

Supplementary Materials

Negative density-dependence characterize mutualistic interactions between birds and fruiting plants across latitudes

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This PDF file includes:

Figures S1 to S8

Tables S1 to S4¹

Code S1 to S3

¹ Tables S6–8 containing the randomization results can be found in a separate supplementary spreadsheet file.

Supplementary figures

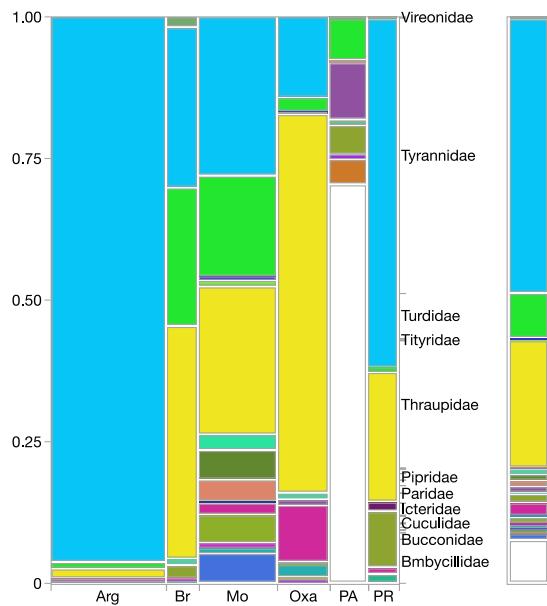


Figure S1 – Mosaic plot showing the proportional contribution of bird families to the total number of frugivory visits to fruiting plant species registered in each study site. In all sites except Pennsylvania, Tyrannidae (blue) and Thraupidae (yellow) accounted for most frugivory interactions. Turdidae (green) were also proportionally important in Brazil, Moyobamba, and Pennsylvania.

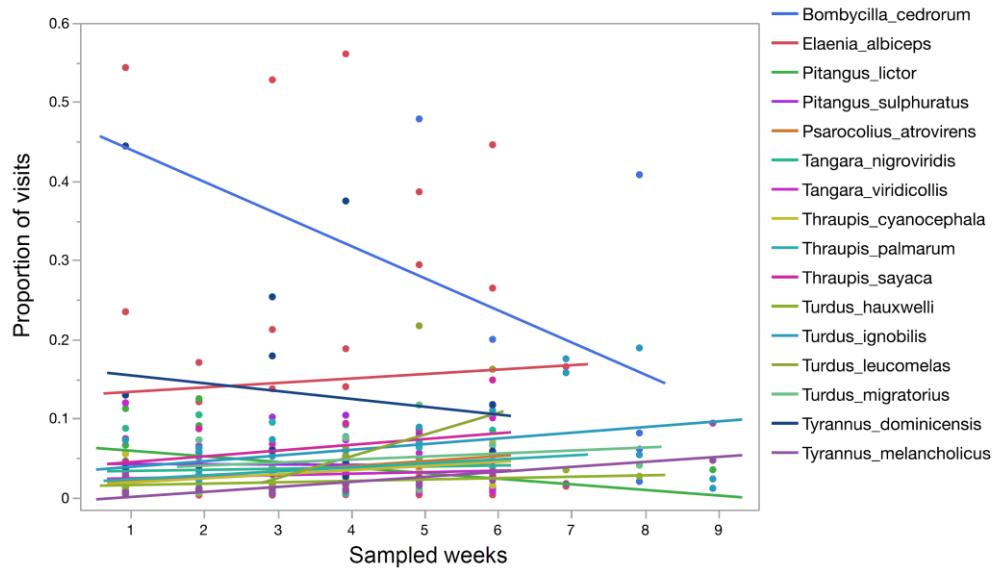


Figure S2 – Sixteen most dominant bird species that accounted for most frugivory records across the sampled communities. Regression lines show the temporal variation of the contribution of a given bird species to the total frugivory records (proportion of visits) across the sampled weeks. These most dominant bird species remained dominant throughout the sampling period.

Regression lines were fitted through a binomial GLMM with the proportion of visits as response variable, sampled weeks as fixed effect, and the interaction between bird species and sampled week as random effect. The analysis indicates that the relationship between the proportion of visits and sampled weeks is not significant ($\alpha = -3.14$, $\beta = 0.04$, Wald $\chi^2 = 0.729$, $p = 0.393$).

