1 **Title:** Does phenology explain plant-pollinator interactions at different latitudes? An assessment of its

2 explanatory power in plant-hoverfly networks in French calcareous grasslands

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27 **Author contributions**

28 NDM and FM conceived the project, formulated and implemented the model. NDM conducted the

29 analysis and prepared the manuscript. FM supervised the analysis and edited the manuscript. NH, YP,

30 CV and BS contributed substantially to all later versions. NDM, NH, YP and BS conducted the fieldwork

31 and provided the data. CV identified the hoverflies.

32 **Data accessibility**

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

34

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 phenological 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

50 Understanding how phenology determines species interactions is a central question in the case of

51 mutualistic networks. In plant-pollinator networks, phenology shapes their temporal and spatial limits,

52 thus defining the area and the period along the season in which interactions preferably occur (Olesen

53 *et al.* 2011; Ogilvie & Forrest 2017). Since plant and pollinator phenologies are not equally affected by

54 changes in environmental cues, partial or total phenological mismatches can occur as a result of

55 environmental changes such as climate change (Parmesan 2007; Rafferty 2017). Phenological advances

56 indeed increase at higher latitudes, as a response to the acceleration of warming temperature along

57 the same gradient (Post *et al.* 2018), increase phenological mismatch, and have the potential to

58 threaten the synchrony needed for effective pollination (Hutchings *et al.* 2018). Such environmental

59 changes can thus drastically alter pollinator interactions through modified temporal overlap between

60 pollinators and their floral resources leading, in extreme cases, to local extinctions (Memmott *et al.*

61 2007) and the ensuing absence of the partner species at the location and/or time at which the

62 interaction should have taken place (Willmer 2012; Miller-Struttmann *et al.* 2015; Rafferty *et al.* 2015;

63 Hutchings *et al.* 2018).

64 Because phenological match is crucial to plant-pollinator interactions, and thus ultimately to

65 pollinators' fitness, pollinators have to adapt to phenological shifts either through interaction with

66 other plant species (Rafferty *et al.* 2015) or through changes of their own phenology (Bartomeus *et al.*

67 2011). Phenology can then influence dynamical network properties, such as the stability and the

68 coexistence of species, through changes in network topology (Encinas-Viso *et al.* 2012). Moreover,

69 phenology predictably affects network compartmentalization as different phenophases likely

70 correspond to different compartments when networks are considered on an annual scale (Martín

71 González *et al.* 2012).

72 Despite considerable theoretical advances, there are few models available to predict the probability

73 of interaction in plant-pollinator networks (Staniczenko *et al.* 2017; Cirtwill *et al.* 2019) and fewer still

74 able to make comparisons between networks. Due to their complexity and variation among years

75 (Chacoff *et al.* 2017), most studies of mutualistic networks have focused on predicting and comparing

76 classic network metrics (nestedness, connectance, modularity, etc.) which are all influenced by

77 network size, *i.e.* the number of plant and insect species (Fortuna *et al.* 2010; Staniczenko *et al.* 2013;

78 Poisot & Gravel 2014; Astegiano *et al.* 2015). Moreover, few studies have compared interaction

79 networks along environmental gradients (Devoto *et al.* 2005; Schleuning *et al.* 2012; Sebastián-

80 González *et al.* 2015; Pellissier *et al.* 2017). In order to compare networks of different sizes, a better

81 alternative is to switch from network-derived metrics to the comparison of the probability of

82 interaction given by regression models, which can consider multiple factors and latent variables and

83 assume that the sampled data are just part of a larger unobserved dataset (Grace *et al.* 2010).

84 Calcareous grasslands are characterized by highly diverse plant communities with a high proportion of

85 entomophilous species (Baude *et al.* 2016), thus they are a convenient model for such studies. Most

86 plant-insect pollinator networks involve bee species (Anthophila), but recent studies have also pointed

87 out the importance of hoverflies (Diptera: Syrphidae), which pollinate a large spectrum of wild

88 flowering species (Klecka *et al.* 2018a) and crops (Jauker & Wolters 2008; Rader *et al.* 2011). They

89 usually behave opportunistically, *i.e.* from being pollen generalists to specialists, only limited by

90 morphological constraints (Iler *et al.* 2013; Klecka *et al.* 2018a; Lucas *et al.* 2018). Indeed, their

91 generalist behaviour, at the species level, could be the result of individually specialized diets, since

92 most pollen retrieved on hoverfly individuals usually comes from a single plant taxon (Lucas *et al.* 2018)

93 and depends on flower availability and phenology (Cowgill *et al.* 1993; Colley & Luna 2000; Lucas *et al.*

94 2018). Moreover, some hoverflies have preferences regarding plant colour, morphology and

95 inflorescence height (Branquart & Hemptinne 2000; Colley & Luna 2000; Lunau 2014; Klecka *et al.*

96 2018b, a).

97 Here we study the consequences of environmental gradients on plant-pollinator interactions, focusing

98 on how phenology overlap affects interactions between plants and insects in six calcareous grassland

99 sites distributed along a latitudinal gradient. We obtained plant and insect phenologies, abundances,

100 and interactions in all sites from April to October 2016. We modelled plant-pollinator interaction

101 networks following a Bayesian Structural Equation Modelling approach (SEM) using latent variables,

102 *i.e.* unobserved variables (Grace *et al.* 2010). SEM is a multivariate technique used to test several

103 hypotheses in ecological studies. SEM analysis involves cause-effect equations to evaluate multiple

104 causal relationship (Grace 2006; Eisenhauer *et al.* 2015) using observed and latent variables to explain

105 some other observed variables (Grace 2006). SEM can be used to choose among competing models

106 (Grace & Bollen 2008). Thus, SEM are well suited for studying the complexity of ecological networks.

107 To test whether phenology affects network compartmentalization, we looked for species subgroups

108 using a latent block model (LBM) which is among the best clustering methods for weighted networks

109 (Leger *et al.* 2015).

110 The comparison of 16 SEMs and the analysis of LBMs of sampled networks evinced that phenology

111 overlap is an important determinant of plant-pollinator interactions, but is less informative than

112 species abundances and performs heterogeneously among sites. Our results suggest that the use of

113 SEMs to compare networks of different sizes along an environmental gradient is an innovative

114 approach which can help understand the structure of plant-pollinator networks.

115 **MATERIALS AND METHODS**

116 <u>Study sites</u>

117 We sampled plant and hoverfly species in six areas (Fig. S1) of 1 hectare each in different French

118 regions: two sites in Hauts-de-France (Les Larris de Grouches-Luchuel, thereafter noted LAR,

119 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

120 2°12'05.56"E, in départements Pas-de-Calais and Somme), two sites in Normandie (Château Gaillard –

121 le Bois Dumont, noted CG, 49°14'7.782"N 1°24'16.445"E and les Falaises d'Orival, noted FAL,

122 49°04'40.08"N 1°33'07.254"E, départements: Eure and Seine Maritime) and two sites in Occitanie

123 (Fourches, noted F, 43°56'07.00"N 3°30'46.1"E and Bois de Fontaret, noted BF, 43°55'17.71"N

124 3°30'06.06"E, départment: Gard). The six sites are included in the European NATURA 2000 network, a

125 network of preserved areas designated to protect a number of habitats and species representative of

126 European biodiversity. The four sites in Hauts-de-France and Normandie are managed by the

127 Conservatoire d'espaces naturels of Normandie, Picardie and Nord – Pas-de-Calais and the sites in

128 Occitanie by the CPIE Causses méridionaux. We sampled each site once a month from April to October

129 2016, except for the site of Riez that was sampled from May to October.

130 <u>Plant-hoverfly observations and sampling</u>

131 To collect information at the community level, in each site and at each session we realized: (i) a botanic

132 inventory of the flowering species, recorded their abundances and the total flower covering in the area

133 and (ii) a pollinator sampling using a hand net along a variable transect walk.

134 Flowering plants were identified at the species level. We recorded the abundances of all flowering

135 species. At first, we estimated the total percentage of surface covered by all flowering species in the

136 selected area. We then estimated the relative abundance of each flowering species. We used Braun-

137 Blanquet coefficients of abundance-dominance, ranked from i to 5 (most abundant coefficient class)

138 (van der Maarel 1975, 1979; Mucina *et al.* 2000), to rank flowering species. We converted the

139 coefficients to percentage intervals and then in mean values of percentage cover classes (Table S1):

140 coefficient *5* = 75-100%, coeff *4* = 50-75%, coeff *3*=25-50%, coeff *2* = 10-25%, coeff *1* = 1-10%, coeff *+*

141 = few individuals less than < 1%, coeff *i* = 1 individual. All inventories were realized by the same

142 surveyors to avoid biases.

