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

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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.

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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 (Staniczenko *et al.* 2017; Cirtwill *et al.* 2019) and fewer still

able to make comparisons between networks. Due to their complexity and variation among years (Chacoff *et al.* 2017), 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.* 2017). In order to compare networks of different sizes, a better alternative is to switch from network-derived metrics to the comparison of the probability of interaction given by 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).

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 to specialists, only limited by morphological constraints (Iler *et al.* 2013; Klecka *et al.* 2018a; Lucas *et al.* 2018). Indeed, their generalist behaviour, at the species level, could be the result of individually 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; Lucas *et al.* 2018). 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

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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, *i.e.* unobserved variables (Grace *et al.* 2010). SEM is a multivariate technique used to test several hypotheses in ecological studies. SEM analysis involves cause-effect equations to evaluate multiple causal relationship (Grace 2006; Eisenhauer *et al.* 2015) using observed and latent variables to explain some other observed variables (Grace 2006). SEM can be used to choose among competing models (Grace & Bollen 2008). Thus, SEM are well suited for studying the complexity of ecological networks. To test whether phenology affects network compartmentalization, we looked for species subgroups using a latent block model (LBM) which is among the best clustering methods for weighted networks (Leger *et al.* 2015).

The comparison of 16 SEMs and the analysis of LBMs 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 hoverfly 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

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3°30'06.06"E, département: Gard). The six sites are included in the European NATURA 2000 network, a network of preserved areas designated to protect a number of habitats and species representative of European biodiversity. 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, ranked from i to 5 (most abundant coefficient class) (Van Der Maarel 1975, 1979; Mucina *et al.* 2000), to rank flowering species. We converted the coefficients to percentage intervals and then in mean values of percentage cover classes (Table S1): 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 hoverflies only (since at the moment of the study bees were not identified at the species level yet). 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 and even if hoverflies are known to prefer open flowers (Branquart & Hemptinne 2000), we also considered the interactions between hoverflies and plant species of the Fabaceae family because 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).

Plant – hoverfly networks

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_{ij} when we recorded v_{ij} 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 obtained 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) and the *dmax*-value (maximum d-value theoretically possible given the observed number of interactions in the network) using the `dfun` function in the `bipartite` package (Dormann *et al.* 2009). 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 then manually

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calculated the standardized specialization index *d'* (Blüthgen *et al.* 2006) for each plant and insect species as the ratio of the *d*-value to its corresponding *dmax*-value.

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 identify strong, simple divisions of a network into relatively independent sub-networks by looking for highly interconnected 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 corresponding 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. For hoverflies, we used the recorded number of visiting individuals (total abundance) and their presence (recorded months) along the season to calculate their average abundance during months when they were present (A_H).

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Déplacé vers le haut [3]: 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).

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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)

SEM is a confirmatory technique that involves cause-effect equations to evaluate multivariate hypotheses in ecological networks (Grace 2006). The primary interest of SEM analyses lies in its ability to compare different causal models between the same sets of explanatory and explained variables. Another important feature of SEM is that they can relate data through latent variables, *i.e.* variables which are not measured in the model and which represent underlying causes or effects, coupled with observed variables (Grace 2006; Grace *et al.* 2010). SEM can now be assessed using Bayesian approaches and parameters estimated using MCMC (Markov Chain Monte Carlo)(Grace *et al.* 2010; Fan *et al.* 2016).

In our study, we modelled hoverfly-plant interaction networks using a SEM approach (Fig. 1) with latent variables linking the number of visits per plant-pollinator species pair 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 species pair (*i.e.* the intensity of interactions). We used the term latent

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tables to describe latent variables organized as insect x plant tables, such as the expected number of visit matrix.

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, E_i and E_j), to represent heterogeneity of species degrees (*i.e.* the number of links) in the network. We modelled the possibility 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 probability μ_{ij} given by:

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

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 visits V_{ij} 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"). Please note that we only linked abundances to the number of visits, V_{ij}, and not to the possibility of interaction I_{ij}, because the aim of the latter latent table is to capture "forbidden links", while detectability and sampling effects are supposed to be captured by the statistical model of the number of interactions. We integrated species abundances as predictor variables in order to assess the effect of PO on the number of visits on top of a "null model" that already includes sensible drivers of the numbers of visits, such as species abundances. 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:

$$\log(\lambda_{ij}) = \lambda_0 + \lambda_H A_{H,i} + \lambda_P A_{P,j} + \lambda_{PO} \log(1 + PO_{ij})$$

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

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 all combinations of 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` using Pareto smoothed importance sampling for regularizing importance weights (Vehtari *et al.* 2017). The LOO criterion is a fully Bayesian method to compare models of different complexities and to estimate prediction accuracy using the log-likelihood evaluated at the posterior simulations of the parameter values (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, which are used to compare frequentist models, but can instead be applied to Bayesian models, without suffering the

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instability issues of the Deviance Information Criterion which used to be the main information criterion for Bayesian models(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).

Predictive power analysis

We tested the predictive power of the models we built by making predictions for the I_{ij} table and checking their validity using a binarized version of the visit table V_{ij}. Predictions were obtained by defining a threshold on interaction probability μ_{ij}: values found above the threshold were predicted as occurring interactions, values below the threshold as no interaction. The threshold probability value was found by maximizing the sum of model specificity and sensitivity. We computed accuracy statistics (sensitivity, specificity, omission rate, area under the ROC curve [AUC]) in two situations: (i) when predicting data for the site that was used to build the model (self-validation; e.g. predicting interaction data in the site of Riez based on the model developed for this site) and (ii) when predicting data for the other site from the same region (cross-validation; e.g. predicting data for the LAR site based on the model for the R site). We performed theses analyses using the `SDMTools` package in R. We only used

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the set of best models (LOO < 4) found for each site to predict the interactions in the other site through a multimodel averaging approach. We obtained the threshold probability using `optim.tresh` function with option `max.sensitivity+specificity`.

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) and the maximum number of visits recorded in the site of FAL was 47 (between *Helophilus pendulus* and *Scabiosa columbaria*, Fig. S3) and in the site of CG was 22 (between *Eristalis tenax* and *S. columbaria* and between *Sphaerophoria scripta* and *Leontodon hispidus*, Fig. 3). 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 total number of interactions recorded in these sites (BF and F) is not the highest recorded in the field (Table 1): the maximum number of visits in the site of BF was 10 (between *Spherophoria scripta* and *Helichrysum stoechas*, Fig. S2) and 12 in the site of F (between *Syrphus ribesii* and *Bellis perennis*, Fig. 2). In the two southern sites we also recorded the lowest connectance values (BF: 0.07 and F: 0.08) of all six sites, with the highest connectance observed in the site of R (R 0.16; LAR 0.13; CG 0.13; FAL 0.12). The maximum number of visits recorded in the site of LAR was 12 (between *Syrphus ribesii* and *L. hispidus*, Fig. S4) and in the site of R was 17 (between *Syritta pipiens* and *Asperula cynanchica*, Fig. S5).

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, Effects weight). 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

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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 (w_{H_P} = 0.59, Table 2; standardised coefficient = 0.67, Fig. 4). The effects of phenological overlap on the probability of interaction (PO → I_{ij}) and the intensity of visits (PO → λ_{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 showing a low effect size of phenology on interaction probability and intensity (Fig. 4).

When assessing the predictive power of the best models, we observed that the sensitivity and specificity values, both for the self-validation and the cross-validation, were higher than 0.5 (Table S2), which means that the interactions predicted by the models are better than predicted by chance. While area under the curve (AUC) values were all higher than 0.75 for self-validation, cross-validation tests yielded intermediate values (AUC between 0.62 and 0.73), reflecting the fact that abundances and phenology are certainly not sufficient to make accurate predictions on the occurrence of plant-pollinator interactions.

DISCUSSION

Latitude affects the seasonality, with 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.* 2017). One of the main problems of comparing networks

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along gradients is the dependence of network metrics on network size (Staniczenko *et al.* 2013; Astegiano *et al.* 2015; Tylianakis & Morris 2017). In this study, to avoid the problem of comparing networks with different dimensions, we decided to focus on the determinants of the probability of interaction and the number of visits, rather than the overall structure. We employed Bayesian Structural Equation Models (SEM) which 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). In our study we used SEM to link the numbers of visits to phenology overlap (PO) and species abundance through latent probabilities of species interaction and expected numbers of visits per plant-pollinator species pair. We tested different models with variable numbers of effects and compared them in each site. In our models, we used species abundances to construct a sensible null model to test whether phenology overlap could help explain the probability and intensity of interactions when the effects of species abundances are already taken into account. In all sites, we found that models that included both PO and abundances had always better goodness-of-fit than models that included only abundances. Abundances indeed provided a sensible null model since the goodness-of-fit of models that did not include abundances were always quite worse than the ones which did.

