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"))

## `summarise()` has grouped output by 'Crop\_ID', 'Corn\_weed\_management'. You can  
## override using the `.groups` argument.

## Warning: `funs()` was deprecated in dplyr 0.8.0.  
## Please use a list of either functions or lambdas:   
##   
## # Simple named list:   
## list(mean = mean, median = median)  
##   
## # Auto named with `tibble::lst()`:   
## tibble::lst(mean, median)  
##   
## # Using lambdas  
## list(~ mean(., trim = .2), ~ median(., na.rm = TRUE))  
## This warning is displayed once every 8 hours.  
## Call `lifecycle::last\_lifecycle\_warnings()` to see where this warning was generated.

Table 1: Added control efficacy (with respect to the original control efficacy reflected by the unmanipulated seed production) averaged over 10000 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 seeds in the bottom 2 - 20 cm soil stratum.

| Crop ID | Corn weed management | cohort 1 | cohort 2 | cohort 2 | cohort 4 | cohort 5 | cohort 6 |
| --- | --- | --- | --- | --- | --- | --- | --- |
| C2 | conventional | 1.00 | 0.99 | 0.99 | 0.00 | 0 | 0 |
| C2 | low | 1.00 | 0.99 | 0.98 | 0.00 | 0 | 0 |
| S2 | conventional | 1.00 | 1.00 | 1.00 | 0.00 | 0 | 0 |
| S2 | low | 1.00 | 1.00 | 1.00 | 0.00 | 0 | 0 |
| C3 | conventional | 1.00 | 1.00 | 0.99 | 0.00 | 0 | 0 |
| C3 | low | 0.93 | 0.96 | 0.59 | 0.00 | 0 | 0 |
| S3 | conventional | 1.00 | 1.00 | 1.00 | 1.00 | 1 | 1 |
| S3 | low | 1.00 | 1.00 | 0.99 | 0.00 | 0 | 0 |
| O3 | conventional | 0.00 | 0.00 | 0.00 | 0.00 | 0 | 0 |
| O3 | low | 0.00 | 0.00 | 0.00 | 0.00 | 0 | 0 |
| C4 | conventional | 1.00 | 1.00 | 1.00 | 0.00 | 0 | 0 |
| C4 | low | 1.00 | 0.99 | 0.97 | 0.00 | 0 | 0 |
| S4 | conventional | 1.00 | 1.00 | 1.00 | 0.77 | 0 | 0 |
| S4 | low | 1.00 | 1.00 | 1.00 | 1.00 | 1 | 0 |
| O4 | conventional | 0.00 | 0.00 | 0.00 | 0.00 | 0 | 0 |
| O4 | low | 0.00 | 0.00 | 0.00 | 0.00 | 0 | 0 |
| A4 | conventional | 0.00 | 0.00 | 0.00 | 0.00 | 0 | 0 |
| A4 | low | 0.00 | 0.00 | 0.00 | 0.00 | 0 | 0 |

seed\_allowance\_sim\_df %>%   
 group\_by(Crop\_ID, Corn\_weed\_management, cohort) %>%  
 summarise(mean\_seed\_per\_capita\_threshold = mean(seed\_per\_capita\_threshold)) %>%  
 pivot\_wider(names\_from = cohort, values\_from = mean\_seed\_per\_capita\_threshold) %>%  
 mutate(phase\_order = ifelse(str\_detect(Crop\_ID, "C"), 1,  
 ifelse(str\_detect(Crop\_ID, "S"), 2,  
 ifelse(str\_detect(Crop\_ID, "O"), 3, 4)))) %>%  
 mutate(Rot = substr(Crop\_ID,2,2))%>%  
 arrange(Rot, phase\_order, Corn\_weed\_management)

## `summarise()` has grouped output by 'Crop\_ID', 'Corn\_weed\_management'. You can  
## override using the `.groups` argument.

## # A tibble: 18 × 10  
## # Groups: Crop\_ID, Corn\_weed\_management [18]  
## Crop\_ID Corn\_weed\_…¹ `1` `2` `3` `4` `5` `6` phase…² Rot   
## <chr> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>  
## 1 C2 conventional 111. 1.10e2 8.40e1 6.30e3 2.19e+3 2.72e2 1 2   
## 2 C2 low 21.2 2.10e1 2.12e1 5.06e2 2.24e+2 3.48e1 1 2   
## 3 S2 conventional 111. 1.11e2 8.49e1 1.90e4 6.50e+3 1.76e3 2 2   
## 4 S2 low 21.5 2.14e1 2.13e1 2.17e4 5.37e+3 1.40e3 2 2   
## 5 C3 conventional 21.6 2.16e1 2.13e1 1.66e2 2.71e+2 7.52e1 1 3   
## 6 C3 low 21.2 2.14e1 8.41e1 1.44e2 3.55e+1 5.12e1 1 3   
## 7 S3 conventional 20.8 2.14e1 2.13e1 2.13e1 2.13e+1 2.10e1 2 3   
## 8 S3 low 21.7 2.10e1 1.13e3 3.14e4 2.80e+4 5.62e3 2 3   
## 9 O3 conventional 3354. 8.49e2 4.25e2 2.18e2 1.23e+2 7.96e1 3 3   
## 10 O3 low 658 2.37e2 3.08e2 2.06e2 1.61e+2 1.05e2 3 3   
## 11 C4 conventional 20.8 2.12e1 2.15e1 7.22e2 5.01e+2 2.73e2 1 4   
## 12 C4 low 21.5 2.12e1 2.09e1 1.65e2 5.22e+1 1.88e1 1 4   
## 13 S4 conventional 21.3 2.13e1 2.12e1 1.70e3 5.40e+3 1.89e4 2 4   
## 14 S4 low 20.9 2.15e1 2.11e1 2.13e1 2.14e+1 4.67e3 2 4   
## 15 O4 conventional 3697. 1.02e3 2.67e2 2.27e2 3.63e+2 6.52e1 3 4   
## 16 O4 low 3362. 2.11e3 8.91e2 7.22e2 4.32e+2 1.55e2 3 4   
## 17 A4 conventional 460. 1.47e1 1 e0 1.32e1 1.25e+0 4.25e0 4 4   
## 18 A4 low 10.7 8.25e0 9.25e0 2.5 e0 5 e-1 1.25e0 4 4   
## # … with abbreviated variable names ¹​Corn\_weed\_management, ²​phase\_order

## `summarise()` has grouped output by 'Crop\_ID', 'Corn\_weed\_management'. You can  
## override using the `.groups` argument.

