Title: Does phenology explain plant-pollinator interactions at different latitudes? An assessment of its explanatory power in plant-hoverfly networks in French calcareous grasslands

Authors: Natasha de Manincor[1]*, Nina Hautekeete[1], Yves Piquot[1], Bertrand Schatz[2], Cédric Vanappelghem[3], François Massol[1,4]

[1]Université de Lille, CNRS, UMR 8198 - Evo-Eco-Paleo, 59000 Lille, France

[2]CEFE, EPHE-PSL, CNRS, University of Montpellier, University of Paul Valéry Montpellier 3, IRD, Montpellier, France

[3]Conservatoire d'espaces naturels Nord et du Pas-de-Calais, 160 rue Achille Fanien - ZA de la Haye, 62190 LILLERS

[4]Univ. Lille, CNRS, Inserm, CHU Lille, Institut Pasteur de Lille, U1019 - UMR 8204 - CIIL - Center for Infection and Immunity of Lille, F-59000 Lille, France

E-mail addresses and ORCID numbers:

Natasha de Manincor: natasha.de-manincor@univ-lille.fr, 0000-0001-9696-125X

Nina Hautekeete: nina.hautekeete@univ-lille.fr, 0000-0002-6071-5601

Yves Piquot: yves.piquot@univ-lille.fr, 0000-0001-9977-8936

Bertrand Schatz: bertrand.schatz@cefe.cnrs.fr, 0000-0003-0135-8154

Cédric Vanappelghem: cedric.vanappelghem@espaces-naturels.fr

François Massol: francois.massol@univ-lille.fr, 0000-0002-4098-955X

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*Correspoinding author information: Natasha de Manincor, e-mail: natasha.de-manincor@univ-lille.fr, phone: +330362268530

Author contributions

NDM and FM conceived the project, formulated and implemented the model. NDM conducted the analysis and prepared the manuscript. FM supervised the analysis and edited the manuscript. NH, YP, CV and BS contributed substantially to all later versions. NDM, NH, YP and BS conducted the fieldwork and provided the data. CV identified the hoverflies.

Data accessibility

The data supporting the results are archived on Zenodo (DOI: 10.5281/zenodo.2542845).

Abstract

For plant-pollinator interactions to occur, the flowering of plants and the flying period of pollinators (i.e. their phenologies) have to overlap. Yet, few models make use of this principle to predict interactions and fewer still are able to compare interaction networks of different sizes. Here, we tackled both challenges using Bayesian Structural Equation Models (SEM), incorporating the effect of phenology overlap, in six plant-hoverfly networks. Insect and plant abundances were strong determinants of the number of visits, while phenology overlap alone was not sufficient, but significantly improved model fit. Phenology overlap was a stronger determinant of plant-pollinator interactions in sites where the average overlap was longer and network compartmentalization was weaker, i.e. at higher latitudes. Our approach highlights the advantages of using Bayesian SEMs to compare interaction networks of different sizes along environmental gradients and articulates the various steps needed to do so.

INTRODUCTION

Understanding how phenology determines species interactions is a central question in the case of mutualistic networks. In plant-pollinator networks, phenology shapes their temporal and spatial limits, thus defining the area and the period along the season in which interactions preferably occur (Olesen *et al.* 2011; Ogilvie & Forrest 2017). Since plant and pollinator phenologies are not equally affected by changes in environmental cues, partial or total phenological mismatches can occur as a result of environmental changes such as climate change (Parmesan 2007; Rafferty 2017). Phenological advances indeed increase at higher latitudes, as a response to the acceleration of warming temperature along the same gradient (Post *et al.* 2018), increase phenological mismatch, and have the potential to threaten the synchrony needed for effective pollination(Hutchings *et al.* 2018). Such environmental changes can thus drastically alter pollinator interactions through modified temporal overlap between pollinators and their floral resources leading, in extreme cases, to local extinctions (Memmott *et al.* 2007) and the ensuing absence of the partner species at the location and/or time at which the interaction should have taken place (Willmer 2012; Miller-Struttmann *et al.* 2015; Rafferty *et al.* 2015; Hutchings *et al.* 2018).

Because phenological match is crucial to plant-pollinator interactions, and thus ultimately to pollinators' fitness, pollinators have to adapt to phenological shifts either through interaction with other plant species (Rafferty *et al.* 2015) or through changes of their own phenology (Bartomeus *et al.* 2011). Phenology can then influence dynamical network properties, such as the stability and the coexistence of species, through changes in network topology (Encinas-Viso *et al.* 2012). Moreover, phenology predictably affects network compartmentalization as different phenophases likely correspond to different compartments when networks are considered on an annual scale (Martín González *et al.* 2012).

Despite considerable theoretical advances, there are few models available to predict the probability of interaction in plant-pollinator networks and fewer still able to make comparisons between networks. Due to their complexity and variation among years (Chacoff *et al.* 2018), most studies of mutualistic networks have focused on predicting and comparing classic network metrics (nestedness, connectance, modularity, etc.) which are all influenced by network size, *i.e.* the number of plant and insect species (Fortuna *et al.* 2010; Staniczenko *et al.* 2013; Poisot & Gravel 2014; Astegiano *et al.* 2015). Moreover, few studies have compared interaction networks along environmental gradients (Devoto *et al.* 2005; Schleuning *et al.* 2012; Sebastián-González *et al.* 2015; Pellissier *et al.* 2018). In order to compare networks of different sizes, a better alternative is to switch from network-derived metrics to the comparison of output of regression models, which can consider multiple factors and latent variables and assume that the sampled data are just part of a larger unobserved dataset (Grace *et al.* 2010). Large datasets allowing relevant comparisons of networks are rare; they require parallel investigations in rich communities of plants and insects to favour interactions between them. Calcareous grasslands are characterized by highly diverse plant communities with a high proportion of entomophilous species (Baude *et al.* 2016), thus they are a convenient model for such studies. Most plant-insect pollinator networks involve bee species (Anthophila), but recent studies have also pointed out the importance of hoverflies (Diptera: Syrphidae), which pollinate a large spectrum of wild flowering species (Klecka *et al.* 2018a) and crops (Jauker & Wolters 2008; Rader *et al.* 2011). They usually behave opportunistically, *i.e.* from being pollen generalists as well as pollen or nectar specialists, only limited by morphological constraints (Iler *et al.* 2013; Klecka *et al.* 2018a; Lucas *et al.* 2018). Indeed, their generalisation could be the result of serial specialized diets, since most pollen retrieved on hoverfly individuals usually comes from a single plant taxon (Lucas *et al.* 2018) and depends on flower availability and phenology (Cowgill *et al.* 1993; Colley & Luna 2000). Moreover, some hoverflies have preferences regarding plant colour, morphology and inflorescence height (Branquart & Hemptinne 2000; Colley & Luna 2000; Lunau 2014; Klecka *et al.* 2018b, a).

Here we study the consequences of environmental gradients on plant-pollinator interactions, focusing on how phenology overlap affects interactions between plants and insects in six calcareous grassland sites distributed along a latitudinal gradient. We obtained plant and insect phenologies, abundances, and interactions in all sites from April to October 2016. We modelled plant-pollinator interaction networks following a Bayesian Structural Equation Modelling approach (SEM) using latent variables. The comparison of 16 SEM models and the analysis of latent block models (LBM) of sampled networks evinced that phenology overlap is an important determinant of plant-pollinator interactions, but is less informative than species abundances and performs heterogeneously among sites. Our results suggest that the use of SEMs to compare networks of different sizes along an environmental gradient is an innovative approach which can help understand the structure of plant-pollinator networks.

MATERIALS AND METHODS

Study sites

We sampled plant and pollinator species in six areas (Fig. S1) of 1 hectare each in different French regions: two sites in Hauts-de-France (Les Larris de Grouches-Luchuel, thereafter noted LAR, 50°11'22.5"N 2°22'02.9"E and Regional natural reserve Riez de Noeux les Auxi, noted R, 50°14’51.85”N 2°12’05.56”E, in départements Pas-de-Calais and Somme), two sites in Normandie (Château Gaillard – le Bois Dumont, noted CG, 49°14'7.782"N 1°24'16.445"E and les Falaises d’Orival, noted FAL, 49°04'40.08"N 1°33'07.254"E, départements: Eure and Seine Maritime) and two sites in Occitanie (Fourches, noted F, 43°56'07.00"N 3°30'46.1"E and Bois de Fontaret, noted BF, 43°55'17.71"N 3°30'06.06"E, départment: Gard). The six sites are included in the European NATURA 2000 network; the four sites in Hauts-de-France and Normandie are managed by the Conservatoire d’espaces naturels of Normandie, Picardie and Nord – Pas-de-Calais and the sites in Occitanie by the CPIE Causses méridionaux. We sampled each site once a month from April to October 2016, except for the site of Riez that was sampled from May to October.

Plant-hoverfly observations and sampling

To collect information at the community level, in each site and at each session we realized: (i) a botanic inventory of the flowering species, recorded their abundances and the total flower covering in the area and (ii) a pollinator sampling using a hand net along a variable transect walk.

Flowering plants were identified at the species level. We recorded the abundances of all flowering species. At first, we estimated the total percentage of surface covered by all flowering species in the selected area. We then estimated the relative abundance of each flowering species. We used Braun-Blanquet coefficients of abundance-dominance to rank flowering species: coefficient ***5*** = 75-100%, coeff ***4*** = 50-75%, coeff ***3***=25-50%, coeff ***2*** = 10-25%, coeff ***1*** = 1-10%, coeff ***+*** = few individuals less than < 1%, coeff ***i*** = 1 individual. All inventories were realized by the same surveyors to avoid biases.

Pollinator observations were performed by the same team of 3-5 persons each day. The surveyors walked slowly around any potential attractive resource patch included in the selected 1-hectare area for 4h each day. We split the sampling period into 2 hours in the morning (about 10-12h) and 2 hours in the afternoon (about 14-16h) to cover the daily variability of both pollinator (bees and hoverflies, which are more active in the morning than in the afternoon; D'Amen *et al.* 2013) and flower communities. Sampling took place when we had suitable weather conditions for pollinators (following Westphal *et al.* 2008). We sampled all flower-visiting insects and we recorded observed interactions. All sampled insects were immediately put individually in a killing vial with ethyl acetate and were later prepared and pinned in the laboratory and identified at the species level by expert taxonomists. Even if we collected both bees and hoverflies, in this study we focus on syrphids only. Overall, we sampled for 41 days, equivalent to about 164 hours in the field (all the surveyors collected at the same time). For all analyses described here, we only used the list of visited herbaceous plant species and hoverflies which were found visiting a plant. Despite their rarity, we also considered the interactions between hoverflies and plant species of the Fabaceae family because we did not want to exclude data in the absence of the proof of no interaction, even if hoverflies are known to prefer open flowers (Branquart & Hemptinne 2000). However, we observed in the field that they visited Fabaceae species that were already opened by other insects, *e.g.* by large bee species, such as *Eucera* sp. (De Manincor, personal observation).

<u>Plant – hoverfly networks</u>

For each site, we constructed an interaction network consisting of all pairs of interacting plant and insect species, pooling data from all months. A pair of species (*i,j*) was connected with intensity *v* when we recorded *v* visits of insect species *i* on plant species *j* in the site. We calculated the network specialization index, H2' (Blüthgen *et al.* 2006) using the `H2fun` function implemented in the `bipartite` package (Dormann *et al.* 2009; R Core Team 2018). We also calculated the standardized specialization index *d'* (Blüthgen *et al.* 2006) for each plant and insect species as the ratio of the *d*-value (Kullback-Leibler divergence between the interactions of the focal species and the interactions predicted by the weight of potential partner species in the overall network) to its corresponding *dmax*-value (maximum d-value theoretically possible given the observed number of interactions in the network). We obtained these values using the `dfun` function in the `bipartite` package (Dormann *et al.* 2009), but we did not use the *d'* values provided by this package as they sometimes yielded spurious results based on the computation of the minimal *d* value (e.g. reporting low *d'* for species with only one partner in the network).

We calculated the modularity of the network and the associated partition of species into modules using the `cluster_leading_eigen` method for modularity optimization implemented in the `igraph` package (Csardi & Nepusz 2006; Newman 2006). Modularity optimization can help gauge strong, simple divisions of a network in relatively independent sub-networks by looking for densest sub-networks. However, modules are not meant to inform about more subtle groupings among the species, *e.g.* particular avoidance of interactions between insects of group A and plants of group 1. In order to detect such groups, we implemented latent block models (LBM) using the `BM_poisson` method for Poisson probability distribution implemented in the `blockmodels` package (Leger *et al.* 2015). Blocks are calculated separately for the two groups (insect and plant) based on the number of visits (*i.e.* a weighted network). The algorithm finds the best divisions of insects and plants through fitting one Poisson parameter in each block of the visit matrix, thus essentially maximizing the ICL (Integrated Completed Likelihood; Biernacki *et al.* 2000; Daudin *et al.* 2008). The LBM script is given in

Supplementary Information (Appendix S3). All analyses were performed in R version 3.3.3 (R Core Team 2018).

Plant and hoverfly abundances and phenology overlap

We calculated plant abundance using information about the abundance-dominance recorded in the field following the methodology of Braun-Blanquet presented above. We transformed the coefficients of abundance in percentages (Table S1): we used the mean of the percentage which correspond to each class. We then calculated the relative abundance (A_P) of each flowering plant species as the ratio of the focal species cumulated abundance to total flower abundance during its flowering season. We used the recorded number of visiting hoverflies and their presence (recorded months) along the season to calculate their average abundance during months when they were present (A_H).