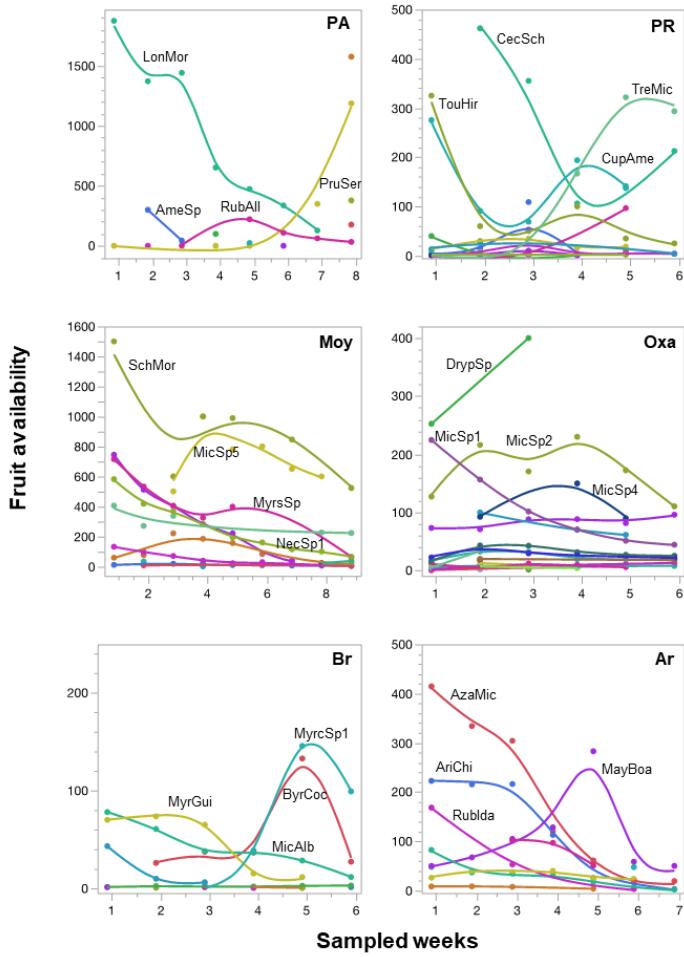


Figure S3 – Temporal variation in fruit availability (cumulative ripe fruit counts of plant species) of dominant fruiting species across the sampled weeks of the six study sites. It is evident that temporal turnover of fruit resources was a common feature of all study sites. In each panel, the four fruiting plant species experiencing the most drastic changes in fruit availability over time are indicated by a six-letter code. Pennsylvania (PA): *Lonicera morrowii* (LonMor), *Prunus serotina* (PruSer), *Rubus allegheniensis* (RubAll), and *Amelanchier* sp. (AmeSp). Puerto Rico (PR): *Tournefortia hirsutissima* (TouHir), *Cecropia schreberiana* (CecSch), *Trema micrantha* (TreMic), *Cupania americana* (CupAme). Moyobamba (Moy): *Schefflera morototoni* (SchMor), *Miconia* sp.5 (MicSp5), *Myrsini* sp. (MyrsSp), *Nectandra* sp.1 (NecSp1). Oxapampa (Oxa): *Drypetes* sp. (DrypSp), *Miconia* sp.2 (MicSp2), *Miconia* sp.1 (MicSp1), *Miconia* sp.4 (MicSp4). Brazil (Br): *Myrcia guianensis* (MyrGui), *Miconia albicans* (MicAlb), *Myrcia* sp.1 (MyrcSp1), *Byrsonima coccobifolia* (ByrCoc). Argentina (Ar): *Azara microphylla* (AzaMic), *Aristotelia chilensis* (AriChi), *Rubus idaeus* (RubIda), *Maytenus boaria* (MayBoa).

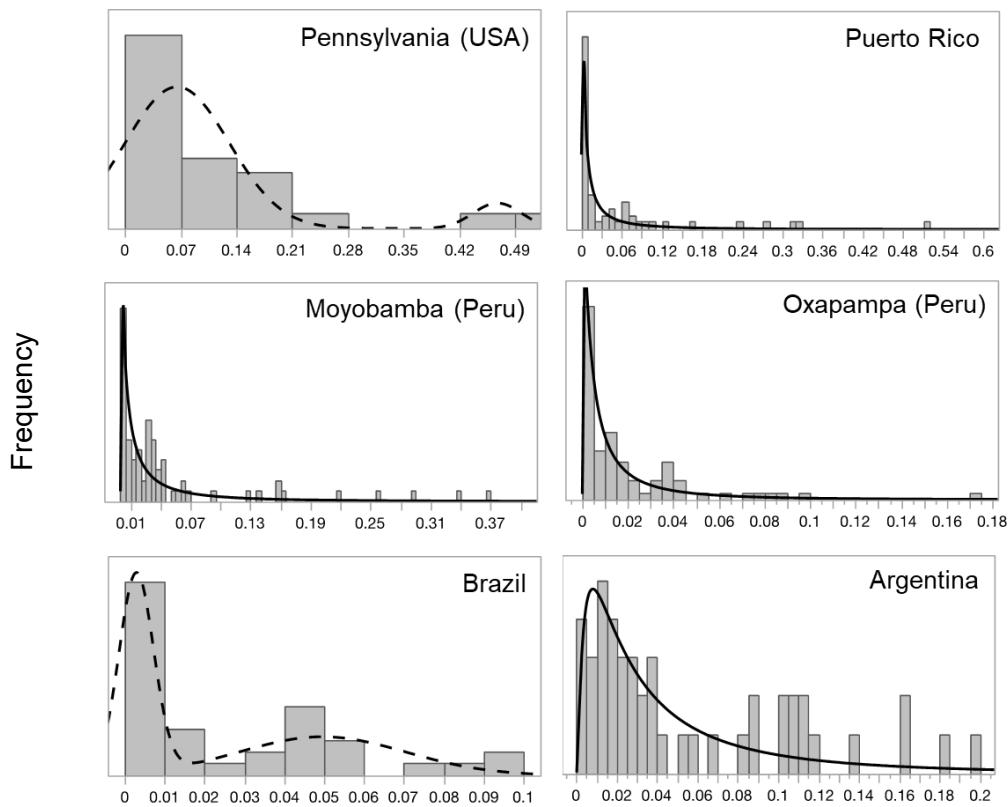


Figure S4 – Histograms showing the frequency distributions of plant species' relative fruit abundances at each sampled bird-plant community. All fruiting plant communities were characterized by a few plant species being dominant at any given week, and most species being proportionally rare, as indicated by a highly skewed distribution towards the rare species. We fitted first lognormal distributions (solid lines) and tested for goodness of fit, and if data was not lognormally distributed, we adjusted a mixture of two normal distributions (dashed lines).