143 Pollinator observations were performed by the same team of 3-5 persons each day. The surveyors

144 walked slowly around any potential attractive resource patch included in the selected 1-hectare area

145 for 4h each day. We split the sampling period into 2 hours in the morning (about 10-12h) and 2 hours

146 in the afternoon (about 14-16h) to cover the daily variability of both pollinator (bees and hoverflies,

147 which are more active in the morning than in the afternoon; D'Amen *et al.* 2013) and flower

148 communities. Sampling took place when we had suitable weather conditions for pollinators (following

149   Westphal *et al.* 2008). We sampled all flower-visiting insects and we recorded observed interactions.

150   All sampled insects were immediately put individually in a killing vial with ethyl acetate and were later

151   prepared and pinned in the laboratory and identified at the species level by expert taxonomists. Even

152   if we collected both bees and hoverflies, in this study we focus on hoverflies only (since at the moment

153   of the study bees were not identified at the species level yet). Overall, we sampled for 41 days,

154   equivalent to about 164 hours in the field (all the surveyors collected at the same time). For all analyses

155   described here, we only used the list of visited herbaceous plant species and hoverflies which were

156   found visiting a plant. Despite their rarity and even if hoverflies are known to prefer open flowers

157   (Branquart & Hemptinne 2000), we also considered the interactions between hoverflies and plant

158   species of the Fabaceae family because we observed in the field that they visited Fabaceae species

159   that were already opened by other insects, *e.g.* by large bee species, such as *Eucera* sp. (de Manincor,

160   personal observation).

161   <u>Plant – hoverfly networks</u>

162   For each site, we constructed an interaction network consisting of all pairs of interacting plant and

163   insect species, pooling data from all months. A pair of species (i,j) was connected with intensity v_{ij} when

164   we recorded v_{ij} visits of insect species i on plant species j in the site. We calculated the network

165   specialization index, H2' (Blüthgen *et al.* 2006) using the `H2fun` function implemented in the

166   `bipartite` package (Dormann *et al.* 2009; R Core Team 2018). We obtained the *d*-value (Kullback-

167   Leibler divergence between the interactions of the focal species and the interactions predicted by the

168   weight of potential partner species in the overall network) and the *dmax*-value (maximum d-value

169   theoretically possible given the observed number of interactions in the network) using the `dfun`

170   function in the `bipartite` package (Dormann *et al.* 2009). We did not use the *d'* values provided by

171   this package as they sometimes yielded spurious results based on the computation of the minimal *d*

172   value (e.g. reporting low *d'* for species with only one partner in the network).We then manually

173 calculated the standardized specialization index *d'* (Blüthgen *et al.* 2006) for each plant and insect

174 species as the ratio of the *d*-value to its corresponding *dmax*-value.

175 We calculated the modularity of the network and the associated partition of species into modules

176 using the `cluster_leading_eigen` method for modularity optimization implemented in the

177 `igraph` package (Csardi & Nepusz 2006; Newman 2006). Modularity optimization can help identify

178 strong, simple divisions of a network into relatively independent sub-networks by looking for highly

179 interconnected sub-networks. However, modules are not meant to inform about more subtle

180 groupings among the species, *e.g.* particular avoidance of interactions between insects of group A and

181 plants of group 1. In order to detect such groups, we implemented latent block models (LBM) using

182 the `BM_poisson` method for Poisson probability distribution implemented in the `blockmodels`

183 package (Leger *et al.* 2015). Blocks are calculated separately for the two groups (insect and plant) based

184 on the number of visits (*i.e.* a weighted network). The algorithm finds the best divisions of insects and

185 plants through fitting one Poisson parameter in each block of the visit matrix, thus essentially

186 maximizing the ICL (Integrated Completed Likelihood; Biernacki *et al.* 2000; Daudin *et al.* 2008). The

187 LBM script is given in Supplementary Information (Appendix S3). All analyses were performed in R

188 version 3.3.3 (R Core Team 2018).

189 <u>Plant and hoverfly abundances and phenology overlap</u>

190 We calculated plant abundance using information about the abundance-dominance recorded in the

191 field following the methodology of Braun-Blanquet presented above. We transformed the coefficients

192 of abundance in percentages (Table S1): we used the mean of the percentage corresponding to each

193 class. We then calculated the relative abundance (A_P) of each flowering plant species as the ratio of

194 the focal species cumulated abundance to total flower abundance during its flowering season. For

195 hoverflies, we used the recorded number of visiting individuals (total abundance) and their presence

196 (recorded months) along the season to calculate their average abundance during months when they

197 were present (A_H).

198 We refer to plant phenology as their flowering period and insect phenology as the flying period. We

199 considered only flowering plants which had been visited by pollinators. For the pollinators, we

200 considered only hoverflies which were found in interaction. To build the species phenology tables for

201 both plants and hoverflies, we merged the information provided by two sources of data (field data and

202 the literature): we used the observed phenology of both plants and insects during the field session as

203 the only source of information for plants (plants visited by insects and plants found in the botanic

204 inventory in the site at that date), and we complemented the hoverfly phenology with information

205 provided by the Syrph the Net Database (Speight *et al.* 2016). We then built the phenology overlap

206 (PO) matrix based on the species phenology tables by calculating the number of phenologically active

207 months that are shared by each pair of insect and plant species along the season.

208 Bayesian Structural Equation Modelling (SEM)

209 SEM is a confirmatory technique that involves cause-effect equations to evaluate multivariate

210 hypotheses in ecological networks (Grace 2006). The primary interest of SEM analyses lies in its ability

211 to compare different causal models between the same sets of explanatory and explained variables.

212 Another important feature of SEM is that they can relate data through latent variables, *i.e.* variables

213 which are not measured in the model and which represent underlying causes or effects, coupled with

214 observed variables (Grace 2006; Grace *et al.* 2010). SEM can now be assessed using Bayesian

215 approaches and parameters estimated using MCMC (Markov Chain Monte Carlo)(Grace *et al.* 2010;

216 Fan *et al.* 2016).

217 In our study, we modelled hoverfly-plant interaction networks using a SEM approach (Fig. 1) with latent

218 variables linking the number of visits per plant-pollinator species pair to abundance and phenology

219 overlap (PO) data through a first latent table representing probabilities of interactions, another latent

220 table representing the possible interactions between plant and pollinators (as a realization of the

221 aforementioned interaction probability matrix), and a third latent table yielding the expected number

222 of visits per plant-pollinator species pair (*i.e.* the intensity of interactions). We used the term latent

10

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

224 visit matrix.

225 In this model, we considered that PO had an effect on possible interactions (I_{ij}) and the number of visits

226 (λ_{ij}) – a longer overlap is intuitively expected to drive a higher probability of interaction and a larger

227 number of visits. Interaction probabilities were also assumed to depend on two random effects (plant

228 and insect species identities, E_i and E_j), to represent heterogeneity of species degrees (*i.e.* the number

229 of links) in the network. We modelled the possibility of interaction I_{ij} between insect species *i* and plant

230 species *j* (*i.e.* $I_{ij} = 1$ when species *i* and *j* can interact) as a Bernoulli random variable of probability μ_{ij}

231 given by:

232
$$\text{logit}(\mu_{ij}) = \mu_0 + \mu_{PO}PO_{ij} + E_i + E_j$$

233 where logit is the usual logistic transformation (log(x/(1-x)), μ_0 is the intercept of this relation, μ_{PO} is

234 the coefficient measuring the effect of PO, and E_i and E_j are the random effects associated with insect

235 species i and plant species j respectively.

236 The number of visits V_{ij} was assumed to depend on plant and hoverfly abundances, as more abundant

237 species are expected to be more often sampled (and thus more often recorded "in interaction"). Please

238 note that we only linked abundances to the number of visits, V_{ij}, and not to the possibility of interaction

239 I_{ij}, because the aim of the latter latent table is to capture "forbidden links", while detectability and

240 sampling effects are supposed to be captured by the statistical model of the number of interactions.

241 We integrated species abundances as predictor variables in order to assess the effect of PO on the

242 number of visits on top of a "null model" that already includes sensible drivers of the numbers of visits,

243 such as species abundances. V_{ij} was modelled as a Poisson random variable to allow for sampling

244 variability, with a conditional mean λ_{ij} (the intensity of visits that can occur) given by:

245
$$\log(\lambda_{ij}) = \lambda_0 + \lambda_H A_{H,i} + \lambda_P A_{P,j} + \lambda_{PO}\log(1 + PO_{ij})$$

246 where λ_0 is the intercept of this relation, λ_H is the coefficient measuring the effect of hoverfly

247 abundance A_H, λ_P is that of plant abundance A_P, and λ_{PO} is the coefficient of the effect of PO.

248 Possible interactions (I_{ij}) and the intensity of visits (λ_{ij}) are multiplied to obtain the unconditional mean

249 number of recorded visits, *i.e.* V_{ij} is then obtained as a Poisson draw of mean $I_{ij} \lambda_{ij}$.

250 Overall we estimated four main parameters: the effect of phenology overlap on the probability of

251 interaction ($PO \rightarrow I_{ij}$, μ_{PO}), the effect of phenology overlap on the intensity of interactions ($PO \rightarrow \lambda_{ij}$,

252 λ_{PO}), the effect of plant abundance on the intensity of interactions ($A_P \rightarrow \lambda_{ij}$, coefficient λ_P) and the

253 effect of insect (hoverflies) abundance on the intensity of interactions ($A_H \rightarrow \lambda_{ij}$, λ_H).

