Supplementary online material

Article: Defaunation effects on plant recruitment depend on size matching and size trade-offs in seed-dispersal networks

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Appendix S1. Structure of simulated seed-dispersal networks

**Figure S1.** Simulated seed dispersal networks displaying the distribution of interactions for each of the six scenarios considered in this study (i.e. structured or not by size matching, crossed with the consideration of a negative size-quantity relationship in plants only, birds only, both or none). Frugivore species appear on the top row of each network, whereas plant species are on the bottom row. All species are ordered by decreasing size (see blue and green arrows for frugivores and plants, respectively).
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Appendix S1. Results from sensitivity analysis.

Versions of Fig. 2-4 after selecting different values for the undercompensation parameter ($\beta$) (Fig. S1-S6), specialization parameter ($s$) (Fig. S7-S12), and a different niche shape (Fig. S13-S15).

Figure S1. Defaunation effects on seedling abundance under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=10$ and no undercompensation parameter $\beta$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S2. Defaunation effects on seedling diversity under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=10$ and no undercompensation parameter $\beta$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S3. Defaunation effects on **mean seed size** of recruited seedlings under different scenarios of **size matching** and **size trade-offs** using a **skewed** niche shape, specialization parameter $s=10$ and **no undercompensation** parameter $\beta$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line; grey areas representing the confidence intervals, which extend to outside the plotting area). Model scenarios were defined as explained in Fig 2. of the main text.
Figure S4. Defaunation effects on seedling abundance under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=10$ and undercompensation parameter $\beta$ set to 50% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S5. Defaunation effects on seedling diversity under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=10$ and undercompensation parameter $\beta$ set to 50% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
**Figure S6.** Defaunation effects on mean seed size of recruited seedlings under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=10$ and undercompensation parameter $\beta$ set to 50% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line; grey areas representing the confidence intervals, which extend to outside the plotting area). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S7. Defaunation effects on seedling abundance under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=2$ and undercompensation parameter $\beta$ set to $10\%$ of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
**Figure S8.** Defaunation effects on seedling diversity under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=2$ and undercompensation parameter $\beta$ set to 10% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S9. Defaunation effects on mean seed size of recruited seedlings under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=2$ and undercompensation parameter $\beta$ set to 10% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line; grey areas representing the confidence intervals, which extend to outside the plotting area). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S10. Defaunation effects on seedling abundance under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=50$ and undercompensation parameter $\beta$ set to 10% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S11. Defaunation effects on seedling diversity under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=50$ and undercompensation parameter $\beta$ set to 10% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S12. Defaunation effects on mean seed size of recruited seedlings under different scenarios of size matching and size trade-offs using a skewed niche shape, specialization parameter $s=50$ and undercompensation parameter $\beta$ set to 10% of the maximum value $1/x$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line; grey areas representing the confidence intervals, which extend to outside the plotting area). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S13. Defaunation effects on seedling abundance under different scenarios of size matching and size trade-offs using a symmetric (Gaussian) niche shape, specialization parameter $s=10$ and undercompensation parameter $\beta$ set to 10% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
Figure S14. Defaunation effects on seedling diversity under different scenarios of size matching and size trade-offs using a symmetric (Gaussian) niche shape, specialization parameter $s=10$ and undercompensation parameter $\beta$ set to 10% of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line, with grey areas representing the confidence intervals). Model scenarios were defined as explained in Fig. 2 of the main text.
Fig S15. Defaunation effects on mean seed size of recruited seedlings under different scenarios of size matching and size trade-offs using a symmetric (Gaussian) niche shape, specialization parameter $s=10$ and undercompensation parameter $\beta$ set to $10\%$ of the maximum value $1/x_j$. We compared consequences of size-structured bird extinction (red line; defaunation) and random extinction (black dashed line; grey areas representing the confidence intervals, which extend to outside the plotting area). Model scenarios were defined as explained in Fig. 2 of the main text.
### Supplementary online material

**Article**: Defaunation effects on plant recruitment depend on size matching and size trade-offs in seed-dispersal networks

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**Appendix S2. Source Code for simulations in the R language for statistical computing**

Explanatory comments (#)

## 1) R version 3.3.1 (2016-06-21)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 7 x64 (build 7601) Service Pack 1

## 2) Load Packages
## require(vegan)# to calculate Shannon diversity index
## require(Hmisc)# to calculate the community weighted mean of seed size

-----------------------------------------------
Functions to create our simulated seed dispersal networks -----------------------------------------------
Modified from Fründ et. al. (2016) -----------------------------------------------

