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Figure A1-A3

Table A1

Appendix 1–4

Figure A1 . Workflow followed to perform the network analyses.

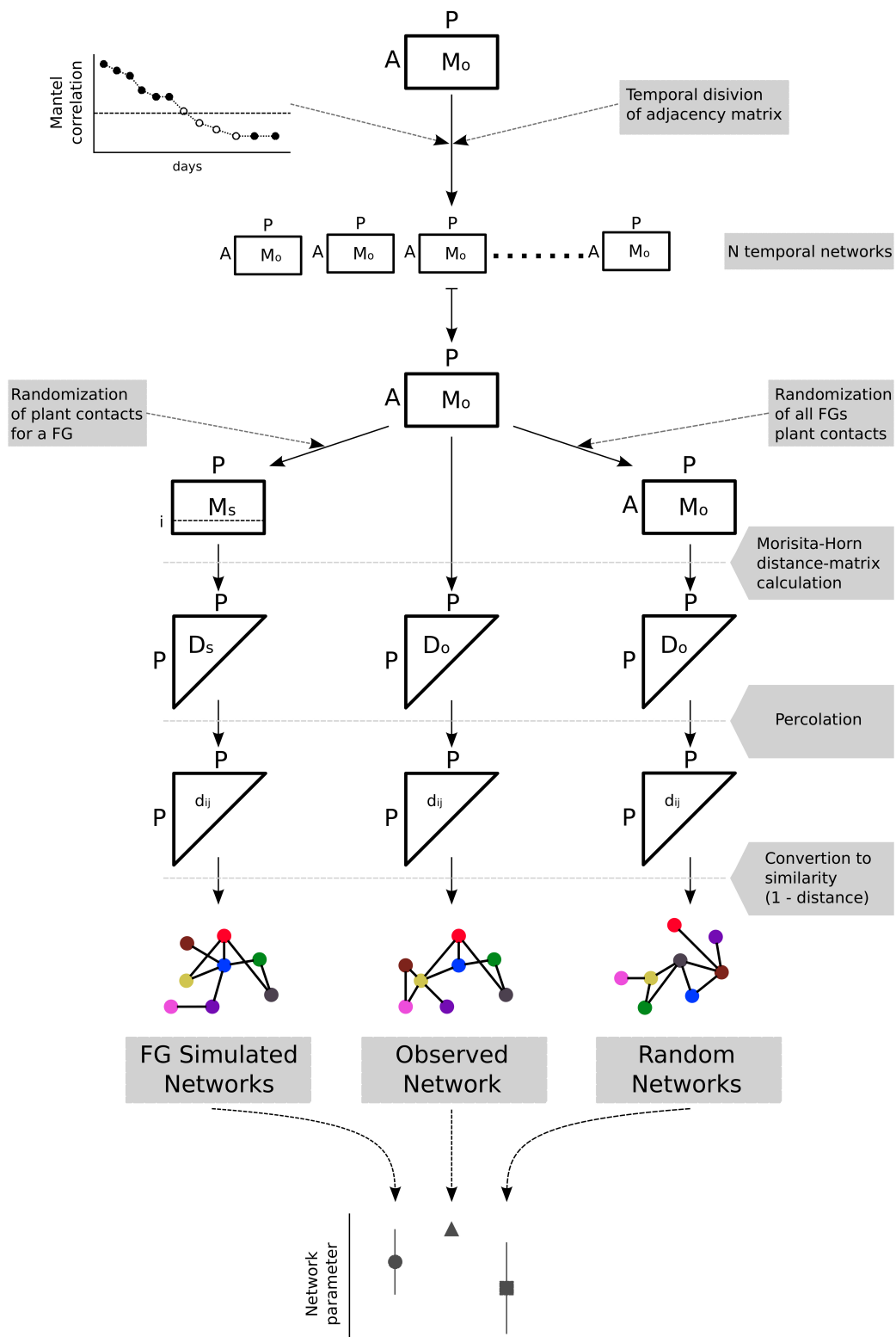


Figure A2. Intraseasonal temporal evolution of functional group richness and diversity measured as Hurlbert's PIE index. Dashed lines denote values for year 2010 while continuous lines values for year 2011. Envelopes indicate 95% confidence intervals. Values correspond to overlapping rolling windows spanning 3 days. See Appendix 3 for a detailed explanation.

