The data in the model projection was used in this simulation. 100 iterations of simulation were run per each rotation crossed with corn weed management regime. Different simulation outputs are collected at different chunks: x-lambda-x-x for population growth rate, x-seed-production-per-capita for manipulated seed production per plant, x-plant-density-fixed for mature plant density as empirically measure, and x-all-output for all the outputs combined.

# event sequence: seed dropped - field cultivator - emerge - survive - new seed - chisel - overwinter   
  
# create a function   
# vec: starting seed column  
# prt: pre-planting-tillage  
# em: emergence  
# sv: seed survival rate and seedling to maturity success rate  
# seed: fecundity  
# poh: post-harvest tillage  
# ow: over winter seed survival  
##### with corn under conventional weed management {-}  
  
### Output: seedbank at top and bottom strata at the end of each crop phase  
  
N\_2yr\_conv\_lambda <- list() # blank data frame to save loop output   
N\_2yr\_conv\_lambda[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_2yr\_conv\_lambda[[i]] = rot\_2year\_conv\_lambda(vec = N\_2yr\_conv\_lambda[[i-1]],  
 poh\_C = fall\_tillage$C2\_conv,  
 ow\_C = overwinter$C2\_conv,  
 prt\_C = spring\_tillage$C2\_conv,  
 em\_C = emergence$C2\_conv,  
 sv\_C = summer\_survival$C2\_conv,  
 seed\_C = fecundity18$C2\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S2\_conv,  
 ow\_S = overwinter$S2\_conv,  
 prt\_S = spring\_tillage$S2\_conv,  
 em\_S = emergence$S2\_conv,  
 sv\_S = summer\_survival$S2\_conv,  
 seed\_S = fecundity18$S2\_conv)  
}  
  
N\_2yr\_conv\_lambda\_df <- N\_2yr\_conv\_lambda %>%   
 unlist(recursive = TRUE) %>%  
 data.frame() %>%  
 dplyr::rename(seedbank\_counts = ".") %>%  
 dplyr::mutate(stratum = rep(c("top", "bottom",   
 "cohort\_1", "cohort\_2",   
 "cohort\_3", "cohort\_4",  
 "cohort\_5", "cohort\_6"),t)) %>%  
 filter(stratum %in% c("top", "bottom")) %>%  
 unnest(cols = everything()) %>%  
 mutate(cycle\_no = as.character(rep(1:t, each = 2))) %>%  
 pivot\_wider(names\_from = stratum, values\_from = seedbank\_counts) %>%  
 mutate(total\_seedbank\_counts = top + bottom) %>%  
 mutate(lambda\_cycle = total\_seedbank\_counts/lag(total\_seedbank\_counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "2-year",  
 Corn\_weed\_management = "conventional")   
  
##### with corn under low herbicide weed management {-}  
N\_2yr\_low\_lambda <- list() # blank data frame to save loop output   
  
N\_2yr\_low\_lambda[[1]] <- starting\_point   
for (i in 2:t) {   
 N\_2yr\_low\_lambda[[i]] = rot\_2year\_low\_lambda(vec = N\_2yr\_low\_lambda[[i-1]],  
 poh\_C = fall\_tillage$C2\_low,  
 ow\_C = overwinter$C2\_low,  
 prt\_C = spring\_tillage$C2\_low,  
 em\_C = emergence$C2\_low,  
 sv\_C = summer\_survival$C2\_low,  
 seed\_C = fecundity18$C2\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S2\_low,  
 ow\_S = overwinter$S2\_low,  
 prt\_S = spring\_tillage$S2\_low,  
 em\_S = emergence$S2\_low,  
 sv\_S = summer\_survival$S2\_low,  
 seed\_S = fecundity18$S2\_low)  
}  
  
N\_2yr\_low\_lambda\_df <- N\_2yr\_low\_lambda %>%   
 unlist(recursive = TRUE) %>%  
 data.frame() %>%  
 dplyr::rename(seedbank\_counts = ".") %>%  
 dplyr::mutate(stratum = rep(c("top", "bottom",   
 "cohort\_1", "cohort\_2",   
 "cohort\_3", "cohort\_4",  
 "cohort\_5", "cohort\_6"),t)) %>%  
 filter(stratum %in% c("top", "bottom")) %>%  
 unnest(cols = everything()) %>%  
 mutate(cycle\_no = as.character(rep(1:t, each = 2))) %>%  
 pivot\_wider(names\_from = stratum, values\_from = seedbank\_counts) %>%  
 mutate(total\_seedbank\_counts = top + bottom) %>%  
 mutate(lambda\_cycle = total\_seedbank\_counts/lag(total\_seedbank\_counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "2-year",  
 Corn\_weed\_management = "low")