254 We used the `jags` function (`R2jags` package), which provides an interface from R to the JAGS library

255 for Bayesian data analysis, to estimate model parameters. JAGS (Plummer 2003) uses a Markov Chain

256 Monte Carlo algorithm to generate samples from the posterior distribution of the parameters. We ran

257 two Markov chains with 10^6 iterations per chain to check for model convergence. The code of the

258 model is given in Supplementary Material (Appendix S1 and S2).

259 <u>Model and parameter comparison</u>

260 We estimated the 16 models that included all combinations of 0 and 4 of the above-mentioned effects

261 to understand which effects were more likely to play a role in the structuring of the network. The

262 goodness-of-fit of these models were compared using the leave-one-out cross-validation criterion

263 (LOO) calculated using the R package `loo` using Pareto smoothed importance sampling for regularizing

264 importance weights (Vehtari *et al.* 2017). The LOO criterion is a fully Bayesian method to compare

265 models of different complexities and to estimate prediction accuracy using the log-likelihood evaluated

266 at the posterior simulations of the parameter values (Vehtari *et al.* 2017). Models can thus be ranked

267 according to their LOO scores, with the best model being the one with the lowest LOO value. The LOO

268 criterion is analogous to the classic Akaike and Bayesian Information Criteria, which are used to

269 compare frequentist models, but can instead be applied to Bayesian models, without suffering the

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270 instability issues of the Deviance Information Criterion which used to be the main information criterion

271 for Bayesian models(Vehtari *et al.* 2017). To rank the models, we then calculated the *ΔLOO* (noted Δ_i)

272 as $\Delta_i = LOO_i - LOO_{min}$ (following Burnham & Anderson 2004), where LOO_{min} is the minimum of the LOO_i

273 values among the 16 models. We used Δ_i to obtain model weights ω_i, following the Akaike weight

274 methodology (Burnham & Anderson 2002):

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

275

276 We then summed weights (w_H) over all models that incorporated a given focal parameter to ascertain

277 the plausibility of the effect associated to this parameter. We used this sum to evaluate the null

278 hypothesis (H0) that a given factor has no effect on the plant-pollinator interactions by comparing the

279 sum of weights to null expectations, based on the fact that each tested effect is incorporated in exactly

280 half of the tested models. The effect is considered *plausible* when $w_H > 0.5$, *implausible* otherwise,

281 *likely* when $w_H > 0.73$, and *unlikely* when it corresponds to a value of 0.27 or lower, following Massol

282 *et al.* (2007).

283 <u>Predictive power analysis</u>

284 We tested the predictive power of the models we built by making predictions for the I_{ij} table and

285 checking their validity using a binarized version of the visit table V_{ij}. Predictions were obtained by

286 defining a threshold on interaction probability μ_{ij}: values found above the threshold were predicted as

287 occurring interactions, values below the threshold as no interaction. The threshold probability value

288 was found by maximizing the sum of model specificity and sensitivity. We computed accuracy statistics

289 (sensitivity, specificity, omission rate, area under the ROC curve [AUC]) in two situations: (i) when

290 predicting data for the site that was used to build the model (self-validation; e.g. predicting interaction

291 data in the site of Riez based on the model developed for this site) and (ii) when predicting data for

292 the other site from the same region (cross-validation; e.g. predicting data for the LAR site based on the

293 model for the R site). We performed theses analyses using the `SDMTools` package in R. We only used

13

294 the set of best models (LOO < 4) found for each site to predict the interactions in the other site through

295 a multimodel averaging approach. We obtained the threshold probability using `optim.tresh`

296 function with option `max.sensitivity+specificity`.

RESULTS

Plant-hoverfly networks and phenology overlap

299 At the end of the field campaign we had collected 1584 hoverflies and recorded 1668 interactions

300 between 76 hoverfly species and 115 plant species overall (Table 1, Table S2). The number of sampled

301 hoverfly and plant species varied between sites and among regions. In Normandie we generally

302 sampled a higher number of hoverflies than in the other two regions (Table 1) and the maximum

303 number of visits recorded in the site of FAL was 47 (between *Helophilus pendulus* and *Scabiosa*

304 *columbaria*, Fig. S2) and in the site of CG was 22 (between *Eristalis tenax* and *S. columbaria* and

305 between *Sphaerophoria scripta* and *Leontodon hispidus*, Fig. 2). We observed the highest diversity of

306 both plants and hoverflies in Occitanie and the lowest diversity of hoverflies in Hauts-de-France.

307 Despite the high species diversity in Occitanie, the total number of interactions recorded in these sites

308 (BF and F) is not the highest recorded in the field (Table 1): the maximum number of visits in the site

309 of BF was 10 (between *Spherophoria scripta* and *Helichrysum stoechas*, Fig. S3) and 12 in the site of F

310 (between *Syrphus ribesii* and *Bellis perennis*, Fig. 3). In the two southern sites we also recorded the

311 lowest connectance values (BF: 0.07 and F: 0.08) of all six sites, with the highest connectance observed

312 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

313 site of LAR was 12 (between *Syrphus ribesii* and *L. hispidus*, Fig. S4) and in the site of R was 17 (between

314 *Syritta pipiens* and *Asperula cynanchica*, Fig. S5).

315 In spite of differences in diversity and the number of interactions, the overall level of specialization (H2

316 index) did not show a high variation among the 6 networks (range: 0.32 – 0.37). However, we found

317 that the sites in Occitanie (BF and F) had a higher average degree of specialization (d') for both insect

318 (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

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324 modularity (BF 0.51 and F 0.48) than the ones in Normandie (CG 0.34 and FAL 0.23) and Hauts-de-

325 France (LAR 0.37 and R 0.34; Table 1). Given that these statistics only compare 6 sites, none of these

326 assessments can be properly statistically tested, but the importance of the differences among sites is

327 highly suggestive of a difference in average specialization and modularity. We found that plant

328 phenology is generally shorter in all sites than that of hoverflies (Table 1). The phenology overlap was

329 shorter in Occitanie (BF and F) than in the other sites (Table 1).

330 Illustrations of the block clustering provided by the LBM analysis (Latent Block Model) are shown in

331 Fig. 2 and 3 in the main text and in Fig. S2 to S5 in Supplementary Information. We found different

332 numbers of blocks in plants and hoverflies among sites: the BF site had 2 insect blocks and 2 plant

333 blocks (Fig. S3); the F site had 4 of both (Fig. 3); the CG and R sites had 3 blocks for the plants and 4

334 blocks for the insects in (Fig. 2 and S5); the FAL site had 4 plant blocks and 3 insect blocks (Fig. S2); the

335 LAR site had 3 blocks for the plants and 2 for the insects (Fig. S4).

336 <u>Model ranking and comparison of parameters in each site</u>

337 For each site we compared the 16 models using the LOO criterion (Table 2, ΔLOO values). We found

338 that models 1, 2 and 4 had consistently better goodness-of-fit than the others. The model

339 incorporating all effects except the effect of phenological overlap on the probability of interaction

340 (Model 4: λ_{ij} ~ A_H + A_P + PO, Table 2) was the best model in the sites of CG, FAL and LAR. In the two

341 southern sites (BF and F), we found that the model incorporating all effects except that of phenological

342 overlap on the intensity of visits (Model 1: λ_{ij} ~ A_H + A_P / I_{ij} ~ PO, Table 2), was the best one. The model

343 incorporating all effects (Model 0: λ_{ij} ~ A_H + A_P + PO / I_{ij} ~ PO, Table 2) was found as the best one only in

344 the site of R, but was a suitable model (ΔLOO <4) in all the other sites (Table 2). We also compared the

345 sum of model weights of the four parameters among sites (Table 2, Effects weight). We found that the

346 effect of insect abundance on the intensity of interaction (A_H → λ_{ij}) is always likely (*i.e.* the sum of their

347 weights is always higher than 0.73, Table 2) and of large effect size in all sites (standardised coefficient

348 higher than 1, Fig. 4). Likewise, we found that the effect of plant abundance on the intensity of

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353 interaction ($A_P \rightarrow \lambda_{ij}$) was always likely and had large effect size in most part of sites, except in the site

354 of F (w_H = 0.59, Table 2; standardised coefficient = 0.67, Fig. 4). The effects of phenological overlap on

355 the probability of interaction (PO $\rightarrow$ I_{ij}) and the intensity of visits (PO $\rightarrow$ λ_{ij}), however, had variable

356 plausibility among sites. The effect of phenological overlap on the probability of interaction was *likely*

357 only in half of the sites (Table 2 and Fig. 4). The effect of phenological overlap on the intensity of visits

358 was *not plausible* only in the two southern sites (BF and F) and *plausible* in the other four sites (LAR, R

359 CG and FAL, Table 2 and Fig. 4). In all sites, the standardised coefficients of PO effects were always less

360 than 1, thus showing a low effect size of phenology on interaction probability and intensity (Fig. 4).