Table 2: Seed production thresholds averaged over 10000 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 seeds in the bottom 2 - 20 cm soil stratum.

| Crop ID | Corn weed management | cohort 1 | cohort 2 | cohort 3 | cohort 4 | cohort 5 | cohort 6 |
| --- | --- | --- | --- | --- | --- | --- | --- |
| C2 | conventional | 454.86 | 2,861.28 | 3.27 | 20.45 | 7.12 | 0.22 |
| C2 | low | 2,874.41 | 8,190.58 | 777.33 | 1,116.92 | 394.41 | 14.59 |
| S2 | conventional | 1,232.38 | 313.85 | 21.09 | 1,771.20 | 12.75 | 4.52 |
| S2 | low | 891.19 | 209.31 | 13.92 | 1,369.89 | 1.86 | 0.48 |
| C3 | conventional | 106.98 | 544.28 | 0.59 | 6.49 | 0.63 | 0.04 |
| C3 | low | 3,102.25 | 7,784.20 | 2,896.20 | 646.98 | 52.25 | 18.85 |
| S3 | conventional | 221.86 | 45.48 | 3.47 | 0.30 | 0.02 | 0.05 |
| S3 | low | 418.93 | 79.75 | 308.23 | 37.04 | 29.66 | 19.33 |
| O3 | conventional | 4,629.98 | 2,147.01 | 3,435.82 | 1,122.19 | 74.96 | 10.20 |
| O3 | low | 2,469.09 | 1,553.85 | 6,670.59 | 2,972.25 | 771.23 | 170.52 |
| C4 | conventional | 100.07 | 545.46 | 0.61 | 1.71 | 1.18 | 0.16 |
| C4 | low | 3,224.09 | 8,401.50 | 612.16 | 313.26 | 82.43 | 7.15 |
| S4 | conventional | 194.66 | 39.25 | 0.30 | 162.58 | 19.86 | 69.59 |
| S4 | low | 346.77 | 112.40 | 15.90 | 7.76 | 0.30 | 83.03 |
| O4 | conventional | 3,752.11 | 2,928.32 | 2,590.26 | 1,262.50 | 1,252.16 | 21.70 |
| O4 | low | 16,086.05 | 24,621.11 | 36,657.54 | 18,593.19 | 9,482.49 | 1,602.32 |
| A4 | conventional | 7,271.06 | 520.98 | 0.30 | 356.69 | 8.13 | 7.60 |
| A4 | low | 1,499.39 | 2,587.35 | 43.00 | 595.41 | 33.52 | 32.12 |

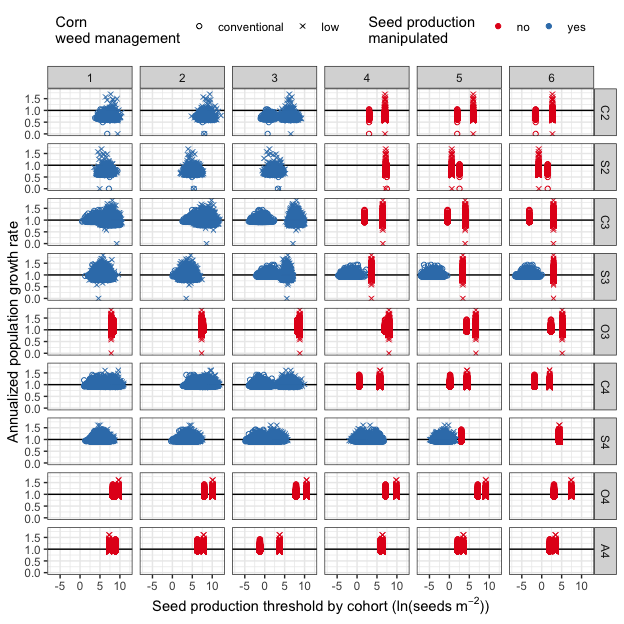


Figure 1: Cohort-based seed production threshold on natural logarithm scale for waterhemp population stabilization over 10000 rotational cycles (the 2-year rotation cycled over two years and ended at the soybean phase, the 3-year rotation cycled over three years and ended at the oat phase, and the 4-year 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 meet annualized lambda = 1. The dots colored blue are where control measures extended beyond waterhemp cohort 3 would be necessary. The relationships of aboveground mass and fecundity in Nguyen and Liebman (2022a) were used to estimate per-capita seed production threshold in each cohort. The black horizontal lines mark annualized lambda = 1. The right-hand-side panel labels indicate the crop identities, which are the combinations of the first letter in crop species names and the rotation to which the crops belonged (C2, corn in the 2-year rotation; C3, corn in the 3-year rotation; C4, corn in the 4-year rotation; S2, soybean in the 2-year rotation; S3, soybean in the 3-year rotation; S4, soybean in the 4-year rotation; O3, oat in the 3-year rotation; O4, oat in the 4-year rotation; and A4, alfalfa in the 4-year rotation).