### Output: Mature plant densities until seed production (B\_h = sv\_C or sv\_S)  
### 1 iteration only because no randomization at any matrix  
N\_2yr\_conv\_mature\_plant\_density\_fixed <- rot\_2year\_conv\_plant\_density\_fixed(vec = starting\_point ,  
 poh\_C = fall\_tillage$C2\_conv,  
 ow\_C = overwinter$C2\_conv,  
 prt\_C = spring\_tillage$C2\_conv,  
 em\_C = emergence$C2\_conv,  
 sv\_C = summer\_survival$C2\_conv,  
 seed\_C = fecundity18$C2\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S2\_conv,  
 ow\_S = overwinter$S2\_conv,  
 prt\_S = spring\_tillage$S2\_conv,  
 em\_S = emergence$S2\_conv,  
 sv\_S = summer\_survival$S2\_conv,  
 seed\_S = fecundity18$S2\_conv)  
  
N\_2yr\_conv\_mature\_plant\_density\_fixed\_df <- N\_2yr\_conv\_mature\_plant\_density\_fixed %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(plant\_counts\_fixed = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"),2)) %>%  
 mutate(Crop\_ID = c(rep("C2", 6), rep("S2", 6)))  
  
  
### Output: Mature plant densities until seed production (B\_h = sv\_C or sv\_S)  
### 1 iteration only because no randomization at any matrix  
  
N\_2yr\_low\_mature\_plant\_density\_fixed <- rot\_2year\_low\_plant\_density\_fixed(vec = starting\_point ,  
 poh\_C = fall\_tillage$C2\_low,  
 ow\_C = overwinter$C2\_low,  
 prt\_C = spring\_tillage$C2\_low,  
 em\_C = emergence$C2\_low,  
 sv\_C = summer\_survival$C2\_low,  
 seed\_C = fecundity18$C2\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S2\_low,  
 ow\_S = overwinter$S2\_low,  
 prt\_S = spring\_tillage$S2\_low,  
 em\_S = emergence$S2\_low,  
 sv\_S = summer\_survival$S2\_low,  
 seed\_S = fecundity18$S2\_low)  
  
N\_2yr\_low\_mature\_plant\_density\_fixed\_df <- N\_2yr\_low\_mature\_plant\_density\_fixed %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(plant\_counts\_fixed = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"),2)) %>%  
 mutate(Crop\_ID = c(rep("C2", 6), rep("S2", 6)))

### CONV Output: seed production, after manipulation by cohort x crop phase x iteration  
  
N\_2yr\_conv\_seed\_production\_per\_capita <- list() # blank data frame to save loop output   
  
for (i in 1:t) {   
 N\_2yr\_conv\_seed\_production\_per\_capita[[i]] =  
 rot\_2year\_conv\_seed\_production\_per\_cap(seed\_C = fecundity18$C2\_conv,  
 seed\_S = fecundity18$S2\_conv)  
}  
  
# original per capita seed production in fecundity18$C2\_conv[1,3:8] and fecundity18$S2\_conv[1,3:8]  
N\_2yr\_conv\_seed\_production\_per\_capita\_df <- N\_2yr\_conv\_seed\_production\_per\_capita %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(seed\_per\_capita\_threshold = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), t\*2)) %>%  
 mutate(cycle\_no = as.character(rep(1:t, each = 12))) %>% # 12 = 6 cohorts x 2 phases  
 mutate(Crop\_ID = rep(c(rep("C2", 6), rep("S2", 6)), t)) %>%  
 mutate(seed\_per\_capita\_original = rep(c(fecundity18$C2\_conv[1,3:8],  
 fecundity18$S2\_conv[1,3:8]), t)) %>%  
 mutate(seed\_production\_manipulated = ifelse(seed\_per\_capita\_threshold == seed\_per\_capita\_original, "no", "yes"))  
   
  
### LOW output  
  
N\_2yr\_low\_seed\_production\_per\_capita <- list() # blank data frame to save loop output   
  
for (i in 1:t) {   
 N\_2yr\_low\_seed\_production\_per\_capita[[i]] =  
 rot\_2year\_low\_seed\_production\_per\_cap(seed\_C = fecundity18$C2\_low,  
 seed\_S = fecundity18$S2\_low)  
}  
  
  
N\_2yr\_low\_seed\_production\_per\_capita\_df <- N\_2yr\_low\_seed\_production\_per\_capita %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(seed\_per\_capita\_threshold = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), t\*2)) %>%  
 mutate(cycle\_no = as.character(rep(1:t, each = 12))) %>% # 12 = 6 cohorts x 2 phases  
 mutate(Crop\_ID = rep(c(rep("C2", 6), rep("S2", 6)), t)) %>%  
 mutate(seed\_per\_capita\_original = rep(c(fecundity18$C2\_low[1,3:8],  
 fecundity18$S2\_low[1,3:8]), t)) %>%  
 mutate(seed\_production\_manipulated = ifelse(seed\_per\_capita\_threshold == seed\_per\_capita\_original, "no", "yes"))