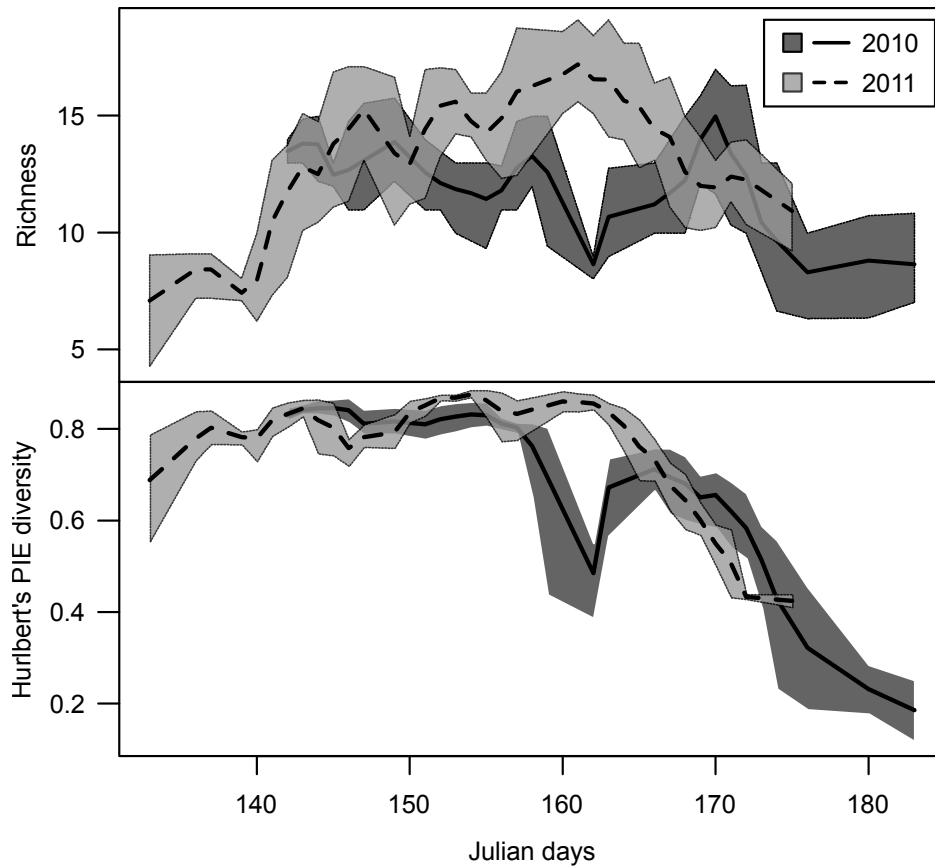


Figure A3. Linear regression of Morisita-Horn dissimilarity index over temporal distance among surveys for both years.

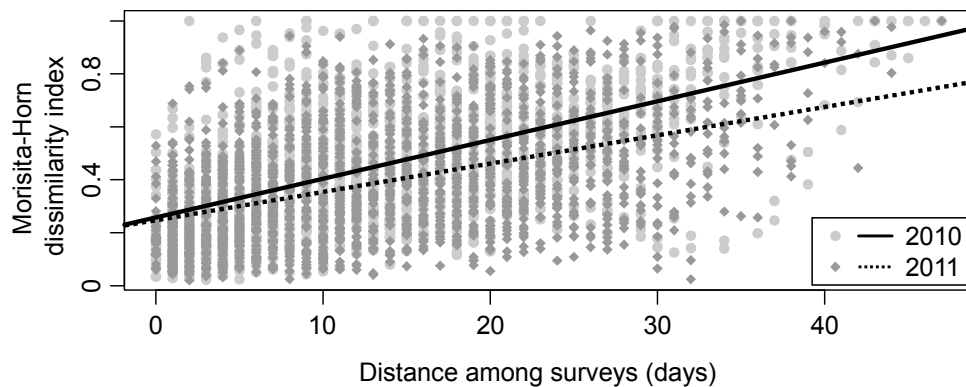


Table A1. Flowering phenological parameters for each year.

Year	Flowering days	Number flowers per individual at flowering peak	Flowering peak		Pairwise synchrony	
			Population level	Individual level	Augspurger X_{ij}	Jaccard type Chao index J
2010	34.15 ± 10.33	10.14 ± 6.92	153	154.82 ± 6.87	0.62 ± 0.18	0.25 ± 0.21
2011	30.71 ± 5.81	14.90 ± 10.89	156	155.16 ± 5.08	0.69 ± 0.14	0.14 ± 0.14

Appendix 1

Flowering curve estimations

To estimate the individual flowering curves we fitted a polynomial function for the number of open flowers per day. These functions take the form:

$$f(x) = a_n x^n + a_{n-1} x^{n-1} + \dots + a_1 x + a_0$$

Where each a is an independent real number, and n the degree of the function (i.e. the highest power of x in its expression). This kind of functions allows for multimodality in the flowering patterns.