We also found that in all sites the most important factor affecting pollinator visits was insect abundance (Table 2). Likewise, we found that plant abundance was also a very important effect in most sites, except in the site of F (Table 2). Since insect abundances are given by visitation data, it is not surprising that the intensity of interactions positively depends on these abundances. Species abundance often explain the linkage level in pollination network studies (Olesen *et al.* 2008; Bartomeus *et al.* 2016; Chacoff *et al.* 2017; Pellissier *et al.* 2017) 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

Déplacé (insertion) [1]

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Déplacé vers le haut [1]: 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).

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incorporated the effect of PO on either the probability or the intensity of interactions (Table 2), and the model that only considered species abundance (model 5 in Table 2) was not the best one in any site. 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. However, our objective was not to compare the effect of phenology overlap to that of species abundance – for such an endeavour, one would need estimates of species abundances independent of visitation data. Because models which consider the effect of PO on the intensity and/or probability of interactions are the best models for all sites evinces a clear effect of PO. 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 → λ_{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 hoverflies may undergo selection

Déplacé vers le bas [2]: 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).

Déplacé (insertion) [2]

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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) but also the lower connectance. 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). Moreover, in our study we only considered as "true absence" of the interaction the lack of phenological coupling between species (*i.e.* plant and hoverfly species which are not present at the same moment along the season cannot interact). We did not consider "false absences", *i.e.* missing links, since not all the potential links among species are recorded in the field (Olesen *et al.* 2011) which may introduce bias in the estimation of the probability of interactions (Bartomeus *et al.* 2016; Cirtwill *et al.* 2019).

To conclude, plant phenology here drives the duration of the phenology overlap between plant and hoverflies, 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.* 2017) 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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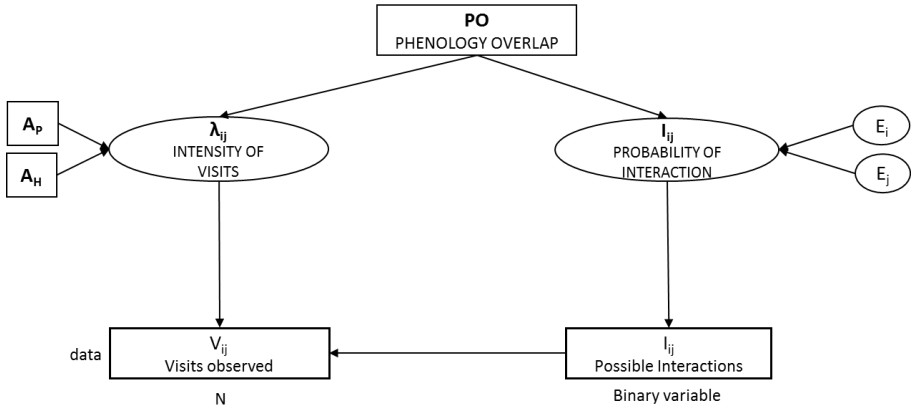

Figure 1. Summary diagram of the SEM model. We estimated 4 effects: the effect of plant abundance (AP → λij, coefficient λP), the effect of insect (hoverflies) abundance on the intensity of visits (AH → λij, λH), the effect of phenology overlap on the intensity of visits (PO → λij, λPO) and the effect 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 species identities. 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.

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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.

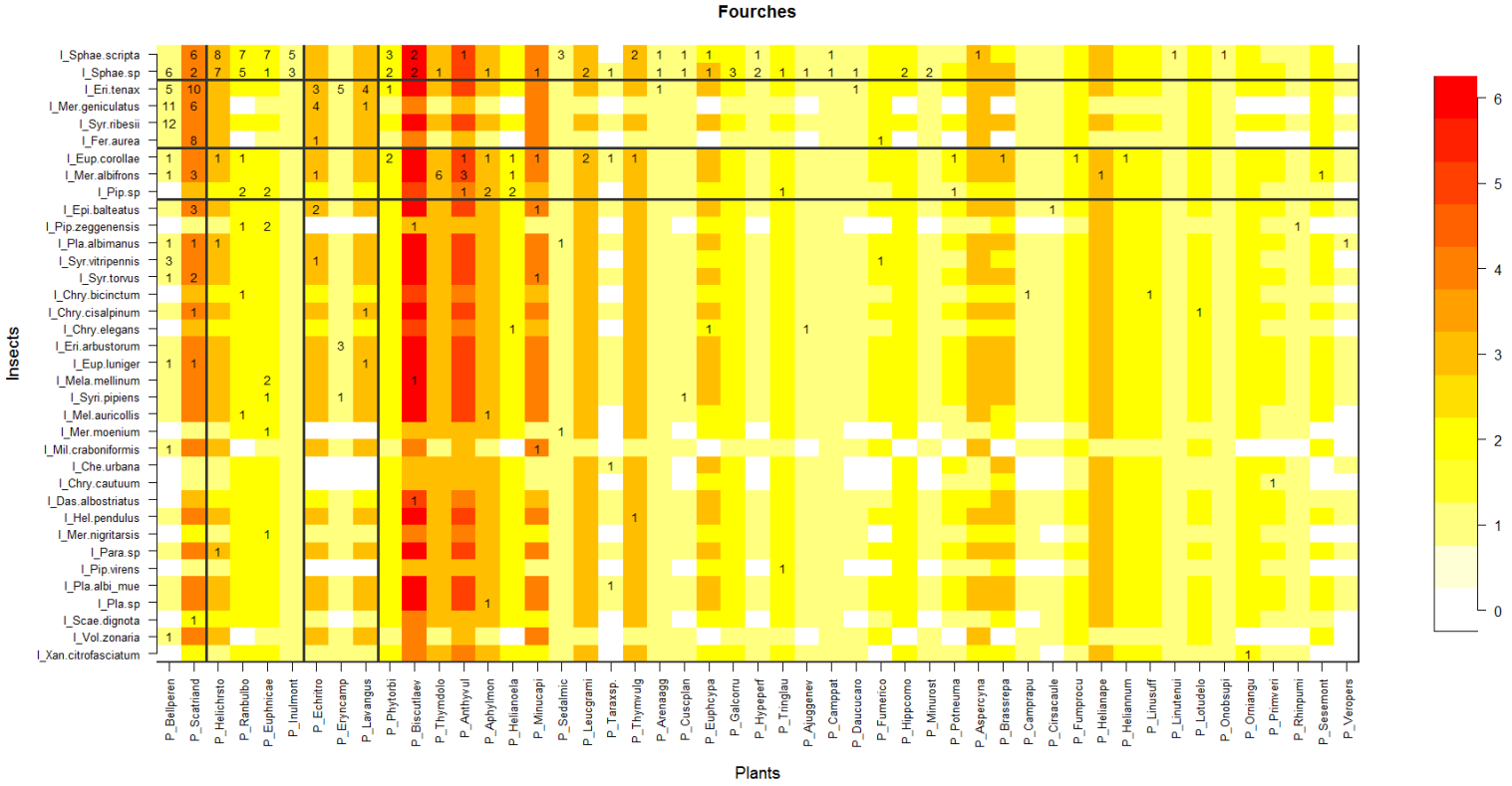

Figure 3. Block clustering provided by LBM in the site of Chateau Gaillard (CG, Normandie) overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants 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.