We refer to plant phenology as their flowering period and insect phenology as the flying period. We considered only flowering plants which had been visited by pollinators. For the pollinators, we considered only hoverflies which were found in interaction. To build the species phenology tables for both plants and hoverflies, we merged the information provided by two sources of data (field data and the literature): we used the observed phenology of both plants and insects during the field session as the only source of information for plants (plants visited by insects and plants found in the botanic inventory in the site at that date), and we complemented the hoverfly phenology with information provided by the Syrph the Net Database (Speight *et al.* 2016). We then built the phenology overlap (PO) matrix based on the species phenology tables by calculating the number of phenologically active months that are shared by each pair of insect and plant species along the season.

Bayesian Structural Equation Modelling (SEM)

We modelled the hoverfly-plant interaction network using a Bayesian Structural Equation Modelling approach (SEM, Fig. 1) with latent variables linking the number of visits per plant-pollinator dyad to abundance and phenology overlap (PO) data through a first latent table representing probabilities of interactions, another latent table representing the possible interactions between plant and pollinators (as a realization of the aforementioned interaction probability matrix), and a third latent table yielding the expected number of visits per plant-pollinator dyad (*i.e.* the intensity of interactions).

In this model, we considered that PO had an effect on possible interactions (I_{ij}) and the number of visits (λ_{ij}) – a longer overlap is intuitively expected to drive a higher probability of interaction and a larger number of visits. Interaction probabilities were also assumed to depend on two random effects (plant and insect species identities), to represent heterogeneity of species degrees in the network. We modelled the probability of interaction I_{ij} between insect species i and plant species j (*i.e.* I_{ij} = 1 when species i and j can interact) as a Bernoulli random variable of mean μ_{ij} given by:

$$\mathrm{logit}(\mu_{ij}) = \mu_0 + \mu_{PO} PO_{ij} + E_i + E_j$$

where logit is the usual logistic transformation (log(x/(1-x)), μ_0 is the intercept of this relation, μ_{PO} is the coefficient measuring the effect of PO, and E_i and E_j are the random effects associated with insect species i and plant species j respectively.

The number of interactions was assumed to depend on plant and hoverfly abundances, as more abundant species are expected to be more often sampled (and thus more often recorded "in interaction"). The number of visits V_{ij} was modelled as a Poisson random variable to allow for sampling variability, with a conditional mean λ_{ij} (the intensity of visits that can occur) given by:

$$\log(\lambda_{ij}) = \lambda_0 + \lambda_H A_H + \lambda_P A_P + \lambda_{PO} \log(1 + PO)$$

where λ_0 is the intercept of this relation, λ_H is the coefficient measuring the effect of hoverfly abundance A_H, λ_P is that of plant abundance A_P, and λ_{PO} is the coefficient of the effect of PO.

Possible interactions (I_{ij}) and the intensity of visits (λ_{ij}) are multiplied to obtain the unconditional mean number of recorded visits, *i.e.* V_{ij} is then obtained as a Poisson draw of mean $I_{ij}\,\lambda_{ij}$.

Overall we thus estimated four main parameters: the effect of plant abundance on the intensity of interactions ($A_P \rightarrow \lambda_{ij}$, coefficient λ_P), the effect of insect (hoverflies) abundance on the intensity of interactions ($A_H \rightarrow \lambda_{ij}$, λ_H), the effect of phenology overlap on the intensity of interactions ($PO \rightarrow \lambda_{ij}$, λ_{PO}) and the effect of phenology overlap on the probability of interaction ($PO \rightarrow I_{ij}$, μ_{PO}).

We used the `jags` function (`R2jags` package), which provides an interface from R to the JAGS library for Bayesian data analysis, to estimate model parameters. JAGS (Plummer 2003) uses a Markov Chain Monte Carlo algorithm to generate samples from the posterior distribution of the parameters. We ran two Markov chains with 10^6 iterations per chain to check for model convergence. The code of the model is given in Supplementary Material (Appendix S1 and S2).

Model and parameter comparison

We estimated the 16 models that included between 0 and 4 of the above-mentioned effects to understand which effects were more likely to play a role in the structuring of the network. The goodness-of-fit of these models were compared using the leave-one-out cross-validation criterion (LOO) calculated using the R package `loo` (Vehtari *et al.* 2017). Models can thus be ranked according to their LOO scores, with the best model being the one with the lowest LOO value. The LOO criterion is analogous to the classic Akaike and Bayesian Information Criteria, but can be applied to Bayesian models without suffering the same instability issues of the Deviance Information Criterion (Vehtari *et al.* 2017). To rank the models, we then calculated the ΔLOO (noted Δ_i) as $\Delta_i = LOO_i - LOO_{min}$ (following Burnham & Anderson 2004), where LOO_{min} is the minimum of the LOO_i values among the 16 models. We used Δ_i to obtain model weights ω_i, following the Akaike weight methodology (Burnham & Anderson 2002):

$$\omega_i = \frac{e^{-\Delta_i/2}}{\sum e^{-\Delta_i/2}}$$

We then summed weights (w_H) over all models that incorporated a given focal parameter to ascertain the plausibility of the effect associated to this parameter. We used this sum to evaluate the null hypothesis (H0) that a given factor has no effect on the plant-pollinator interactions by comparing the sum of weights to null expectations, based on the fact that each tested effect is incorporated in exactly half of the tested models. The effect is considered *plausible* when $w_H > 0.5$, *implausible* otherwise, *likely* when $w_H > 0.73$, and *unlikely* when it corresponds to a value of 0.27 or lower, following Massol *et al.* (2007).

RESULTS

Plant-hoverfly networks and phenology overlap

At the end of the field campaign we had collected 1584 hoverflies and recorded 1668 interactions between 76 hoverfly species and 117 plant species overall (Table 1). The number of sampled hoverfly and plant species varied between sites and among regions. In Normandie we generally sampled a higher number of hoverflies than in the other two regions (Table 1). We observed the highest diversity of both plants and hoverflies in Occitanie and the lowest diversity of hoverflies in Hauts-de-France. Despite the high species diversity in Occitanie, the number of interactions recorded in these sites (BF and F) is not the highest recorded in the field (Table 1).

In spite of differences in diversity and the number of interactions, the overall level of specialization (H2 index) did not show a high variation among the 6 networks (range: 0.32 – 0.37). However, we found that the sites in Occitanie (BF and F) had a higher average degree of specialization (d') for both insect (BF 0.63 and F 0.57) and plant species (BF 0.58 and F 0.48). The sites in Occitanie also had a higher modularity (BF 0.51 and F 0.48) than the ones in Normandie (CG 0.34 and FAL 0.23) and Hauts-de-France (LAR 0.37 and R 0.34; Table 1). Given that these statistics only compare 6 sites, none of these assessments can be properly statistically tested, but the importance of the differences among sites is highly suggestive of a difference in average specialization and modularity. We found that plant phenology is generally shorter in all sites than that of hoverflies (Table 1). The phenology overlap was shorter in Occitanie (BF and F) than in the other sites (Table 1).

Illustrations of the block clustering provided by the LBM analysis (Latent Block Model) are shown in Fig. 2 and 3 in the main text and in Fig. S2 to S5 in Supplementary Information. We found different numbers of blocks in plants and hoverflies among sites: the BF site had 2 insect blocks and 2 plant blocks (Fig. S2); the F site had 4 of both (Fig. 2); the CG and R sites had 3 blocks for the plants and 4 blocks for the insects in (Fig. 3 and S5); the FAL site had 4 plant blocks and 3 insect blocks (Fig. S3); the LAR site had 3 blocks for the plants and 2 for the insects (Fig. S4).

Model ranking and comparison of parameters in each site

For each site we compared the 16 models using the LOO criterion (Table 2, ΔLOO values). We found that models 1, 2 and 4 had consistently better goodness-of-fit than the others. The model incorporating all effects except the effect of phenological overlap on the probability of interaction (Model 4: $\lambda_{ij} \sim A_H + A_P$ + PO, Table 2) was the best model in the sites of CG, FAL and LAR. In the two southern sites (BF and F), we found that the model incorporating all effects except that of phenological overlap on the intensity of visits (Model 1: $\lambda_{ij} \sim A_H + A_P$ / $I_{ij} \sim$ PO, Table 2), was the best one. The model incorporating all effects (Model 0: $\lambda_{ij} \sim A_H + A_P$ + PO / $I_{ij} \sim$ PO, Table 2) was found as the best one only in the site of R, but was a suitable model (ΔLOO <4) in all the other sites (Table 2). We also compared the sum of model weights of the four parameters among sites (Table 2, Evidence ratio). We found that the effect of insect abundance on the intensity of interaction ($A_H \rightarrow \lambda_{ij}$) is always likely (*i.e.* the sum of their weights is always higher than 0.73, Table 2) and of large effect size in all sites (standardised coefficient higher than 1, Fig. 4). Likewise, we found that the effect of plant abundance on the intensity of interaction ($A_P \rightarrow \lambda_{ij}$) was always likely and had large effect size in most part of sites, except in the site of F (ER = 0.59, Table 2; standardised coefficient = 0.67, Fig. 4). The effects of phenological overlap on the probability of interaction (PO $\rightarrow I_{ij}$) and the intensity of visits (PO $\rightarrow \lambda_{ij}$), however, had variable plausibility among sites. The effect of phenological overlap on the probability of interaction was *likely* only in half of the sites (Table 2 and Fig. 4). The effect of phenological overlap on the intensity of visits was *not plausible* only in the two southern sites (BF and F) and *plausible* in the other four sites (LAR, R CG and FAL, Table 2 and Fig. 4). In all sites, the standardised coefficients of PO effects were always less than 1, thus suggesting a low effect size of phenology on interaction probability and intensity (Fig. 4).

DISCUSSION

Latitude affects the seasonality, advancing species phenologies at higher latitudes, and thus, can be a limiting factor for the phenological coupling of interacting species (Post *et al.* 2018). In this study we explored the effect of phenology overlap on a large network of species interactions in calcareous grasslands and how this effect could vary along a latitudinal gradient in France using empirical data on six plant-hoverfly networks. We identified plants and insects at the species level to build detailed interaction networks and hence avoid spurious generalisation levels. In order to better understand the determinants of variation in species interactions in space and time, we used the latitudinal gradient to consider variations linked to environmental cues and the entire flowering period to allow for seasonal variation (Valverde *et al.* 2016; Pellissier *et al.* 2018). One of the main problems of comparing networks along gradients is the dependence of networks metrics on network size (Staniczenko *et al.* 2013; Astegiano *et al.* 2015; Tylianakis & Morris 2017). In this study, we employed Bayesian Structural Equation Models (SEM) to link the numbers of visits to abundance and phenology overlap (PO) through latent probabilities of species interaction and expected numbers of visits per plant-pollinator dyad. We tested different models with variable numbers of effects and compared them in each site. SEM is an emergent approach increasingly used to investigate complex networks of relationship in ecological studies (Grace *et al.* 2010; Eisenhauer *et al.* 2015; Fan *et al.* 2016; Theodorou *et al.* 2017).

We found that in all sites the most important effect affecting pollinator visits was insect abundance (Table 2). Likewise we found that plant abundance was also a very important effect in most part of sites, except in the site of F (Table 2). Species abundance often explain the linkage level in pollination network studies (Olesen *et al.* 2008; Bartomeus *et al.* 2016; Chacoff *et al.* 2018; Pellissier *et al.* 2018) but it is often associated with the length of the phenology to better assess the general properties of the interaction network (Vázquez *et al.* 2009; Olito & Fox 2015). In accordance with this verbal prediction, we indeed found that the best models incorporated the effect of PO on either the probability or the intensity of interactions (Table 2). Phenology overlap generally cannot predict the probability of interaction on its own (Encinas-Viso *et al.* 2012; CaraDonna *et al.* 2017). Our findings do agree with this general predicament since no site favoured a model that only incorporated PO effects and because these effects always display lower effect sizes than the other variables. In our model, the effect of PO on the probability of interaction and the expected number of visits also vary along the latitudinal gradient (Fig. 4).

In general, we observed that southern sites (BF and F) showed shorter plant phenology and phenology overlap (PO) than the other four sites (Table 1). In these sites, plant species richness is higher and fewer visits were sampled, probably because the presence of specialist species with short phenophases may increase the number of forbidden or undetected links (Olesen *et al.* 2011; Martín González *et al.* 2012). Conversely, in sites where plant phenology is longer, PO is longer too, as observed in Normandie and Hauts-de-France (CG, FAL, LAR and R, Table 1). Moreover, when plant richness and specialization are lower, a higher number of visits can be observed (Table 1) because generalist species could interact without constraints. Indeed, in Normandie and Hauts-de-France we found that the effect of phenology overlap on the intensity of visits was always likely (PO $\rightarrow \lambda_{ij}$, Table 2) and we observed higher numbers of interactions in the first two/three blocks of insects and plants which also corresponded to blocks with longer PO (Fig. 3, S3, S4 and S5). A higher phenological overlap is expected to drive a higher probability of interactions and a larger number of visits (Olesen *et al.* 2011). In Occitanie, we did not find any effect of PO on the number of visits because the more densely visited blocks do not correspond to those with longer phenology overlap. Plant phenology can therefore drive the probability and the intensity of interactions in networks in which plant phenology is shorter, thus suggesting that syrphid flies may undergo selection for behavioural flexibility in order to maintain synchrony with their foraging resources (Iler *et al.* 2013; Ogilvie & Forrest 2017).

