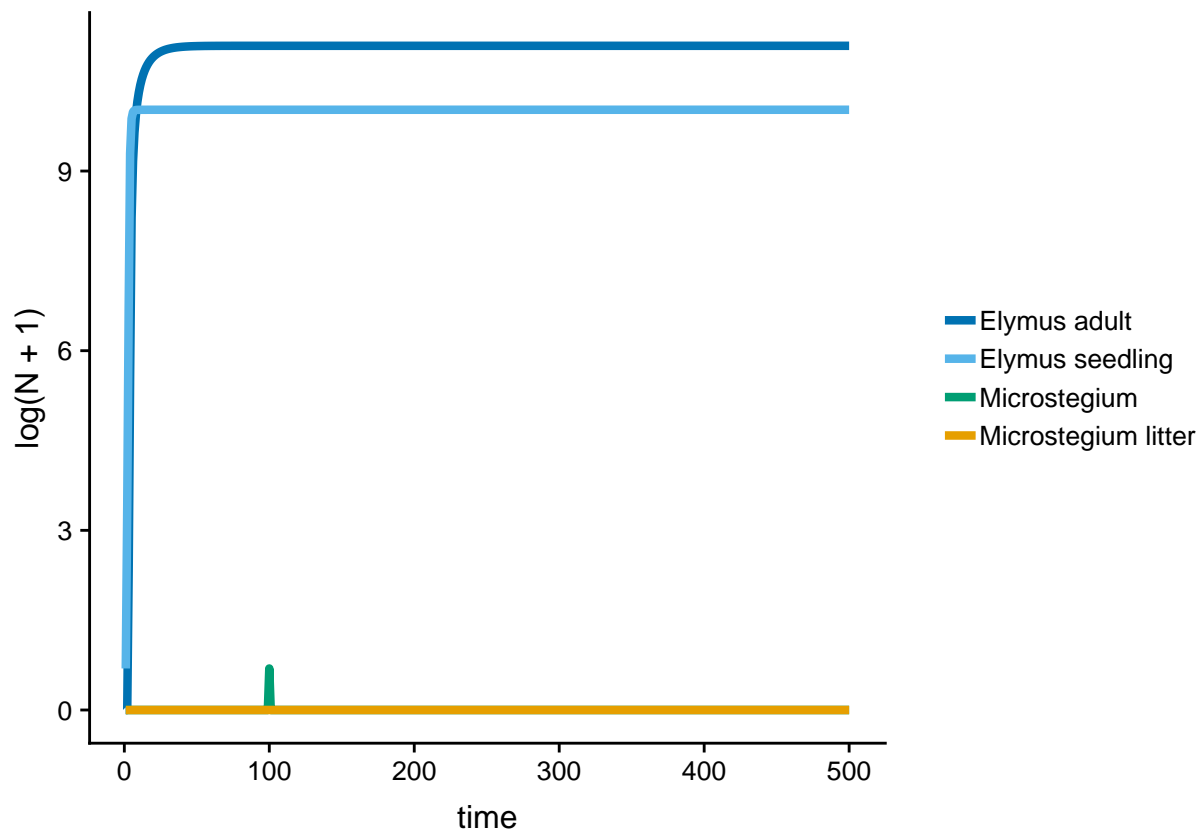
6 Simulations

6.1 No disease

```

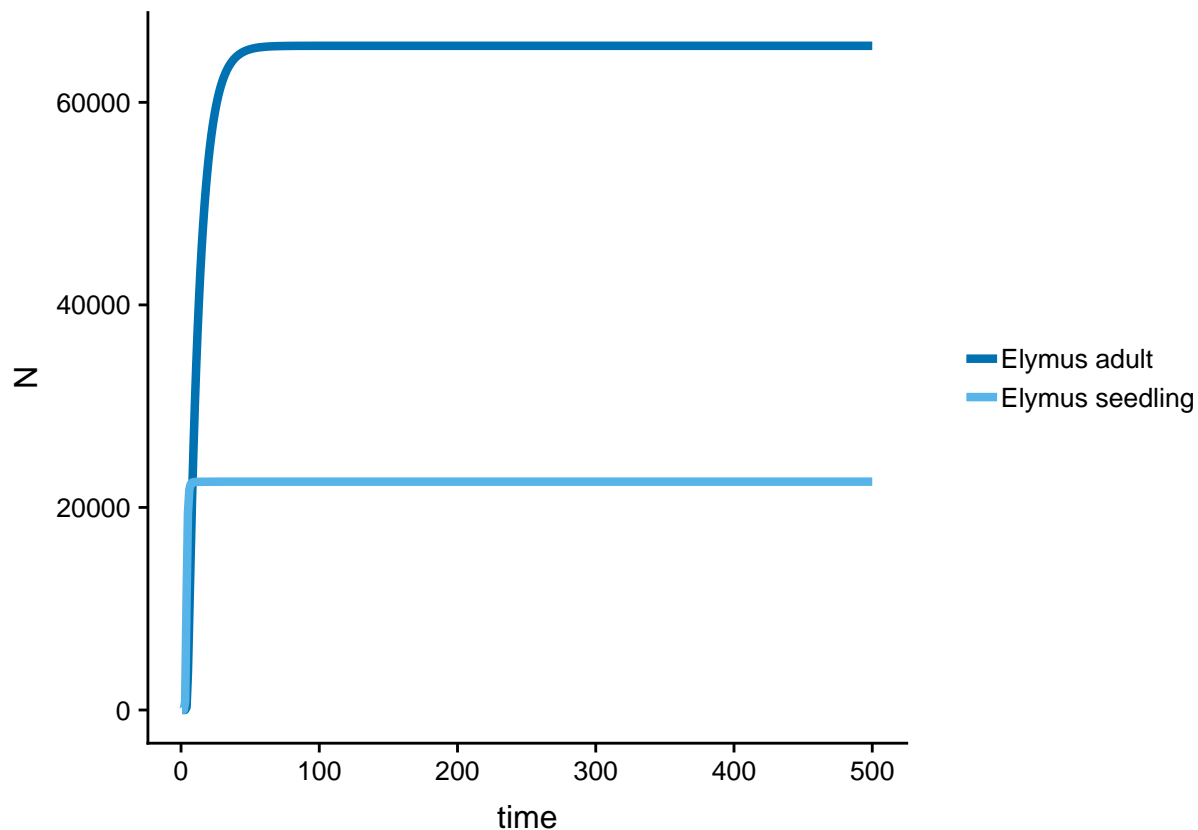
nodisSim <- simFun(params, NO.A, NO.S, NO.P, L0, Ni.A, simtime, invtime, distime = simtime + 10)
nodisSim %>%
  ggplot(aes(x = time, y = log(N+1), color = species)) +
  geom_line(size = 1.5) +
  theme(axis.text = element_text(size = axisText),
    axis.title = element_text(size = axisTitle),
    legend.text = element_text(size = legendText),
    legend.title = element_text(size = legendTitle)) +
  scale_color_manual(values = colPal)

```



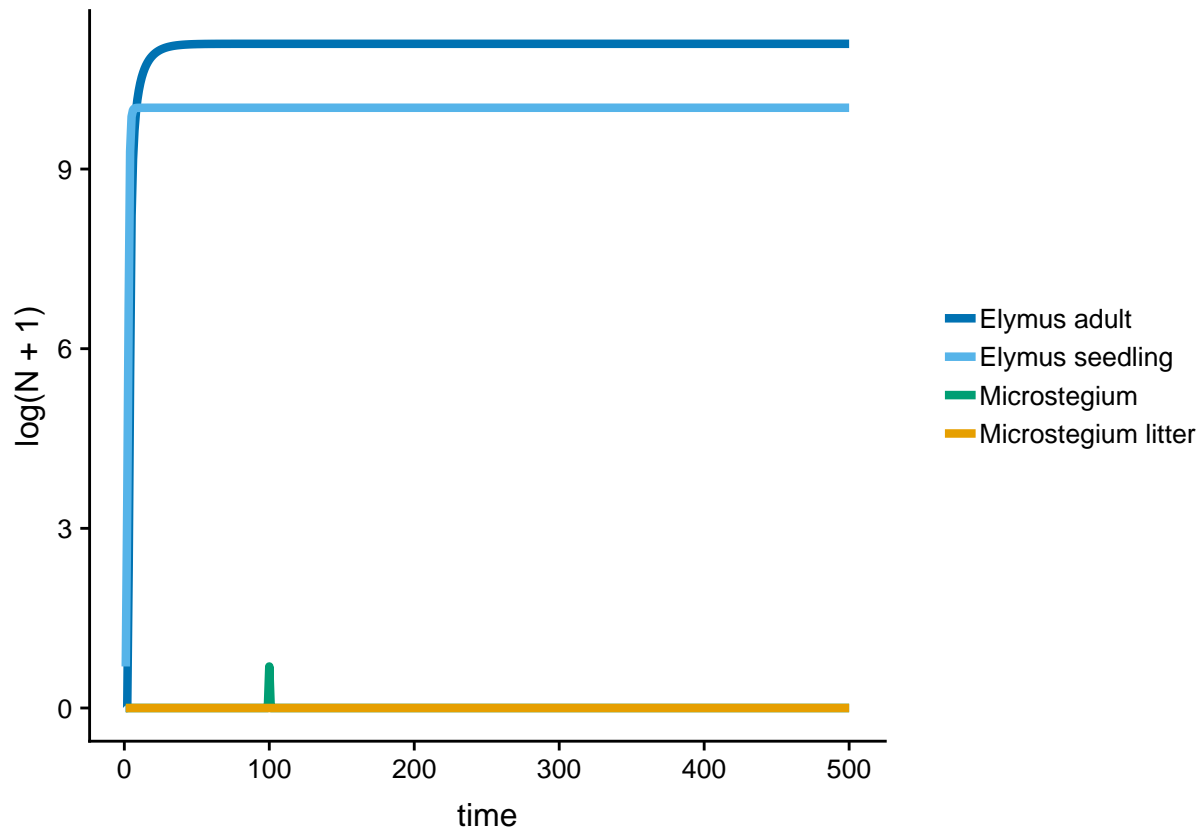