# total stratified seedbank density and lambdas in N\_2yr\_conv\_lambda\_df  
# manipulated seed production in N\_2yr\_conv\_seed\_production\_per\_capita\_df  
# fixed mature plant density in N\_2yr\_conv\_mature\_plant\_density\_fixed\_df   
  
N\_2yr\_conv\_all\_df <- N\_2yr\_conv\_seed\_production\_per\_capita\_df %>%   
 left\_join(N\_2yr\_conv\_lambda\_df, by = "cycle\_no") %>%  
 left\_join(N\_2yr\_conv\_mature\_plant\_density\_fixed\_df, by = c("Crop\_ID", "cohort"))   
  
  
N\_2yr\_low\_all\_df <- N\_2yr\_low\_seed\_production\_per\_capita\_df %>%   
 left\_join(N\_2yr\_low\_lambda\_df, by = "cycle\_no") %>%  
 left\_join(N\_2yr\_low\_mature\_plant\_density\_fixed\_df, by = c("Crop\_ID", "cohort"))

##### with corn under conventional weed management {-}  
N\_3yr\_conv\_lambda <- list() # blank dataframe to save loop output   
  
N\_3yr\_conv\_lambda[[1]] <- starting\_point   
  
  
for (i in 2:t) {   
 N\_3yr\_conv\_lambda[[i]] = rot\_3year\_conv\_lambda(vec = N\_3yr\_conv\_lambda[[i-1]],  
 poh\_C = fall\_tillage$C3\_conv,  
 ow\_C = overwinter$C3\_conv,  
 prt\_C = spring\_tillage$C3\_conv,  
 em\_C = emergence$C3\_conv,  
 sv\_C = summer\_survival$C3\_conv,  
 seed\_C = fecundity18$C3\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S3\_conv,  
 ow\_S = overwinter$S3\_conv,  
 prt\_S = spring\_tillage$S3\_conv,  
 em\_S = emergence$S3\_conv,  
 sv\_S = summer\_survival$S3\_conv,  
 seed\_S = fecundity18$S3\_conv,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O3\_conv,  
 ow\_O = overwinter$O3\_conv,  
 prt\_O = spring\_tillage$O3\_conv,  
 em\_O = emergence$O3\_conv,  
 sv\_O = summer\_survival$O3\_conv,  
 seed\_O = fecundity18$O3\_conv)  
}  
  
N\_3yr\_conv\_lambda\_df <- N\_3yr\_conv\_lambda %>%   
 unlist(recursive = TRUE) %>%  
 data.frame() %>%  
 dplyr::rename(seedbank\_counts = ".") %>%  
 dplyr::mutate(stratum = rep(c("top", "bottom",  
 "cohort\_1", "cohort\_2",  
 "cohort\_3", "cohort\_4",  
 "cohort\_5", "cohort\_6"),t)) %>%  
 filter(stratum %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = as.character(rep(1:t, each = 2))) %>%  
 pivot\_wider(names\_from = stratum, values\_from = seedbank\_counts) %>%  
 mutate(total\_seedbank\_counts = top + bottom) %>%  
 mutate(lambda\_cycle = total\_seedbank\_counts/lag(total\_seedbank\_counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "3-year",  
 Corn\_weed\_management = "conventional")   
  
##### with corn under low herbicide weed management {-}   
N\_3yr\_low\_lambda <- list() # blank dataframe to save loop output   
  
N\_3yr\_low\_lambda[[1]] <- starting\_point   
  
  
for (i in 2:t) {   
 N\_3yr\_low\_lambda[[i]] = rot\_3year\_low\_lambda(vec = N\_3yr\_low\_lambda[[i-1]],  
 poh\_C = fall\_tillage$C3\_low,  
 ow\_C = overwinter$C3\_low,  
 prt\_C = spring\_tillage$C3\_low,  
 em\_C = emergence$C3\_low,  
 sv\_C = summer\_survival$C3\_low,  
 seed\_C = fecundity18$C3\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S3\_low,  
 ow\_S = overwinter$S3\_low,  
 prt\_S = spring\_tillage$S3\_low,  
 em\_S = emergence$S3\_low,  
 sv\_S = summer\_survival$S3\_low,  
 seed\_S = fecundity18$S3\_low,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O3\_low,  
 ow\_O = overwinter$O3\_low,  
 prt\_O = spring\_tillage$O3\_low,  
 em\_O = emergence$O3\_low,  
 sv\_O = summer\_survival$O3\_low,  
 seed\_O = fecundity18$O3\_low)  
}  
  