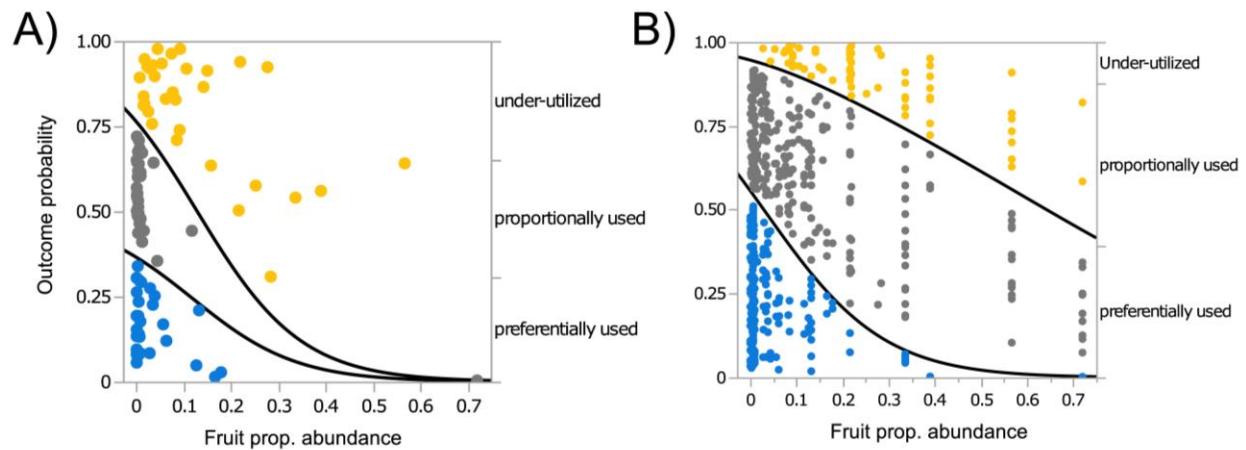


Figure S5 – Multinomial logistic regression plots where the selection probability of a plant be under-utilized, proportionally used, or preferentially used (blue dots) was modelled in function of the proportional fruit abundance at the global (A) and global pairwise (B) scale of analysis. In both models the selection probabilities in relation to fruit relative abundance were statistically significant (Wald $\chi^2 = 14.067$, $p = 0.0009$; Wald $\chi^2 = 108.80$, $p < 0.0001$, respectively), with the probability of being under-utilized (yellow dots) increasing as the proportional fruit abundance increases.

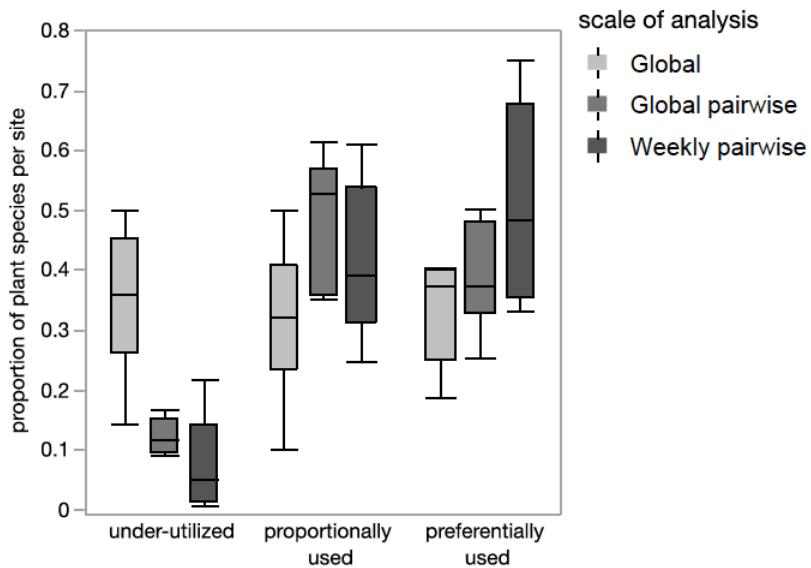


Figure S6 – Summary of three possible fruit selection outcomes across the six sampled communities based on randomizations testing the null hypothesis of proportional interactions between birds and plants using three different scale of data analysis. Each boxplot summarizes the proportion of selection outcomes for each category in each study site. Global tests averaged fruit availability data for plant species across the entire sampling period of sites and pool interactions from all bird species to each plant species in a site. Global pairwise test analysed selection at the scale of individual bird-plant species pairs for the average plant availability, while weekly pairwise test conducted pairwise selection tests at the scale of each week of sampling at the sites.