361 When assessing the predictive power of the best models, we observed that the sensitivity and

362 specificity values, both for the self-validation and the cross-validation, were higher than 0.5 (Table S3),

363 which means that the interactions predicted by the models are better than predicted by chance. While

364 area under the curve (AUC) values were all higher than 0.75 for self-validation, cross-validation tests

365 yielded intermediate values (AUC between 0.62 and 0.73), reflecting the fact that abundances and

366 phenology are certainly not sufficient to make accurate predictions on the occurrence of plant-

367 pollinator interactions.

368 **DISCUSSION**

369 Latitude affects the seasonality, with advancing species phenologies at higher latitudes, and thus, can

370 be a limiting factor for the phenological coupling of interacting species (Post *et al.* 2018). In this study

371 we explored the effect of phenology overlap on a large network of species interactions in calcareous

372 grasslands and how this effect could vary along a latitudinal gradient in France using empirical data on

373 six plant-hoverfly networks. We identified plants and insects at the species level to build detailed

374 interaction networks and hence avoid spurious generalisation levels. In order to better understand the

375 determinants of variation in species interactions in space and time, we used the latitudinal gradient to

376 consider variations linked to environmental cues and the entire flowering period to allow for seasonal

377 variation (Valverde *et al.* 2016; Pellissier *et al.* 2017). One of the main problems of comparing networks

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379 along gradients is the dependence of network metrics on network size (Staniczenko *et al.* 2013;

380 Astegiano *et al.* 2015; Tylianakis & Morris 2017). In this study, to avoid the problem of comparing

381 networks with different dimensions, we decided to focus on the determinants of the probability of

382 interaction and the number of visits, rather than the overall structure. We employed Bayesian

383 Structural Equation Models (SEM) which is an emergent approach increasingly used to investigate

384 complex networks of relationship in ecological studies (Grace *et al.* 2010; Eisenhauer *et al.* 2015; Fan

385 *et al.* 2016; Theodorou *et al.* 2017). In our study we used SEM to link the numbers of visits to phenology

386 overlap (PO) and species abundance through latent probabilities of species interaction and expected

387 numbers of visits per plant-pollinator species pair. We tested different models with variable numbers

388 of effects and compared them in each site. In our models, we used species abundances to construct a

389 sensible null model to test whether phenology overlap could help explain the probability and intensity

390 of interactions when the effects of species abundances are already taken into account. In all sites, we

391 found that models that included both PO and abundances had always better goodness-of-fit than

392 models that included only abundances. Abundances indeed provided a sensible null model since the

393 goodness-of-fit of models that did not include abundances were always quite worse than the ones

394 which did.

395 We also found that in all sites the most important factor affecting pollinator visits was insect

396 abundance (Table 2). Likewise, we found that plant abundance was also a very important effect in most

397 sites, except in the site of F (Table 2). Since insect abundances are given by visitation data, it is not

398 surprising that the intensity of interactions positively depends on these abundances. Species

399 abundance often explain the linkage level in pollination network studies (Olesen *et al.* 2008; Bartomeus

400 *et al.* 2016; Chacoff *et al.* 2017; Pellissier *et al.* 2017) but it is often associated with the length of the

401 phenology to better assess the general properties of the interaction network (Vázquez *et al.* 2009;

402 Olito & Fox 2015). In accordance with this verbal prediction, we indeed found that the best models

403 incorporated the effect of PO on either the probability or the intensity of interactions (Table 2), and

404 the model that only considered species abundance (model 5 in Table 2) was not the best one in any

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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, this 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. 2, S2, 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 for behavioural flexibility in order to maintain synchrony with their foraging resources (Iler et al. 2013; Ogilvie & Forrest 2017).

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433 We also found that modularity decreased along the latitudinal gradient, with richer sites (BF and F)

434 displaying higher modularity (as in Sebastián-González *et al.* 2015) but also the lower connectance. In

435 the two southern sites, higher modularity could be related to shorter phenologies and higher

436 proportions of non-overlapping sets of species, which induce some form of temporal short-term

437 specialisation (Lucas *et al.* 2018). However, modularity also seems to be influenced by species

438 abundances and degrees (Schleuning *et al.* 2014), and is expected to increase with link specificity

439 (Morente-López *et al.* 2018). Indeed, in these sites, species blocks match species degrees (Fig. 3 and

440 S3), with generalist and specialist species forming separate blocks among both plants and insects

441 (Martín González *et al.* 2012). With lower modularity and more generalist species, we expect a stronger

442 relationship between phenology and the intensity of interactions because interactions are less

443 influenced by insect preferences and more by seasonal rhythm and flower availability (Dormann *et al.*

444 2017). Thus, different phenophases might correspond to different compartments (Martín González *et*

445 *al.* 2012; Morente-López *et al.* 2018), as observed in CG, FAL, LAR and R where higher overlap

446 corresponded to higher numbers of observed visits. Although phenology improved model fit (Table 2),

447 its effect size was modest (Fig. 4), which suggests that other types of data such as traits and phylogenies

448 might help predict specific interactions. In our study, we did not consider competition among studied

449 insect species or with other group of insects, such as bees which were present in all sites. Different

450 types of pollinators with different abundances could have context-dependent effects on network

451 topology (Valverde *et al.* 2016). Moreover, in our study we only considered as "true absence" of the

452 interaction the lack of phenological coupling between species (*i.e.* plant and hoverfly species which are

453 not present at the same moment along the season cannot interact). We did not consider "false

454 absences", *i.e.* missing links, since not all the potential links among species are recorded in the field

455 (Olesen *et al.* 2011) which may introduce bias in the estimation of the probability of interactions

456 (Bartomeus *et al.* 2016; Cirtwill *et al.* 2019).

457 To conclude, plant phenology here drives the duration of the phenology overlap between plant and

458 hoverflies, which in turn influences either the probability of interaction or the expected number of
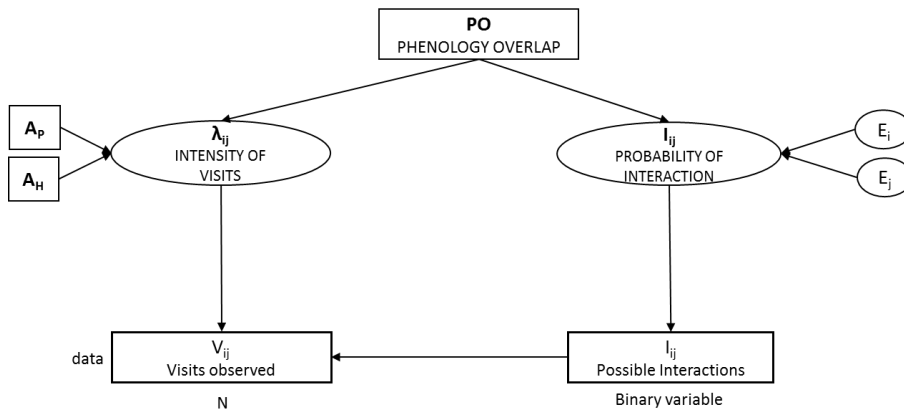
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461 visits, as well as network compartmentalization. Longer phenologies correspond to less constrained

462 interactions (lower modularity), shorter phenologies to more constrained interactions (higher

463 modularity), which in turn restrict the number of visits. Phenology overlap alone was not sufficient to

464 explain interactions, as suggested elsewhere (CaraDonna *et al.* 2017). Plant and insect abundances

465 played a substantial role to explain the number of visits (as in Chacoff *et al.* 2017) since abundances

466 may affect partner choice (Trøjelsgaard *et al.* 2015). Our results, and the ability of the method used

467 here to compare different effects on interaction patterns, suggest that the use of Bayesian SEM to

468 compare networks of different sizes is a valuable tool which can help understand plant-pollinator

469 networks (Eisenhauer *et al.* 2015). The use of latent variables can help predict the probability of

470 interaction and the expected number of visits while avoiding circularity – the introduction of plant and

471 insect specific random effects played the role of an implicit "degree" effect. Our results demonstrate

472 the importance of considering differences in plant and insect phenologies to better predict their

473 interactions in pollination networks at different latitudes. The use of morphological traits (*e.g.* tongue

474 length, inter-tegular distance, …) together with species richness and phylogenies, on top of variables

475 already used, might improve the modelling of interactions and could help better understand some