We also found that modularity decreased along the latitudinal gradient, with richer sites (BF and F) displaying higher modularity (as in Sebastián-González *et al.* 2015). In the two southern sites, higher modularity could be related to shorter phenologies and higher proportions of non-overlapping sets of species, which induce some form of temporal short-term specialisation (Lucas *et al.* 2018). However, modularity also seems to be influenced by species abundances and degrees (Schleuning *et al.* 2014), and is expected to increase with link specificity (Morente-López *et al.* 2018). Indeed, in these sites, species blocks match species degrees (Fig. 2 and S2), with generalist and specialist species forming separate blocks among both plants and insects (Martín González *et al.* 2012). With lower modularity and more generalist species, we expect a stronger relationship between phenology and the intensity of interactions because interactions are less influenced by insect preferences and more by seasonal rhythm and flower availability (Dormann *et al.* 2017). Thus, different phenophases might correspond to different compartments (Martín González *et al.* 2012; Morente-López *et al.* 2018), as observed in CG, FAL, LAR and R where higher overlap corresponded to higher numbers of observed visits. Although phenology improved model fit (Table 2), its effect size was modest (Fig. 4), which suggests that other types of data such as traits and phylogenies might help predict specific interactions. In our study, we did not consider competition among studied insect species or with other group of insects, such as bees which were present in all sites. Different types of pollinators with different abundances could have context-dependent effects on network topology (Valverde *et al.* 2016).

To conclude, plant phenology here drives the duration of the phenology overlap between plant and insects, which in turn influences either the probability of interaction or the expected number of visits, as well as network compartmentalization. Longer phenologies correspond to less constrained interactions (lower modularity), shorter phenologies to more constrained interactions (higher modularity), which in turn restrict the number of visits. Phenology overlap alone was not sufficient to explain interactions, as suggested elsewhere (CaraDonna *et al.* 2017). Plant and insect abundances played a substantial role to explain the number of visits (as in (Chacoff *et al.* 2018)) since abundances may affect partner choice (Trøjelsgaard *et al.* 2015). Our results, and the ability of the method used here to compare different effects on interaction patterns, suggest that the use of Bayesian SEM to compare networks of different sizes is a valuable tool which can help understand plant-pollinator networks (Eisenhauer *et al.* 2015). The use of latent variables can help predict the probability of interaction and the expected number of visits while avoiding circularity – the introduction of plant and insect specific random effects played the role of an implicit “degree” effect. Our results demonstrate the importance of considering differences in plant and insect phenologies to better predict their interactions in pollination networks at different latitudes. The use of morphological traits (*e.g.* tongue length, inter-tegular distance, …) together with species richness and phylogenies, on top of variables already used, might improve the modelling of interactions and could help better understand some forbidden or missing links in richer communities or considering other pollinators (*e.g.* wild bees).

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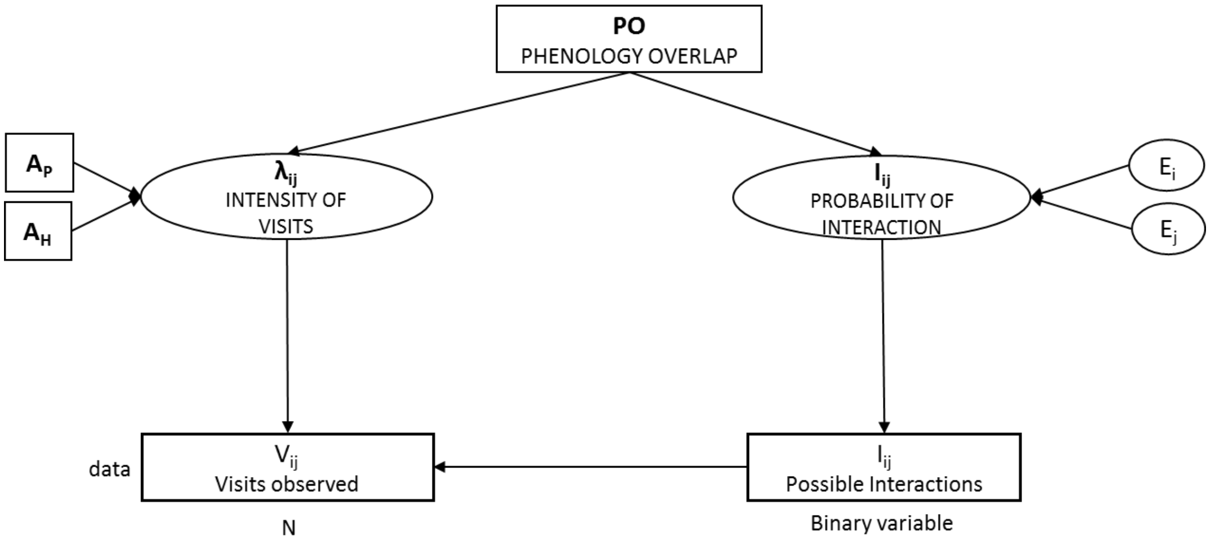

Figure 1. Summary diagram of the SEM model. We estimated 4 effects: the effect of plant abundance (AP → λij, coefficient λP), the effect of insect (hoverflies) abundance on the intensity of visits (AH → λij, λH), the effect of phenology overlap on the intensity of visits (PO → λij, λPO) and the effect of phenology overlap on the probability of interaction (PO → Iij, μPO). The phenology overlap (PO) is the number of phenologically active months that are shared by each pair of insect and plant species along the season. The intensity of visits (λij) and the probability of interaction are latent variables in the model. Effect-i and effect-p are random effects calculated by the model which represent the insect and plant degrees. The Iij (Possible interactions) is a binary variable and the Vij (visits observed) follow a Poisson distribution with an expected value given when the probability of interaction is predicted as "true". Rectangles represent observed variables while ovals represent unobserved influences.

Figure 2. Block clustering provided by LBM in the site of Fourches (F, Occitanie), overlaid on a heatmap of species phenology overlap. The LBM algorithm finds the best division for the group of insects and plants independently through fitting Poisson parameters in each block maximizing the likelihood (ICL). Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are separated by solid black lines. Colours correspond to the number of months that are shared by each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker colours. Numbers are the number of visits observed in the field for a given plant-insect pair.

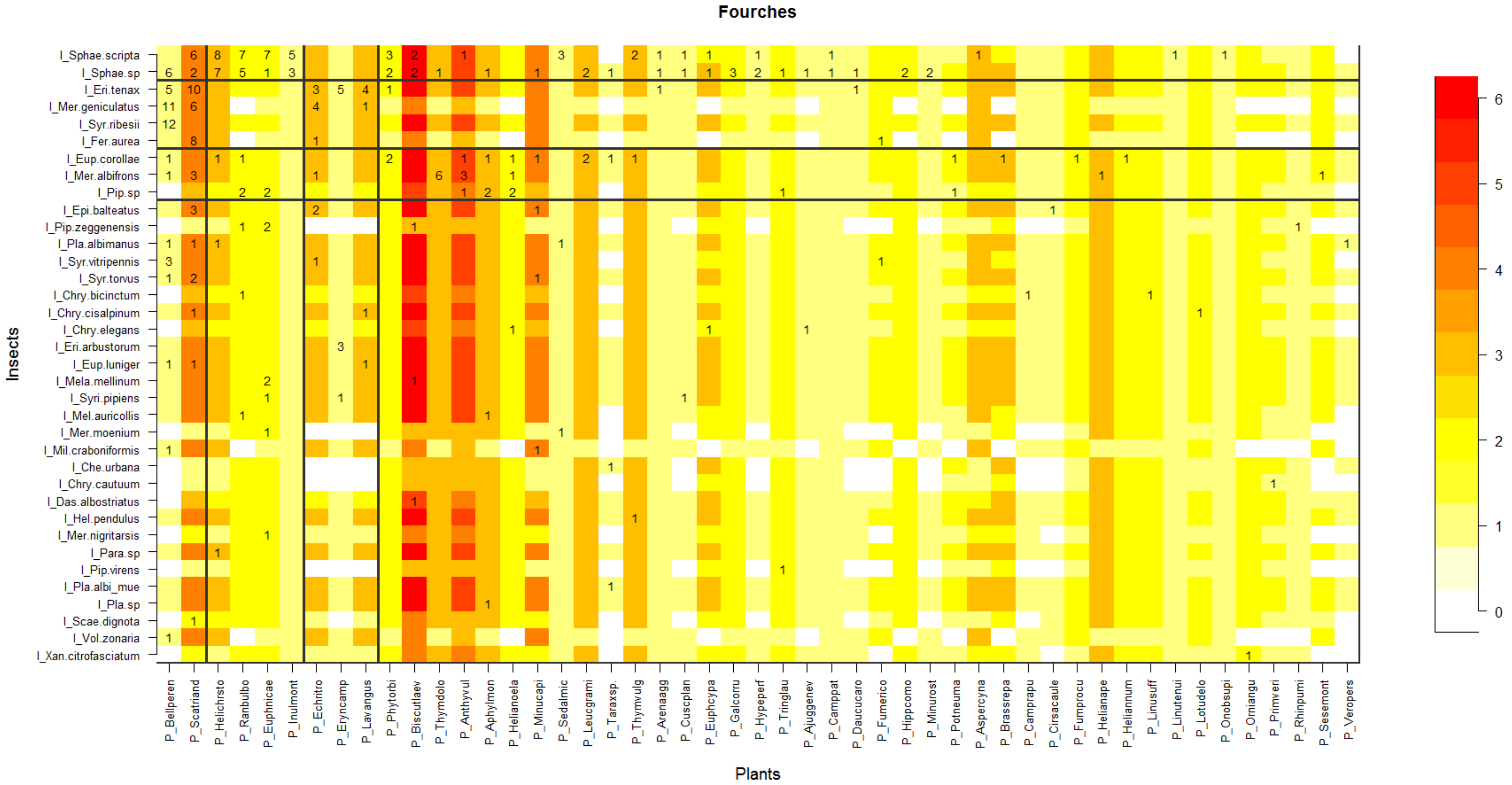

Figure 3. Block clustering provided by LBM in the site of Chateau Gaillard (CG, Normandie) overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are separated by solid black lines. Colours correspond to the number of months that are shared by each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker colours. Numbers are the number of visits observed in the field for a given plant-insect pair.

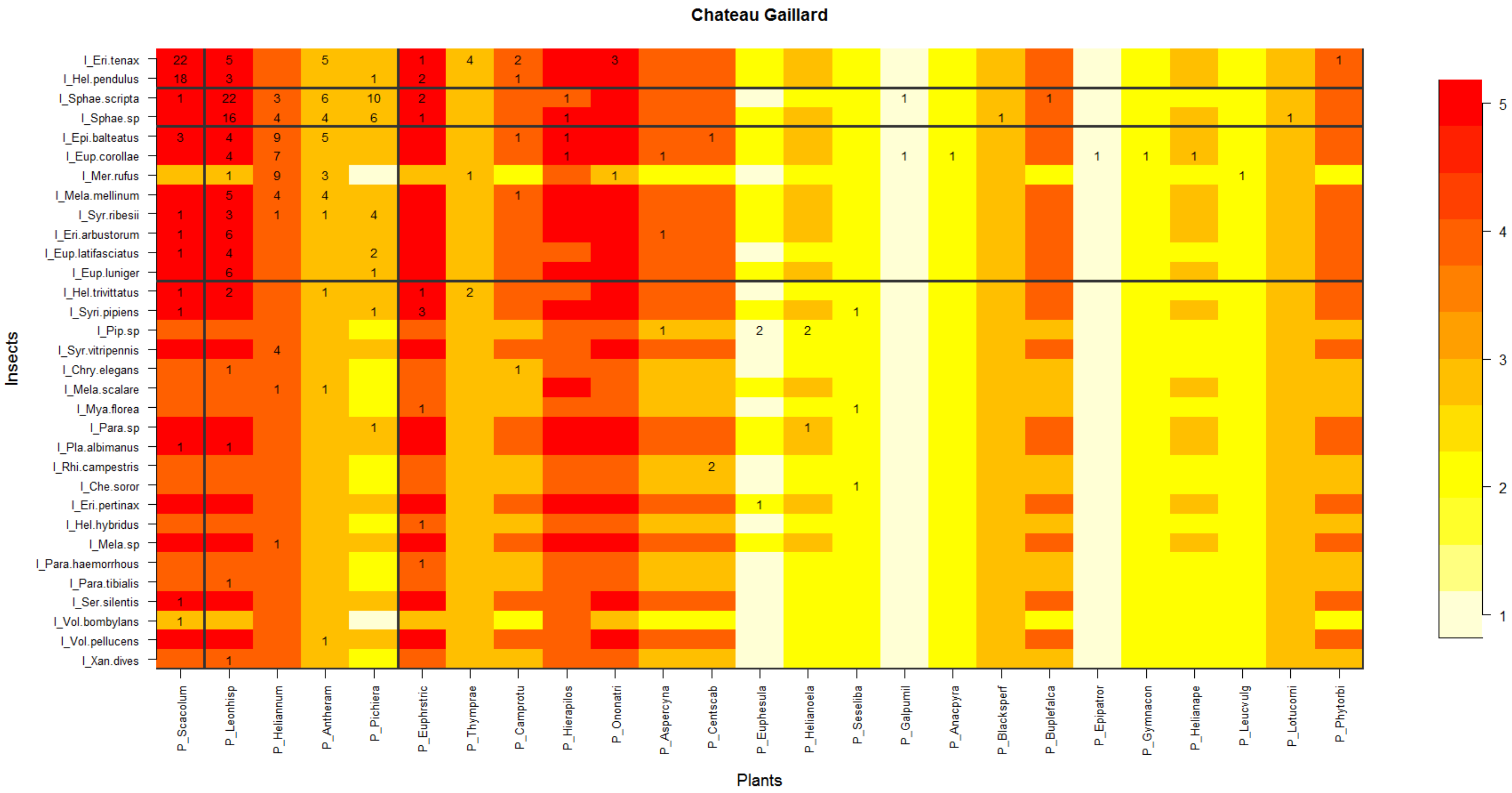

Figure 4. Summary diagram of the best models in all sites. The thickness of the arrows is scaled to Akaike weights (thin ER < 0.73; thick ER > 0.73, cf. Table 2). Standardised coefficients of the model average (computed based on the Akaike weighted model average) are reported next to the arrows. PO is the phenology overlap, I_{ij} is the probability of interaction, λ_{ij} is the intensity of visits, A_H and A_P are the hoverflies and plant abundances respectively.