#--- web generator (quantitative (weighted) niche model) ---
makeweb <- function(specpar = 1, birdtraits, planttraits, nicheshape="normal"){
  # function to generate web with defined "specialization", based on a trait matching concept
  # the output web has interaction probabilities for all species (assuming equal abundances)
  # specpar is the specialization parameter (always increases with specialization)
  # nicheshape: the function calculating pref.values from trait differences; the default 'normal' uses gaussian/bell-shaped niches
  fun_pref <- function(traitdif){
    if (nicheshape == "normal") {
      prefs <- dnorm(traitdif,mean=0,sd=1/specpar)
    } else if (nicheshape == "skewed") {
      # a simple skewed function, lognormal shifted to mode=0 (scaling by stretching x)
      prefs <- dlnorm(traitdif * specpar + exp(-1))
    }
    prefs
  }
  Nplant <- length(planttraits)
  Nbird <- length(birdtraits)
  web <- fun_pref(outer(planttraits,birdtraits,"-")) # adjusted this so that traitdif is defined as birdtrait-planttrait
  web <- web / matrix(colSums(web),nrow=Nplant,ncol=Nbird,byrow=TRUE) # standardize link weights to probability;
  web
}

#--- create skewed traits --- (same as get_skewabuns function in Fründ et. al. (2016))
get_skewtr <- function(myN, tr_meanlog=2, tr_sdlog=1.5){
  # generate traits that match a log-normal distribution (but without introducing noise):
  # divide quantile distribution in N+1 regular intervals, and take the N non-0or1 intvl borders as trait values
  # it is rescaled in the second step (line70) to really have the intended mean trait (not log-mean)
  tr <- qlnorm(seq(0, 1, length.out=myN+2), tr_meanlog, tr_sdlog) [-c(1,myN+2)] # takes equidistant points of the quantile function, removing the extremes that would be 0 and Inf
  tr <- sort(tr, decr=TRUE)
}

#--- make true web from preferences and interaction frequencies ---
make_trueweb <- function(web_p, plantfreq, birdfreq){
  # first step: prepare a web that's used to multiply with the web_p:
  web_relfreq <- {plantfreq %*% t(birdfreq)} / mean(plantfreq)
  # second step: multiply preference web with interaction frequencies
  web_p * web_relfreq
#------------------ STEP 1: GENERATE SEED DISPERSAL NETWORKS ------------------

---(I) Generate the simulated sps pool ---

NBird <- 60
Nplant <- 50

---(II) Draw trait (SIZE) values using lognormal distributions but with parameters matching the empirical distributions of fruit volume and bird body mass presented in Dehling et al. (2014) ----

# For the sake of simplicity, we will make available just the final fitted traits (lines 100-115). However, from lines 80-95, we show how to reproduce it with other empirical trait data.

# Get the mean and sdlog for any empirical traits (parameters to change afterwards within the functions). “volume” and “Bodymass” would be the empirical variables

# FRUIT SIZE
# vol_meanlog <- mean(log(volume^(1/3)))
# vol_sdllog <- sd(log(volume^(1/3)))
# BIRD BODY MASS
# mass_meanlog <- mean(log(Bodymass^(1/3))) # taking the cubic root of mass translates it into a linear (instead of volume)
# mass_sdllog <- sd(log(Bodymass^(1/3)))

# Change the values of the parameters mean and sdLog within the function by those empirical ones

## vector x in the main text
# fit_pltr <- get_skewtr(Nplant, vol_meanlog, vol_sdllog) ## vector x in the main text
# fit_birdtr <- get_skewtr(Nbird, mass_meanlog, mass_sdllog) 

# These are the trait values we obtained (matching the empirical distributions of fruit volume and bird body mass presented in Dehling et al. 2014)


--- (III) Once having the trait values... Estimation of the interaction frequency for birds and plants if there is a negative relationship (“YES” scenarios; following f=1/y+b for birds, and following f=1/x in the case of plants) or if there is no relationship between size-int freq (“NO” scenarios). All the outputs were scale dividing by the mean ---

### "YES"

# PLANTS. We assume a negative relationship: y=1/x

YES_pl_freq <- (1/fit_pltr)/mean((1/fit_pltr)) # vector fi in the main text

# BIRDS: We assume a negative relationship: y=(1/x)+b (where b is the undercompensation parameter set to the 10% of the maximum value of 1/x

v10 <- max(1/fit_birdtr)/10

YES_bird_freq <- (1/fit_birdtr)+v10)/mean((1/fit_birdtr)+v10) # vector gj in the main text

### "NO". Fixed to the value representing the mean freq of the YES scenarios but as we scale dividing by the mean, the mean freq value is 1

# PLANTS

mfreqY_pl <- 1

NO_pl_freq <- rep(mfreqY_pl, 50)

# BIRDS

mfreqY_bird <- 1

NO_bird_freq <- rep(mfreqY_bird, 60)

#------------------ END: GENERATE SEED DISPERSAL NETWORKS ------------------
#IV Generate the final simulated seed dispersal networks