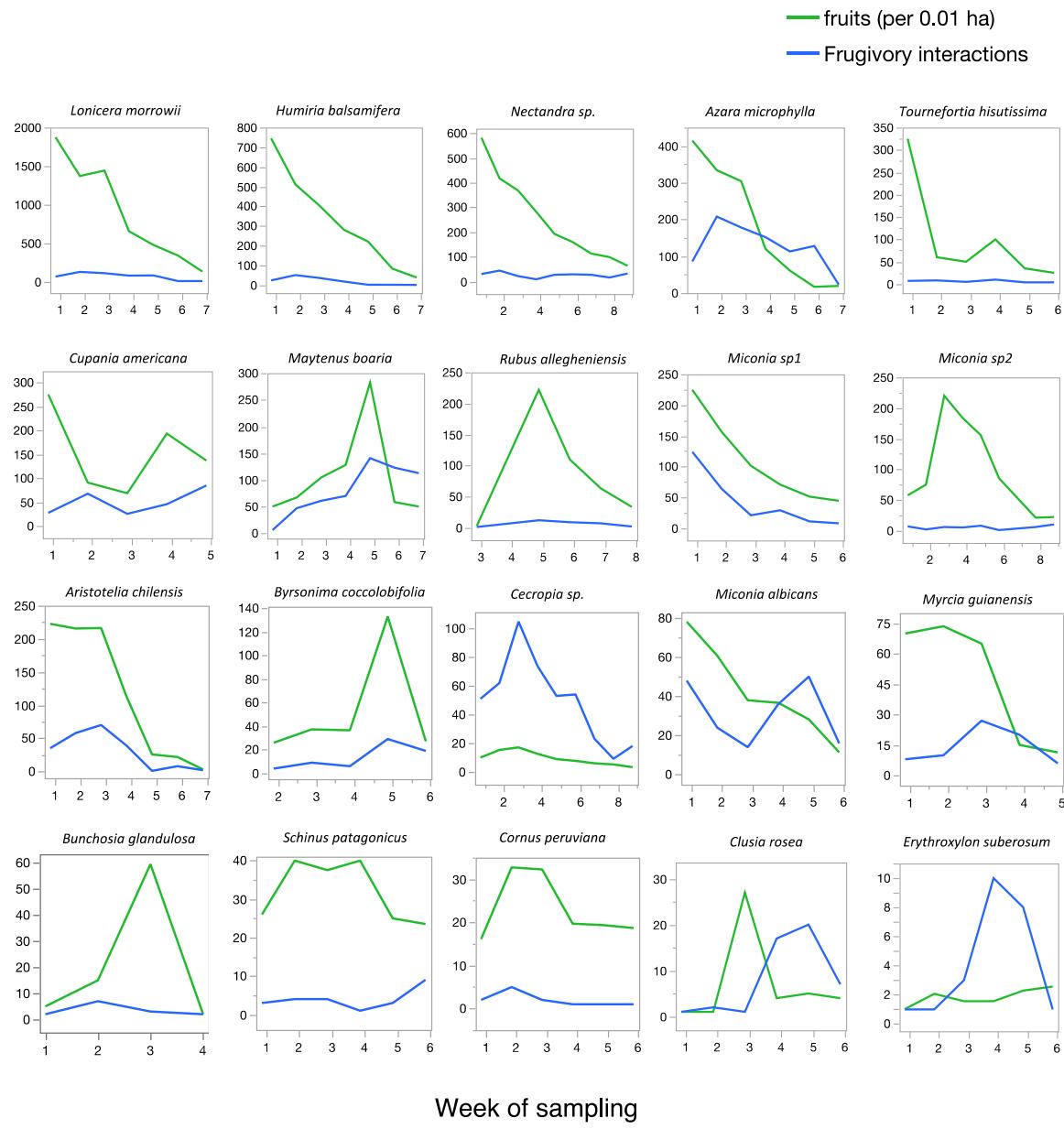


Figure S7 – Selection of plant species from all study sites for which there were at least five weeks of abundance and frugivory interaction data. See that the magnitude of the changes of fruit abundance is much greater than the magnitude of the changes in frugivory interactions as plant had more fruit. Note that study sites measured between 1.0 and 1.75 ha, and the fruit abundance data presented is the average density at the level of the 10 x 10 m cells (0.01 ha) of each plot. Thus, frugivory interactions are about two orders of magnitude below the fruit abundance value scale.

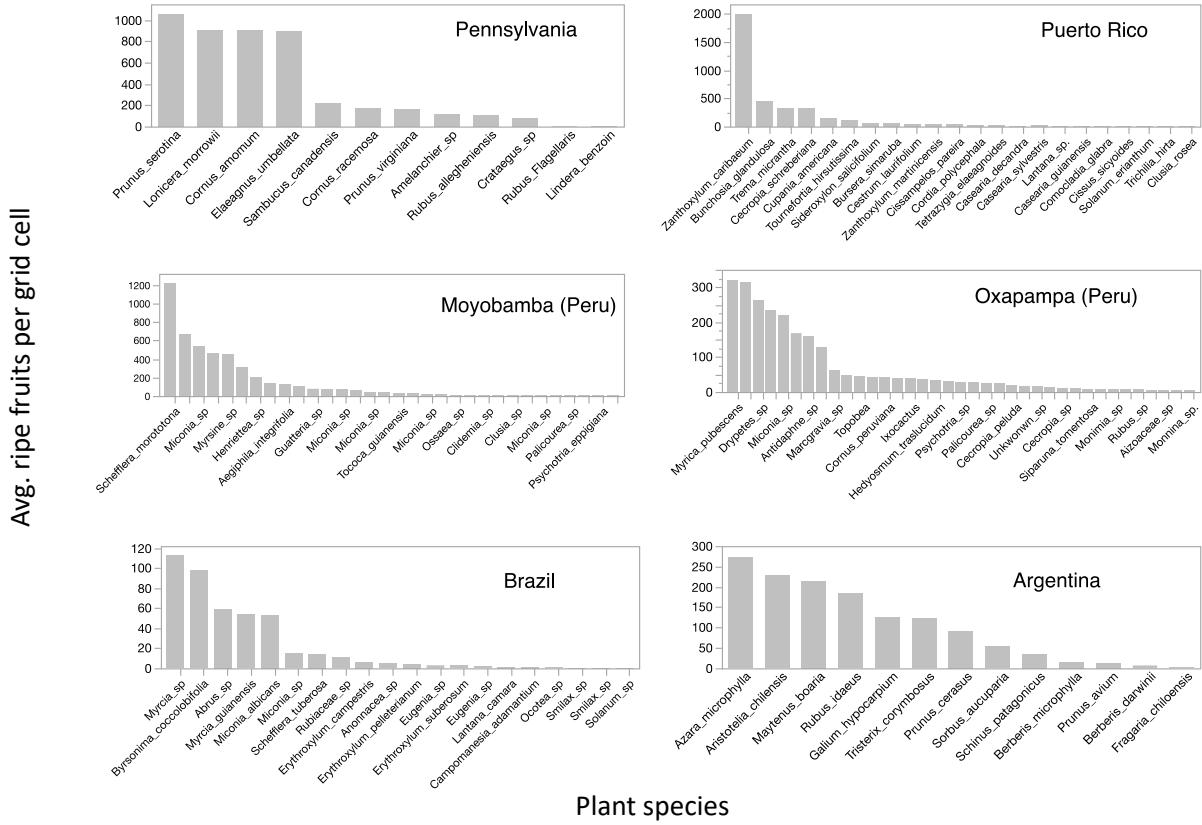


Figure S8 – Average fruit abundance of fruiting plant species per grid cell (10 x10 meter) detected during the weekly phenology surveys at study sites: Pennsylvania, Puerto Rico, Moyobamba (Peru), Oxapampa (Peru), Brazil (Cerrado), and Argentina (Bariloche). Some plant species of trace fruit abundance were detected only through foraging interactions (e.g., Tables S5-S7 contain a few extra very rare fruiting plant species not detected during phenology surveys. At the same time, most but not exactly all the above fruiting species accumulated at least one frugivory record, and thus can be missing from Tables S5-S7).