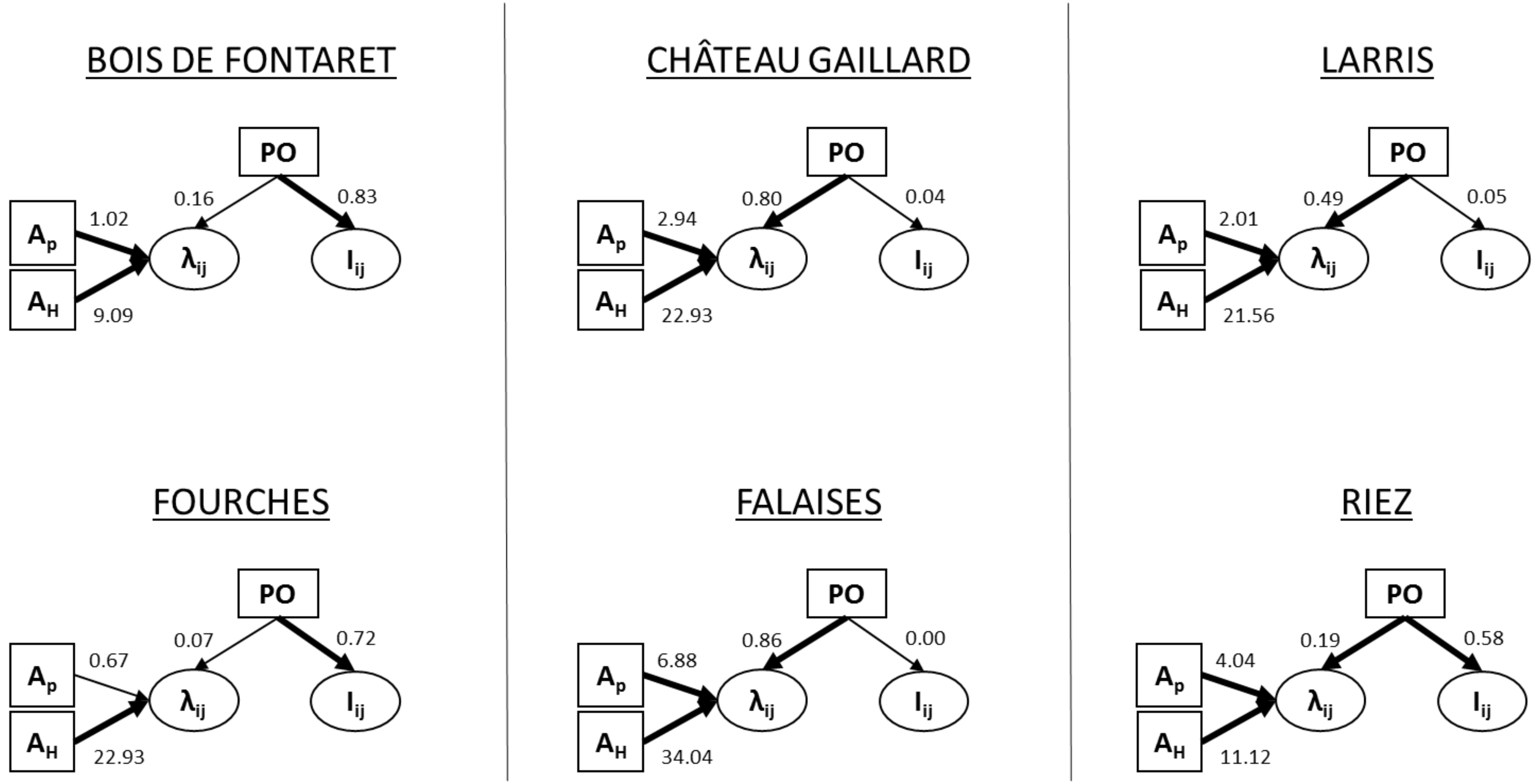

Table 1. Summary table of results obtained in each site (Bois de Fontaret [BF] and Fourches [F] in Occitanie, Château Gaillard [CG] and Falaises [FAL] in Normandie, Larris [LAR] and Riez [R] in Hauts-de-France). `H2'` and `d’` indices refer to specialization indices described by Blüthgen *et al.* (2006) and implemented in the R package `bipartite` (Dormann *et al.* 2009). The modularity score was obtained using the `leading-eigenvector` method described by Newman (2006) and implemented in the `igraph` package (Csardi & Nepusz 2006). LBM refers to latent block modelling as implemented in the R package `blockmodels` (Leger *et al.* 2015).

		Collected data				Specialization index			Species phenology			Modularity analysis	LBM	
Site	Region	Sampled insects	Insect species	Plant species	Recorded Interactions	H2' index	d' Insects (average + sd)	d' Plants (average + sd)	Insect (average + sd)	Plant (average + sd)	Phenology overlap (PO) (average + sd)	modularity score	blocks I	blocks P
BF	Occitanie	197	40	43	198	0.37	0.63 ± 0.17	0.58 ± 0.17	5.25 ± 1.51	2.14 ± 1.04	1.77 ± 1.03	0.53	2	2
F	Occitanie	223	36	49	286	0.33	0.57 ± 0.18	0.48 ± 0.19	5.61 ± 1.54	2.08 ± 1.13	1.78 ± 1.14	0.48	4	4
CG	Normandie	295	32	25	297	0.34	0.40 ± 0.21	0.47 ± 0.18	6.03 ± 1.00	3.28 ± 1.24	3.02 ± 1.17	0.34	4	3
FAL	Normandie	363	34	30	374	0.32	0.40 ± 0.18	0.41 ± 0.18	6.06 ± 1.13	3.57 ± 1.59	3.23 ± 1.51	0.23	3	4
LAR	Hauts-de-France	220	24	33	220	0.36	0.48 ± 0.19	0.45 ± 0.15	6.38 ± 0.82	3.18 ± 1.38	2.99 ± 1.36	0.37	2	3
R	Hauts-de-France	286	22	29	293	0.32	0.39 ± 0.16	0.40 ± 0.16	5.55 0.74	3.38 ± 1.47	3.11 ± 1.45	0.34	4	3
	Total	**1584**	**76**	**117**	**1668**									

Table 2. (i) Comparison of SEM models using the leave-one-out cross-validation criterion (LOO); (ii) evidence ratios (ER) of model effects in each site. (i) Models are ranked depending on the number of parameters used (from 0 to 4). The best models are the ones with ΔLOO=0 (underlined and bold values). The other suitable models are the ones with ΔLOO <4 (underlined and italic values). λ_{ij} is the intensity of visits, I_{ij} is the probability of interaction, A_H is the insect abundance, A_P is the plant abundance and PO is the phenology overlap. (ii) We compared 4 model effects: PO → I_{ij}, effect of the phenology overlap on the probability of interaction; PO → λ_{ij} effect of the phenology overlap on the intensity of visits; A_H → $\boldsymbol{\lambda_{ij}}$ and A_P → $\boldsymbol{\lambda_{ij}}$ effects of the hoverflies and plant abundances on the intensity of interaction. The ER limits for unlikelihood is 0.27, plausibility 0.5 and likelihood 0.73. Underlined and bold values represent the likely hypothesis only.

			Sites					
			BF	F	CG	FAL	LAR	R
	Model	*Nb of parameters*	*ΔLOO values*					
0	**λ_{ij} ~ A_H + A_P + PO / I_{ij} ~ PO**	4	*2.98*	*2.04*	*3.54*	*2.54*	*2.86*	**0.00**
1	**λ_{ij} ~ A_H + A_P / I_{ij} ~ PO**	3	**0.00**	**0.00**	36.75	64.04	10.37	*2.90*
2	λ_{ij} ~ A_P + PO / I_{ij} ~ PO	3	8.66	78.23	106.46	184.02	44.60	17.00
3	λ_{ij} ~ A_H + PO / I_{ij} ~ PO	3	6.63	*1.71*	8.09	73.62	11.24	11.42
4	**λ_{ij} ~ A_H + A_P + PO**	3	*2.86*	8.06	**0.00**	**0.00**	**0.00**	*2.24*
5	λ_{ij} ~ PO / I_{ij} ~ PO	2	14.69	73.20	109.85	223.86	55.67	23.09
6	λ_{ij} ~ A_H / I_{ij} ~ PO	2	*1.45*	*1.31*	33.53	119.04	27.23	19.76
7	λ_{ij} ~ A_P / I_{ij} ~ PO	2	9.84	72.16	156.61	256.04	47.99	21.53
8	λ_{ij} ~ A_H + PO	2	11.49	8.18	5.25	71.97	10.28	13.80
9	λ_{ij} ~ A_P + PO	2	10.71	88.67	103.46	182.14	44.36	17.94
10	λ_{ij} ~ A_H + A_P	2	24.36	14.04	36.10	66.82	10.51	4.26
11	I_{ij} ~ PO	1	11.78	68.52	154.26	272.98	64.12	32.39
12	λ_{ij} ~ PO	1	19.99	86.20	108.46	219.66	54.64	25.73
13	λ_{ij} ~ A_H	1	25.58	14.41	36.12	123.30	28.27	22.78
14	λ_{ij} ~ A_P	1	32.99	87.70	157.74	256.39	48.82	22.87
15	-	0	34.39	83.89	155.68	274.80	64.78	33.52
	Model effects		Evidence ratio (ER)					
	PO → I_{ij}		**0.88**	**0.98**	0.15	0.22	0.20	**0.74**
	PO → λ_{ij}		0.26	0.35	**1.00**	**1.00**	**0.99**	**0.79**
	A_H → λ_{ij}		**0.99**	**1.00**	**1.00**	**1.00**	**1.00**	**1.00**
	A_P → λ_{ij}		**0.74**	0.59	**0.93**	**1.00**	**0.99**	**1.00**

Supporting Information

The following Supporting Information is available for this article:

Appendix S1. Model code.

Appendix S2. Model script for the 16 models.

Appendix S3. Script modularity and latent block model analysis (LBM).

Figure S1. Sites location in France.

Figure S2. Block clustering provided by LBM in the site of Bois de Fontaret (BF, Occitanie), overlaid on a heatmap of species phenology overlap.

Figure S3. Block clustering provided by LBM in the site of Falaises (FAL, Normandie), overlaid on a heatmap of species phenology overlap.

Figure S4. Block clustering provided by LBM in the site of Larris (LAR, Hauts-de-France), overlaid on a heatmap of species phenology overlap.

Figure S5. Block clustering provided by LBM in the site of Riez (R, Hauts-de-France), overlaid on a heatmap of species phenology overlap.

Table S1. Table of transformed plant abundances.

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Supplementary Information

Does phenology explain plant-pollinator interactions at different latitudes? An assessment of its explanatory power in plant-hoverfly networks in French calcareous grasslands

N. de Manincor[1]*, N. Hautekeete[1], Y. Piquot[1], B. Schatz[2], C. Vanappelghem[3], F. Massol[1,4]

[1] Université de Lille, CNRS, UMR 8198 - Evo-Eco-Paleo, 59000 Lille, France
[2] CEFE, EPHE-PSL, CNRS, University of Montpellier, University of Paul Valéry Montpellier 3, IRD, Montpellier, France
[3] Conservatoire d'espaces naturels Nord et du Pas-de-Calais, 160 rue Achille Fanien - ZA de la Haye, 62190 LILLERS
[4] Univ. Lille, CNRS, Inserm, CHU Lille, Institut Pasteur de Lille, U1019 - UMR 8204 - CIIL - Center for Infection and Immunity of Lille, F-59000 Lille, France

Natasha de Manincor ORCID: 0000-0001-9696-125X
Nina Hautekeete ORCID: 0000-0002-6071-5601
Yves Piquot ORCID: 0000-0001-9977-8936
Bertrand Schatz ORCID: 0000-0003-0135-8154
François Massol ORCID: 0000-0002-4098-955X

*Corresponding author

E-mail adresses: natasha.de-manincor@univ-lille.fr, francois.massol@univ-lille.fr, nina.hautekeete@univ-lille.fr, yves.piquot@univ-lille.fr, Bertrand.SCHATZ@cefe.cnrs.fr, cedric.vanappelghem@espaces-naturels.fr

Appendix S1: Model Code

The model code (in JAGS language) given in this supplementary material refers to the “model Z0” which considers all four parameters (model effects, Table 2 in the main text). Overall, we estimated 16 models that included between 0 and 4 of the above-mentioned effects. To create the code for these other models, parameters should be removed following the order in the Tab. 2. The four parameters tested in the model are: (i) alpha: effect of the phenology overlap (cooc) on the probability of interaction; (ii) epsilon: effect of the phenology overlap on the intensity of visits; (iii) gamma: effect of the insect abundances (ab_I) on the intensity of visits; and (iv) delta: effect of the plant abundances (ab_P) on the intensity of visits.

```
model
{
  for( i in 1 : dim1 ) {
    for( p in 1 : dim2 ) {
      inter[i , p] ~ dbern(mu[i , p])
          logit(mu[i , p]) <- beta + alpha*cooc[i , p] + effet_I[i] + effet_P[p]
          lambda[i,p] <- exp(theta[i,p])
          theta[i,p] <- theta0 + gamma*ab_I[i] + delta*ab_P[p] + epsilon*log(1+cooc[i,p])
          visit[i,p] ~ dpois( inter[i,p]*lambda[i,p] )
          loglik[i,p] <- log(ifelse(visit[i,p]==0,1-mu[i,p]+mu[i , p]*dpois(visit[i,p],lambda[i,p]),mu[i ,
p]*dpois(visit[i,p],lambda[i,p])))
    }
  }

  for( i in 1 : dim1 ) {
    effet_I[i] ~ dnorm( 0.0,tau_I)
```

```
    }

    for( p in 1 : dim2 ) {
      effet_P[p] ~ dnorm( 0.0,tau_P)
    }

            tau_I ~ dexp( 10)
            tau_P ~ dexp( 10)
            alpha ~ dnorm(0,0.01)
            beta ~  dnorm(0,0.01)
            theta0 ~ dnorm(0,0.01)
            gamma ~ dnorm(0,0.01)
            delta ~ dnorm(0,0.01)
            epsilon ~ dnorm(0,0.01)
  }
```

Appendix 2: Model script for the 16 models – LOO values

The following generic script was applied to all the study sites using all 16 models. The script is separated in three blocks which communicate among them: the script options, the model definitions and the execution (model inference). We defined three options to set (i) the name of the directory (-d), (ii) the site (-s) and (iii) the type of model (-m).

