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.

Goal: manipulate mature plant density for cohorts 1 through 3 via survival rate manipulation

# event sequence: seed dropped - field cultivator - emerge - survive - new seed - chisel - overwinter   
  
# create a function   
# vec: starting seed column  
# poh: post-harvest tillage  
# ow: over winter seed survival  
# prt: pre-planting-tillage  
# em: emergence  
# sv: seed survival rate and seedling to maturity success rate  
# seed: fecundity  
  
rot\_2year\_conv <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,  
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S){  
   
  
 sv\_C[3,3] <- .006 #99.4 % efficacy wrt plant density  
 sv\_C[4,4] <- .006  
 sv\_C[5,5] <- .006  
 # sv\_C[6,6] <- .01  
# sv\_C[7,7] <- .01  
  
  
  
 sv\_S[3,3] <- .006  
 sv\_S[4,4] <- .006  
 sv\_S[5,5] <- .006  
# sv\_S[6,6] <- .01  
# sv\_S[7,7] <- .01  
  
  
 # corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
  
   
# soybean phase dynamics  
  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn   
  
 after\_soy  
}  
  
rot\_2year\_low <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,  
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S){  
   
  
  
 sv\_C[3,3] <- .001 #99.9 % efficacy  
 sv\_C[4,4] <- .002  
 sv\_C[5,5] <- .003 # 99.8% efficacy  
 # sv\_C[6,6] <- .01  
# sv\_C[7,7] <- .01  
  
  
  
 sv\_S[3,3] <- .001  
 sv\_S[4,4] <- .002  
 sv\_S[5,5] <- .003  
# sv\_S[6,6] <- .01  
# sv\_S[7,7] <- .01  
  
 # corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
# soybean phase dynamics  
  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn   
  
 after\_soy  
}

##### with corn under conventional weed management {-}  
t <- 100  
N\_2yr\_conv <- list() # blank data frame to save loop output   
N\_2yr\_conv[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_2yr\_conv[[i]] = rot\_2year\_conv(vec = N\_2yr\_conv[[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\_df <- N\_2yr\_conv %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "2-year",  
 Corn\_weed\_management = "conventional") %>%  
 na.omit()

##### with corn under low herbicide weed management {-}  
N\_2yr\_low <- list() # blank dataframe to save loop output   
  
N\_2yr\_low[[1]] <- starting\_point   
for (i in 2:t) {   
 N\_2yr\_low[[i]] = rot\_2year\_low(vec = N\_2yr\_low[[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\_df <- N\_2yr\_low %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "2-year",  
 Corn\_weed\_management = "low") %>%  
 na.omit()

rot\_3year\_conv <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,   
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S ,  
 poh\_O, ow\_O, prt\_O, em\_O, sv\_O, seed\_O){  
   
  
  
 sv\_C[3,3] <- .0001  
 sv\_C[4,4] <- .0001  
 sv\_C[5,5] <- .0001  
 sv\_C[6,6] <- .0001  
 sv\_C[7,7] <- .0001  
 sv\_C[8,8] <- .0001  
  
  
  
 sv\_S[3,3] <- .0001  
 sv\_S[4,4] <- .0001  
 sv\_S[5,5] <- .0001  
 sv\_S[6,6] <- .0001  
 sv\_S[7,7] <- .0001  
 sv\_S[8,8] <- .0001  
   
## Extra control efficacy in oat is now needed   
 sv\_O[5,5] <- .01  
 sv\_O[6,6] <- .01  
 sv\_O[7,7] <- .01  
 sv\_O[8,8] <- .01  
  
# corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
 # soybean phase dynamics  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn  
# oat phase dynamics  
 after\_oat <- ow\_O %\*% poh\_O %\*% seed\_O %\*% sv\_O %\*% em\_O %\*% prt\_O %\*% after\_soy   
   
 after\_oat  
}  
  
### low herbicide weed management  
## Manipulation note: if cohorts 1 through 3 were reduced to rlnorm(1, 2.65, 0.89), alphas are around 0.5 --> super "safe", but hard  
## cohorts 1 through 3 at rlnorm(1, 5.2, 0.51): more realistic  
rot\_3year\_low <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,   
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S ,  
 poh\_O, ow\_O, prt\_O, em\_O, sv\_O, seed\_O){  
   