476 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.
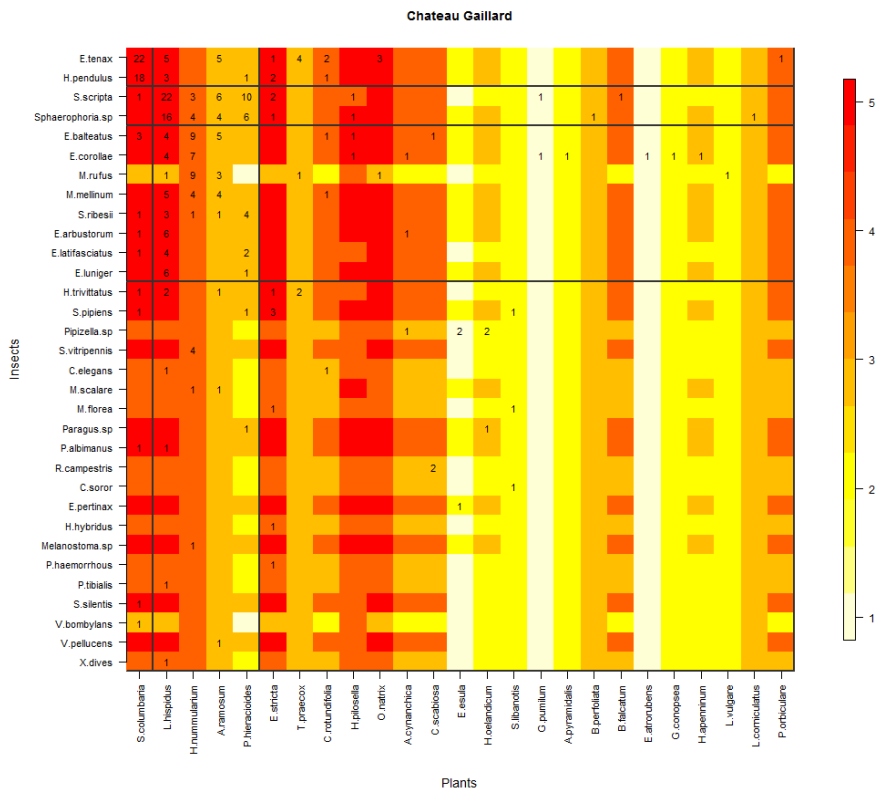
Figure 2. Block clustering provided by LBM in the site of Chateau Gaillard (CG, Normandie) overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants 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. Complete species names are reported in Table S2.

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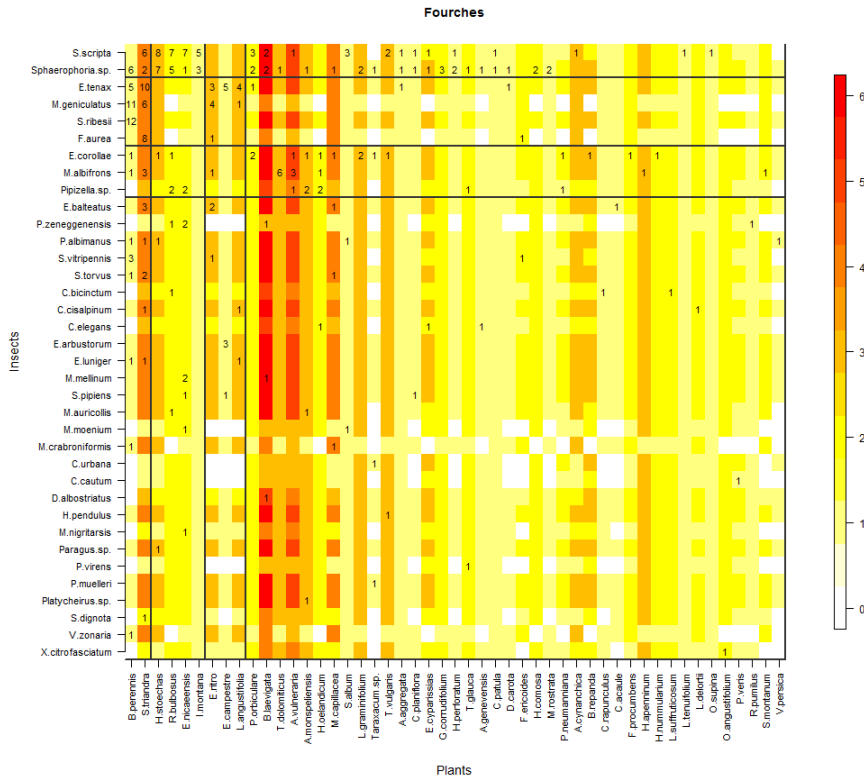
Figure 3. Block clustering provided by LBM in the site of Fourches (F, Occitanie), overlaid on a heatmap of species phenology overlap. The LBM algorithm finds the best division for the group of insects and plants independently through fitting Poisson parameters in each block maximizing the likelihood (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. Complete species names are reported in Table S2.

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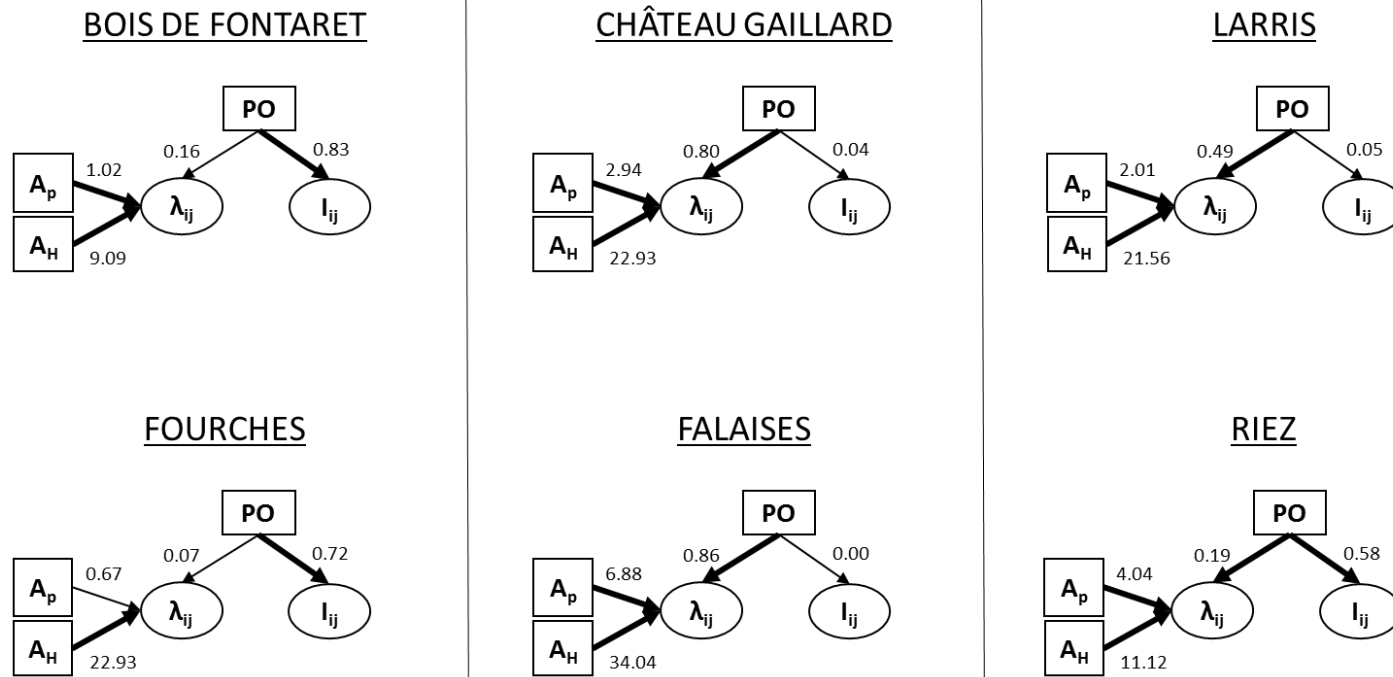
Figure 4. Summary diagram of the best models in all sites. The thickness of the arrows is scaled to Akaike weights (thin ER < 0.73; thick ER > 0.73, cf. Table 2). Standardised coefficients of the model average (computed based on the Akaike weighted model average) are reported next to the arrows. PO is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

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524 **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
525 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
526 implemented in the R package `bipartite` (Dormann *et al.* 2009). The modularity score was obtained using the `leading-eigenvector` method
527 described by Newman (2006) and implemented in the `igraph` package (Csardi & Nepusz 2006). LBM refers to latent block modelling as implemented in the
528 R package `blockmodels` (Leger *et al.* 2015).

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Site	Region	Collected data				Specialization index			Species phenology			Modularity analysis	LBM	
		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									

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

543 **Supporting Information**

544 The following Supporting Information is available for this article:

545 Figure S1. Sites location in France.

546 Figure S2. Block clustering provided by LBM in the site of Falaises (FAL, Normandie), overlaid on a

547 heatmap of species phenology overlap.

548 Figure S3. Block clustering provided by LBM in the site of Bois de Fontaret (BF, Occitanie), overlaid on

549 a heatmap of species phenology overlap.

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

551 heatmap of species phenology overlap.

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

553 heatmap of species phenology overlap.