We used, as an example, the information for the site of Bois de Fontaret (BF).

Exemple: Rscript (name) “script-SEMLOO_generique.R” “-d o-BFs-2016” “-s BFs”

In order to calculate the standardised coefficients for each parameters used, at the end of the third block, we added the functions to get the parameter values for each site and each model.

```
############################### BLOCK 1 – SCRIPT OPTION ###############################
library(optparse)
option_list = list(
    make_option(c("-d", "--dir"), type="character", default=NULL, help="directory",
metavar="character"),
    make_option(c("-s", "--site"), type="character", default=NULL, help="site name",
metavar="character"),
        make_option(c("-m", "--modele"), type="character", default="all", help="modele name",
metavar="character"))
opt_parser = OptionParser(option_list=option_list);
opt = parse_args(opt_parser);
site<-opt$site
dossier<-opt$dir
################################## Librairies #########################
library(bipartite)
library(vegan)
library(igraph)
```

```
library(magrittr)
library(dummies)
library(MuMIn)
library(rjags)
library(boot)
library(R2jags)
library(coda)
library(lattice)
library(ggplot2)
library(loo)
library(matrixStats)
########################## Function to record the LOO values ########################
write_values<-function(x, f, app)
{
        write.table(x, append=app, file=f, sep="\t", row.names=T, col.names=T, quote=F)
}
######################### BLOCK 2 – MODEL FUNCTIONS ###########################
#Model function and model initialization: one function for each model from model Z15, with 0
parameters, to Z00 with all the parameters#
### MODEL Z015
mZ015<-function(){
        init.funZ015 <-function(){
          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "theta0" =
rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
        }
```

```
	mod.Z015<<-jags(inits=init.funZ015,model.file = "modelZ015_code.txt",data =
list("visit","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","beta","theta0", "loglik"),n.chains = 1, n.iter=1000000,
n.burnin = 250000, n.thin = 250)
	mod.Z015.mcmc<-as.mcmc(mod.Z015)
	mZ015<-mod.Z015$BUGSoutput$sims.list
	mZ015.deviance<-mZ015$deviance
	mZ015.loglik<-mZ015$loglik
	dimSEM<-dim(mZ015.loglik)[1]
	list.mZ015<-sapply(1:dimSEM,function(x) matrix(mZ015.loglik[x,,],nrow=dim1*dim2))
	list.tmZ015<-(t(list.mZ015))
	mZ015.loo<-loo(list.tmZ015)
	loo_file<-paste(dossier, "/", site, "_Z015_loo.txt", sep="")
	write_values("mZ015", app=F, loo_file)
	mZ015_loo_pointwise<-mZ015.loo$pointwise
	mZ015_loo_pareto_k<-mZ015.loo$pareto_k
	mZ015.loo$pareto_k<-NULL
	mZ015.loo$pointwise<-NULL
	write_values(as.matrix(mZ015.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z015.RData", sep=""))
}
### MODEL Z014
mZ014<-function(){
	init.funZ014 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "delta" = rnorm(1,0,1),
"theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
```

```
		}
		mod.Z014<<-jags(inits=init.funZ014,model.file = "modelZ014_code.txt",data =
list("visit","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","delta","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z014.mcmc<-as.mcmc(mod.Z014)
		mZ014<-mod.Z014$BUGSoutput$sims.list
		mZ014.deviance<-mZ014$deviance
		mZ014.loglik<-mZ014$loglik
		dimSEM<-dim(mZ014.loglik)[1]
		list.mZ014<-sapply(1:dimSEM,function(x) matrix(mZ014.loglik[x,,],nrow=dim1*dim2))
		list.tmZ014<-(t(list.mZ014))
		mZ014.loo<-loo(list.tmZ014)
		mZ014.loo
		loo_file<-paste(dossier, "/", site, "_Z014_loo.txt", sep="")
		write_values("mZ014", app=T, loo_file)
		mZ014_loo_pointwise<-mZ014.loo$pointwise
		mZ014_loo_pareto_k<-mZ014.loo$pareto_k
		mZ014.loo$pareto_k<-NULL
		mZ014.loo$pointwise<-NULL
		write_values(as.matrix(mZ014.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z014.RData", sep=""))
}
### MODEL Z013
mZ013<-function(){
		init.funZ013 <-function(){
```

```
            list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =
rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
"inter"=inter0)
        }
        mod.Z013<<-jags(inits=init.funZ013,model.file = "modelZ013_code.txt",data =
list("visit","ab_I","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","gamma","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
        mod.Z013.mcmc<-as.mcmc(mod.Z013)
        mZ013<-mod.Z013$BUGSoutput$sims.list
        mZ013.deviance<-mZ013$deviance
        mZ013.loglik<-mZ013$loglik
        dimSEM<-dim(mZ013.loglik)[1]
        list.mZ013<-sapply(1:dimSEM,function(x) matrix(mZ013.loglik[x,,],nrow=dim1*dim2))
        list.tmZ013<-(t(list.mZ013))
        mZ013.loo<-loo(list.tmZ013)
        mZ013.loo
        loo_file<-paste(dossier, "/", site, "_Z013_loo.txt", sep="")
        write_values("mZ013", app=T, loo_file)
        mZ013_loo_pointwise<-mZ013.loo$pointwise
        mZ013_loo_pareto_k<-mZ013.loo$pareto_k
        mZ013.loo$pareto_k<-NULL
        mZ013.loo$pointwise<-NULL
        write_values(as.matrix(mZ013.loo), app=T, loo_file)
        save.image(paste(dossier, "/", site, "_Z013.RData", sep=""))
}
```

```
### MODEL Z012
mZ012<-function(){
	init.funZ012 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "theta0" =
rnorm(1,0,1), "epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
"inter"=inter0)
	}
	mod.Z012<<-jags(inits=init.funZ012,model.file = "modelZ012_code.txt",data =
list("cooc","visit","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z012.mcmc<-as.mcmc(mod.Z012)
	mZ012<-mod.Z012$BUGSoutput$sims.list
	mZ012.deviance<-mZ012$deviance
	mZ012.loglik<-mZ012$loglik
	dimSEM<-dim(mZ012.loglik)[1]
	list.mZ012<-sapply(1:dimSEM,function(x) matrix(mZ012.loglik[x,,],nrow=dim1*dim2))
	list.tmZ012<-(t(list.mZ012))
	mZ012.loo<-loo(list.tmZ012)
	mZ012.loo
	loo_file<-paste(dossier, "/", site, "_Z012_loo.txt", sep="")
	write_values("mZ012", app=T, loo_file)
	mZ012_loo_pointwise<-mZ012.loo$pointwise
	mZ012_loo_pareto_k<-mZ012.loo$pareto_k
	mZ012.loo$pareto_k<-NULL
	mZ012.loo$pointwise<-NULL
```

```
		write_values(as.matrix(mZ012.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z012.RData", sep=""))
}
### MODEL Z011
mZ011<-function(){
		init.funZ011 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z011<<-jags(inits=init.funZ011,model.file = "modelZ011_code.txt",data = list("cooc","visit","dim1","dim2"),parameters.to.save = c("mu","effet_I","effet_P","tau_I","tau_P","alpha","beta","theta0","loglik"),n.chains = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z011.mcmc<-as.mcmc(mod.Z011)
		mZ011<-mod.Z011$BUGSoutput$sims.list
		mZ011.deviance<-mZ011$deviance
		mZ011.loglik<-mZ011$loglik
		dimSEM<-dim(mZ011.loglik)[1]
		list.mZ011<-sapply(1:dimSEM,function(x) matrix(mZ011.loglik[x,,],nrow=dim1*dim2))
		list.tmZ011<-(t(list.mZ011))
		mZ011.loo<-loo(list.tmZ011)
		mZ011.loo
		loo_file<-paste(dossier, "/", site, "_Z011_loo.txt", sep="")
		write_values("mZ011", app=T, loo_file)
		mZ011_loo_pointwise<-mZ011.loo$pointwise
		mZ011_loo_pareto_k<-mZ011.loo$pareto_k
```

```
	mZ011.loo$pareto_k<-NULL
	mZ011.loo$pointwise<-NULL
	write_values(as.matrix(mZ011.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z011.RData", sep=""))
}
### MODEL Z010
mZ010<-function(){
	init.funZ010 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =
rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
	mod.Z010<<-jags(inits=init.funZ010,model.file = "modelZ010_code.txt",data =
list("visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","gamma","delta","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z010.mcmc<-as.mcmc(mod.Z010)
	mZ010<-mod.Z010$BUGSoutput$sims.list
	mZ010.deviance<-mZ010$deviance
	mZ010.loglik<-mZ010$loglik
	dimSEM<-dim(mZ010.loglik)[1]
	list.mZ010<-sapply(1:dimSEM,function(x) matrix(mZ010.loglik[x,,],nrow=dim1*dim2))
	list.tmZ010<-(t(list.mZ010))
	mZ010.loo<-loo(list.tmZ010)
	mZ010.loo
	loo_file<-paste(dossier, "/", site, "_Z010_loo.txt", sep="")
```

```
		write_values("mZ010", app=T, loo_file)
		mZ010_loo_pointwise<-mZ010.loo$pointwise
		mZ010_loo_pareto_k<-mZ010.loo$pareto_k
		mZ010.loo$pareto_k<-NULL
		mZ010.loo$pointwise<-NULL
		write_values(as.matrix(mZ010.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z010.RData", sep=""))
}
### MODEL Z09
mZ09<-function(){
		init.funZ09 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "delta" = rnorm(1,0,1),
"theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z09<<-jags(inits=init.funZ09,model.file = "modelZ09_code.txt",data =
list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","delta","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z09.mcmc<-as.mcmc(mod.Z09)
		mZ09<-mod.Z09$BUGSoutput$sims.list
		mZ09.deviance<-mZ09$deviance
		mZ09.loglik<-mZ09$loglik
		dimSEM<-dim(mZ09.loglik)[1]
		list.mZ09<-sapply(1:dimSEM,function(x) matrix(mZ09.loglik[x,,],nrow=dim1*dim2))
		list.tmZ09<-(t(list.mZ09))
```

```
		mZ09.loo<-loo(list.tmZ09)
		mZ09.loo
		loo_file<-paste(dossier, "/", site, "_Z09_loo.txt", sep="")
		write_values("mZ09", app=T, loo_file)
		mZ09_loo_pointwise<-mZ09.loo$pointwise
		mZ09_loo_pareto_k<-mZ09.loo$pareto_k
		mZ09.loo$pareto_k<-NULL
		mZ09.loo$pointwise<-NULL
		write_values(as.matrix(mZ09.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z09.RData", sep=""))
}
### MODEL Z08
mZ08<-function(){
		init.funZ08 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =
rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z08<<-jags(inits=init.funZ08,model.file = "modelZ08_code.txt",data =
list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","gamma","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z08.mcmc<-as.mcmc(mod.Z08)
		mZ08<-mod.Z08$BUGSoutput$sims.list
		mZ08.deviance<-mZ08$deviance
		mZ08.loglik<-mZ08$loglik
```

```
		dimSEM<-dim(mZ08.loglik)[1]
		list.mZ08<-sapply(1:dimSEM,function(x) matrix(mZ08.loglik[x,,],nrow=dim1*dim2))
		list.tmZ08<-(t(list.mZ08))
		mZ08.loo<-loo(list.tmZ08)
		mZ08.loo
		loo_file<-paste(dossier, "/", site, "_Z08_loo.txt", sep="")
		write_values("mZ08", app=T, loo_file)
		mZ08_loo_pointwise<-mZ08.loo$pointwise
		mZ08_loo_pareto_k<-mZ08.loo$pareto_k
		mZ08.loo$pareto_k<-NULL
		mZ08.loo$pointwise<-NULL
		write_values(as.matrix(mZ08.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z08.RData", sep=""))
}
### MODEL Z07
mZ07<-function(){
		init.funZ07 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "delta" =
rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
"inter"=inter0)
		}
		mod.Z07<<-jags(inits=init.funZ07,model.file = "modelZ07_code.txt",data =
list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","delta","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z07.mcmc<-as.mcmc(mod.Z07)
```

```
		mZ07<-mod.Z07$BUGSoutput$sims.list
		mZ07.deviance<-mZ07$deviance
		mZ07.loglik<-mZ07$loglik
		dimSEM<-dim(mZ07.loglik)[1]
		list.mZ07<-sapply(1:dimSEM,function(x) matrix(mZ07.loglik[x,,],nrow=dim1*dim2))
		list.tmZ07<-(t(list.mZ07))
		mZ07.loo<-loo(list.tmZ07)