Appendix 2

Equations used on this manuscript

Eq. A1. Augspurger synchrony index (X_{ij}) (1983):

Augspurger synchrony measures the flowering synchrony of a plant with the rest of the population:

$$X_i = \frac{1}{n-1} \frac{1}{f_i} \sum_{j \neq i}^n e_j$$

In this equation, n denotes the number of individuals in the population, f_i the number of flowering days and e_j the number of co-flowering days of individuals i and j .

When making pairwise comparisons the index turns asymmetric in the sense that the values obtained differ depending of which plant is been compared with the other. This is because the flowering duration of each plant differs. To overcome this, we used a modified version of the Augspurger metric which corrects for this asymmetry:

$$X_{i,j} = \frac{e_j}{f_i + f_j - e_j}$$

In this modified version of the index, f_j indicates the number of flowering days of individual j . Note that the denominator defines the number of days where either one, another, or both plants are flowering.

Eq. A2. Jaccard-type Chao dissimilarity index (J):

We used this index proposed by Chao et al. (2005) as a proxy for a weighted flowering synchrony among pairs of plants:

$$J = \frac{UV}{U+V-UV}$$

Here U and V express the relative abundances of flowers belonging to the coflowering days for

plant 1 and 2 respectively. This index ranges from 0 to 1, where 0 means no temporal overlap among a pair of individuals, and 1 complete temporal overlap.

Eq. A3. Hurlbert's PIE diversity index ($D_{Hurlbert}$):

We used this algorithm to study the pollinator visits along each flowering season. This index was proposed by Hurlbert (1971) as a modification of the Simpson diversity index. We chose this index because it is insensitive to sample size:

$$D_{Hurlbert} = 1 - \sum \left(\frac{n_i}{N} \right) \left[\frac{(n_i - 1)}{(N - 1)} \right]$$

Here, n_i refers to abundance of the i th species, and N is total abundance.

Eq. A4. Morisita-Horn dissimilarity index (S_{M-H}):

In order to study the seasonal turnover of the pollinator community by comparing temporal distances among all pairs of surveys with their community dissimilarity, we chose the Morisita-Horn dissimilarity index (Morisita 1959, Horn 1966). This index has a low sensitivity to rare species allowing us to eliminate the effect of relative meaningless flower contacts by some FGs:

$$S_{M-H} = \frac{2 \sum_{i=1}^S p_{i1} p_{i2}}{\left[\sum_{i=1}^S p_{i1}^2 + \sum_{i=1}^S p_{i2}^2 \right]}$$

Here, S is the total number of species in both compared assemblages, p_{i1} and p_{i2} denotes the relative abundance of species i in assemblage 1 and 2 respectively.

Eq. A5. Modularity index (Q):

This metric measures the degree to which a network is structured in subgroups of highly

connected nodes (modules) (Newman 2004). It measures the observed fraction of links within groups minus that expected from a random distribution of the links:

$$Q = \frac{1}{2m} \sum_{i,j} \left[A_{ij} - \frac{k_i k_j}{2m} \right] \delta(c_i c_j)$$

For a given structure in modules, A_{ij} denotes the connexion among nodes i and j taking the value of 1 if these are connected, and 0 if not. k_i and k_j are the linkage degree, m is the number of links in the graph, c_i and c_j the modules into which nodes i and j are respectively assigned, and $\delta(c_i c_j)$ is a function which value is 1 when $c_i = c_j$, and 0 otherwise (Newman and Girvan 2004, Newman 2004).

Eq. A6. Weighted clustering coefficient (C_w):

This metric, proposed by Opsahl and Panzarasa (2009) as an extension of the global clustering coefficient (Newman 2003) was used to measure network transitivity. It measures the tendency of nodes to cluster together into tight groups using the proportion of closed triads of nodes over the overall number of all triads (open and close) in the network. A triad is a group of three nodes interconnected. Depending on how these are connected they are closed triads: if all of the three nodes are fully interconnected; or open triads: if two of the nodes are not inter-connected. The weighted extension used here weights each triad with the geometric mean of all links forming it.

$$C_w = \frac{\sum_{\tau_A} \omega}{\sum_{\tau} \omega}$$

In this formula ω are the link weights forming all tripets (τ) and the subset of closed triplets (τ_A).

Eq. A7. Assortative mixing by node degree (r):

This metric was introduced in graph theory by Newman (2003). It is a measure of network centralization and denotes to what extent nodes tend to be connected with nodes of similar degree. For undirected networks this metric is defined as:

$$r = \frac{\sum_{jk} jk (e_{jk} - q_j q_k)}{\sigma_q^2}$$

Where e_{jk} is the fraction of nodes that connect nodes of degree j with nodes of degree k . q_j are the degree distributions of nodes with degree j attached to nodes of degree k and vice-versa for q_k .