##TWO INTERACTION RULES

1. **NO SIZE MATCHING** (neutral case)

   ```r
   web_neutral <- matrix(1, nPlant, nBird)
   ```

2. **SIZE MATCHING**

   ```r
   web_p <- makeweb(web_p = web_neutral, birdfreq=NO_bird_freq, plantfreq=NO_pl_freq)
   ```

###NO SIZE MATCHING SCENARIOS

- None

###SIZE MATCHING SCENARIOS

- Birds only

## Estimation of seed fate

From seed dispersal networks to seedling recruitment networks

###STEP 2: GENERATE 3 DIMENSIONS OF SEEDLING RECRUITMENT

---

###V Generate the final simulated seed dispersal networks

####Observe the effect of size-matching

- Calculate final seed dispersal networks incorporating interaction frequencies according to different scenarios: no size matching vs. size matching, crossed with “YES” and “NO” scenarios for the size-interaction frequency relationship in plants only, birds only, none or both. We further fixed the exact bird frequencies and let plant frequencies vary in each scenario.

```
# NO SIZE MATCHING SCENARIOS
# NO SIZE MATCHING
# in BIRDS ONLY
sc1 <- make_trueweb(web_p = web_neutral, birdfreq=NO_bird_freq, plantfreq=NO_pl_freq)
sc1b <- sc1/ matrix(colSums(sc1)/NO_bird_freq,nrow=Nplant, ncol=Nbird,byrow=TRUE)

# in PLANTS ONLY
sc2 <- make_trueweb(web_p = web_neutral, birdfreq=YES_bird_freq, plantfreq=NO_pl_freq)

# in BOTH
sc3 <- make_trueweb(web_p = web_neutral, birdfreq=NO_bird_freq, plantfreq=YES_pl_freq)
sc3b <- sc3/ matrix(colSums(sc3)/NO_bird_freq,nrow=Nplant, ncol=Nbird,byrow=TRUE)

# SIZE MATCHING SCENARIOS
# NONE
sc4 <- make_trueweb(web_p = web_neutral, birdfreq=YES_bird_freq, plantfreq=YES_pl_freq)
sc4b <- sc4/ matrix(colSums(sc4)/YES_bird_freq,nrow=Nplant, ncol=Nbird,byrow=TRUE)

# BIRDS
# in BIRDS ONLY
sc5 <- make_trueweb(web_p = web_neutral, birdfreq=NO_bird_freq, plantfreq=NO_pl_freq)
sc5b <- sc5/ matrix(colSums(sc5)/NO_bird_freq,nrow=Nplant, ncol=Nbird,byrow=TRUE)

# in PLANTS ONLY
sc6 <- make_trueweb(web_p = web_neutral, birdfreq=YES_bird_freq, plantfreq=NO_pl_freq)
sc6b <- sc6/ matrix(colSums(sc6)/YES_bird_freq,nrow=Nplant, ncol=Nbird,byrow=TRUE)

# in BOTH
sc7 <- make_trueweb(web_p = web_neutral, birdfreq=NO_bird_freq, plantfreq=YES_pl_freq)
sc7b <- sc7/ matrix(colSums(sc7)/NO_bird_freq,nrow=Nplant, ncol=Nbird,byrow=TRUE)

# BIRDS
# in BOTH
sc8 <- make_trueweb(web_p = web_neutral, birdfreq=YES_bird_freq, plantfreq=YES_pl_freq)
sc8b <- sc8/ matrix(colSums(sc8)/YES_bird_freq,nrow=Nplant, ncol=Nbird,byrow=TRUE)
```

---

####Observe the effect of size-matching

Premature extinction or immigration from birds and plants if there is a positive relationship which exactly cancels out the negative interaction frequency-size relationships from step 1 (**YES** scenarios: following $y = ax/(1+bx)$ for birds, and following $y=x$ in the case of plants) or if there is no relationship between seed-size fate (**NO** scenarios). These outputs were also scaled by the respective mean.

####Observe the effect of size-matching

```
### "YES"
# PLANTS: we assume $y=x$
YES_fate_pl <- fit_pltr ## vector qi in the main text

# BIRDS: we assume $y=ax/(1+bx)$
YES_fate_bird <- fit_birdtr/(1+v10*fit_birdtr) ## vector rj in the main text

### "NO"
# PLANTS
NO_fate_pl <- rep(mean(YES_fate_pl),50)

# BIRDS
NO_fate_bird <- rep(mean(YES_fate_bird),60)

# GENERATE the final 6 FULL SCENARIOS
# Size-quantity (int freq) and size-quality (seed fate) relationships together constituted a potential quantity-quality trade-off for both plants and birds. For simplicity, we finally excluded “plants only” and “birds only” trade-off scenarios for the no size matching case, as these did not differ from the other neutral scenarios (i.e., those potentially calculated with sc2 and sc3 of step1).

####Observe the effect of size-matching