Supplementary tables

Table S1 – Parameter estimates (posterior means), credible intervals, and effective sample sizes of the regression modelling the number of bird-plant interactions under a Poisson distribution in response to fruit abundance (scaled) and frugivory degree (scaled) (fixed effects), and bird and plant species as random effects for the global pairwise datasets. This result shows a positive (although small effect) relationship between interactions and fruit abundance. (This table accompany the results presented in Fig. 2A).

	Mean	2.50%	97.50%	N Eff.
Fixed effects				
Intercept	0.39584	0.20022	0.58311	1600
Fruit abundance	0.13499	0.05121	0.21757	1600
Frugivory degree	0.08043	-0.0353	0.20298	1419
Random effects				
Bird species	0.2558	0.1731	0.3588	1751
Plant species	0.3155	0.1899	0.4814	1600

Table S2 – Parameter estimates (posterior means), credible intervals, and effective sample sizes of the multinomial logistic regression that examined the probabilities of fruit selection types (preferential, proportional, under-utilized) of plant species as a function of their fruit abundance. We modelled the proportion of cases (successes and failures) with a multinomial distribution as a function of selection type and the fruit abundance (scaled) of plant species (fixed effects), including their interaction term. Study sites were set as a random effect. (This table accompany the results presented in Fig. 2B)

	Mean	2.50%	97.50%	N Eff.
Fixed effects				
Intercept (Under utilized)	-4.3539	-4.9097	-3.8571	581.6
Proportionally used	3.4612	2.8985	4.0296	886.7
Preferentially used	4.5701	3.9653	5.1966	720.5
Fruit prop. abundance	1.1473	0.7728	1.5233	793.4
Proportionally used : Fruit prop. Abundance	-0.3046	-0.8056	0.1861	1600
Preferentially used : Fruit prop. Abundance	-3.6417	-4.3619	-2.9876	790.7
Random effects				
Sampling site	0.00294	6.68E-17	0.007193	810.5

Table S3 – Parameter estimates (posterior means), credible intervals, and effective sample sizes of the regression modelling the selection strength under a Gaussian distribution in response to fruit abundance (scaled) and frugivory degree (scaled) (fixed effects), and bird phylogeny and plant species as random effects. This result shows a negative relationship between selection strength and fruit abundance in all sites, indicating that as fruit abundance increases selection strength decreases towards under-utilization. (This table accompanies the results presented in Fig. 2D).

Site		Mean	2.50%	97.50%	N Eff.
Pennsylvania	Fixed effects				
	Intercept	2.43066	0.69819	4.63866	1600
	Fruit abundance	-2.34792	-3.37616	-1.30407	1600
	Frugivory degree	-0.91844	-1.79549	0.01938	1753
	Random effects				
	Bird phylogeny	0.06658	9.74E-17	0.1845	469.9
	Plant species	5.504	1.16E-15	16.2	891.9
Puerto Rico	Fixed effects				
	Intercept	6.5663	3.5925	9.5012	704.1
	Fruit abundance	-2.4909	-4.6931	-0.6139	1600
	Frugivory degree	2.6607	0.7872	4.491	1600
	Random effects				
	Bird phylogeny	0.4347	2.14E-17	1.26	893.1
	Plant species	12.68	8.41E-17	51.94	227.5
Moyobamba	Fixed effects				
	Intercept	8.4531	1.903	14.4142	1600
	Fruit abundance	-1.9242	-3.4087	-0.5421	1600
	Frugivory degree	0.368	-0.6642	1.435	1484
	Random effects				
	Bird phylogeny	11.32	2.043	23.99	1464
	Plant species	87.21	20.5	181.4	1755
Oxapampa	Fixed effects				
	Intercept	4.87011	2.60959	6.89324	1522
	Fruit abundance	-1.56477	-2.82039	-0.31105	1600
	Frugivory degree	-0.08329	-0.79489	0.72689	1600
	Random effects				
	Bird phylogeny	1.383	1.42E-16	11.31	25.65
	Plant species	13.14	2.262	26.81	1600
Brazil	Fixed effects				
	Intercept	6.1478	1.9999	10.0003	1600
	Fruit abundance	-0.7555	-1.3454	-0.1518	1600
	Frugivory degree	-0.126	-0.5902	0.3565	1600
	Random effects				
	Bird phylogeny	0.01709	5.31E-17	0.04831	270.2
	Plant species	46.44	15.55	94.06	1723

Argentina	Fixed effects				
	Intercept	-2.1573	2.9889	1600	
Fruit abundance		-1.1909	-2.1819	-0.1989	1488
Frugivory degree		-0.5076	-1.4489	0.36	1600
Random effects					
Bird phylogeny		0.04285	2.18E-17	0.02605	402.7
Plant species		11.21	0.548	27.35	1600

Table S4 – Network-level metrics calculated for the weekly pairwise interaction dataset sampled in each bird-plant community. For each weekly interaction network, we calculated nestedness ($wNODF_{obs}$), modularity (Q_{obs}), and niche overlap (NO_{obs}). The significance of the departure of observed values from those expected by chance was assessed with a bootstrapping procedure (bold indicates that observed values were statistically different from expected by chance, $p < 0.05$). Mean ($wNODF_{exp}$, Q_{exp} , NO_{exp}) and standard deviation ($wNODF_{expSD}$, Q_{expSD} , NO_{expSD}) of expected values are reported. Similar to the results obtained for the global pairwise network analysis, the overall pattern of high nestedness, low modularity, and extensive niche overlap is also present in the vast majority of weekly frugivory networks.