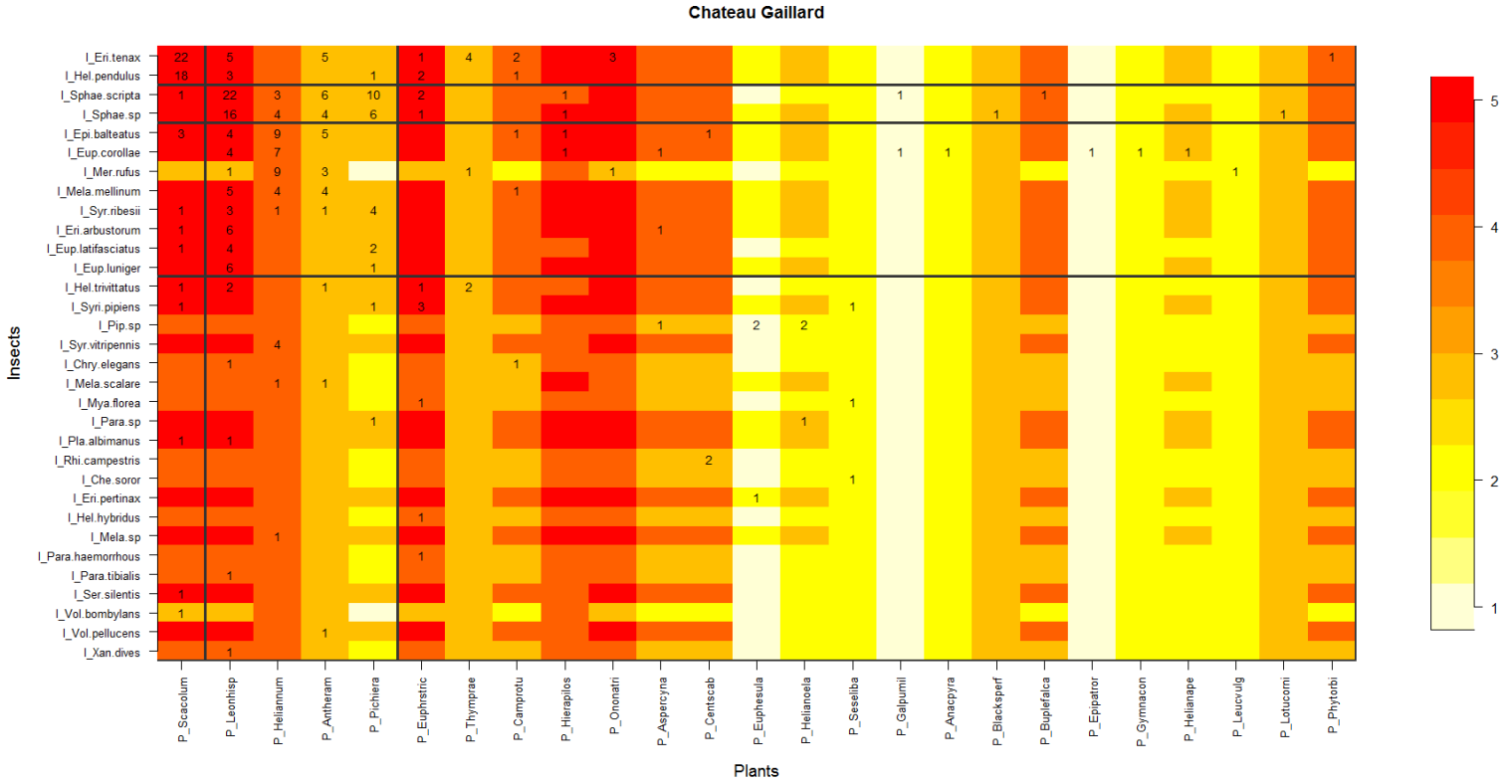

Figure 4. Summary diagram of the best models in all sites. The thickness of the arrows is scaled to Akaike weights (thin ER < 0.73; thick ER > 0.73, cf. Table 2). Standardised coefficients of the model average (computed based on the Akaike weighted model average) are reported next to the arrows. PO is 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.

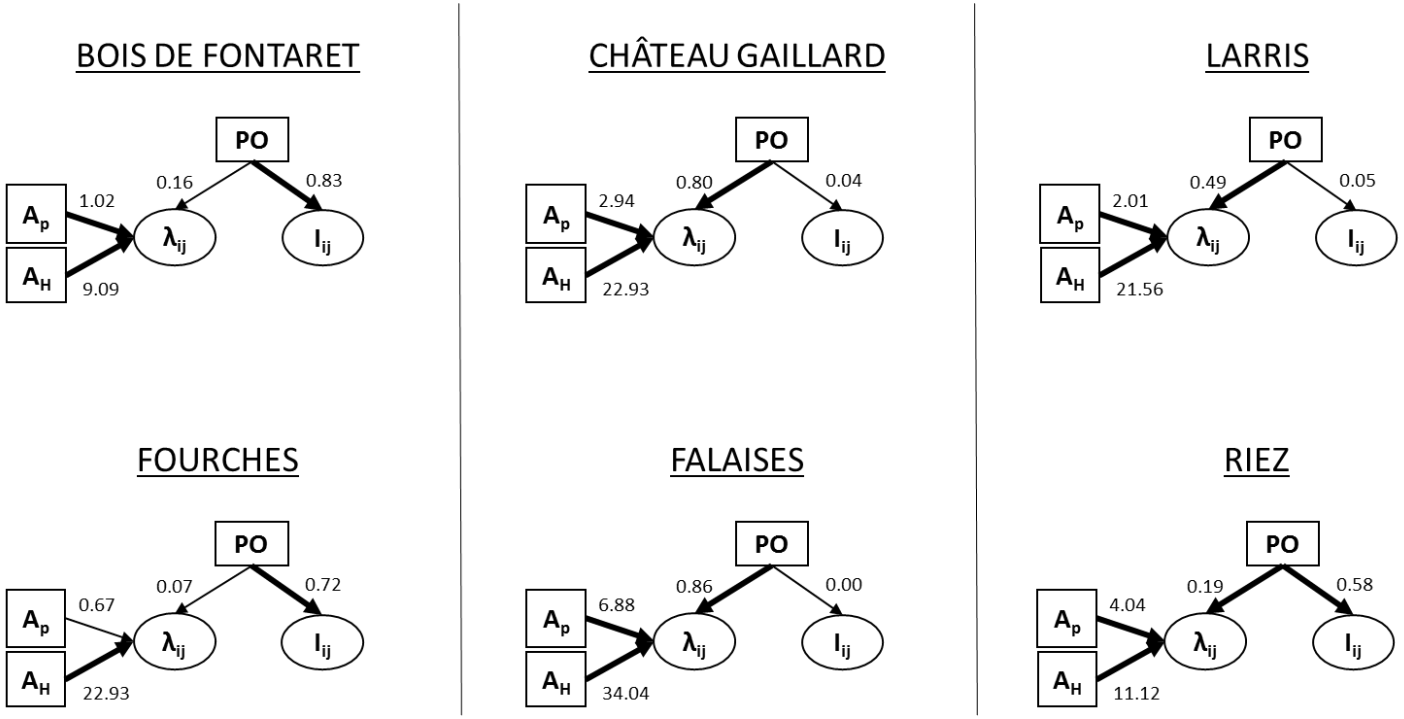

Table 1. Summary table of results obtained in each site (Bois de Fontaret [BF] and Fourches [F] in Occitanie, Château Gaillard [CG] and Falaises [FAL] in Normandie, Larris [LAR] and Riez [R] in Hauts-de-France). `H2'` and `d'` indices refer to specialization indices described by Blüthgen *et al.* (2006) 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 w_H 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	$\boldsymbol{\lambda_{ij} \sim A_H + A_P + PO / I_{ij} \sim PO}$	4	*2.98*	*2.04*	*3.54*	*2.54*	*2.86*	**0.00**
1	$\boldsymbol{\lambda_{ij} \sim A_H + A_P / I_{ij} \sim PO}$	3	**0.00**	**0.00**	36.75	64.04	10.37	*2.90*
2	$\lambda_{ij} \sim A_P + PO / I_{ij} \sim PO$	3	8.66	78.23	106.46	184.02	44.60	17.00
3	$\lambda_{ij} \sim A_H + PO / I_{ij} \sim PO$	3	6.63	*1.71*	8.09	73.62	11.24	11.42
4	$\boldsymbol{\lambda_{ij} \sim A_H + A_P + PO}$	3	*2.86*	8.06	**0.00**	**0.00**	**0.00**	*2.24*
5	$\lambda_{ij} \sim PO / I_{ij} \sim PO$	2	14.69	73.20	109.85	223.86	55.67	23.09
6	$\lambda_{ij} \sim A_H / I_{ij} \sim PO$	2	*1.45*	*1.31*	33.53	119.04	27.23	19.76
7	$\lambda_{ij} \sim A_P / I_{ij} \sim PO$	2	9.84	72.16	156.61	256.04	47.99	21.53
8	$\lambda_{ij} \sim A_H + PO$	2	11.49	8.18	5.25	71.97	10.28	13.80
9	$\lambda_{ij} \sim A_P + PO$	2	10.71	88.67	103.46	182.14	44.36	17.94
10	$\lambda_{ij} \sim A_H + A_P$	2	24.36	14.04	36.10	66.82	10.51	4.26
11	$I_{ij} \sim PO$	1	11.78	68.52	154.26	272.98	64.12	32.39
12	$\lambda_{ij} \sim PO$	1	19.99	86.20	108.46	219.66	54.64	25.73
13	$\lambda_{ij} \sim A_H$	1	25.58	14.41	36.12	123.30	28.27	22.78
14	$\lambda_{ij} \sim A_P$	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		Effects weight (w_H)					
	$\boldsymbol{PO \rightarrow I_{ij}}$		**0.88**	**0.98**	0.15	0.22	0.20	**0.74**
	$\boldsymbol{PO \rightarrow \lambda_{ij}}$		0.26	0.35	**1.00**	**1.00**	**0.99**	**0.79**
	$\boldsymbol{A_H \rightarrow \lambda_{ij}}$		**0.99**	**1.00**	**1.00**	**1.00**	**1.00**	**1.00**
	$\boldsymbol{A_P \rightarrow \lambda_{ij}}$		**0.74**	0.59	**0.93**	**1.00**	**0.99**	**1.00**

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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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759

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

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Mis en forme : Anglais (Royaume-Uni)