```
# NO SIZE MATCHING SCENARIOS
recr_web_1 <- sc1b * outer(NO_fate_pl,NO_fate_bird)
recr_web_2 <- sc4b * outer(NO_fate_pl,YES_fate_bird)
recr_web_3 <- NO_fate_pl * outer(NO_fate_pl,NO_fate_bird)
recr_web_4 <- NO_fate_pl * outer(NO_fate_pl,YES_fate_bird)
```
recr.web.5 <- sc7b * outer(YES_fate_pl,NO_fate_bird)
recr.web.6 <- sc8b * outer(YES_fate_pl,YES_fate_bird)

# create a list with the 6 final webs of seedling recruitment
recr.webs_tot <- list(recr.web.1, recr.web.2, recr.web.3, recr.web.4, recr.web.5, recr.web.6)

#---- (VI) Calculate the 3 dimensions of seedling recruitment (Abundance and Diversity of seedlings and mean seed size)----
dimnames(alldata_def)[[3]] <- dimnames(alldata_def)[[2]] <- dimnames(alldata_def)[[1]] <- "# Define the names of the dimensions of the arrays

for (i in 1:6) {
  Abund <- sum(recr.webs_tot[[i]])  # abundance
  Div <- diversity(rowSums(recr.webs_tot[[i]]), index = "shannon")  # Shannon diversity (for plants)
  mean_size <- wtd.mean(fit_pltr, rowSums(recr.webs_tot[[i]]))  # mean seed size
  dimensionsSdl[[i]] <- cbind(Abund, Div, mean_size)
}

# table with values of the three dimensions of seedling recruitment for each of the 6 scenarios
csn_recr.values <- as.data.frame(do.call("rbind", dimensionsSdl))

#------------------- STEP 3: GENERATE THE DEFAUNATION SCENARIOS ------------------

#---------------- RANDOM EXTINCTION SCENARIO ----

Nrep=10000  # number of replicates
alldata <- array(NA, dim=c(6,60,3,Nrep))

# Define the names of the dimensions of the arrays
dimnames(alldata)[[1]] <- paste("Full_Scn",1:6,sep="")
dimnames(alldata)[[2]] <- paste("Bird_Rich",60:1,sep="")
dimnames(alldata)[[3]] <- c("abun","div","meansize")

# Create a unique loop for all the scenarios
for (i in 1:6) {
  # put the names of the birds and plants for the whole list with all the recruitment webs
  recr.webs_tot[[i]] <- list(paste("p",1:50,sep=''),paste("b",1:60,sep=''))
}

# Calculate 3 dimensions of seedling recruitment for each value of species richness along a random extinction sequence
for (k in 1:6) {
  for (n in 1:Nrep) {
    seq.ran <- sample(colnames(recr.webs_tot[[k]]), drop=FALSE)
    web.old <- recr.webs_tot[[k]]
    for(i in 1:60) {
      alldata[k, i, "abun", n] <- sum(web.old)
      alldata[k, i, "div", n] <- diversity(rowSums(web.old), index="shannon")
      alldata[k, i, "meansize", n] <- wtd.mean(fit_pltr, rowSums(web.old))
      web.old <- web.old[,which(colnames(web.old)==seq.ran[i]), drop=FALSE]
    }
  }
}

# mean and confidence intervals of all the replicates for each scenario, bird richness and dimension of seedling recruitment.
alldata.ranCI.mean <- apply(alldata,1:3, mean)  # mean
alldata.ranCI_low <- apply(alldata,1:3, quantile, probs=0.025,na.rm=T)  # L CI
alldata.ranCI_high <- apply(alldata,1:3, quantile, probs=0.975,na.rm=T)  # H CI

#---------------- DETERMINISTIC EXTINCTION SCENARIO (size-structured defaunation) ----

alldata_def <- array(NA, dim=c(6,60,3))

# Define the names of the dimensions of the arrays
dimnames(alldata_def)[[1]] <- paste("Full_Scn",1:6,sep="")
dimnames(alldata_def)[[2]] <- paste("Bird_Rich",60:1,sep="")
dimnames(alldata_def)[[3]] <- c("abun","div","meansize")
for (k in 1:6){
    seq_def <- colnames(recr.webs_tot[[k]])
    web.old <- recr.webs_tot[[k]]
    for(i in 1:60){
        alldata_def[k, i, "abun"] <- sum(web.old)
        alldata_def[k, i, "div"] <- diversity(rowSums(web.old))
        alldata_def[k, i, "meansize"] <- wtd.mean(fit_pltr,rowSums(web.old))
        web.old <- web.old[,which(colnames(web.old)==seq_def[i]), drop=FALSE]
    }
}

#---- References ----