554 Table S1. Table of transformed plant abundances.

555 Table S2. Table of hoverfly and plant species names and abbreviations used in the LBM figures.

556 Table S3. Table of model accuracy.

557 Appendix S1. Model code.

558 Appendix S2. Model script for the 16 models.

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

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Supplementary Information

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

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Figures and Tables
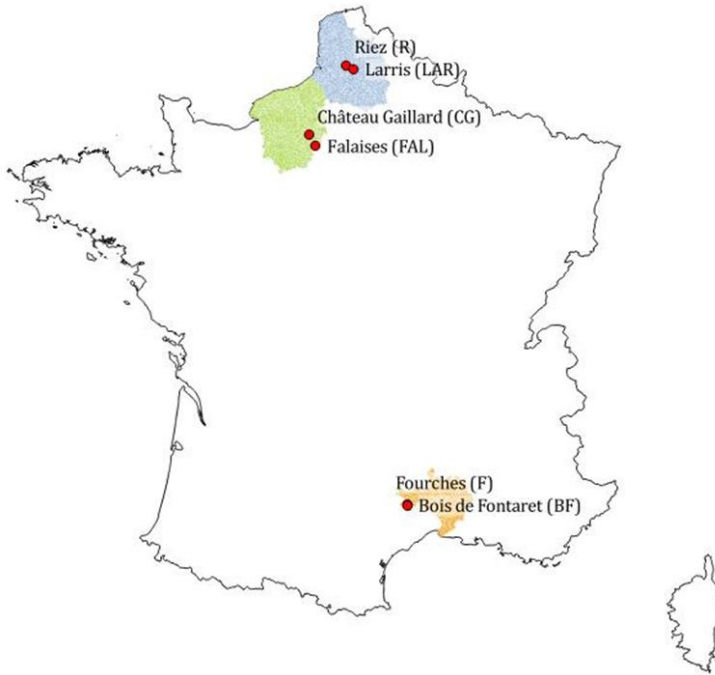
Figure S1. Site location in France: in blue the French départements Pas-de-Calais and Somme (Hauts-de-France region), in green the départements Eure and Seine Maritime (Normandie region), in orange the départment Gard (Occitanie region). The six sites correspond to the red dots (with the sites of Fourches and Bois de Fontaret represented by same dot due to their closeness).

Figure S2. 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. Complete species names are reported in Table S2.

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Bois de Fontaret

766

767 **Figure S3.** Block clustering provided by LBM in the site of Bois de Fontaret (BF, Occitanie), overlaid on
768 a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in
769 columns, following their degree (number of partners). The blocks of insects and the blocks of plants
770 are separated by solid black lines. Colours correspond to the number of months that are shared by
771 each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker
772 colours. Numbers are the number of visits observed in the field for a given plant-insect pair. Complete
773 species names are reported in Table S2.

Larris

775

776　**Figure S4.** Block clustering provided by LBM in the site of Larris (LAR, Hauts-de-France), overlaid on a
777　heatmap of species phenology overlap. Insect species are displayed in rows and plant species in
778　columns, following their degree (number of partners). The blocks of insects and the blocks of plants
779　are separated by solid black lines. Colours correspond to the number of months that are shared by
780　each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker
781　colours. Numbers are the number of visits observed in the field for a given plant-insect pair. Complete
782　species names are reported in Table S2.

Riez
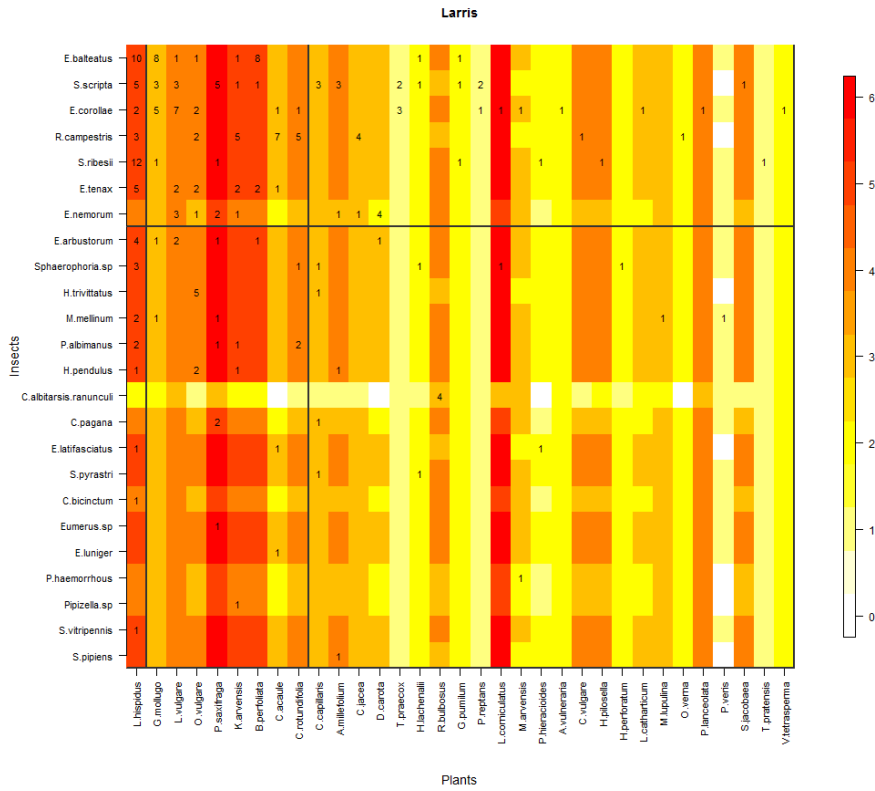
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Figure S5. Block clustering provided by LBM in the site of Riez (R, Hauts-de-France), overlaid on a
heatmap of species phenology overlap. Insect species are displayed in rows and plant species in
columns, following their degree (number of partners). 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. Complete
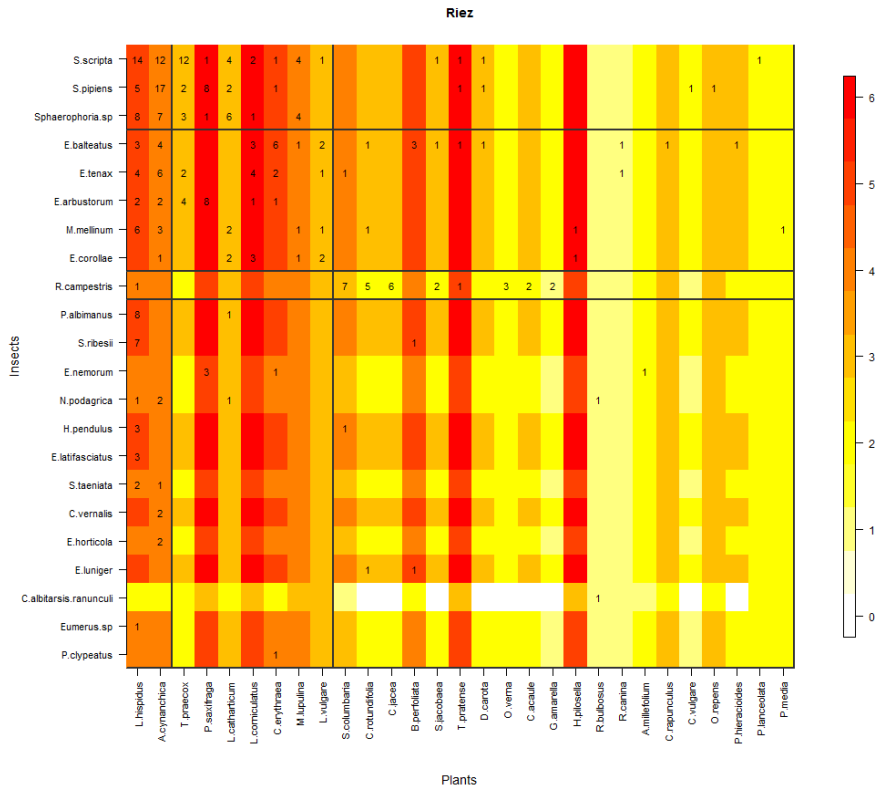species names are reported in Table S2.

Supplementary Information: Phenology and plant-hoverfly interactions

791 **Table S1.** Table of transformed plant abundances. The first column shows the Braun-Blanquet
792 coefficients of, the second column, their percentages, and the third column, the transformed
793 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%

794

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Table S2. Table of hoverfly and plant species names and abbreviations used in the LBM Figures.