Site	Week	Network metrics								
		$wNODF_{obs}$	$wNODF_{exp}$	$wNODF_{expSD}$	Q_{obs}	Q_{exp}	Q_{expSD}	NO_{obs}	NO_{exp}	NO_{expSD}
Pennsylvania	1	100.00	100.00	0	0.0005	0.0862	0.0960	0.99	0.56	0.41
	2	64.81	41.16	9.63	0.0139	0.2041	0.0761	0.99	0.19	0.16
	3	57.95	38.76	6.14	0.1845	0.3305	0.1087	0.32	0.15	0.14
	4	20.51	17.11	7.51	0.0492	0.3051	0.1147	0.01	0.08	0.12
	5	40.28	34.70	6.88	0.1644	0.4424	0.0862	0.17	0.16	0.08
	6	40.74	33.02	6.71	0.4089	0.4359	0.0744	0.13	0.20	0.10
	7	100.00	48.23	33.1	0.1065	0.2638	0.0701	0.63	0.52	0.14
	8	52.00	28.21	9.26	0.2062	0.4634	0.0808	0.46	0.21	0.07
Puerto Rico	1	19.18	16.22	3.01	0.4160	0.5619	0.0651	0.16	0.18	0.03
	2	39.96	22.60	4.34	0.3032	0.4389	0.0413	0.35	0.18	0.03
	3	37.50	23.55	4.90	0.2337	0.5510	0.0602	0.36	0.18	0.04
	4	47.11	29.63	5.35	0.4309	0.5177	0.0717	0.38	0.21	0.04
	5	44.14	25.36	5.14	0.3527	0.4071	0.0536	0.23	0.18	0.04
	6	34.41	23.17	6.92	0.4325	0.5101	0.0552	0.19	0.17	0.05
Moyobamba	1	37.47	19.47	2.06	0.4037	0.6186	0.0312	0.13	0.10	0.02
	2	37.64	17.72	1.93	0.3940	0.6479	0.0340	0.16	0.08	0.02
	3	38.94	15.42	1.54	0.4029	0.6608	0.0274	0.14	0.07	0.02
	4	31.69	10.63	1.21	0.4173	0.7179	0.0292	0.11	0.05	0.01
	5	23.70	10.97	1.24	0.4927	0.7115	0.0320	0.21	0.05	0.02
	6	22.32	10.72	1.41	0.4173	0.7028	0.0317	0.17	0.05	0.02
	7	21.17	11.02	1.70	0.3934	0.6806	0.0474	0.11	0.05	0.02
	8	10.68	8.85	1.79	0.6034	0.7118	0.0361	0.19	0.05	0.02
	9	24.95	13.41	1.85	0.5412	0.6791	0.0390	0.16	0.07	0.02
Oxapampa	1	37.43	17.77	1.95	0.3480	0.6214	0.0288	0.13	0.10	0.02
	2	28.52	17.99	1.84	0.4008	0.5868	0.0273	0.14	0.12	0.02
	3	19.64	12.30	1.66	0.5419	0.6506	0.0287	0.08	0.08	0.01
	4	31.95	15.79	2.03	0.4201	0.6233	0.0328	0.15	0.10	0.02
	5	22.85	14.51	2.06	0.5001	0.6539	0.0366	0.14	0.08	0.02
	6	37.06	19.81	3.08	0.4847	0.5966	0.0435	0.17	0.12	0.03
Brazil	1	66.45	34.27	6.07	0.2312	0.4733	0.0495	0.26	0.22	0.06
	2	51.39	41.07	7.95	0.2183	0.3919	0.0409	0.40	0.32	0.06

3	54.68	28.38	4.94	0.3232	0.5144	0.0460	0.31	0.18	0.04	
4	65.42	34.24	4.91	0.2551	0.4794	0.0402	0.39	0.21	0.04	
5	66.84	31.49	4.30	0.2400	0.5387	0.0459	0.42	0.16	0.04	
6	42.61	33.29	6.42	0.3234	0.4990	0.0625	0.14	0.21	0.06	
Argentina	1	57.68	35.44	8.32	0.2122	0.4151	0.1192	0.40	0.27	0.06
	2	85.71	55.13	11.74	0.0444	0.3308	0.1227	0.80	0.37	0.09
	3	63.53	33.31	8.46	0.1014	0.4290	0.1272	0.58	0.28	0.06
	4	72.67	32.81	9.53	0.1135	0.4167	0.1327	0.94	0.22	0.08
	5	83.33	35.67	7.79	0.1942	0.4890	0.1237	0.82	0.22	0.06
	6	48.98	22.58	5.69	0.2252	0.5150	0.1149	0.49	0.14	0.05
	7	59.38	28.88	11.51	0.0558	0.3323	0.1212	0.49	0.18	0.10

Supplementary code

Below you will find the code written in the R programming language regarding the randomization tests developed to determine whether fruiting plant species were preferentially used, proportionally used, or under-utilized based on their fruit availability. Randomization tests were performed at three analytical scales: global (Code S1), global pairwise (Code S2), and weekly pairwise (Code S3). The results from these analyses can be found on the spreadsheet file containing Tables S5–7.