N\_3yr\_low\_lambda\_df <- N\_3yr\_low\_lambda %>%   
 unlist(recursive = TRUE) %>%  
 data.frame() %>%  
 dplyr::rename(seedbank\_counts = ".") %>%  
 dplyr::mutate(stratum = rep(c("top", "bottom",  
 "cohort\_1", "cohort\_2",  
 "cohort\_3", "cohort\_4",  
 "cohort\_5", "cohort\_6"),t)) %>%  
 filter(stratum %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = as.character(rep(1:t, each = 2))) %>%  
 pivot\_wider(names\_from = stratum, values\_from = seedbank\_counts) %>%  
 mutate(total\_seedbank\_counts = top + bottom) %>%  
 mutate(lambda\_cycle = total\_seedbank\_counts/lag(total\_seedbank\_counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "3-year",  
 Corn\_weed\_management = "low")

### Output: Mature plant densities until seed production (B\_h = sv\_C or sv\_S)  
### 1 iteration only because no randomization at any matrix  
N\_3yr\_conv\_mature\_plant\_density\_fixed <- rot\_3year\_conv\_plant\_density\_fixed(vec = starting\_point ,  
 poh\_C = fall\_tillage$C3\_conv,  
 ow\_C = overwinter$C3\_conv,  
 prt\_C = spring\_tillage$C3\_conv,  
 em\_C = emergence$C3\_conv,  
 sv\_C = summer\_survival$C3\_conv,  
 seed\_C = fecundity18$C3\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S3\_conv,  
 ow\_S = overwinter$S3\_conv,  
 prt\_S = spring\_tillage$S3\_conv,  
 em\_S = emergence$S3\_conv,  
 sv\_S = summer\_survival$S3\_conv,  
 seed\_S = fecundity18$S3\_conv,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O3\_conv,  
 ow\_O = overwinter$O3\_conv,  
 prt\_O = spring\_tillage$O3\_conv,  
 em\_O = emergence$O3\_conv,  
 sv\_O = summer\_survival$O3\_conv,  
 seed\_O = fecundity18$O3\_conv)  
  
N\_3yr\_conv\_mature\_plant\_density\_fixed\_df <- N\_3yr\_conv\_mature\_plant\_density\_fixed %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(plant\_counts\_fixed = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), 3)) %>% # 3 phases  
 mutate(Crop\_ID = c(rep("C3", 6), rep("S3", 6), rep("O3", 6)))  
  
  
### Output: Mature plant densities until seed production (B\_h = sv\_C or sv\_S)  
### 1 iteration only because no randomization at any matrix  
N\_3yr\_low\_mature\_plant\_density\_fixed <- rot\_3year\_low\_plant\_density\_fixed(vec = starting\_point,  
 poh\_C = fall\_tillage$C3\_low,  
 ow\_C = overwinter$C3\_low,  
 prt\_C = spring\_tillage$C3\_low,  
 em\_C = emergence$C3\_low,  
 sv\_C = summer\_survival$C3\_low,  
 seed\_C = fecundity18$C3\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S3\_low,  
 ow\_S = overwinter$S3\_low,  
 prt\_S = spring\_tillage$S3\_low,  
 em\_S = emergence$S3\_low,  
 sv\_S = summer\_survival$S3\_low,  
 seed\_S = fecundity18$S3\_low,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O3\_low,  
 ow\_O = overwinter$O3\_low,  
 prt\_O = spring\_tillage$O3\_low,  
 em\_O = emergence$O3\_low,  
 sv\_O = summer\_survival$O3\_low,  
 seed\_O = fecundity18$O3\_low)  
  
N\_3yr\_low\_mature\_plant\_density\_fixed\_df <- N\_3yr\_low\_mature\_plant\_density\_fixed %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(plant\_counts\_fixed = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), 3)) %>% #3 phases  
 mutate(Crop\_ID = c(rep("C3", 6), rep("S3", 6), rep("O3", 6)))

### CONV Output: seed production, after manipulation by cohort x crop phase x iteration  
N\_3yr\_conv\_seed\_production\_per\_capita <- list() # blank data frame to save loop output   
  
  
for (i in 1:t) {   
 N\_3yr\_conv\_seed\_production\_per\_capita[[i]] =  
 rot\_3year\_conv\_seed\_production\_per\_cap(seed\_C = fecundity18$C3\_conv,  
 seed\_S = fecundity18$S3\_conv,  
 seed\_O = fecundity18$O3\_conv)  
}  
  