Type	Short name	Scientific name	Notes
Syrphidae	C.albitarsis.ranunculi	*Cheilosia albitarsis* (Meigen), 1822 / *Cheilosia ranunculi* (Doczkal), 2000	the identification is not possible, could be both species - in the analysis we used as one species
Syrphidae	C.pagana	*Cheilosia pagana* (Meigen), 1822	
Syrphidae	C.scutellata	*Cheilosia scutellata* (Fallen), 1817	
Syrphidae	C.soror	*Cheilosia soror* (Zetterstedt), 1843	
Syrphidae	C.urbana	*Cheilosia urbana* (Meigen), 1822	
Syrphidae	C.vernalis	*Cheilosia vernalis* (Fallen), 1817	
Syrphidae	C.bicinctum	*Chrysotoxum bicinctum* (L.), 1758	
Syrphidae	C.cautum	*Chrysotoxum cautum* (Harris), 1776	
Syrphidae	C.cisalpinum	*Chrysotoxum cisalpinum* (Rondani), 1845	
Syrphidae	C.elegans	*Chrysotoxum elegans* (Loew), 1841	
Syrphidae	C.octomaculatum	*Chrysotoxum octomaculatum* (Curtis), 1837	
Syrphidae	D.albostriatus	*Dasysyrphus albostriatus* (Fallen), 1817	
Syrphidae	E.balteatus	*Episyrphus balteatus* (De Geer), 1776	
Syrphidae	E.arbustorum	*Eristalis arbustorum* (L.), 1758	
Syrphidae	E.horticola	*Eristalis horticola* (De Geer), 1776	
Syrphidae	E.nemorum	*Eristalis nemorum* (L.), 1758	
Syrphidae	E.pertinax	*Eristalis pertinax* (Scopoli), 1763	
Syrphidae	E.similis	*Eristalis similis* (Fallen), 1817	
Syrphidae	E.tenax	*Eristalis tenax* (L.), 1758	
Syrphidae	E.clavatus	*Eumerus clavatus* (Becker), 1923	
Syrphidae	Eumerus sp.	*Eumerus* sp.	the identification is not possible
Syrphidae	E.corollae	*Eupeodes corollae* (Fabricius), 1794	
Syrphidae	E.latifasciatus	*Eupeodes latifasciatus* (Macquart), 1829	
Syrphidae	E.luniger	*Eupeodes luniger* (Meigen), 1822	
Syrphidae	F.aurea	*Ferdinandea aurea* (Rondani), 1844	
Syrphidae	H.hybridus	*Helophilus hybridus* (Loew), 1846	
Syrphidae	H.pendulus	*Helophilus pendulus* (L.), 1758	
Syrphidae	H.trivittatus	*Helophilus trivittatus* (Fabricius), 1805	
Syrphidae	M.mellinum	*Melanostoma mellinum* (L.), 1758	
Syrphidae	M.scalare	*Melanostoma scalare* (Fabricius), 1794	
Syrphidae	Melanostoma sp.	*Melanostoma* sp.	the identification is not possible
Syrphidae	M.auricollis	*Meliscaeva auricollis* (Meigen), 1822	
Syrphidae	M.albifrons	*Merodon albifrons* (Meigen), 1822	
Syrphidae	M.avidus	*Merodon avidus* (Rossi), 1790	
Syrphidae	M.elegans	*Merodon elegans* (Hurkmans), 1993	
Syrphidae	M.equestris	*Merodon equestris* (Fabricius), 1794	
Syrphidae	M.geniculatus	*Merodon geniculatus* Strobl, 1909	
Syrphidae	M.moenium	*Merodon moenium* (Wiedemann), 1822	
Syrphidae	M.nigritarsis	*Merodon nigritarsis* Rondani, 1845	
Syrphidae	M.rufus	*Merodon rufus* Meigen, 1838	
Syrphidae	M.serratulus	*Merodon serrulatus* Wiedemann in Meigen, 1822	
Syrphidae	M.analis	*Microdon analis* (Macquart), 1842	
Syrphidae	M.crabroniformis	*Milesia crabroniformis* (Fabricius), 1775	
Syrphidae	M.florea	*Myathropa florea* (L.), 1758	
Syrphidae	N.podagrica	*Neoascia podagrica* (Fabricius), 1775	
Syrphidae	P.haemorrhous	*Paragus haemorrhous* Meigen, 1822	

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Syrphidae	P.tibialis	*Paragus tibialis* (Fallen), 1817	
Syrphidae	Paragus sp.	*Paragus* sp.	the identification is not possible
Syrphidae	P.pruinosomaculata	*Pelecocera pruinosomaculata* Strobl, 1906	
Syrphidae	P.tricincta	*Pelecocera tricincta* Meigen, 1822	
Syrphidae	P.austriaca	*Pipiza austriaca* Meigen, 1822	
Syrphidae	P.divicoi	*Pipizella divicoi* (Goeldlin), 1974	
Syrphidae	P.virens	*Pipizella virens* (Fabricius), 1805	
Syrphidae	P.zeneggenensis	*Pipizella zeneggenensis* (Goeldlin), 1974	
Syrphidae	Pipizella sp.	*Pipizella* sp.	
Syrphidae	P.albimanus	*Platycheirus albimanus* (Fabricius), 1781	
Syrphidae	P.albimanus.muelleri	*Platycheirus albimanus* (Fabricius), 1782 / *Platycheirus muelleri* (Marcuzzi), 1941	the identification is not possible, could be both species
Syrphidae	P.clypeatus	*Platycheirus clypeatus* (Meigen), 1822	
Syrphidae	P.Platycheirus	*Platycheirus* sp.	the identification is not possible
Syrphidae	R.campestris	*Rhingia campestris* Meigen, 1822	
Syrphidae	S.dignota	*Scaeva dignota* (Rondani, 1857)	
Syrphidae	S.pyrastri	*Scaeva pyrastri* (L.), 1758	
Syrphidae	S.silentis	*Sericomyia silentis* (Harris), 1776	
Syrphidae	S.scripta	*Sphaerophoria scripta* (L.), 1758	
Syrphidae	S.taeniata	*Sphaerophoria taeniata* (Meigen), 1822	
Syrphidae	S.Sphaerophoria	*Sphaerophoria* sp.	the female identification is not possible
Syrphidae	S.pipiens	*Syritta pipiens* (L.), 1758	
Syrphidae	S.ribesii	*Syrphus ribesii* (L.), 1758	
Syrphidae	S.torvus	*Syrphus torvus* (Osten-Sacken), 1875	
Syrphidae	S.vitripennis	*Syrphus vitripennis* (Meigen), 1822	
Syrphidae	V.bombylans	*Volucella bombylans* (L.), 1758	
Syrphidae	V.inanis	*Volucella inanis* (L.), 1758	
Syrphidae	V.pellucens	*Volucella pellucens* (L.), 1758	
Syrphidae	V.zonaria	*Volucella zonaria* (Poda), 1761	
Syrphidae	X.citrofasciatum	*Xanthogramma citrofasciatum* (De Geer), 1776	
Syrphidae	X.dives	*Xanthogramma dives* (Rondani), 1857	
Plants	A.millefolium	*Achillea millefolium*	
Plants	A.genevensis	*Ajuga genevensis*	
Plants	A.sphaerocephalon	*Allium sphaerocephalon*	
Plants	A.pyramidalis	*Anacamptis pyramidalis*	
Plants	A.ramosum	*Anthericum ramosum*	
Plants	A.montana	*Anthyllis montana*	
Plants	A.vulneraria	*Anthyllis vulneraria*	
Plants	A.monspeliensis	*Aphyllanthes monspeliensis*	
Plants	A.aggregata	*Arenaria aggregata*	
Plants	A.cynanchica	*Asperula cynanchica*	
Plants	A.linosyris	*Aster linosyris*	
Plants	B.perennis	*Bellis perennis*	
Plants	B.laevigata	*Biscutella laevigata*	
Plants	B.perfoliata	*Blackstonia perfoliata*	
Plants	B.repanda	*Brassica repanda*	
Plants	B.falcatum	*Bupleurum falcatum*	
Plants	C.patula	*Campanula patula*	
Plants	C.rapunculus	*Campanula rapunculus*	
Plants	C.rotundifolia	*Campanula rotundifolia*	

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Plants	C.erythraea	*Centaurium erythraea*	
Plants	C.jacea	*Centaurea jacea*	
Plants	C.scabiosa	*Centaurea scabiosa*	
Plants	C.acaule	*Cirsium acaule*	
Plants	C.vulgare	*Clinopodium vulgare*	
Plants	C.cantabrica	*Convolvulus cantabrica*	
Plants	C.minima	*Coronilla minima*	
Plants	C.capillaris	*Crepis capillaris*	
Plants	C.foetida	*Crepis foetida*	
Plants	C.planiflora	*Cuscuta planiflora var. godronii*	
Plants	D.carota	*Daucus carota*	
Plants	D.pentaphyllum	*Dorycnium pentaphyllum*	
Plants	E.vulgare	*Echium vulgare*	
Plants	E.ritro	*Echinops ritro*	
Plants	E.atrorubens	*Epipactis atrorubens*	
Plants	E.campestre	*Eryngium campestre*	
Plants	E.cyparissias	*Euphorbia cyparissias*	
Plants	E.esula	*Euphorbia esula*	
Plants	E.exigua	*Euphorbia exigua*	
Plants	E.nicaeensis	*Euphorbia nicaeensis*	
Plants	E.stricta	*Euphrasia stricta*	
Plants	F.ericoides	*Fumana ericoides*	
Plants	F.procumbens	*Fumana procumbens*	
Plants	G.corrudifolium	*Galium corrudifolium*	
Plants	G.mollugo	*Galium mollugo*	
Plants	G.pumilum	*Galium pumilum*	
Plants	G.amarella	*Gentianella amarella*	
Plants	G.vulgaris	*Globularia vulgaris*	
Plants	G.conopsea	*Gymnadenia conopsea*	
Plants	H.apenninum	*Helianthemum apenninum*	
Plants	H.nummularium	*Helianthemum nummularium*	
Plants	H.oelandicum	*Helianthemum oelandicum*	
Plants	H.stoechas	*Helichrysum stoechas*	
Plants	H.lachenalii	*Hieracium lachenalii*	
Plants	H.pilosella	*Hieracium pilosella* (synonyms)	Pilosella officinarum (accepted name)
Plants	H.comosa	*Hippocrepis comosa*	
Plants	H.perforatum	*Hypericum perforatum*	
Plants	I.montana	*Inula montana*	
Plants	K.arvensis	*Knautia arvensis*	
Plants	L.angustifolia	*Lavandula angustifolia*	
Plants	L.hispidus	*Leontodon hispidus*	
Plants	L.graminifolium	*Leucanthemum graminifolium*	
Plants	L.vulgare	*Leucanthemum vulgare*	
Plants	L.catharticum	*Linum catharticum*	
Plants	L.narbonense	*Linum narbonense*	
Plants	L.tenuifolium	*Linum tenuifolium*	
Plants	L.corniculatus	*Lotus corniculatus*	
Plants	L.delortii	*Lotus delortii*	
Plants	M.lupulina	*Medicago lupulina*	
Plants	M.minima	*Medicago minima*	
Plants	M.capillacea	*Minuartia capillacea*	
Plants	M.rostrata	*Minuartia rostrata*	
Plants	M.arvensis	*Myosotis arvensis*	