Code S1 Randomization for global dataset

```
data <- read.table("GlobalData.txt", h=T)
SITE_NAME <- subset(data, community == "SITE_NAME")
#After importing the data, we subset the dataset for each sampled community (here the generic "SITE_NAME" indicates the name of the chosen site to perform the first randomization test. E.g., "Brazil")
SITE_NAME$PropAvgAvail <-
  SITE_NAME$availability_avgweek/sum(SITE_NAME$availability_avgweek) #Calculating the average proportional fruit availability
SITE_NAME <- SITE_NAME[order(SITE_NAME$PropAvgAvail, decreasing = T),] #Ordering the data.frame in the decreasing order of proportional availability
SITE_NAME$prop_band <- cumsum(SITE_NAME$PropAvgAvail) #Defining proportional bands as the cumulative sum of the ordered proportional availabilities

#Creating objects of each parameter that will be used on the randomization
visits = SITE_NAME$visits #number of frugivore visits received by each plant species
visit.tot = sum(SITE_NAME$visits) #total number of visits of the community
prop.bands <- SITE_NAME$prop_band #proportional bands
plts <- SITE_NAME$plant_sp #plant species
nplts <- length(SITE_NAME$plant_sp) #number of plant species
tot.rnd <- 10^4 #total number of iterations of the randomization

#Below we create an empty matrix and vectors to store the results of each iteration of the randomization
bt <- matrix(0, nrow = nplts, ncol = tot.rnd) #Randomization results matrix where plant species are in the rows, and each randomization iteration in the columns
select.strength <- numeric() #Selection strength
rndMean <- numeric() #Mean expected number of visits
rndSD <- numeric() #Standard deviation of the expected number of visits
rnd2.5Quant <- numeric() #2.5% confidence interval of the distribution of expected visits
rnd97.5Quant <- numeric() #97.5% confidence interval of the distribution of expected visits
pvalue <- numeric() #P-value of the significance whether the observed values were higher, lower, or equal the expected value
```

```

#Below starts the randomization procedure
set.seed(123)
for (j in 1:ncol(bt)) {
  x <- runif(visit.tot) #generating random values between 0 and 1 that are equal to
  the total number of visits documented
  for (i in 1:length(x)){
    tmp <- which(x[i]>prop.bands) #this returns how many proportional bands each
    random value encompass, and its position in relation to the bands
    bt[length(tmp)+1,j] <- bt[length(tmp)+1,j]+1 #this assigns a visit to the plant
    species according to its proportional band
  }
}

#Below we extract the randomization results
for (i in 1:length(visits)) {
  rndMean[i] <- round(mean(bt[i,]),3)
  rndSD[i] <- round(sd(bt[i,]),3)
  select.strength[i] <- round(((visits[i]-rndMean[i])/rndSD[i]),3)
  rnd2.5Quant[i] <- quantile(bt[i,], probs = 0.025)
  rnd97.5Quant[i] <- quantile(bt[i,], probs = 0.975)
  pvalue[i] <- round(2*pnorm(-abs(select.strength[i])),3)
}
#Creating a data.frame with the final results of the randomization
GlobalResults.SITE_NAME <- data.frame(SITE_NAME, rndMean, rndSD,
rnd2.5Quant,rnd97.5Quant,select.strength, pvalue)

```

Code S2 Randomization for global pairwise dataset

```
data <- read.table("GlobalPairwiseData.txt", h=T)
SITE_NAME <- subset(data, community == "SITE_NAME")
#After importing the data, we subset the dataset for each sampled community (here the generic "SITE_NAME" indicates the name of the chosen site to perform the first randomization test. E.g., "Brazil")

tot.rnd <- 10^4 #total number of iterations of the randomization
brds <- data.frame(bird_sp = unique(BR$bird_sp), visits = tapply(SITE_NAME$visits, SITE_NAME$bird_sp, sum)) #Creating a data.frame where each row contains a unique bird species and its respective total number of visits
plts <- unique(SITE_NAME$plant_sp) #Extracting the plant species

PltsAvail <- unique(SITE_NAME[,c(2,4)]) #Extracting the fruit availability of each plant species
PltsAvail$PropAvail <- PltsAvail$availability/sum(PltsAvail$availability) #Calculating the proportional fruit availability
PltsAvail <- PltsAvail[order(PltsAvail$PropAvail, decreasing = T),] #Ordering the plant species in the decreasing order of proportional availability
PltsAvail$prop_band <- cumsum(PltsAvail$PropAvail) #Defining proportional bands as the cumulative sum of the ordered proportional availabilities

res <- list() #Creating an empty list to store the results of the randomization

#Below starts the randomization procedure
for (k in 1:tot.rnd) {
  bt <- matrix(0, nrow = length(PltsAvail$plant_sp), ncol = length(brds$bird_sp))
  #Creating an empty interaction matrix where each pairwise randomized interaction will be stored
  rownames(bt) <- PltsAvail$plant_sp; colnames(bt) <- brds$bird_sp #Naming the rows of the matrix with plants species names and the columns with bird species names

  for (j in 1:length(brds$bird_sp)) {
    x <- runif(brds[j, 2]) #generating random values between 0 and 1 that are equal to the total number of visits documented for each bird species

    for (i in 1:length(x)){
      tmp <- which(x[i]>PltsAvail$prop_band) #this returns how many proportional bands each random value encompasses, and its position in relation to the bands
      bt[length(tmp)+1,j] <- bt[length(tmp)+1,j]+1 #this assigns a visit to the plant species according to its proportional band
    }
  }
  res[[k]] <- bt #Storing each randomized bird-plant interaction matrix as an element of the list created to store the randomization results
}

rndmean <- apply(simplify2array(res), c(1, 2), mean) #Calculating the mean expected number of visits
```

```

rndsd <- apply(simplify2array(res), c(1, 2), sd) #Standard deviation of the expected
number of visits

rnd2.5Quant <- apply(simplify2array(res), c(1, 2), quantile, probs = 0.025) #2.5%
confidence interval of the distribution of expected visits

rnd97.5Quant <- apply(simplify2array(res), c(1, 2), quantile, probs = 0.975) #97.5%
confidence interval of the distribution of expected visits

#Below we convert the matrices into pairwise interaction dataframes

tmean <- reshape2::melt(rndmean)

tsd <- reshape2::melt(rndsd)

t25 <- reshape2::melt(rnd2.5Quant)

t97 <- reshape2::melt(rnd97.5Quant)

#Creating a data.frame with the final results of the randomization

GlobalPairwiseResults_SITE_NAME <- data.frame(SITE_NAME,
                                              RndMean = tmean$value[match(paste(SITE_NAME$bird_sp,
                                              SITE_NAME$plant_sp), paste(tmean$Var2, tmean$Var1))],
                                              RndSD = tsd$value[match(paste(SITE_NAME$bird_sp,
                                              SITE_NAME$plant_sp), paste(tsd$Var2, tsd$Var1))],
                                              Rnd2.5Quant = t25$value[match(paste(SITE_NAME$bird_sp,
                                              SITE_NAME$plant_sp), paste(tsd$Var2, tsd$Var1))],
                                              Rnd97.5Quant = t97$value[match(paste(SITE_NAME$bird_sp,
                                              SITE_NAME$plant_sp), paste(tsd$Var2, tsd$Var1))]

GlobalPairwiseResults_SITE_NAME$select.strength <-
round(((GlobalPairwiseResults_SITE_NAME$visits-
GlobalPairwiseResults_SITE_NAME$RndMean)/GlobalPairwiseResults_SITE_NAME$RndSD),3)

GlobalPairwiseResults_SITE_NAME$pvalue <- round(2*pnorm(-
abs(GlobalPairwiseResults_SITE_NAME$Zscore)),3)