These distribution are related to e_{jk} through:

$$\sum_k e_{jk} = q_j.$$

σ_q^2 is the standard deviation of the distribution of q_k . This metric r takes value of 1 if there is a perfect assortative mixing, 0 if there is no assortative mixing and close to -1 when is disassortative. Values close to 0 describe star-like networks while values close to 1 describe networks with a core of highly connected nodes against a periphery of nodes with lower degree (Newman 2010).

Eq. A8. Standarized effect size (SES):

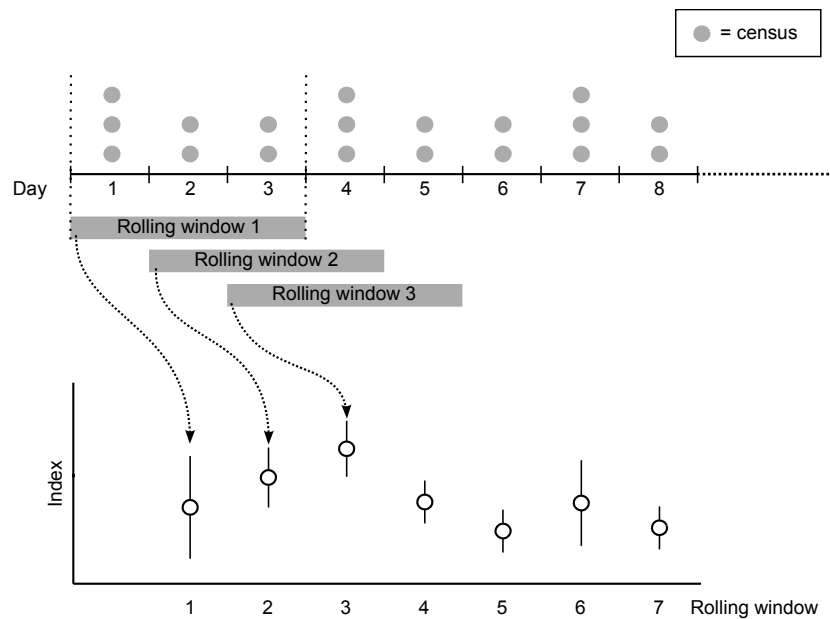
$$SES = \frac{o - \tilde{e}}{std(e)}$$

Here o denotes the empirical value, e the expected distribution (obtained by reshuffling), and \tilde{e} the median of the expected distribution. We used the median instead of the mean due to the lack of normality in the expected distributions.

Appendix 3

Visualization of the temporal variation of richness and diversity

To visualize temporal trends in richness and diversity of FGs, we used an overlapping rolling window spanning three days. For each combination of two surveys contained in a given window, we calculated the richness and diversity of FGs. Therefore, for each window we were able to calculate an average and 95% confidence interval. See figure below. Here, the variation in sampling effort per day depended mainly on weather conditions.