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)
```

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```
809     }
810
811     for( p in 1 : dim2 ) {
812       effet_P[p] ~ dnorm( 0.0,tau_P)
813     }
814
815           tau_I ~ dexp( 10)
816           tau_P ~ dexp( 10)
817           alpha ~ dnorm(0,0.01)
818           beta ~  dnorm(0,0.01)
819           theta0 ~ dnorm(0,0.01)
820           gamma ~ dnorm(0,0.01)
821           delta ~ dnorm(0,0.01)
822           epsilon ~ dnorm(0,0.01)
823   }
824
```

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Mis en forme : Anglais (Royaume-Uni)

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)
```

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Mis en forme : Anglais (Royaume-Uni)

```
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)
        }
```

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Mis en forme : Anglais (Royaume-Uni)

```
        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)
```

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Mis en forme : Anglais (Royaume-Uni)

```
902             }
903             mod.Z014<<-jags(inits=init.funZ014,model.file = "modelZ014_code.txt",data =
904 list("visit","ab_P","dim1","dim2"),parameters.to.save =
905 c("mu","effet_I","effet_P","tau_I","tau_P","delta","beta","theta0","loglik"),n.chains = 1,
906 n.iter=1000000, n.burnin = 250000, n.thin = 250)
907             mod.Z014.mcmc<-as.mcmc(mod.Z014)
908             mZ014<-mod.Z014$BUGSoutput$sims.list
909             mZ014.deviance<-mZ014$deviance
910             mZ014.loglik<-mZ014$loglik
911             dimSEM<-dim(mZ014.loglik)[1]
912             list.mZ014<-sapply(1:dimSEM,function(x) matrix(mZ014.loglik[x,,],nrow=dim1*dim2))
913             list.tmZ014<-(t(list.mZ014))
914             mZ014.loo<-loo(list.tmZ014)
915             mZ014.loo
916             loo_file<-paste(dossier, "/", site, "_Z014_loo.txt", sep="")
917             write_values("mZ014", app=T, loo_file)
918             mZ014_loo_pointwise<-mZ014.loo$pointwise
919             mZ014_loo_pareto_k<-mZ014.loo$pareto_k
920             mZ014.loo$pareto_k<-NULL
921             mZ014.loo$pointwise<-NULL
922             write_values(as.matrix(mZ014.loo), app=T, loo_file)
923             save.image(paste(dossier, "/", site, "_Z014.RData", sep=""))
924 }
925 ### MODEL Z013
926 mZ013<-function(){
927             init.funZ013 <-function(){
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
928                 list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =
929 rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
930 "inter"=inter0)
931             }
932             mod.Z013<<-jags(inits=init.funZ013,model.file = "modelZ013_code.txt",data =
933 list("visit","ab_I","dim1","dim2"),parameters.to.save =
934 c("mu","effet_I","effet_P","tau_I","tau_P","gamma","beta","theta0","loglik"),n.chains = 1,
935 n.iter=1000000, n.burnin = 250000, n.thin = 250)
936             mod.Z013.mcmc<-as.mcmc(mod.Z013)
937             mZ013<-mod.Z013$BUGSoutput$sims.list
938             mZ013.deviance<-mZ013$deviance
939             mZ013.loglik<-mZ013$loglik
940             dimSEM<-dim(mZ013.loglik)[1]
941             list.mZ013<-sapply(1:dimSEM,function(x) matrix(mZ013.loglik[x,,],nrow=dim1*dim2))
942             list.tmZ013<-(t(list.mZ013))
943             mZ013.loo<-loo(list.tmZ013)
944             mZ013.loo
945             loo_file<-paste(dossier, "/", site, "_Z013_loo.txt", sep="")
946             write_values("mZ013", app=T, loo_file)
947             mZ013_loo_pointwise<-mZ013.loo$pointwise
948             mZ013_loo_pareto_k<-mZ013.loo$pareto_k
949             mZ013.loo$pareto_k<-NULL
950             mZ013.loo$pointwise<-NULL
951             write_values(as.matrix(mZ013.loo), app=T, loo_file)
952             save.image(paste(dossier, "/", site, "_Z013.RData", sep=""))
953 }
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
### 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
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
980             write_values(as.matrix(mZ012.loo), app=T, loo_file)
981             save.image(paste(dossier, "/", site, "_Z012.RData", sep=""))
982     }
983     ### MODEL Z011
984     mZ011<-function(){
985             init.funZ011 <-function(){
986               list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "theta0"
987     = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
988             }
989             mod.Z011<<-jags(inits=init.funZ011,model.file = "modelZ011_code.txt",data =
990     list("cooc","visit","dim1","dim2"),parameters.to.save =
991     c("mu","effet_I","effet_P","tau_I","tau_P","alpha","beta","theta0","loglik"),n.chains = 1,
992     n.iter=1000000, n.burnin = 250000, n.thin = 250)
993             mod.Z011.mcmc<-as.mcmc(mod.Z011)
994             mZ011<-mod.Z011$BUGSoutput$sims.list
995             mZ011.deviance<-mZ011$deviance
996             mZ011.loglik<-mZ011$loglik
997             dimSEM<-dim(mZ011.loglik)[1]
998             list.mZ011<-sapply(1:dimSEM,function(x) matrix(mZ011.loglik[x,,],nrow=dim1*dim2))
999             list.tmZ011<-(t(list.mZ011))
1000            mZ011.loo<-loo(list.tmZ011)
1001            mZ011.loo
1002            loo_file<-paste(dossier, "/", site, "_Z011_loo.txt", sep="")
1003            write_values("mZ011", app=T, loo_file)
1004            mZ011_loo_pointwise<-mZ011.loo$pointwise
1005            mZ011_loo_pareto_k<-mZ011.loo$pareto_k
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1006            mZ011.loo$pareto_k<-NULL
1007            mZ011.loo$pointwise<-NULL
1008            write_values(as.matrix(mZ011.loo), app=T, loo_file)
1009            save.image(paste(dossier, "/", site, "_Z011.RData", sep=""))
1010    }
1011    ### MODEL Z010
1012    mZ010<-function(){
1013            init.funZ010 <-function(){
1014              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =
1015    rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1),
1016    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
1017            }
1018            mod.Z010<<-jags(inits=init.funZ010,model.file = "modelZ010_code.txt",data =
1019    list("visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =
1020    c("mu","effet_I","effet_P","tau_I","tau_P","gamma","delta","beta","theta0","loglik"),n.chains = 1,
1021    n.iter=1000000, n.burnin = 250000, n.thin = 250)
1022            mod.Z010.mcmc<-as.mcmc(mod.Z010)
1023            mZ010<-mod.Z010$BUGSoutput$sims.list
1024            mZ010.deviance<-mZ010$deviance
1025            mZ010.loglik<-mZ010$loglik
1026            dimSEM<-dim(mZ010.loglik)[1]
1027            list.mZ010<-sapply(1:dimSEM,function(x) matrix(mZ010.loglik[x,,],nrow=dim1*dim2))
1028            list.tmZ010<-(t(list.mZ010))
1029            mZ010.loo<-loo(list.tmZ010)
1030            mZ010.loo
1031            loo_file<-paste(dossier, "/", site, "_Z010_loo.txt", sep="")
```


Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1032            write_values("mZ010", app=T, loo_file)
1033            mZ010_loo_pointwise<-mZ010.loo$pointwise
1034            mZ010_loo_pareto_k<-mZ010.loo$pareto_k
1035            mZ010.loo$pareto_k<-NULL
1036            mZ010.loo$pointwise<-NULL
1037            write_values(as.matrix(mZ010.loo), app=T, loo_file)
1038            save.image(paste(dossier, "/", site, "_Z010.RData", sep=""))
1039    }
1040    ### MODEL Z09
1041    mZ09<-function(){
1042            init.funZ09 <-function(){
1043              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "delta" = rnorm(1,0,1),
1044    "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
1045    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
1046            }