```

Code S3 Randomization for weekly pairwise dataset

```
data <- read.table("weeklyPairwiseData.txt", h=T)
SITE_NAME <- subset(data, community == "SITE_NAME")
#After importing the data, we subset the dataset for each sampled community (here the generic "SITE_NAME" indicates the name of the chosen site to perform the first randomization test. E.g., "Brazil")

SITE_NAMEW <- list() #Creating an empty list where each element of the list will be the dataset corresponding to each sampled week
for (w in 1:max(SITE_NAME$week)) { #for loop to separate the dataset per sampled week
  SITE_NAMEW[[w]] <- subset(SITE_NAME, week == w)
}

tot.rnd <- 10^4 #total number of iterations of the randomization
SITE_NAME.Results <- list() #empty list to store the final results

for (w in 1:length(SITE_NAMEW)) {
  brds <- data.frame(frug_name = unique(SITE_NAMEW[[w]]$frug_name), interactions = tapply(SITE_NAMEW[[w]]$interactions, SITE_NAMEW[[w]]$frug_name, sum)) #Creating a data.frame where each row contains a unique bird species and its respective total number of visits
  plts <- unique(SITE_NAMEW[[w]]$Plant_name) #Extracting the plant species

  PltsAvail <- unique(SITE_NAMEW[[w]][,c(3,6)]) #Extracting the fruit availability of each plant species
  PltsAvail$PropAvail <- PltsAvail$Mean.Ripe_fruits./sum(PltsAvail$Mean.Ripe_fruits.) #Calculating the proportional fruit availability
  PltsAvail <- PltsAvail[order(PltsAvail$PropAvail, decreasing = T),] #Ordering the plant species in the decreasing order of proportional availability
  PltsAvail$prop_band <- cumsum(PltsAvail$PropAvail) #Defining proportional bands as the cumulative sum of the ordered proportional availabilities

  res <- list() #Creating an empty list to store the results of the randomization

#Below starts the randomization procedure
  for (k in 1:tot.rnd) {
    bt <- matrix(0, nrow = length(PltsAvail$Plant_name), ncol = length(brds$frug_name)) #Creating an empty interaction matrix where each pairwise randomized interaction will be stored
    rownames(bt) <- PltsAvail$Plant_name; colnames(bt) <- brds$frug_name #Naming the rows of the matrix with plants species names and the columns with bird species names

    for (j in 1:length(brds$frug_name)) {
      x <- runif(brds[j, 2]) #generating random values between 0 and 1 that are equal to the total number of visits documented for each bird species

      for (i in 1:length(x)){
        tmp <- which(x[i]>PltsAvail$prop_band) #this returns how many proportional bands each random value encompass, and its position in relation to the bands
      }
    }
  }
}
```

```

bt[length(tmp)+1,j] <- bt[length(tmp)+1,j]+1 #this assigns a visit to the plant
species according to its proportional band
}

}

res[[k]] <- bt #Storing each randomized bird-plant interaction matrix as an
element of the list created to store the randomization results
}

rndmean <- apply(simplify2array(res), c(1, 2), mean) #Calculating the mean expected
number of visits
rndsd <- apply(simplify2array(res), c(1, 2), sd) #Standard deviation of the expected
number of visits
rnd2.5Quant <- apply(simplify2array(res), c(1, 2), quantile, probs = 0.025) #2.5%
confidence interval of the distribution of expected visits
rnd97.5Quant <- apply(simplify2array(res), c(1, 2), quantile, probs = 0.975) #97.5%
confidence interval of the distribution of expected visits

#Below we convert the matrices into pairwise interaction dataframes
tmean <- reshape2::melt(rndmean)
tsd <- reshape2::melt(rndsd)
t25 <- reshape2::melt(rnd2.5Quant)
t97 <- reshape2::melt(rnd97.5Quant)

#Creating a data.frame with the final results of the randomization
SITE_NAME.Results[[w]] <- data.frame(SITE_NAMEw[[w]],
                                       RndMean =
tmean$value[match(paste(SITE_NAMEw[[w]]$frug_name, SITE_NAMEw[[w]]$Plant_name),
paste(tmean$var2, tmean$var1))],
                                       RndSD = tsd$value[match(paste(SITE_NAMEw[[w]]$frug_name,
SITE_NAMEw[[w]]$Plant_name), paste(tsd$var2, tsd$var1))],
                                       Rnd2.5Quant =
t25$value[match(paste(SITE_NAMEw[[w]]$frug_name, SITE_NAMEw[[w]]$Plant_name),
paste(tsd$var2, tsd$var1))],
                                       Rnd97.5Quant =
t97$value[match(paste(SITE_NAMEw[[w]]$frug_name, SITE_NAMEw[[w]]$Plant_name),
paste(tsd$var2, tsd$var1))]

                                       SITE_NAME.Results[[w]]$select.strength <-
round(((SITE_NAME.Results[[w]]$interactions- SITE_NAME.Results[[w]]$RndMean)/
SITE_NAME.Results[[w]]$RndSD),3)
                                       SITE_NAME.Results[[w]]$pvalue <- round(2*pnorm(-
abs(SITE_NAME.Results[[w]]$Zscore)),3)

}

#Combining the list elements containing the results of each week into a single
data.frame
SITE_NAME.Results <- dplyr::bind_rows(SITE_NAME.Results, .id = "column_label")

```