		mZ07.loo
		loo_file<-paste(dossier, "/", site, "_Z07_loo.txt", sep="")
		write_values("mZ07", app=T, loo_file)
		mZ07_loo_pointwise<-mZ07.loo$pointwise
		mZ07_loo_pareto_k<-mZ07.loo$pareto_k
		mZ07.loo$pareto_k<-NULL
		mZ07.loo$pointwise<-NULL
		write_values(as.matrix(mZ07.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z07.RData", sep=""))
}
### MODEL Z06
mZ06<-function(){
		init.funZ06 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"
= rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
"inter"=inter0)
		}
		mod.Z06<<-jags(inits=init.funZ06,model.file = "modelZ06_code.txt",data =
list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
```

```
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
        mod.Z06.mcmc<-as.mcmc(mod.Z06)
        mZ06<-mod.Z06$BUGSoutput$sims.list
        mZ06.deviance<-mZ06$deviance
        mZ06.loglik<-mZ06$loglik
        dimSEM<-dim(mZ06.loglik)[1]
        list.mZ06<-sapply(1:dimSEM,function(x) matrix(mZ06.loglik[x,,],nrow=dim1*dim2))
        list.tmZ06<-(t(list.mZ06))
        mZ06.loo<-loo(list.tmZ06)
        mZ06.loo
        loo_file<-paste(dossier, "/", site, "_Z06_loo.txt", sep="")
        write_values("mZ06", app=T, loo_file)
        mZ06_loo_pointwise<-mZ06.loo$pointwise
        mZ06_loo_pareto_k<-mZ06.loo$pareto_k
        mZ06.loo$pareto_k<-NULL
        mZ06.loo$pointwise<-NULL
        write_values(as.matrix(mZ06.loo), app=T, loo_file)
        save.image(paste(dossier, "/", site, "_Z06.RData", sep=""))
}
### MODEL Z05
mZ05<-function(){
        init.funZ05 <-function(){
          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "theta0"
= rnorm(1,0,1), "epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
"inter"=inter0)
```

```
	}
	mod.Z05<<-jags(inits=init.funZ05,model.file = "modelZ05_code.txt",data =
list("cooc","visit","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z05.mcmc<-as.mcmc(mod.Z05)
	mZ05<-mod.Z05$BUGSoutput$sims.list
	mZ05.deviance<-mZ05$deviance
	mZ05.loglik<-mZ05$loglik
	dimSEM<-dim(mZ05.loglik)[1]
	list.mZ05<-sapply(1:dimSEM,function(x) matrix(mZ05.loglik[x,,],nrow=dim1*dim2))
	list.tmZ05<-(t(list.mZ05))
	mZ05.loo<-loo(list.tmZ05)
	mZ05.loo
	loo_file<-paste(dossier, "/", site, "_Z05_loo.txt", sep="")
	write_values("mZ05", app=T, loo_file)
	mZ05_loo_pointwise<-mZ05.loo$pointwise
	mZ05_loo_pareto_k<-mZ05.loo$pareto_k
	mZ05.loo$pareto_k<-NULL
	mZ05.loo$pointwise<-NULL
	write_values(as.matrix(mZ05.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z05.RData", sep=""))
}
### MODEL Z04
mZ04<-function(){
	init.funZ04 <-function(){
```

```
            list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =
rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
        }
        mod.Z04<<-jags(inits=init.funZ04,model.file = "modelZ04_code.txt",data =
list("cooc","visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","gamma","delta","beta","theta0","epsilon","loglik"),n.chai
ns = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
        mod.Z04.mcmc<-as.mcmc(mod.Z04)
        mZ04<-mod.Z04$BUGSoutput$sims.list
        mZ04.deviance<-mZ04$deviance
        mZ04.loglik<-mZ04$loglik
        dimSEM<-dim(mZ04.loglik)[1]
        list.mZ04<-sapply(1:dimSEM,function(x) matrix(mZ04.loglik[x,,],nrow=dim1*dim2))
        list.tmZ04<-(t(list.mZ04))
        mZ04.loo<-loo(list.tmZ04)
        mZ04.loo
        loo_file<-paste(dossier, "/", site, "_Z04_loo.txt", sep="")
        write_values("mZ04", app=T, loo_file)
        mZ04_loo_pointwise<-mZ04.loo$pointwise
        mZ04_loo_pareto_k<-mZ04.loo$pareto_k
        mZ04.loo$pareto_k<-NULL
        mZ04.loo$pointwise<-NULL
        write_values(as.matrix(mZ04.loo), app=T, loo_file)
        save.image(paste(dossier, "/", site, "_Z04.RData", sep=""))
}
```

```
### MODEL Z03
mZ03<-function(){
	init.funZ03 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"
= rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
	mod.Z03<<-jags(inits=init.funZ03,model.file = "modelZ03_code.txt",data =
list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","beta","theta0","epsilon","loglik"),n.cha
ins = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z03.mcmc<-as.mcmc(mod.Z03)
	mZ03<-mod.Z03$BUGSoutput$sims.list
	mZ03.deviance<-mZ03$deviance
	mZ03.loglik<-mZ03$loglik
	dimSEM<-dim(mZ03.loglik)[1]
	list.mZ03<-sapply(1:dimSEM,function(x) matrix(mZ03.loglik[x,,],nrow=dim1*dim2))
	list.tmZ03<-(t(list.mZ03))
	mZ03.loo<-loo(list.tmZ03)
	mZ03.loo
	loo_file<-paste(dossier, "/", site, "_Z03_loo.txt", sep="")
	write_values("mZ03", app=T, loo_file)
	mZ03_loo_pointwise<-mZ03.loo$pointwise
	mZ03_loo_pareto_k<-mZ03.loo$pareto_k
	mZ03.loo$pareto_k<-NULL
	mZ03.loo$pointwise<-NULL
```

```
		write_values(as.matrix(mZ03.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z03.RData", sep=""))
}
### MODEL Z02
mZ02<-function(){
		init.funZ02 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1, "beta" = rnorm(1,0,1), "delta" =
rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z02<<-jags(inits=init.funZ02,model.file = "modelZ02_code.txt",data =
list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","delta","beta","theta0","epsilon","loglik"),n.chain
s = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z02.mcmc<-as.mcmc(mod.Z02)
		mZ02<-mod.Z02$BUGSoutput$sims.list
		mZ02.deviance<-mZ02$deviance
		mZ02.loglik<-mZ02$loglik
		dimSEM<-dim(mZ02.loglik)[1]
		list.mZ02<-sapply(1:dimSEM,function(x) matrix(mZ02.loglik[x,,],nrow=dim1*dim2))
		list.tmZ02<-(t(list.mZ02))
		mZ02.loo<-loo(list.tmZ02)
		mZ02.loo
		loo_file<-paste(dossier, "/", site, "_Z02_loo.txt", sep="")
		write_values("mZ02", app=T, loo_file)
		mZ02_loo_pointwise<-mZ02.loo$pointwise
```

```
		mZ02_loo_pareto_k<-mZ02.loo$pareto_k
		mZ02.loo$pareto_k<-NULL
		mZ02.loo$pointwise<-NULL
		write_values(as.matrix(mZ02.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z02.RData", sep=""))
}
### MODEL Z01
mZ01<-function(){
		init.funZ01 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma" = rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z01<<-jags(inits=init.funZ01,model.file = "modelZ01_code.txt",data = list("cooc","visit","ab_I","ab_P", "dim1", "dim2"),parameters.to.save = c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","delta","beta","theta0","loglik"),n.chains = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z01.mcmc<-as.mcmc(mod.Z01)
		mZ01<-mod.Z01$BUGSoutput$sims.list
		mZ01.deviance<-mZ01$deviance
		mZ01.loglik<-mZ01$loglik
		dimSEM<-dim(mZ01.loglik)[1]
		list.mZ01<-sapply(1:dimSEM,function(x) matrix(mZ01.loglik[x,,],nrow=dim1*dim2))
		list.tmZ01<-(t(list.mZ01))
		mZ01.loo<-loo(list.tmZ01)
		mZ01.loo
```

```
		loo_file<-paste(dossier, "/", site, "_Z01_loo.txt", sep="")
		write_values("mZ01", app=T, loo_file)
		mZ01_loo_pointwise<-mZ01.loo$pointwise
		mZ01_loo_pareto_k<-mZ01.loo$pareto_k
		mZ01.loo$pareto_k<-NULL
		mZ01.loo$pointwise<-NULL
		write_values(as.matrix(mZ01.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z01.RData", sep=""))
}
### MODEL Z00
mZ00<-function(){
		init.funZ00 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"
= rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z00<<-jags(inits=init.funZ00,model.file = "modelZ00_code.txt",data =
list("cooc","visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","delta","beta","theta0","epsilon","loglik
"),n.chains = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z00.mcmc<-as.mcmc(mod.Z00)
		mZ00<-mod.Z00$BUGSoutput$sims.list
		mZ00.deviance<-mZ00$deviance
		mZ00.loglik<-mZ00$loglik
		dimSEM<-dim(mZ00.loglik)[1]
		list.mZ00<-sapply(1:dimSEM,function(x) matrix(mZ00.loglik[x,,],nrow=dim1*dim2))
```

```
	list.tmZ00<-(t(list.mZ00))
	mZ00.loo<-loo(list.tmZ00)
	mZ00.loo
	loo_file<-paste(dossier, "/", site, "_Z00_loo.txt", sep="")
	write_values("mZ00", app=T, loo_file)
	mZ00_loo_pointwise<-mZ00.loo$pointwise
	mZ00_loo_pareto_k<-mZ00.loo$pareto_k
	mZ00.loo$pareto_k<-NULL
	mZ00.loo$pointwise<-NULL
	write_values(as.matrix(mZ00.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z00.RData", sep=""))
}
###### end model functions
print("JOB DONE")
####################################################
###	Network information (do not change)	###
####################################################
##############################BLOCK 3 – MODEL EXECUTION #######################
#launch_modele<-function(){
	ntw<-read.table(paste(dossier, "/", site, "_ntw.txt", sep=""),
sep="\t",header=T,row.names=1)
	dim1<-dim(ntw)[1]
	dim2<-dim(ntw)[2]
	web<-as.matrix(ntw,dim1,dim2)
	inter0<-dget(paste(dossier, "/", site, "_web_i.txt", sep=""))
	cooc<-dget(paste(dossier, "/", site, "_co.txt", sep=""))
```

```
	visit<-read.table(paste(dossier, "/", site, "_ntw.txt", sep=""),sep="\t",header=T)
	visit<-as.matrix(visit)
	abundanceI<-read.table(paste(dossier, "/", site, "_abI.txt", sep=""), sep="\t", header=T)
	ab_I <- log(abundanceI[,2])
	abundanceP<-read.table(paste(dossier, "/", site, "_abP.txt", sep=""), sep="\t", header=T)
	ab_P <- log(abundanceP[,2])
	if(opt$modele == "all")
	{
		print("modele: all")
		for(i in 0:15)
		{
			print(paste("COMPUTING MODELE ", i, "\n", sep=""))
			mod<-eval(parse(text=paste("mZ0", i, sep="")))
			mod()

		}
	}else{
		print(paste("modele: ", opt$modele), sep="")
		mod<-eval(parse(text=paste("m", opt$modele, sep="")))		#recupération de la fonction du modele
		mod()
	}
#### end model execution
#launch_modele()

################################PARAMETER VALUES##############################
```

```
library(optparse)
option_list = list(
		make_option(c("-d", "--dir"), type="character", default=NULL, help="model directory", 
metavar="character"),
		make_option(c("-s", "--site"), type="character", default=NULL, help="site name", 
metavar="character"))
opt_parser = OptionParser(option_list=option_list);
opt = parse_args(opt_parser);
rdata<-list.files(opt$dir, pattern="*_Z015.RData")
load(paste(opt$dir, "/", rdata, sep=""))  #chargement du RData qui contient tous les modèles pour un 
site donné
print(paste("RData ", rdata, " loaded", sep=""))
for(mod in ls(pattern="mod.Z0*"))
{
		print(paste("getting values from ", mod, sep=""))
		model<-eval(parse(text=mod))
		if(is.null(model$BUGSoutput$mean$alpha)){model$BUGSoutput$mean$alpha<-NA}
		if(is.null(model$BUGSoutput$mean$beta)){model$BUGSoutput$mean$beta<-NA}
		if(is.null(model$BUGSoutput$mean$delta)){model$BUGSoutput$mean$delta<-NA}
		if(is.null(model$BUGSoutput$mean$epsilon)){model$BUGSoutput$mean$epsilon<-NA}
		if(is.null(model$BUGSoutput$mean$gamma)){model$BUGSoutput$mean$gamma<-NA}
		val<-matrix(c(model$BUGSoutput$mean$alpha, model$BUGSoutput$mean$beta, 
model$BUGSoutput$mean$delta, model$BUGSoutput$mean$epsilon, 
model$BUGSoutput$mean$gamma), 1, 5, dimnames=list("values", c("alpha", "beta", "delta", 
"epsilon", "gamma")))
```

```
		write.table(val, file=paste(opt$dir, "/", opt$site, "_", mod, "_values.txt", sep=""), quote=F,
sep="\t", row.names=F, col.names=T)
}
```