1047            mod.Z09<<-jags(inits=init.funZ09,model.file = "modelZ09_code.txt",data =
1048    list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
1049    c("mu","effet_I","effet_P","tau_I","tau_P","delta","beta","theta0","epsilon","loglik"),n.chains = 1,
1050    n.iter=1000000, n.burnin = 250000, n.thin = 250)
1051            mod.Z09.mcmc<-as.mcmc(mod.Z09)
1052            mZ09<-mod.Z09$BUGSoutput$sims.list
1053            mZ09.deviance<-mZ09$deviance
1054            mZ09.loglik<-mZ09$loglik
1055            dimSEM<-dim(mZ09.loglik)[1]
1056            list.mZ09<-sapply(1:dimSEM,function(x) matrix(mZ09.loglik[x,,],nrow=dim1*dim2))
1057            list.tmZ09<-(t(list.mZ09))
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1058            mZ09.loo<-loo(list.tmZ09)
1059            mZ09.loo
1060            loo_file<-paste(dossier, "/", site, "_Z09_loo.txt", sep="")
1061            write_values("mZ09", app=T, loo_file)
1062            mZ09_loo_pointwise<-mZ09.loo$pointwise
1063            mZ09_loo_pareto_k<-mZ09.loo$pareto_k
1064            mZ09.loo$pareto_k<-NULL
1065            mZ09.loo$pointwise<-NULL
1066            write_values(as.matrix(mZ09.loo), app=T, loo_file)
1067            save.image(paste(dossier, "/", site, "_Z09.RData", sep=""))
1068    }
1069    ### MODEL Z08
1070    mZ08<-function(){
1071            init.funZ08 <-function(){
1072              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =
1073    rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
1074    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
1075            }
1076            mod.Z08<<-jags(inits=init.funZ08,model.file = "modelZ08_code.txt",data =
1077    list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
1078    c("mu","effet_I","effet_P","tau_I","tau_P","gamma","beta","theta0","epsilon","loglik"),n.chains = 1,
1079    n.iter=1000000, n.burnin = 250000, n.thin = 250)
1080            mod.Z08.mcmc<-as.mcmc(mod.Z08)
1081            mZ08<-mod.Z08$BUGSoutput$sims.list
1082            mZ08.deviance<-mZ08$deviance
1083            mZ08.loglik<-mZ08$loglik
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1084            dimSEM<-dim(mZ08.loglik)[1]
1085            list.mZ08<-sapply(1:dimSEM,function(x) matrix(mZ08.loglik[x,,],nrow=dim1*dim2))
1086            list.tmZ08<-(t(list.mZ08))
1087            mZ08.loo<-loo(list.tmZ08)
1088            mZ08.loo
1089            loo_file<-paste(dossier, "/", site, "_Z08_loo.txt", sep="")
1090            write_values("mZ08", app=T, loo_file)
1091            mZ08_loo_pointwise<-mZ08.loo$pointwise
1092            mZ08_loo_pareto_k<-mZ08.loo$pareto_k
1093            mZ08.loo$pareto_k<-NULL
1094            mZ08.loo$pointwise<-NULL
1095            write_values(as.matrix(mZ08.loo), app=T, loo_file)
1096            save.image(paste(dossier, "/", site, "_Z08.RData", sep=""))
1097    }
1098    ### MODEL Z07
1099    mZ07<-function(){
1100            init.funZ07 <-function(){
1101              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "delta" =
1102    rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
1103    "inter"=inter0)
1104            }
1105            mod.Z07<<-jags(inits=init.funZ07,model.file = "modelZ07_code.txt",data =
1106    list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
1107    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","delta","beta","theta0","loglik"),n.chains = 1,
1108    n.iter=1000000, n.burnin = 250000, n.thin = 250)
1109            mod.Z07.mcmc<-as.mcmc(mod.Z07)
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1110            mZ07<-mod.Z07$BUGSoutput$sims.list
1111            mZ07.deviance<-mZ07$deviance
1112            mZ07.loglik<-mZ07$loglik
1113            dimSEM<-dim(mZ07.loglik)[1]
1114            list.mZ07<-sapply(1:dimSEM,function(x) matrix(mZ07.loglik[x,,],nrow=dim1*dim2))
1115            list.tmZ07<-(t(list.mZ07))
1116            mZ07.loo<-loo(list.tmZ07)
1117            mZ07.loo
1118            loo_file<-paste(dossier, "/", site, "_Z07_loo.txt", sep="")
1119            write_values("mZ07", app=T, loo_file)
1120            mZ07_loo_pointwise<-mZ07.loo$pointwise
1121            mZ07_loo_pareto_k<-mZ07.loo$pareto_k
1122            mZ07.loo$pareto_k<-NULL
1123            mZ07.loo$pointwise<-NULL
1124            write_values(as.matrix(mZ07.loo), app=T, loo_file)
1125            save.image(paste(dossier, "/", site, "_Z07.RData", sep=""))
1126    }
1127    ### MODEL Z06
1128    mZ06<-function(){
1129            init.funZ06 <-function(){
1130              list("tau_l" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"
1131    = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_l"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
1132    "inter"=inter0)
1133            }
1134            mod.Z06<<-jags(inits=init.funZ06,model.file = "modelZ06_code.txt",data =
1135    list("cooc","visit","ab_l","dim1","dim2"),parameters.to.save =
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
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)
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1162            }
1163            mod.Z05<<-jags(inits=init.funZ05,model.file = "modelZ05_code.txt",data =
1164    list("cooc","visit","dim1","dim2"),parameters.to.save =
1165    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","beta","theta0","epsilon","loglik"),n.chains = 1,
1166    n.iter=1000000, n.burnin = 250000, n.thin = 250)
1167            mod.Z05.mcmc<-as.mcmc(mod.Z05)
1168            mZ05<-mod.Z05$BUGSoutput$sims.list
1169            mZ05.deviance<-mZ05$deviance
1170            mZ05.loglik<-mZ05$loglik
1171            dimSEM<-dim(mZ05.loglik)[1]
1172            list.mZ05<-sapply(1:dimSEM,function(x) matrix(mZ05.loglik[x,,],nrow=dim1*dim2))
1173            list.tmZ05<-(t(list.mZ05))
1174            mZ05.loo<-loo(list.tmZ05)
1175            mZ05.loo
1176            loo_file<-paste(dossier, "/", site, "_Z05_loo.txt", sep="")
1177            write_values("mZ05", app=T, loo_file)
1178            mZ05_loo_pointwise<-mZ05.loo$pointwise
1179            mZ05_loo_pareto_k<-mZ05.loo$pareto_k
1180            mZ05.loo$pareto_k<-NULL
1181            mZ05.loo$pointwise<-NULL
1182            write_values(as.matrix(mZ05.loo), app=T, loo_file)
1183            save.image(paste(dossier, "/", site, "_Z05.RData", sep=""))
1184    }
1185    ### MODEL Z04
1186    mZ04<-function(){
1187            init.funZ04 <-function(){
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1188                list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =
1189    rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
1190    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
1191            }
1192            mod.Z04<<-jags(inits=init.funZ04,model.file = "modelZ04_code.txt",data =
1193    list("cooc","visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =
1194    c("mu","effet_I","effet_P","tau_I","tau_P","gamma","delta","beta","theta0","epsilon","loglik"),n.chai
1195    ns = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
1196            mod.Z04.mcmc<-as.mcmc(mod.Z04)
1197            mZ04<-mod.Z04$BUGSoutput$sims.list
1198            mZ04.deviance<-mZ04$deviance
1199            mZ04.loglik<-mZ04$loglik
1200            dimSEM<-dim(mZ04.loglik)[1]
1201            list.mZ04<-sapply(1:dimSEM,function(x) matrix(mZ04.loglik[x,,],nrow=dim1*dim2))
1202            list.tmZ04<-(t(list.mZ04))
1203            mZ04.loo<-loo(list.tmZ04)
1204            mZ04.loo
1205            loo_file<-paste(dossier, "/", site, "_Z04_loo.txt", sep="")
1206            write_values("mZ04", app=T, loo_file)
1207            mZ04_loo_pointwise<-mZ04.loo$pointwise
1208            mZ04_loo_pareto_k<-mZ04.loo$pareto_k
1209            mZ04.loo$pareto_k<-NULL
1210            mZ04.loo$pointwise<-NULL