References

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Appendix 4

R scripts used on this manuscript

```
#####  
## Function to percolate similarity networks and extract network metrics ##  
#####  
  
percolation.and.indices<-  
function(matriz,walktrap.steps=10000,metodo="horn"){  
  # output data frame  
  output <- data.frame(flowering = NA,contacted=NA,connected = NA,  
                        threshold=NA,weighted.density=NA,modularity=NA,assort.mix=NA)  
  
  # Plants flowering (no NAs)  
  matriz<-matriz[, !apply(is.na(matriz), 2, all)]  
  output[1,"flowering"]<-ncol(matriz)  
  
  matriz<-t(matriz)  
  
  # Plants contacted  
  nocontact<-as.numeric(names(which(rowSums(matriz)==0)))  
  output[1,"contacted"]<-output[1,"flowering"]-length(nocontact)  
  matriz<-matriz[rowSums(matriz)!=0,]  
  
  # Disimilarity matrix in pollinator composition  
  dis<-as.matrix(vegdist(matriz,method=metodo)); label = colnames(dis)  
  salida <- matrix(nrow = length(range), ncol = 3)  
  colnames(salida) <- c("Threshold", "<s>", "Clusters")  
  
  # Percolation (this is extracted from Muñoz-Pajares' package SIDIER)  
  cat("\n","percolating...")  
  range = seq(0, 1, 0.01)  
  for (j in range)  
  {  
    cat(".")  
    dis2 <- matrix(1, nrow = nrow(dis), ncol = ncol(dis))  
    lim <- max(dis) * j  
    fuera <- which(dis > lim)  
    dis2[fuera] <- 0  
    G <- graph.adjacency(dis2)  
    A <- as.network.matrix(dis2)  
    Res <- clusters(G)  
    noGrande <- sort(Res$csizes)[-length(sort(Res$csizes))]  
    N <- sum(noGrande)  
    repes <- unique(noGrande[which(duplicated(noGrande))])  
  }
```

```

if (Res$no > 1)
{
  if (length(repes) > 0)
  {
    n <- c()
    for (o in 1:length(repes))
    {
      n <- c(n, length(which(noGrande == repes[o])))
      sum1 <- repes^2 * n
      noUnic <- c()
      for (y in 1:length(repes))
      {
        noUnic <- c(noUnic, which(noGrande == repes[y]))
        unicos <- noGrande[-noUnic]
        sum2 <- unicos^2
        SUM <- sum(sum1) + sum(sum2)
        S <- SUM/N
      }
    }
  }
  if (length(repes) == 0) S <- sum(noGrande^2)/N
}
if (Res$no == 1)

  S <- 1
  salida[which(range == j), 1] <- j
  salida[which(range == j), 2] <- S
  salida[which(range == j), 3] <- Res$no

  if (is.null(colnames(dis))) label <- c(1:ncol(dis))
}

# Threshold
j <- salida[(max(which(salida[, 2] > 1)) + 1), 1]
output[1,"threshold"]<-j

# convert dissimilarity to similarity matrix
PNW <- matrix(1, nrow = nrow(dis), ncol = ncol(dis)) ;
colnames(PNW)<-rownames(PNW) <- row.names(dis)
PNW[which(dis > max(dis) * j)] <- 0; diag(PNW)<-0
PW<-PNW*(1-dis)

# Connected plants
output[1,"connected"]<-output[1,"contacted"]-length(which(rowSums(PW)==0))

```

```

# Modularity:
G<-graph.adjacency(PW,weighted=TRUE)
cat("\n",paste("calculating best community structure","using",walktrap.steps,"walktrap steps"))
md<-walktrap.community(G,weights = E(G)$weight,steps=walktrap.steps)
output[1,"modules"]<-length(table(md$membership))
output[1,"modularity"]<-modularity(md)

# Weighted clustering:
output[1,"weighted.clustering"]<-clustering_w(PW,measure="gm")
# Assortative mixing by node degree:
output[1,"assort.mix"]<-assortativity.degree(graph.adjacency(PW,weighted=TRUE))
return(output)
}

#####
## Permutation model (model V) ##
#####

# This model permutes the contacts of one or all functional groups along the plants,
# maintaining their number of contacts

# Model.V performs this only on one group
model.V<-function(mat,grupo)
{
  is.integer0 <- function(x)
  {
    is.integer(x) && length(x) == 0L
  }

  mat.p<-mat[-which(mat[,1]==grupo),] # Matrix without the selected FG
  dummy<-mat[which(mat[,1]==grupo),-1] # Dummy FG with randomized flower contacts
  abundance<-sum(dummy,na.rm = T) # Total number of contacs for that FG
  dummy[!is.na(dummy)]<-0
  for(a in 1:abundance) # Randomize all visits of the chosen FG
  {
    j<-sample(which(!is.na(dummy)),1) ; dummy[j]<-dummy[j]+1
  }
  dummy<-(cbind(grupo,dummy)) ; colnames(dummy)[1]<-colnames(mat)[1]
  mat.p<-rbind(mat.p,dummy)
  return(mat.p)
}

# Model.V performs over all groups
model.V.all<-function(mat)

```

```

{
  is.integer0 <- function(x)
  {
    is.integer(x) && length(x) == 0L
  }

  mat.p<-mat
  bichos<-levels(mat[,1])
  for (i in 1:length(bichos))
  {
    mat.p<-mat.p[-which(mat.p[,1]==bichos[i]),] # Matrix without the selected FG
    dummy<-mat[which(mat[,1]==bichos[i]),-1] # Dummy FG with randomized flower contacts
    abundance<-sum(dummy,na.rm = T) # Total number of contacs for that FG
    dummy[!is.na(dummy)]<-0 # Create dummy FG
    for(a in 1:abundance)
    {
      j<-sample(which(!is.na(dummy)),1) ; dummy[j]<-dummy[j]+1
    }
    dummy<-(cbind(bichos[i],dummy)) ; colnames(dummy)[1]<-colnames(mat)[1]
    mat.p<-rbind(mat.p,dummy)
  }
  return(mat.p)
}

```