6.1.1 Elymus on non-transformed scale

```
nodisSim %>%
  filter(species %in% c("Elymus adult", "Elymus seedling")) %>%
  ggplot(aes(x = time, y = N, color = species)) +
  geom_line(size = 1.5) +
  theme(axis.text = element_text(size = axisText),
        axis.title = element_text(size = axisTitle),
        legend.text = element_text(size = legendText),
        legend.title = element_text(size = legendTitle)) +
  scale_color_manual(values = colPal)
```



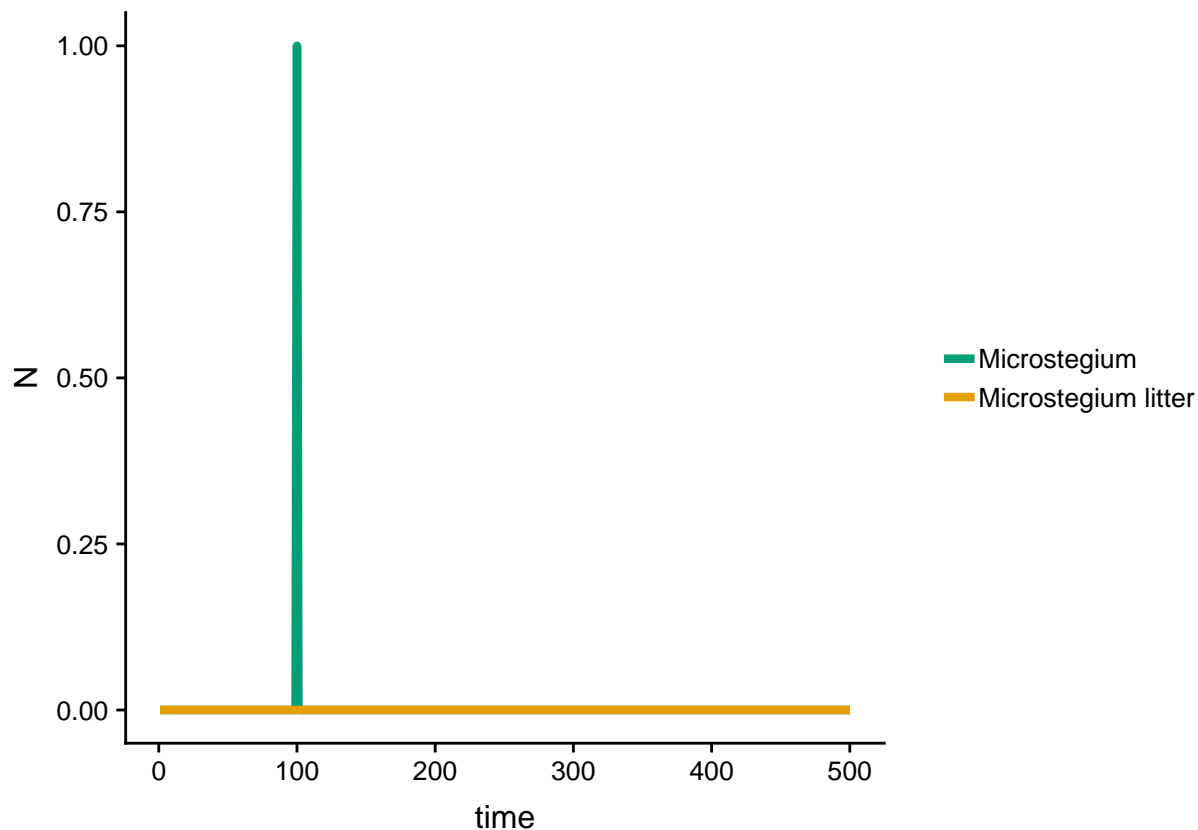
6.2 Add disease

```
disSim <- simFun(params, NO.A, NO.S, NO.P, LO, Ni.A, simtime, invtime, distime)
disSim %>%
  ggplot(aes(x = time, y = log(N+1), color = species)) +
  geom_line(size = 1.5) +
  theme(axis.text = element_text(size = axisText),
        axis.title = element_text(size = axisTitle),
        legend.text = element_text(size = legendText),
        legend.title = element_text(size = legendTitle)) +
  scale_color_manual(values = colPal)
```



6.2.1 Microstegium on non-transformed scale

```
disSim %>%
  filter(species %in% c("Microstegium", "Microstegium litter")) %>%
  ggplot(aes(x = time, y = N, color = species)) +
  geom_line(size = 1.5) +
  theme(axis.text = element_text(size = axisText),
        axis.title = element_text(size = axisTitle),
        legend.text = element_text(size = legendText),
        legend.title = element_text(size = legendTitle)) +
  scale_color_manual(values = colPal[3:4])
```

6.2.2 Time to extinction?

```
nodisSim %>%
  filter(species == "Elymus seedling" & N == 0) %>%
  filter(time == min(time))

## [1] time      N      species
## <0 rows> (or 0-length row.names)

disSim %>%
  filter(species == "Microstegium" & N == 0 & time > invtime) %>%
  filter(time == min(time))

##   time N      species
## 1  101 0 Microstegium
```