1211            write_values(as.matrix(mZ04.loo), app=T, loo_file)
1212            save.image(paste(dossier, "/", site, "_Z04.RData", sep=""))
1213    }
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
### 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
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1240            write_values(as.matrix(mZ03.loo), app=T, loo_file)
1241            save.image(paste(dossier, "/", site, "_Z03.RData", sep=""))
1242    }
1243    ### MODEL Z02
1244    mZ02<-function(){
1245            init.funZ02 <-function(){
1246              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1, "beta" = rnorm(1,0,1), "delta" =
1247    rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
1248    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
1249            }
1250            mod.Z02<<-jags(inits=init.funZ02,model.file = "modelZ02_code.txt",data =
1251    list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
1252    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","delta","beta","theta0","epsilon","loglik"),n.chain
1253    s = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
1254            mod.Z02.mcmc<-as.mcmc(mod.Z02)
1255            mZ02<-mod.Z02$BUGSoutput$sims.list
1256            mZ02.deviance<-mZ02$deviance
1257            mZ02.loglik<-mZ02$loglik
1258            dimSEM<-dim(mZ02.loglik)[1]
1259            list.mZ02<-sapply(1:dimSEM,function(x) matrix(mZ02.loglik[x,,],nrow=dim1*dim2))
1260            list.tmZ02<-(t(list.mZ02))
1261            mZ02.loo<-loo(list.tmZ02)
1262            mZ02.loo
1263            loo_file<-paste(dossier, "/", site, "_Z02_loo.txt", sep="")
1264            write_values("mZ02", app=T, loo_file)
1265            mZ02_loo_pointwise<-mZ02.loo$pointwise
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1266            mZ02_loo_pareto_k<-mZ02.loo$pareto_k
1267            mZ02.loo$pareto_k<-NULL
1268            mZ02.loo$pointwise<-NULL
1269            write_values(as.matrix(mZ02.loo), app=T, loo_file)
1270            save.image(paste(dossier, "/", site, "_Z02.RData", sep=""))
1271    }
1272    ### MODEL Z01
1273    mZ01<-function(){
1274            init.funZ01 <-function(){
1275              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"
1276    = rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1),
1277    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
1278            }
1279            mod.Z01<<-jags(inits=init.funZ01,model.file = "modelZ01_code.txt",data =
1280    list("cooc","visit","ab_I","ab_P", "dim1", "dim2"),parameters.to.save =
1281    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","delta","beta","theta0","loglik"),n.chain
1282    s = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
1283            mod.Z01.mcmc<-as.mcmc(mod.Z01)
1284            mZ01<-mod.Z01$BUGSoutput$sims.list
1285            mZ01.deviance<-mZ01$deviance
1286            mZ01.loglik<-mZ01$loglik
1287            dimSEM<-dim(mZ01.loglik)[1]
1288            list.mZ01<-sapply(1:dimSEM,function(x) matrix(mZ01.loglik[x,,],nrow=dim1*dim2))
1289            list.tmZ01<-(t(list.mZ01))
1290            mZ01.loo<-loo(list.tmZ01)
1291            mZ01.loo
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1292            loo_file<-paste(dossier, "/", site, "_Z01_loo.txt", sep="")
1293            write_values("mZ01", app=T, loo_file)
1294            mZ01_loo_pointwise<-mZ01.loo$pointwise
1295            mZ01_loo_pareto_k<-mZ01.loo$pareto_k
1296            mZ01.loo$pareto_k<-NULL
1297            mZ01.loo$pointwise<-NULL
1298            write_values(as.matrix(mZ01.loo), app=T, loo_file)
1299            save.image(paste(dossier, "/", site, "_Z01.RData", sep=""))
1300    }
1301    ### MODEL Z00
1302    mZ00<-function(){
1303            init.funZ00 <-function(){
1304              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"
1305    = rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
1306    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
1307            }
1308            mod.Z00<<-jags(inits=init.funZ00,model.file = "modelZ00_code.txt",data =
1309    list("cooc","visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =
1310    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","delta","beta","theta0","epsilon","loglik
1311    "),n.chains = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
1312            mod.Z00.mcmc<-as.mcmc(mod.Z00)
1313            mZ00<-mod.Z00$BUGSoutput$sims.list
1314            mZ00.deviance<-mZ00$deviance
1315            mZ00.loglik<-mZ00$loglik
1316            dimSEM<-dim(mZ00.loglik)[1]
1317            list.mZ00<-sapply(1:dimSEM,function(x) matrix(mZ00.loglik[x,,],nrow=dim1*dim2))
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1318            list.tmZ00<-(t(list.mZ00))
1319            mZ00.loo<-loo(list.tmZ00)
1320            mZ00.loo
1321            loo_file<-paste(dossier, "/", site, "_Z00_loo.txt", sep="")
1322            write_values("mZ00", app=T, loo_file)
1323            mZ00_loo_pointwise<-mZ00.loo$pointwise
1324            mZ00_loo_pareto_k<-mZ00.loo$pareto_k
1325            mZ00.loo$pareto_k<-NULL
1326            mZ00.loo$pointwise<-NULL
1327            write_values(as.matrix(mZ00.loo), app=T, loo_file)
1328            save.image(paste(dossier, "/", site, "_Z00.RData", sep=""))
1329    }
1330    ###### end model functions
1331    print("JOB DONE")
1332    ######################################################
1333    ###     Network information (do not change)    ###
1334    ######################################################
1335    ################################BLOCK 3 – MODEL EXECUTION ########################
1336    #launch_modele<-function(){
1337            ntw<-read.table(paste(dossier, "/", site, "_ntw.txt", sep=""),
1338    sep="\t",header=T,row.names=1)
1339            dim1<-dim(ntw)[1]
1340            dim2<-dim(ntw)[2]
1341            web<-as.matrix(ntw,dim1,dim2)
1342            inter0<-dget(paste(dossier, "/", site, "_web_i.txt", sep=""))
1343            cooc<-dget(paste(dossier, "/", site, "_co.txt", sep=""))
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1344            visit<-read.table(paste(dossier, "/", site, "_ntw.txt", sep=""),sep="\t",header=T)
1345            visit<-as.matrix(visit)
1346            abundanceI<-read.table(paste(dossier, "/", site, "_abI.txt", sep=""), sep="\t", header=T)
1347            ab_I <- log(abundanceI[,2])
1348            abundanceP<-read.table(paste(dossier, "/", site, "_abP.txt", sep=""), sep="\t", header=T)
1349            ab_P <- log(abundanceP[,2])
1350            if(opt$modele == "all")
1351            {
1352                    print("modele: all")
1353                    for(i in 0:15)
1354                    {
1355                            print(paste("COMPUTING MODELE ", i, "\n", sep=""))
1356                            mod<-eval(parse(text=paste("mZ0", i, sep="")))
1357                            mod()
1358
1359                    }
1360            }else{
1361                    print(paste("modele: ", opt$modele), sep="")
1362                    mod<-eval(parse(text=paste("m", opt$modele, sep="")))          #recupération de la
1363    fonction du modele
1364                    mod()
1365            }
1366    #### end model execution
1367    #launch_modele()
1368
1369    ################################PARAMETER VALUES################################
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
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")))
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1395                write.table(val, file=paste(opt$dir, "/", opt$site, "_", mod, "_values.txt", sep=""), quote=F,
1396    sep="\t", row.names=F, col.names=T)
1397    }
1398
```


Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

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
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
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)
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
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),]
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
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){
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
  c(((x-1)%%nI)+1,((x-1)%/%nI)+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)
```


Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

```
1529    axis(LEFT<-2,at=1:length(yLabels), labels=as.factor(as.character(yLabels)),las= 2,cex.axis=0.6)
1530    axis(BELOW<-1,at=1:length(xLabels),labels=rep("",length(xLabels)),las =2,cex.axis=0.6)
1531    axis(LEFT<-2,at=1:length(yLabels),labels=rep("",length(yLabels)),las=2,cex.axis<-0.6)
1532    coo<-t(rbind(sapply(indices,function(xx) coord.function(xx,nrow(x),ncol(x)))))
1533    text(coo[,2],nrow(webBFs)+1-coo[,1],labels=visits, cex=0.6)
1534  }
1535  func.plot.matrix(nds,nps)
1536  ######## Black lines to delimit blocks in the plot ######
1537  if (row.nb.gpi>1)
1538  {
1539    ls.class=as.numeric(as.data.frame(table(res.hh.ord2i$mbrshp.hhi))[ls.ord.row.prob,2])
1540    ls.cum=sum(ls.class)-cumsum(ls.class)
1541    abline(h=ls.cum+0.5,col="grey20", lwd=3)
1542  }
1543  if (col.nb.gpi>1)
1544  {
1545    ls.class=as.numeric(as.data.frame(table(res.sp.ord2i$mbrshp.spi))[ls.ord.col.prob,2])
1546    ls.cum=cumsum(ls.class)
1547    abline(v=ls.cum+0.5,col="grey20", lwd=3)
1548  }
```

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

Figures and Tables

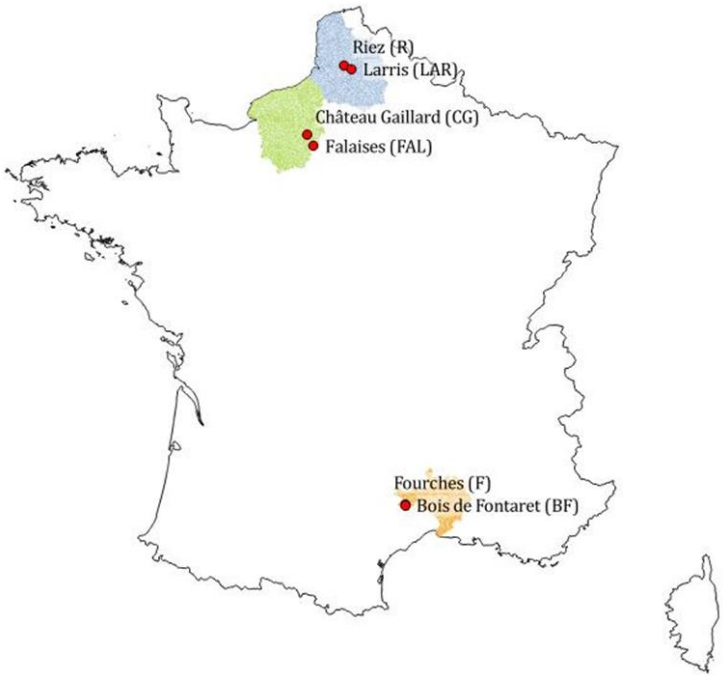

Figure S1. Site location in France: in blue the French départements Pas-de-Calais and Somme (Hauts-de-France region), in green the départements Eure and Seine Maritime (Normandie region), in orange the department Gard (Occitanie region). The six sites correspond to the red dots.

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

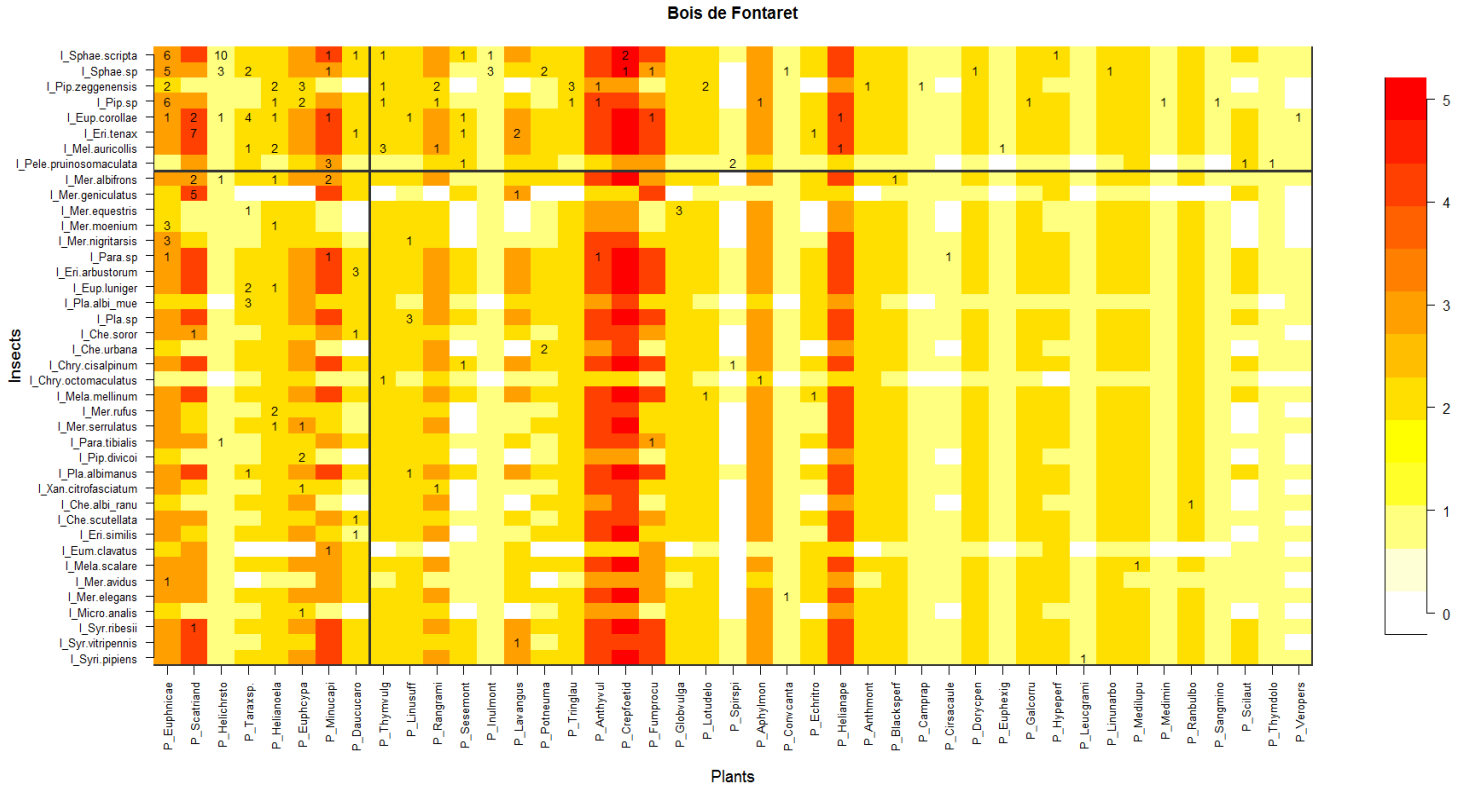

Figure S2. Block clustering provided by LBM in the site of Bois de Fontaret (BF, Occitanie), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants 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.

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

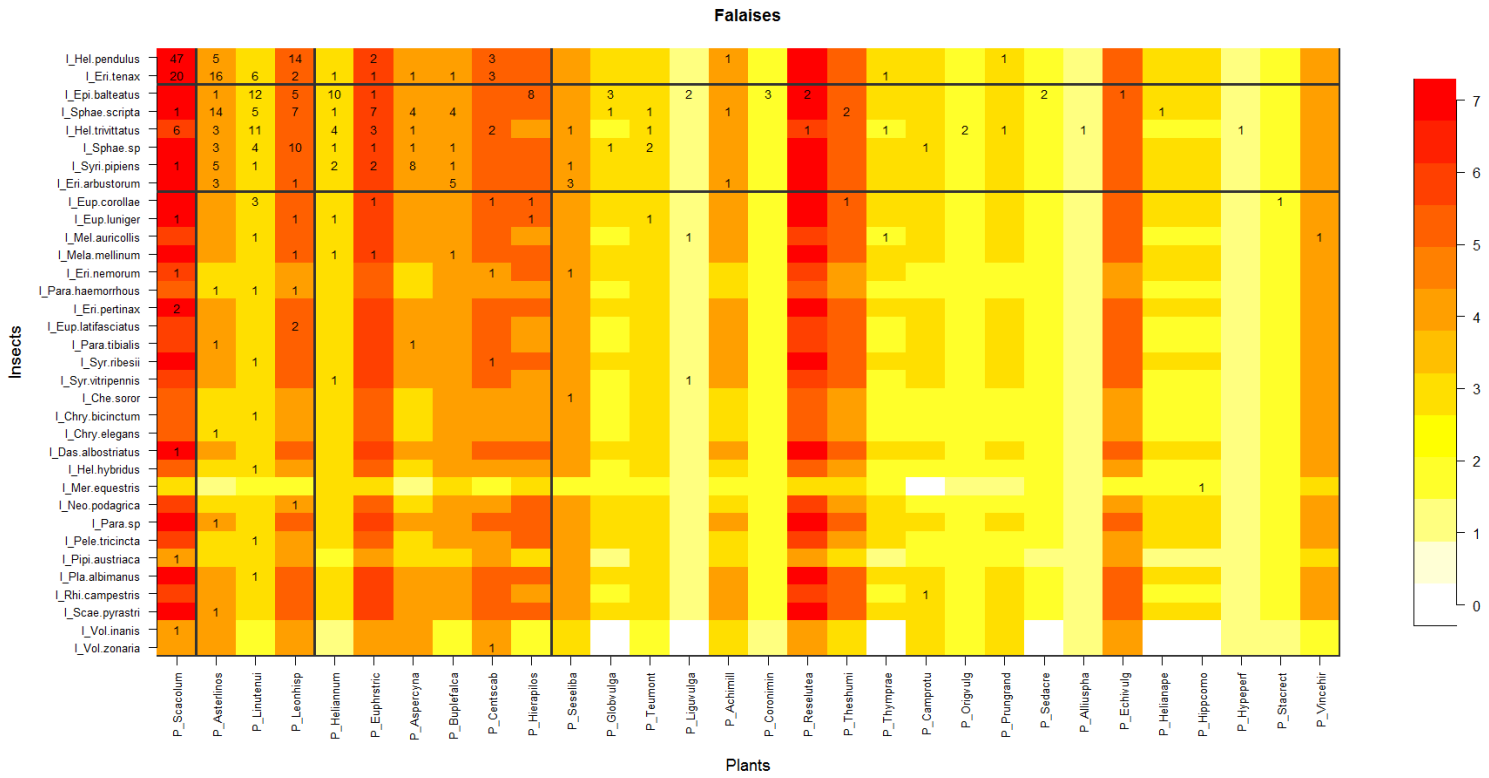

Figure S3. Block clustering provided by LBM in the site of Falaises (FAL, Normandie), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are 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.