Appendix S3: Modularity and latent block model analysis

We calculated the modularity of the network using the `cluster_leading_eigen` method for modularity optimization implemented in the `igraph` package (Csardi and Nepusz 2006, Newman 2006). We then performed latent block models (LBM) using the `BM_poisson` method for quantitative network data implemented in the `blockmodels` package (Leger et al. 2015). Blocks are calculated separately for the two groups (insect and plant) based on the number of visits (*i.e.* a weighted network). The algorithm finds the best divisions of insects and plants through fitting one Poisson parameter in each block of the visit matrix, thus essentially maximizing the ICL (Integrated Completed Likelihood; Biernacki et al. 2000, Daudin et al. 2007).

```
library(bipartite)
library(vegan)
library(igraph)
library(dummies)
library(blockmodels)
library(ade4)
library(fields)

#site data (ex: Bois de Fontaret, BFs)
BFs<-read.table("ntwBFs.txt",header=T,sep="\t")
webBFs <- as.matrix(BFs)
########################## Modularity analysis, binary data ########################
BFs.graph.bin<-graph_from_incidence_matrix(webBFs,multiple=F) #binary
BFs.bin.cle<-cluster_leading_eigen(BFs.graph.bin)
BFs.bin.cle
#get phenology overlap matrix
```

```
coBF<-dget("coBFs.txt")
######################### LBM code: LBM analysis following Poisson ##################
bmi_BFs<-BM_poisson('LBM', webBFs)
bmi_BFs$estimate()
numi_BFs<-which.max(bmi_BFs$ICL)
densi_BFs<-sum(webBFs)/(nrow(webBFs)*ncol(webBFs))
probi_BFs<-bmi_BFs$model_parameters[[numi_BFs]]$lambda
row.nb.gpi<-nrow(probi_BFs)
col.nb.gpi<-ncol(probi_BFs)
prob.rowi<-bmi_BFs$memberships[[numi_BFs]]$Z1
hh.namei<-rownames(webBFs)
mbrshp.hhi<-apply(prob.rowi,1,which.max)
ls.freq.rowi<-rowSums(webBFs)
res.hhi<-cbind.data.frame(hh.namei=hh.namei, mbrshp.hhi=mbrshp.hhi, freq.hhi=ls.freq.rowi)
res.hh.ordi<-res.hhi[order(res.hhi$freq.hhi),]
cpt=0
for(k in 1: (nrow(res.hh.ordi)-1))
{
  if (res.hh.ordi$mbrshp.hhi[k] !=res.hh.ordi$mbrshp.hhi[k+1]) cpt=cpt+1
}
nb.diff.hhi=cpt-(length(levels(as.factor(res.hh.ordi$mbrshp.hhi)))-1)
#write tables
write.table(res.hh.ordi,sep="\t",row.names=FALSE)
prob.coli<-bmi_BFs$memberships[[numi_BFs]]$Z2
sp.namei<-colnames(webBFs)
mbrshp.spi<-apply(prob.coli,1,which.max)
```

```
ls.freq.coli<-colSums(webBFs)
res.spi<-cbind.data.frame(sp.namei=sp.namei, mbrshp.spi=mbrshp.spi, freq.spi=ls.freq.coli)
res.sp.ordi<-res.spi[order(res.spi$freq.spi),]
cpt=0
for (k in 1: (nrow(res.sp.ordi)-1))
{
  if(res.sp.ordi$mbrshp.spi[k] !=res.sp.ordi$mbrshp.spi[k+1]) cpt=cpt+1
}
nb.diff.spi=cpt-(length(levels(as.factor(res.sp.ordi$mbrshp.spi)))-1)
res.sp.ord2i=res.spi[order(res.spi$mbrshp.spi),]
write.table(res.sp.ordi,sep="\t",row.names=FALSE)
write.table(probi_BFs,file="_prob_BFs",sep="\t",row.names=FALSE)

################################ Matrix organization ###############
par(mfrow=c(1,1))
webBFs2<-webBFs
webBFs[which(webBFs>1)]=1
nb.row=nrow(webBFs)
nb.col=ncol(webBFs)
nds=webBFs
nps=coBF
res.prob=read.table("_prob_BFs",sep="\t",h=TRUE)
ls.ord.col.prob=order(colSums(res.prob),decreasing=TRUE)
ls.ord.row.prob=order(rowSums(res.prob),decreasing=TRUE)
ls.ord.hhi=sapply(res.hhi$mbrshp.hhi,function(x) which (x==ls.ord.row.prob))
res.hh.ord2i=res.hhi[order(ls.ord.hhi),]
```

```
row.nb.gpi=length(levels(as.factor(res.hhi$mbrshp.hhi)))
res.hh.ord3i=NULL
for (h in ls.ord.row.prob)
{
  part=res.hh.ord2i[res.hh.ord2i$mbrshp.hhi==h,]
  part.ord=part[order(part$freq.hhi,decreasing=TRUE),]
  res.hh.ord3i=rbind.data.frame(res.hh.ord3i,part.ord)
}
ls.ord.sp=sapply(res.spi$mbrshp.spi,function(x) which (x==ls.ord.col.prob))
res.sp.ord2i=res.spi[order(ls.ord.sp),]
col.nb.gb=length(levels(as.factor(res.spi$mbrshp.spi)))
res.sp.ord3i=NULL
for (h in ls.ord.col.prob)
{
  part=res.sp.ord2i[res.sp.ord2i$mbrshp.spi==h,]
  part.ord=part[order(part$freq.spi,decreasing=TRUE),]
  res.sp.ord3i=rbind.data.frame(res.sp.ord3i,part.ord)
}
nds=nds[as.character(res.hh.ord3i$hh.namei),as.character(res.sp.ord3i$sp.namei)]
nps=nps[as.character(res.hh.ord3i$hh.namei),as.character(res.sp.ord3i$sp.namei)]
webBFs2=webBFs2[as.character(res.hh.ord3i$hh.namei),as.character(res.sp.ord3i$sp.namei)]

######## Plot matrix with heatcolours and the number of visits #######
visits<-matrix(webBFs2,nrow=dim(webBFs2)[1]*dim(webBFs2)[2],ncol=1)
visits<-visits[which(visits>0)] #without the zeros
coord.function<-function(x,nI,nP){
```

```
  c(((x-1)%%nl)+1,((x-1)%/%nl)+1)
}
func.plot.matrix<-function(x,y){
  indices<-which(x==1)
  min<-min(y)
  max<-max(y)
  yLabels<-rownames(x)
  xLabels<-colnames(x)
  title<-c("Bois de Fontaret")
  if(is.null(xLabels)){
    xLabels<-c(1:ncol(x))
  }
  if(is.null(yLabels)){
    yLabels<-c(1:nrow(x))
  }
  reverse<-nrow(x):1
  yLabels<-yLabels[reverse]
  y<-y[reverse,]
  image.plot(1:length(xLabels),1:length(yLabels),t(y),col=c("white",heat.colors(12)[12:1]), xlab="",
ylab="",axes=FALSE,zlim=c(min,max))
  if(!is.null(title)){
    title(ylab="Insects", line=8, cex.lab=1)
    title(xlab="Plants", line=6, cex.lab=1.2)
    title("Bois de Fontaret")
  }
  axis(BELOW<-1,at=1:length(xLabels),labels=as.factor(as.character(xLabels)),las =2, cex.axis=0.6)
```

```
 axis(LEFT<-2,at=1:length(yLabels), labels=as.factor(as.character(yLabels)),las= 2,cex.axis=0.6)
 axis(BELOW<-1,at=1:length(xLabels),labels=rep("",length(xLabels)),las =2,cex.axis=0.6)
 axis(LEFT<-2,at=1:length(yLabels),labels=rep("",length(yLabels)),las=2,cex.axis<-0.6)
 coo<-t(rbind(sapply(indices,function(xx) coord.function(xx,nrow(x),ncol(x)))))
 text(coo[,2],nrow(webBFs)+1-coo[,1],labels=visits, cex=0.6)
}
func.plot.matrix(nds,nps)
####### Black lines to delimit blocks in the plot ######
if (row.nb.gpi>1)
{
 ls.class=as.numeric(as.data.frame(table(res.hh.ord2i$mbrshp.hhi))[ls.ord.row.prob,2])
 ls.cum=sum(ls.class)-cumsum(ls.class)
 abline(h=ls.cum+0.5,col="grey20", lwd=3)
}
if (col.nb.gpi>1)
{
 ls.class=as.numeric(as.data.frame(table(res.sp.ord2i$mbrshp.spi))[ls.ord.col.prob,2])
 ls.cum=cumsum(ls.class)
 abline(v=ls.cum+0.5,col="grey20", lwd=3)
}
```

Figures and Tables

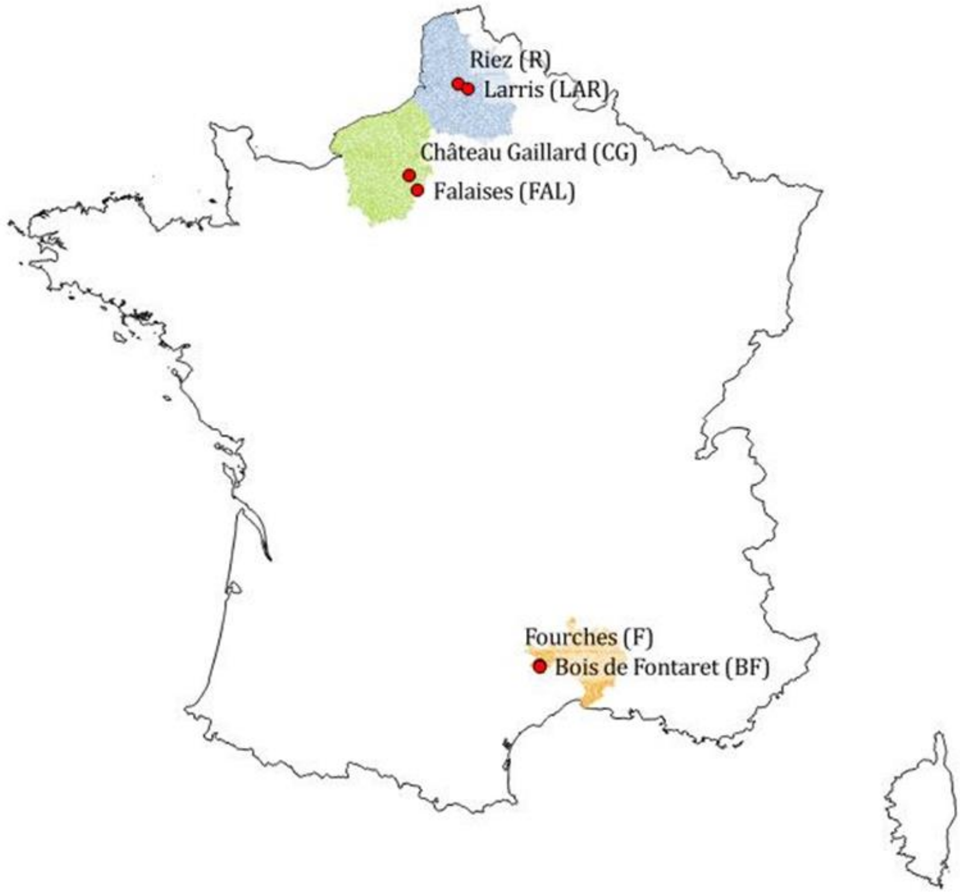

Figure S1. Site location in France: in blue the French départements Pas-de-Calais and Somme (Hauts-de-France region), in green the départements Eure and Seine Maritime (Normandie region), in orange the départment Gard (Occitanie region). The six sites correspond to the red dots.

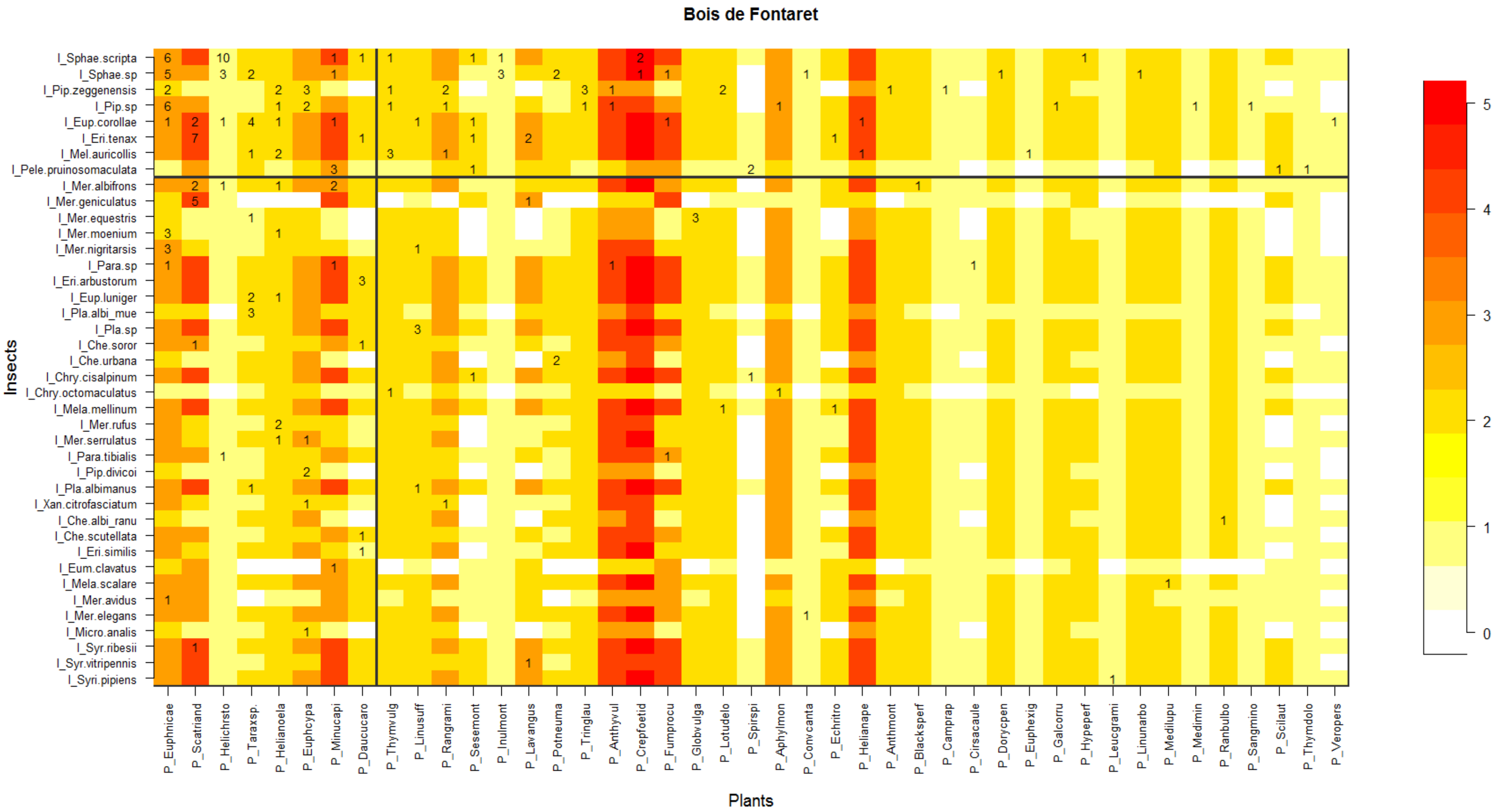

Figure S2. Block clustering provided by LBM in the site of Bois de Fontaret (BF, Occitanie), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are separated by solid black lines. Colours correspond to the number of months that are shared by each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker colours. Numbers are the number of visits observed in the field for a given plant-insect pair.