# original per capita seed production in fecundity18$C3\_conv[1,3:8], fecundity18$S3\_conv[1,3:8], and fecundity18$O3\_conv  
N\_3yr\_conv\_seed\_production\_per\_capita\_df <- N\_3yr\_conv\_seed\_production\_per\_capita %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(seed\_per\_capita\_threshold = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), t\*3)) %>% #\*3 for 3 phases  
 mutate(cycle\_no = as.character(rep(1:t, each = 18))) %>% # 18 = 6 cohorts x 3 phases  
 mutate(Crop\_ID = rep(c(rep("C3", 6), rep("S3", 6), rep("O3", 6)), t)) %>%  
 mutate(seed\_per\_capita\_original = rep(c(fecundity18$C3\_conv[1,3:8],  
 fecundity18$S3\_conv[1,3:8],  
 fecundity18$O3\_conv[1,3:8]), t)) %>%  
 mutate(seed\_production\_manipulated = ifelse(seed\_per\_capita\_threshold == seed\_per\_capita\_original, "no", "yes"))  
  
### LOW output  
  
N\_3yr\_low\_seed\_production\_per\_capita <- list() # blank data frame to save loop output   
  
  
for (i in 1:t) {   
 N\_3yr\_low\_seed\_production\_per\_capita[[i]] =  
 rot\_3year\_low\_seed\_production\_per\_cap(seed\_C = fecundity18$C3\_low,  
 seed\_S = fecundity18$S3\_low,  
 seed\_O = fecundity18$O3\_low)  
}  
  
  
N\_3yr\_low\_seed\_production\_per\_capita\_df <- N\_3yr\_low\_seed\_production\_per\_capita %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(seed\_per\_capita\_threshold = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), t\*3)) %>% #\*3 for 3 phases  
 mutate(cycle\_no = as.character(rep(1:t, each = 18))) %>% # 18 = 6 cohorts x 3 phases  
 mutate(Crop\_ID = rep(c(rep("C3", 6), rep("S3", 6), rep("O3", 6)), t)) %>%  
 mutate(seed\_per\_capita\_original = rep(c(fecundity18$C3\_low[1,3:8],  
 fecundity18$S3\_low[1,3:8],  
 fecundity18$O3\_low[1,3:8]), t)) %>%  
 mutate(seed\_production\_manipulated = ifelse(seed\_per\_capita\_threshold == seed\_per\_capita\_original, "no", "yes"))

# total stratified seedbank density and lambdas in N\_3yr\_conv\_df  
# manipulated seed production in N\_3yr\_conv\_seed\_production\_per\_capita\_df  
# fixed mature plant density in N\_3yr\_conv\_mature\_plant\_density\_fixed\_df   
  
N\_3yr\_conv\_all\_df <- N\_3yr\_conv\_seed\_production\_per\_capita\_df %>%   
 left\_join(N\_3yr\_conv\_mature\_plant\_density\_fixed\_df, by = c("Crop\_ID", "cohort")) %>%  
 left\_join(N\_3yr\_conv\_lambda\_df, by = "cycle\_no")  
  
  
N\_3yr\_low\_all\_df <- N\_3yr\_low\_seed\_production\_per\_capita\_df %>%   
 left\_join(N\_3yr\_low\_lambda\_df, by = "cycle\_no") %>%  
 left\_join(N\_3yr\_low\_mature\_plant\_density\_fixed\_df, by = c("Crop\_ID", "cohort"))

##### with corn under conventional weed management {-}  
N\_4yr\_conv\_lambda <- list() # blank dataframe to save loop output   
  
N\_4yr\_conv\_lambda[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_4yr\_conv\_lambda[[i]] = rot\_4year\_conv\_lambda(vec = N\_4yr\_conv\_lambda[[i-1]],  
 poh\_C = fall\_tillage$C4\_conv,  
 ow\_C = overwinter$C4\_conv,  
 prt\_C = spring\_tillage$C4\_conv,  
 em\_C = emergence$C4\_conv,  
 sv\_C = summer\_survival$C4\_conv,  
 seed\_C = fecundity18$C4\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S4\_conv,  
 ow\_S = overwinter$S4\_conv,  
 prt\_S = spring\_tillage$S4\_conv,  
 em\_S = emergence$S4\_conv,  
 sv\_S = summer\_survival$S4\_conv,  
 seed\_S = fecundity18$S4\_conv,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O4\_conv,  
 ow\_O = overwinter$O4\_conv,  
 prt\_O = spring\_tillage$O4\_conv,  
 em\_O = emergence$O4\_conv,  
 sv\_O = summer\_survival$O4\_conv,  
 seed\_O = fecundity18$O4\_conv,  
   
 #alfalfa dynamics   
 poh\_A = fall\_tillage$A4\_conv,  
 ow\_A = overwinter$A4\_conv,  
 prt\_A = spring\_tillage$A4\_conv,  
 em\_A = emergence$A4\_conv,  
 sv\_A = summer\_survival$A4\_conv,  
 seed\_A = fecundity18$A4\_conv)  
}  
  