  
  
 sv\_C[3,3] <- .0001  
 sv\_C[4,4] <- .003  
 sv\_C[5,5] <- .003  
# sv\_C[6,6] <- .0001  
# sv\_C[7,7] <- .0001  
# sv\_C[8,8] <- .0001  
  
  
  
 sv\_S[3,3] <- .0001  
 sv\_S[4,4] <- .003  
 sv\_S[5,5] <- .003  
 # sv\_S[6,6] <- .0001  
 # sv\_S[7,7] <- .0001  
# sv\_S[8,8] <- .001  
  
   
# corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
 # soybean phase dynamics  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn  
# oat phase dynamics  
 after\_oat <- ow\_O %\*% poh\_O %\*% seed\_O %\*% sv\_O %\*% em\_O %\*% prt\_O %\*% after\_soy   
   
 after\_oat  
}

##### with corn under conventional weed management {-}  
N\_3yr\_conv <- list() # blank dataframe to save loop output   
  
N\_3yr\_conv[[1]] <- starting\_point   
  
  
for (i in 2:t) {   
 N\_3yr\_conv[[i]] = rot\_3year\_conv(vec = N\_3yr\_conv[[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\_df <- N\_3yr\_conv %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = nthroot(lambda\_cycle,3),  
 Rotation = "3-year",  
 Corn\_weed\_management = "conventional") %>%  
 na.omit()

##### with corn under low herbicide weed management {-}   
N\_3yr\_low <- list() # blank dataframe to save loop output   
  
N\_3yr\_low[[1]] <- starting\_point   
  
  
for (i in 2:t) {   
 N\_3yr\_low[[i]] = rot\_3year\_low(vec = N\_3yr\_low[[i-1]],  
 poh\_C = fall\_tillage$C3\_conv,  
 ow\_C = overwinter$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\_df <- N\_3yr\_low %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = nthroot(lambda\_cycle,3),  
 Rotation = "3-year",  
 Corn\_weed\_management = "low") %>%  
 na.omit()

### conventional weed management  
rot\_4year\_conv <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,   
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S ,  
 poh\_O, ow\_O, prt\_O, em\_O, sv\_O, seed\_O,  
 poh\_A, ow\_A, prt\_A, em\_A, sv\_A, seed\_A){  
  
  
 sv\_C[3,3] <- .0001  
 sv\_C[4,4] <- .001  
 sv\_C[5,5] <- .001  
 sv\_C[6,6] <- .005  
 sv\_C[7,7] <- .005  
 sv\_C[8,8] <- .005  
  
  
  
 sv\_S[3,3] <- .0001  
 sv\_S[4,4] <- .001  
 sv\_S[5,5] <- .001  
 sv\_S[6,6] <- .005  
 sv\_S[7,7] <- .005  
 sv\_S[8,8] <- .005  
  
# corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
 # soybean phase dynamics  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn  
# oat phase dynamics  
 after\_oat <- ow\_O %\*% poh\_O %\*% seed\_O %\*% sv\_O %\*% em\_O %\*% prt\_O %\*% after\_soy   
# alfalfa phase dynamics  
after\_alfalfa <- ow\_A %\*% poh\_A %\*% seed\_A %\*% sv\_A %\*% em\_A %\*% prt\_A %\*% after\_oat   
 after\_alfalfa  
}  
  
### low herbicide weed management  
rot\_4year\_low <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,   
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S ,  
 poh\_O, ow\_O, prt\_O, em\_O, sv\_O, seed\_O,  
 poh\_A, ow\_A, prt\_A, em\_A, sv\_A, seed\_A){  
   
  
  
 sv\_C[3,3] <- .0001  
 sv\_C[4,4] <- .001  
 sv\_C[5,5] <- .009  
 sv\_C[6,6] <- .05  
  
  
  
  
 sv\_S[3,3] <- .0001  
 sv\_S[4,4] <- .001  
 sv\_S[5,5] <- .009  
 sv\_S[6,6] <- .05  
  