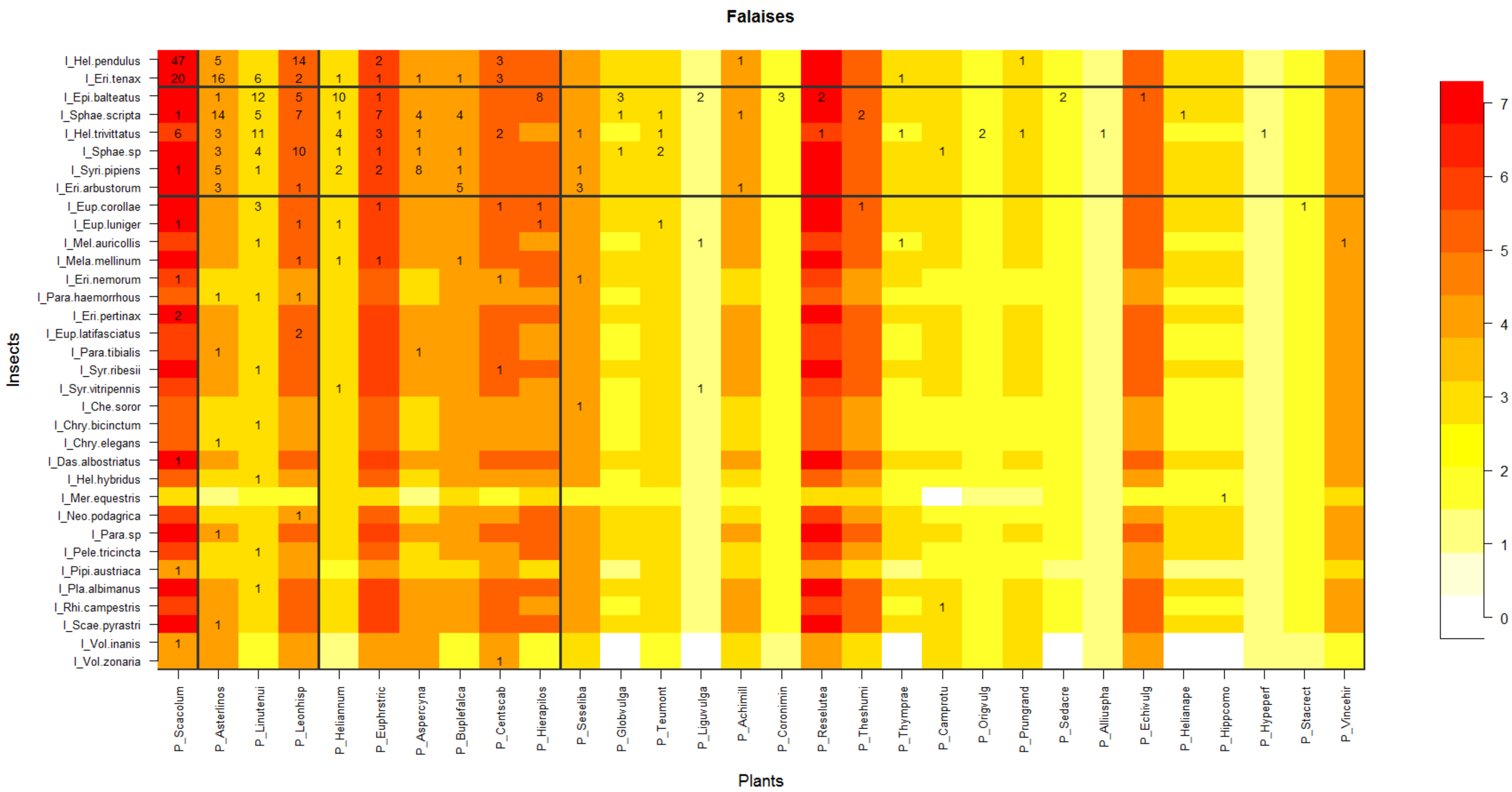

Figure S3. Block clustering provided by LBM in the site of Falaises (FAL, Normandie), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are separated by solid black lines. Colours correspond to the number of months that are shared by each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker colours. Numbers are the number of visits observed in the field for a given plant-insect pair.

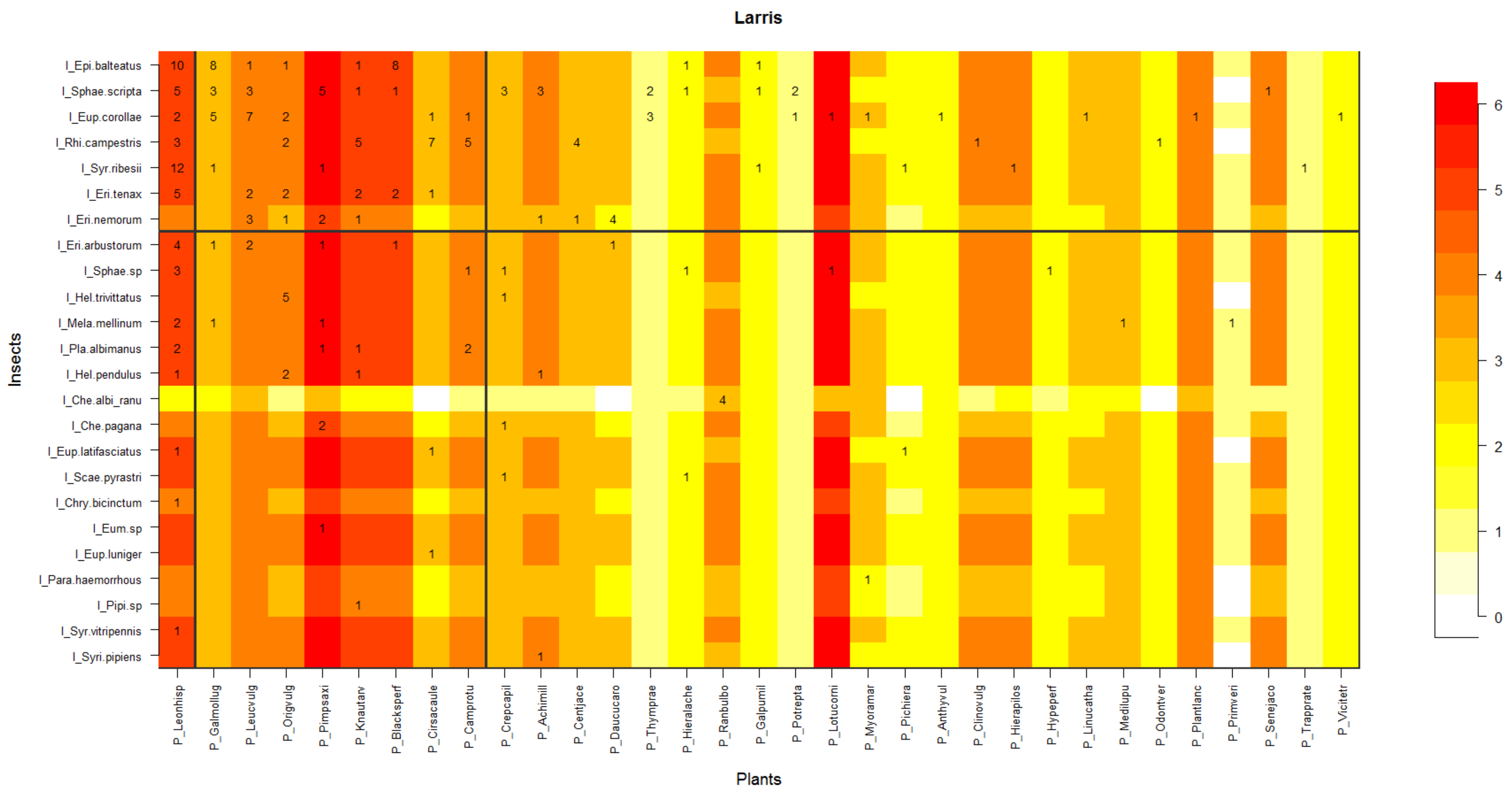

Figure S4. Block clustering provided by LBM in the site of Larris (LAR, Hauts-de-France), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are separated by solid black lines. Colours correspond to the number of months that are shared by each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker colours. Numbers are the number of visits observed in the field for a given plant-insect pair.

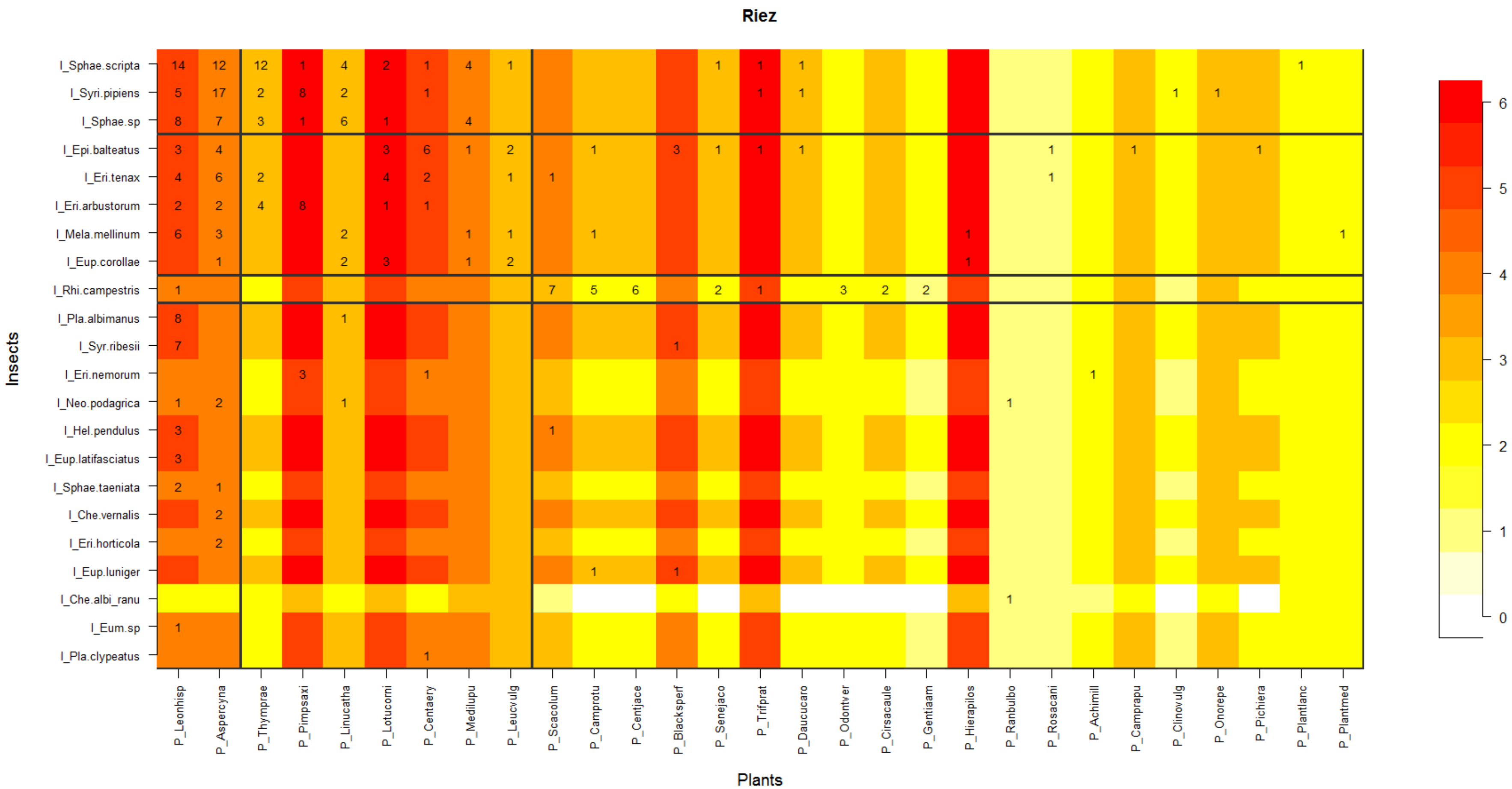

Figure S5. Block clustering provided by LBM in the site of Riez (R, Hauts-de-France), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are separated by solid black lines. Colours correspond to the number of months that are shared by each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker colours. Numbers are the number of visits observed in the field for a given plant-insect pair.

Table S1. Table of transformed plant abundances. The first column shows the Braun-Blanquet coefficients of, the second column, their percentages, and the third column, the transformed abundances used as the plant abundances in the model.

Coefficient Braun-Blanquet	Abundance percentage interval	Abundance percentage
i	1 individual	0.1%
+	< 1 %	0.5%
1	1-10 %	5%
2	10-25 %	15%
3	25-50 %	35%
4	50-75 %	65%
5	75-100 %	85%