N\_4yr\_conv\_lambda\_df <- N\_4yr\_conv\_lambda %>%   
 unlist(recursive = TRUE) %>%  
 data.frame() %>%  
 dplyr::rename(seedbank\_counts = ".") %>%  
 dplyr::mutate(stratum = rep(c("top", "bottom",  
 "cohort\_1", "cohort\_2",  
 "cohort\_3", "cohort\_4",  
 "cohort\_5", "cohort\_6"),t)) %>%  
 filter(stratum %in% c("top", "bottom")) %>%  
 unnest(cols = everything()) %>%  
 mutate(cycle\_no = as.character(rep(1:t, each = 2))) %>%  
 pivot\_wider(names\_from = stratum, values\_from = seedbank\_counts) %>%  
 mutate(total\_seedbank\_counts = top + bottom) %>%  
 mutate(lambda\_cycle = total\_seedbank\_counts/lag(total\_seedbank\_counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "4-year",  
 Corn\_weed\_management = "conventional")   
  
##### with corn under low herbicide weed management {-}   
N\_4yr\_low\_lambda <- list() # blank dataframe to save loop output   
  
N\_4yr\_low\_lambda[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_4yr\_low\_lambda[[i]] = rot\_4year\_low\_lambda(vec = N\_4yr\_low\_lambda[[i-1]],  
 poh\_C = fall\_tillage$C4\_low,  
 ow\_C = overwinter$C4\_low,  
 prt\_C = spring\_tillage$C4\_low,  
 em\_C = emergence$C4\_low,  
 sv\_C = summer\_survival$C4\_low,  
 seed\_C = fecundity18$C4\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S4\_low,  
 ow\_S = overwinter$S4\_low,  
 prt\_S = spring\_tillage$S4\_low,  
 em\_S = emergence$S4\_low,  
 sv\_S = summer\_survival$S4\_low,  
 seed\_S = fecundity18$S4\_low,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O4\_low,  
 ow\_O = overwinter$O4\_low,  
 prt\_O = spring\_tillage$O4\_low,  
 em\_O = emergence$O4\_low,  
 sv\_O = summer\_survival$O4\_low,  
 seed\_O = fecundity18$O4\_low,  
   
 #alfalfa dynamics   
 poh\_A = fall\_tillage$A4\_low,  
 ow\_A = overwinter$A4\_low,  
 prt\_A = spring\_tillage$A4\_low,  
 em\_A = emergence$A4\_low,  
 sv\_A = summer\_survival$A4\_low,  
 seed\_A = fecundity18$A4\_low)  
}  
  
N\_4yr\_low\_lambda\_df <- N\_4yr\_low\_lambda %>%   
 unlist(recursive = TRUE) %>%  
 data.frame() %>%  
 dplyr::rename(seedbank\_counts = ".") %>%  
 dplyr::mutate(stratum = rep(c("top", "bottom",  
 "cohort\_1", "cohort\_2",  
 "cohort\_3", "cohort\_4",  
 "cohort\_5", "cohort\_6"),t)) %>%  
 filter(stratum %in% c("top", "bottom")) %>%  
 unnest(cols = everything()) %>%  
 mutate(cycle\_no = as.character(rep(1:t, each = 2))) %>%  
 pivot\_wider(names\_from = stratum, values\_from = seedbank\_counts) %>%  
 mutate(total\_seedbank\_counts = top + bottom) %>%  
 mutate(lambda\_cycle = total\_seedbank\_counts/lag(total\_seedbank\_counts),  
 lambda\_annualized = nthroot(lambda\_cycle, 4),  
 Rotation = "4-year",  
 Corn\_weed\_management = "low")

### Output: Mature plant densities until seed production (B\_h = sv\_C or sv\_S)  
### 1 iteration only because no randomization at any matrix  
N\_4yr\_conv\_mature\_plant\_density\_fixed <- rot\_4year\_conv\_plant\_density\_fixed(vec = starting\_point ,  
 poh\_C = fall\_tillage$C4\_conv,  
 ow\_C = overwinter$C4\_conv,  
 prt\_C = spring\_tillage$C4\_conv,  
 em\_C = emergence$C4\_conv,  
 sv\_C = summer\_survival$C4\_conv,  
 seed\_C = fecundity18$C4\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S4\_conv,  
 ow\_S = overwinter$S4\_conv,  
 prt\_S = spring\_tillage$S4\_conv,  
 em\_S = emergence$S4\_conv,  
 sv\_S = summer\_survival$S4\_conv,  
 seed\_S = fecundity18$S4\_conv,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O4\_conv,  
 ow\_O = overwinter$O4\_conv,  
 prt\_O = spring\_tillage$O4\_conv,  
 em\_O = emergence$O4\_conv,  
 sv\_O = summer\_survival$O4\_conv,  
 seed\_O = fecundity18$O4\_conv,  
   