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

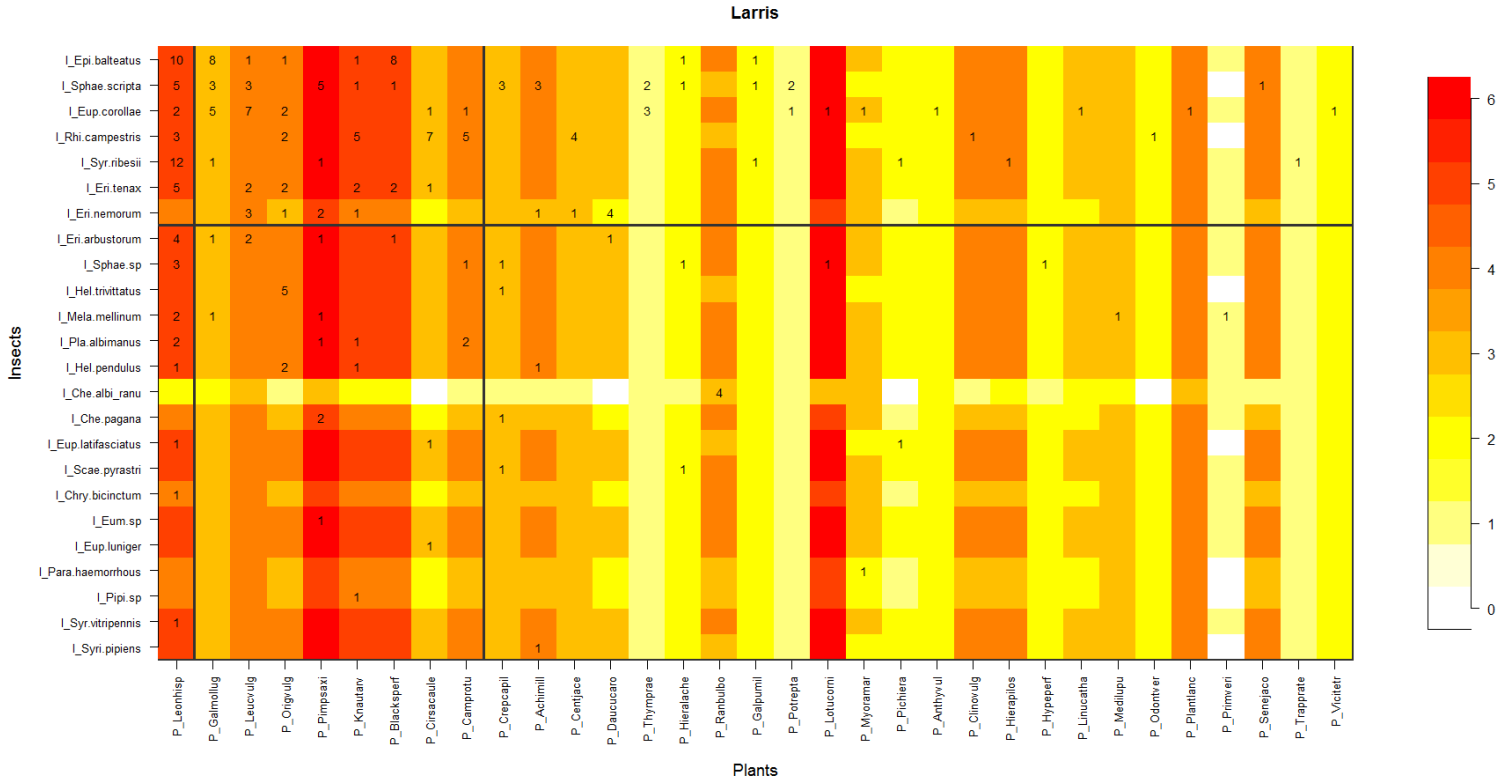

Figure S4. Block clustering provided by LBM in the site of Larris (LAR, Hauts-de-France), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants 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.

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

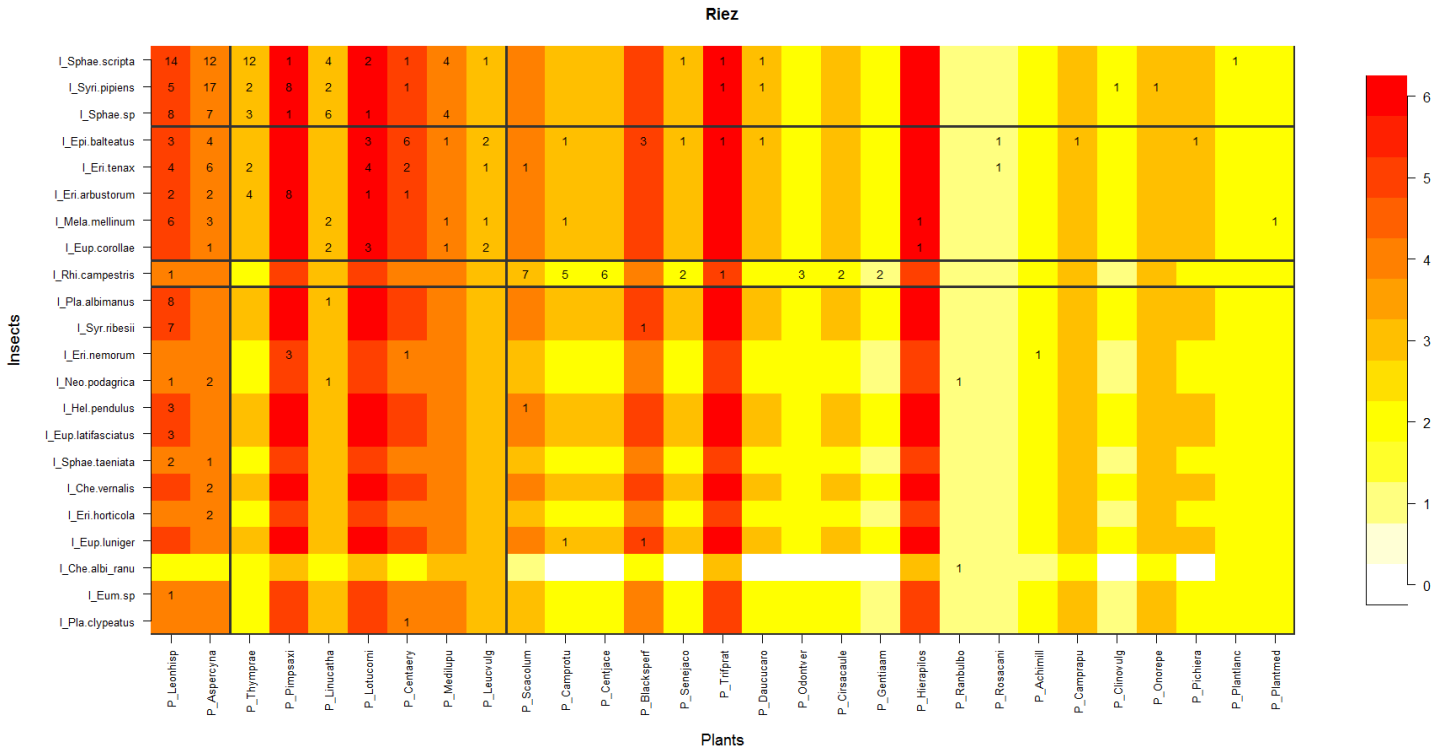

Figure S5. Block clustering provided by LBM in the site of Riez (R, Hauts-de-France), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are 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.

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

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%

Code de champ modifié

Mis en forme : Anglais (Royaume-Uni)

Table S2. Table of model accuracy. The upper part of the table shows the results of the self-validation: in the region Occitanie the self-validation was tested for the site Bois de Fontaret (BF ~ BF) and the site of Fourches (F ~ F); in the region Normandie for the site of Château Gaillard (CG ~ CG) and the sites of Falaises (FAL ~ FAL) ; and in the region Hauts-de-France for the site of Larris (LAR ~ LAR) and for the site of Riez (R ~ R). The lower part of the table shows the results of the cross-validation only between each site of the same region: in the region Occitanie between Bois de Fontaret et Fourches (BF ~ F and vice versa F ~ BF); in the region Normandie between the site of Château Gaillard and Falaises (CG ~ FAL and vice versa FAL ~ CG); and in the region Hauts-de-France between the site of Larris and Riez (LAR ~ R and vice versa R ~ LAR).

Model type	Region	Sites	Threshold	AUC	Omission rate	Sensitivity	Specificity	Prop correct	Kappa
Self-validation	Occitanie	BF ~ BF	0.15	0.78	0.20	0.80	0.75	0.75	0.22
	Occitanie	F ~ F	0.16	0.78	0.19	0.81	0.74	0.75	0.25
	Normandie	CG ~ CG	0.44	0.75	0.29	0.71	0.79	0.78	0.34
	Normandie	FAL ~ FAL	0.37	0.76	0.16	0.84	0.67	0.69	0.27
	Hauts-de-France	LAR ~ LAR	0.29	0.75	0.16	0.84	0.66	0.69	0.27
	Hauts-de-France	R ~ R	0.27	0.81	0.23	0.77	0.86	0.84	0.53
Cross-validation	Occitanie	BF ~ F	0.15	0.73	0.14	0.86	0.59	0.63	0.20
	Occitanie	F ~ BF	0.16	0.67	0.30	0.70	0.64	0.65	0.17
	Normandie	CG ~ FAL	0.44	0.62	0.45	0.55	0.70	0.67	0.21
	Normandie	FAL ~ CG	0.37	0.68	0.24	0.76	0.60	0.63	0.25
	Hauts-de-France	LAR ~ R	0.29	0.63	0.35	0.65	0.61	0.61	0.17
	Hauts-de-France	R ~ LAR	0.27	0.65	0.42	0.58	0.72	0.69	0.22

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