  
# corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
 # soybean phase dynamics  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn  
# oat phase dynamics  
 after\_oat <- ow\_O %\*% poh\_O %\*% seed\_O %\*% sv\_O %\*% em\_O %\*% prt\_O %\*% after\_soy   
# alfalfa phase dynamics  
after\_alfalfa <- ow\_A %\*% poh\_A %\*% seed\_A %\*% sv\_A %\*% em\_A %\*% prt\_A %\*% after\_oat   
   
 after\_alfalfa  
}

##### with corn under conventional weed management {-}  
N\_4yr\_conv <- list() # blank dataframe to save loop output   
  
N\_4yr\_conv[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_4yr\_conv[[i]] = rot\_4year\_conv(vec = N\_4yr\_conv[[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\_df <- N\_4yr\_conv %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_4", "cohort\_3", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = nthroot(lambda\_cycle,4),  
 Rotation = "4-year",  
 Corn\_weed\_management = "conventional") %>%  
 na.omit()

##### with corn under low herbicide weed management {-}   
N\_4yr\_low <- list() # blank dataframe to save loop output   
  
N\_4yr\_low[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_4yr\_low[[i]] = rot\_4year\_low(vec = N\_4yr\_low[[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\_df <- N\_4yr\_low %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = nthroot(lambda\_cycle,4),  
 Rotation = "4-year",  
 Corn\_weed\_management = "low") %>%  
 na.omit()

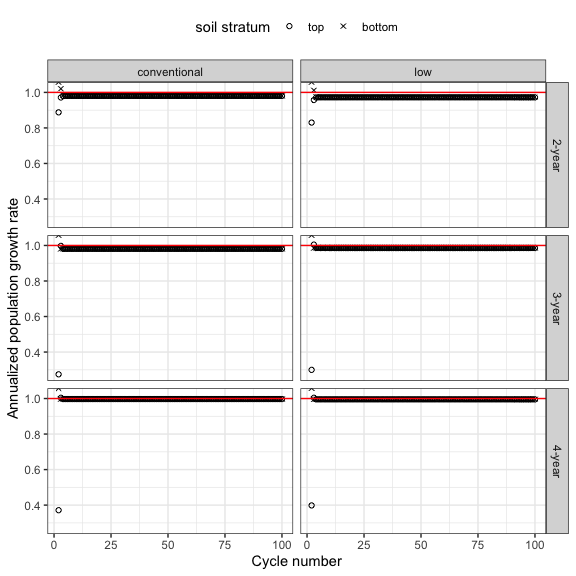


Figure 1: Population growth rates over 100 rotational cycles. All simulations started with a seed column of 10000 female seeds in the top 0 - 2 cm soil stratum and 0 female seed in the bottom 2 - 20 cm soil stratum. The simulation applied weed management on cohorts 1 through 3 in corn and soybean only. It was expected that only the survival rate of cohorts 1 through 3 fecundity in corn and soybean were manipulated to find the mature plant thresholds, and that the survival rates of cohorts 4 and beyond in corn and soybean were kept as they were measured from 2018. However, additional control was neccessary in some crop phases. The crop phases marked with an asterisk (\*) are where control measures extended beyond waterhemp cohort 3 would be neccessary. The crop phases marked with an inverted comma (’) are where no additional control was applied. Each panel was annotated with the average mature plant density (plants/m2) for the first three plant cohorts and the whole crop phase. The red horizontal line marks lambda = 1.