 #alfalfa dynamics   
 poh\_A = fall\_tillage$A4\_conv,  
 ow\_A = overwinter$A4\_conv,  
 prt\_A = spring\_tillage$A4\_conv,  
 em\_A = emergence$A4\_conv,  
 sv\_A = summer\_survival$A4\_conv,  
 seed\_A = fecundity18$A4\_conv)  
  
N\_4yr\_conv\_mature\_plant\_density\_fixed\_df <- N\_4yr\_conv\_mature\_plant\_density\_fixed %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(plant\_counts\_fixed = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), 4)) %>% #4phases  
 mutate(Crop\_ID = c(rep("C4", 6), rep("S4", 6), rep("O4", 6), rep("A4", 6)))  
  
  
### Output: Mature plant densities until seed production (B\_h = sv\_C or sv\_S)  
### 1 iteration only because no randomization at any matrix  
  
  
N\_4yr\_low\_mature\_plant\_density\_fixed <- rot\_4year\_low\_plant\_density\_fixed(vec = starting\_point,  
 poh\_C = fall\_tillage$C4\_low,  
 ow\_C = overwinter$C4\_low,  
 prt\_C = spring\_tillage$C4\_low,  
 em\_C = emergence$C4\_low,  
 sv\_C = summer\_survival$C4\_low,  
 seed\_C = fecundity18$C4\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S4\_low,  
 ow\_S = overwinter$S4\_low,  
 prt\_S = spring\_tillage$S4\_low,  
 em\_S = emergence$S4\_low,  
 sv\_S = summer\_survival$S4\_low,  
 seed\_S = fecundity18$S4\_low,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O4\_low,  
 ow\_O = overwinter$O4\_low,  
 prt\_O = spring\_tillage$O4\_low,  
 em\_O = emergence$O4\_low,  
 sv\_O = summer\_survival$O4\_low,  
 seed\_O = fecundity18$O4\_low,  
   
 #alfalfa dynamics   
 poh\_A = fall\_tillage$A4\_low,  
 ow\_A = overwinter$A4\_low,  
 prt\_A = spring\_tillage$A4\_low,  
 em\_A = emergence$A4\_low,  
 sv\_A = summer\_survival$A4\_low,  
 seed\_A = fecundity18$A4\_low)  
  
N\_4yr\_low\_mature\_plant\_density\_fixed\_df <- N\_4yr\_low\_mature\_plant\_density\_fixed %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(plant\_counts\_fixed = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), 4)) %>% # 4 phases  
 mutate(Crop\_ID = c(rep("C4", 6), rep("S4", 6), rep("O4", 6), rep("A4", 6)))

### CONV Output: seed production, after manipulation by cohort x crop phase x iteration  
  
  
N\_4yr\_conv\_seed\_production\_per\_capita <- list() # blank data frame to save loop output   
  
  
for (i in 1:t) {   
 N\_4yr\_conv\_seed\_production\_per\_capita[[i]] =  
 rot\_4year\_conv\_seed\_production\_per\_cap(seed\_C = fecundity18$C4\_conv,  
 seed\_S = fecundity18$S4\_conv,  
 seed\_O = fecundity18$O4\_conv,  
 seed\_A = fecundity18$A4\_conv)  
}  
  
# original per capita seed production in fecundity18$X4\_conv[1,3:8], X = C, S, O, or A  
N\_4yr\_conv\_seed\_production\_per\_capita\_df <- N\_4yr\_conv\_seed\_production\_per\_capita %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(seed\_per\_capita\_threshold = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), t\*4)) %>% #\*4 for 4 phases  
 mutate(cycle\_no = as.character(rep(1:t, each = 24))) %>% # 24 = 6 cohorts x 4 phases  
 mutate(Crop\_ID = rep(c(rep("C4", 6), rep("S4", 6), rep("O4", 6), rep("A4", 6)), t)) %>%  
 mutate(seed\_per\_capita\_original = rep(c(fecundity18$C4\_conv[1,3:8],  
 fecundity18$S4\_conv[1,3:8],  
 fecundity18$O4\_conv[1,3:8],  
 fecundity18$A4\_conv[1,3:8]), t)) %>%  
 mutate(seed\_production\_manipulated = ifelse(seed\_per\_capita\_threshold == seed\_per\_capita\_original, "no", "yes"))  
  
### LOW output  
  
  
N\_4yr\_low\_seed\_production\_per\_capita <- list() # blank data frame to save loop output   
  
  
for (i in 1:t) {   
 N\_4yr\_low\_seed\_production\_per\_capita[[i]] =  
 rot\_4year\_low\_seed\_production\_per\_cap(seed\_C = fecundity18$C4\_low,  
 seed\_S = fecundity18$S4\_low,  
 seed\_O = fecundity18$O4\_low,  
 seed\_A = fecundity18$A4\_low)  
}  
  
  
N\_4yr\_low\_seed\_production\_per\_capita\_df <- N\_4yr\_low\_seed\_production\_per\_capita %>%   
 unlist(recursive = TRUE) %>% # make a long table  
 data.frame() %>% #corn was listed before soybean in the customized f.  
 dplyr::rename(seed\_per\_capita\_threshold = ".") %>%  
 dplyr::mutate(cohort = rep(c("1", "2", "3", "4", "5", "6"), t\*4)) %>% #\*4 for 4 phases  
 mutate(cycle\_no = as.character(rep(1:t, each = 24))) %>%  
 mutate(Crop\_ID = rep(c(rep("C4", 6), rep("S4", 6), rep("O4", 6), rep("A4", 6)), t)) %>%  
 mutate(seed\_per\_capita\_original = rep(c(fecundity18$C4\_low[1,3:8],  
 fecundity18$S4\_low[1,3:8],  
 fecundity18$O4\_low[1,3:8],  
 fecundity18$A4\_low[1,3:8]), t)) %>%  
 mutate(seed\_production\_manipulated = ifelse(seed\_per\_capita\_threshold == seed\_per\_capita\_original, "no", "yes"))

# total stratified seedbank density and lambdas in N\_4yr\_conv\_lambda\_df  
# manipulated seed production in N\_4yr\_conv\_seed\_production\_per\_capita\_df  
# fixed mature plant density in N\_4yr\_conv\_mature\_plant\_density\_fixed\_df   
  
N\_4yr\_conv\_all\_df <- N\_4yr\_conv\_seed\_production\_per\_capita\_df %>%   
 left\_join(N\_4yr\_conv\_lambda\_df, by = "cycle\_no") %>%  
 left\_join(N\_4yr\_conv\_mature\_plant\_density\_fixed\_df, by = c("Crop\_ID", "cohort"))   
  
  
N\_4yr\_low\_all\_df <- N\_4yr\_low\_seed\_production\_per\_capita\_df %>%   
 left\_join(N\_4yr\_low\_lambda\_df, by = "cycle\_no") %>%  
 left\_join(N\_4yr\_low\_mature\_plant\_density\_fixed\_df, by = c("Crop\_ID", "cohort"))

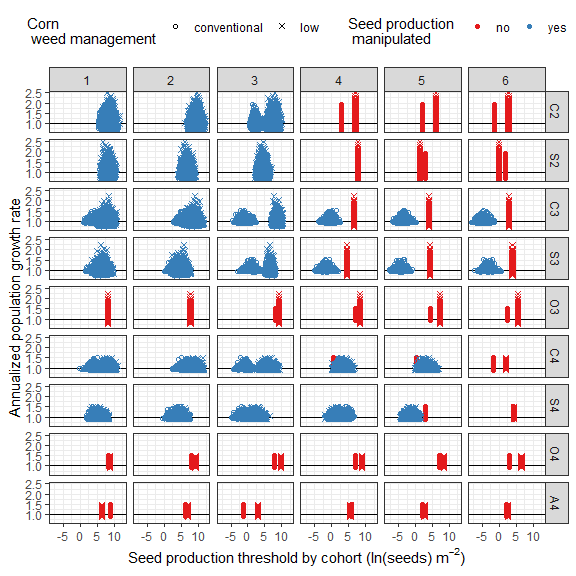


Figure 1: Cohort-based seed production threshold on natural logarithm scale for waterhemp population stabilization over 100 rotational cycles (the 2-year rotation cycled over two years and ended at the soybean phase, the 3-year rotation cycled over three years and ended at the oat phase, and the 4-year rotation cycled over four years and ended at the alfalfa phase). All simulations started with a seed column of 10000 female seeds in the top 0 - 2 cm soil stratum and 0 female seed in the bottom 2 - 20 cm soil stratum. It was expected that no waterhemp cohorts in any crop environments but only the cohorts 1 through 3 in corn and soybean were manipulated to find the seed production thresholds. However, additional control efficacy was needed in some crop phases outside of the expected group to reduce seed production potentials. The dots colored blue are where control measures extended beyond waterhemp cohort 3 would be neccessary. The relationships of aboveground mass and fecundity in Nguyen and Liebman (2022a) were used to estimate per-capita seed production in each cohort. The black horizontal line marks lambda = 1.