## Warning: Removed 4 rows containing missing values (geom\_point).

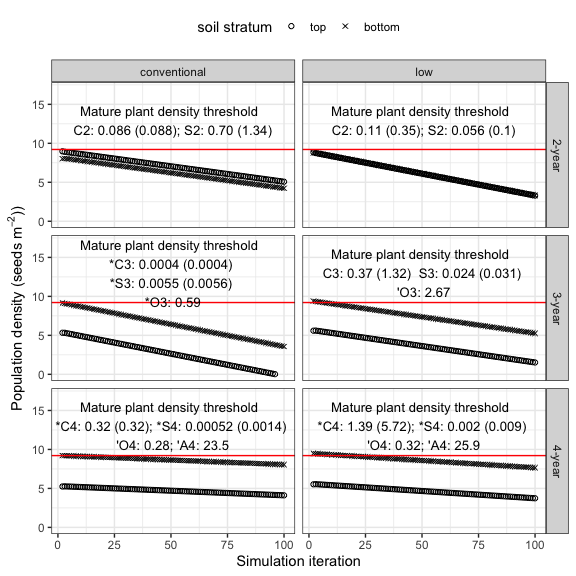


Figure 2: Population size at the end of a rotation cycle over 100 rotational cycles (the 2-year rotation ended at the soybean phase, the 3-year rotation ended at the oat phase, and the 4-year rotation ended at the alfalfa phase). All simulations started with a seed column of 10000 female seeds in the top 0 - 2 cm soil stratum and 0 female seed in the bottom 2 - 20 cm soil stratum. The simulation applied improved weed control efficacy on cohorts 1 through 3 in corn and soybean only. The relationships of aboveground mass and fecundity in Nguyen and Liebman (2022a) were used to estimate cohort-based fecundity. It was expected that no waterhemp cohorts in any crop environments but only the cohorts 1 through 3 in corn and soybean had their survival rates manipulated to find the mature plant density thresholds. However, additional control efficacy was needed in some crop phases outside of the expected groups to reduced the mature plant densities. The crop phases marked with an asterik (\*) are where control measures extended beyond the expected cohorts within the expected crop environments would be neccessary. Each panel was annotated with the average fecundity thresholds for the first three waterhemp cohorts in corn and soybean followed by the whole crop phase. The crop phases marked with an inverted comma (’) are where no additional control was applied. The red horizontal line marks lambda = 1.

## Warning: Removed 4 rows containing missing values (geom\_point).

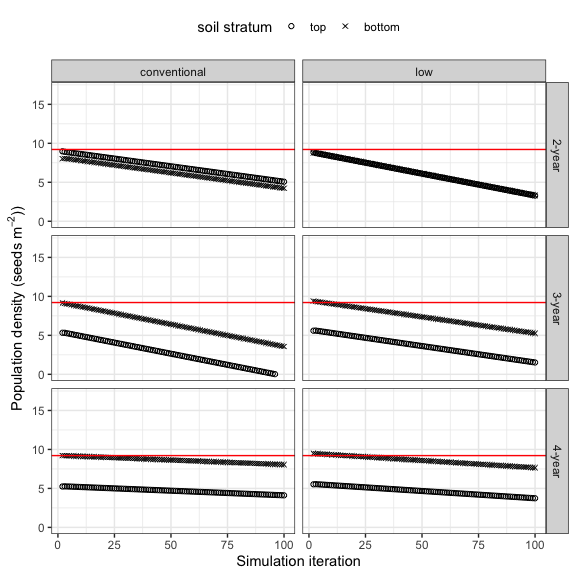


Figure 3: Population size at the end of a rotation cycle over 100 rotational cycles (the 2-year rotation ended at the soybean phase, the 3-year rotation ended at the oat phase, and the 4-year rotation ended at the alfalfa phase). All simulations started with a seed column of 10000 female seeds in the top 0 - 2 cm soil stratum and 0 female seed in the bottom 2 - 20 cm soil stratum. The simulation applied improved weed control efficacy on cohorts 1 through 3 in corn and soybean only. The relationships of aboveground mass and fecundity in Nguyen and Liebman (2022a) were used to estimate cohort-based fecundity. It was expected that no waterhemp cohorts in any crop environments but only the cohorts 1 through 3 in corn and soybean had their survival rates manipulated to find the mature plant density thresholds. However, additional control efficacy was needed in some crop phases outside of the expected groups to reduced the mature plant densities. The crop phases marked with an asterik (\*) are where control measures extended beyond the expected cohorts within the expected crop environments would be neccessary. Each panel was annotated with the average fecundity thresholds for the first three waterhemp cohorts in corn and soybean followed by the whole crop phase. The crop phases marked with an inverted comma (’) are where no additional control was applied. The red horizontal line marks lambda = 1.