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Plants	O.verna	*Odontites verna*
Plants	O.supina	*Onobrychis supina*
Plants	O.natrix	*Ononis natrix*
Plants	O.repens	*Ononis repens*
Plants	O.vulgare	*Origanum vulgare*
Plants	O.angustifolium	*Ornithogalum angustifolium*
Plants	P.orbiculare	*Phyteuma orbiculare*
Plants	P.hieracioides	*Picris hieracioides*
Plants	P.saxifraga	*Pimpinella saxifraga*
Plants	P.lanceolata	*Plantago lanceolata*
Plants	P.media	*Plantago media*
Plants	P.neumanniana	*Potentilla neumanniana*
Plants	P.reptans	*Potentilla reptans*
Plants	P.veris	*Primula veris*
Plants	P.grandiflora	*Prunella grandiflora*
Plants	R.bulbosus	*Ranunculus bulbosus*
Plants	R.gramineus	*Ranunculus gramineus*
Plants	R.lutea	*Reseda lutea*
Plants	R.pumilus	*Rhinanthus pumilus*
Plants	R.canina	*Rosa canina*
Plants	S.minor	*Sanguisorba minor*
Plants	S.columbaria	*Scabiosa columbaria*
Plants	S.triandra	*Scabiosa triandra*
Plants	S.autumnalis	*Scilla autumnalis*
Plants	S.acre	*Sedum acre*
Plants	S.album	*Sedum album subsp. micranthum*
Plants	S.jacobaea	*Senecio jacobaea*
Plants	S.libanotis	*Seseli libanotis*
Plants	S.montanum	*Seseli montanum*
Plants	S.spiralis	*Spiranthes spiralis*
Plants	S.recta	*Stachys recta*
Plants	Taraxacum sp.	*Taraxacum sp.*
Plants	T.montanum	*Teucrium montanum*
Plants	T.humifusum	*Thesium humifusum*
Plants	T.dolomiticus	*Thymus dolomiticus*
Plants	T.praecox	*Thymus praecox*
Plants	T.vulgaris	*Thymus vulgaris*
Plants	T.pratensis	*Tragopogon pratensis*
Plants	T.pratense	*Trifolium pratense*
Plants	T.glauca	*Trinia glauca*
Plants	V.persica	*Veronica persica*
Plants	V.tetrasperma	*Vicia tetrasperma*
Plants	V.hirundinaria	*Vincetoxicum hirundinaria*

796

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797 **Table S3.** 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
798 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
799 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
800 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
801 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
802 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

803

806 **Appendix S1: Model Code**

807 The model code (in JAGS language) given in this supplementary material refers to the "model Z0" which

808 considers all four parameters (model effects, Table 2 in the main text). Overall, we estimated 16

809 models that included between 0 and 4 of the above-mentioned effects. To create the code for these

810 other models, parameters should be removed following the order in the Tab. 2. The four parameters

811 tested in the model are: (i) alpha: effect of the phenology overlap (cooc) on the probability of

812 interaction; (ii) epsilon: effect of the phenology overlap on the intensity of visits; (iii) gamma: effect of

813 the insect abundances (ab_I) on the intensity of visits; and (iv) delta: effect of the plant abundances

814 (ab_P) on the intensity of visits.

815

```
816  model
817  {
818    for( i in 1 : dim1 ) {
819      for( p in 1 : dim2 ) {
820        inter[i , p] ~ dbern(mu[i , p])
821           logit(mu[i , p]) <- beta + alpha*cooc[i , p] + effet_I[i] + effet_P[p]
822           lambda[i,p] <- exp(theta[i,p])
823           theta[i,p] <- theta0 + gamma*ab_I[i] + delta*ab_P[p] + epsilon*log(1+cooc[i,p])
824           visit[i,p] ~ dpois( inter[i,p]*lambda[i,p] )
825           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 ,
826  p]*dpois(visit[i,p],lambda[i,p])))
827      }
828    }
829
830    for( i in 1 : dim1 ) {
831      effet_I[i] ~ dnorm( 0.0,tau_I)
```

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```
832        }

833

834    for( p in 1 : dim2 ) {

835        effet_P[p] ~ dnorm( 0.0,tau_P)

836        }

837

838            tau_I ~ dexp( 10)

839            tau_P ~ dexp( 10)

840            alpha ~ dnorm(0,0.01)

841            beta ~  dnorm(0,0.01)

842            theta0 ~ dnorm(0,0.01)

843            gamma ~ dnorm(0,0.01)

844            delta ~ dnorm(0,0.01)

845            epsilon ~ dnorm(0,0.01)

846    }

847
```

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

849 The following generic script was applied to all the study sites using all 16 models. The script is separated

850 in three blocks which communicate among them: the script options, the model definitions and the

851 execution (model inference). We defined three options to set (i) the name of the directory (-d), (ii) the

852 site (-s) and (iii) the type of model (-m).

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

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

855 In order to calculate the standardised coefficients for each parameters used, at the end of the third

856 block, we added the functions to get the parameter values for each site and each model.

857 ############################ BLOCK 1 – SCRIPT OPTION ############################

858 library(optparse)

859 option_list = list(

860 make_option(c("-d", "--dir"), type="character", default=NULL, help="directory",

861 metavar="character"),

862 make_option(c("-s", "--site"), type="character", default=NULL, help="site name",

863 metavar="character"),

864 make_option(c("-m", "--modele"), type="character", default="all", help="modele name",

865 metavar="character"))

866 opt_parser = OptionParser(option_list=option_list);

867 opt = parse_args(opt_parser);

868 site<-opt$site

869 dossier<-opt$dir

870 ############################ Librairies ############################

871 library(bipartite)

872 library(vegan)

873 library(igraph)

```
874    library(magrittr)

875    library(dummies)

876    library(MuMIn)

877    library(rjags)

878    library(boot)

879    library(R2jags)

880    library(coda)

881    library(lattice)

882    library(ggplot2)

883    library(loo)

884    library(matrixStats)

885    ######################### Function to record the LOO values #######################

886    write_values<-function(x, f, app)

887    {

888            write.table(x, append=app, file=f, sep="\t", row.names=T, col.names=T, quote=F)

889    }

890    ######################### BLOCK 2 – MODEL FUNCTIONS ##########################

891    #Model function and model initialization: one function for each model from model Z15, with 0

892    parameters, to Z00 with all the parameters#

893    ### MODEL Z015

894    mZ015<-function(){

895            init.funZ015 <-function(){

896             list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "theta0" =

897    rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

898            }
```

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```
899        mod.Z015<<-jags(inits=init.funZ015,model.file = "modelZ015_code.txt",data =

900    list("visit","dim1","dim2"),parameters.to.save =

901    c("mu","effet_I","effet_P","tau_I","tau_P","beta","theta0", "loglik"),n.chains = 1, n.iter=1000000,

902    n.burnin = 250000, n.thin = 250)

903        mod.Z015.mcmc<-as.mcmc(mod.Z015)

904        mZ015<-mod.Z015$BUGSoutput$sims.list

905        mZ015.deviance<-mZ015$deviance

906        mZ015.loglik<-mZ015$loglik

907        dimSEM<-dim(mZ015.loglik)[1]

908        list.mZ015<-sapply(1:dimSEM,function(x) matrix(mZ015.loglik[x,,],nrow=dim1*dim2))

909        list.tmZ015<-(t(list.mZ015))

910        mZ015.loo<-loo(list.tmZ015)

911        loo_file<-paste(dossier, "/", site, "_Z015_loo.txt", sep="")

912        write_values("mZ015", app=F, loo_file)

913        mZ015_loo_pointwise<-mZ015.loo$pointwise

914        mZ015_loo_pareto_k<-mZ015.loo$pareto_k

915        mZ015.loo$pareto_k<-NULL

916        mZ015.loo$pointwise<-NULL

917        write_values(as.matrix(mZ015.loo), app=T, loo_file)

918        save.image(paste(dossier, "/", site, "_Z015.RData", sep=""))

919    }

920    ### MODEL Z014

921    mZ014<-function(){

922        init.funZ014 <-function(){

923         list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "delta" = rnorm(1,0,1),

924    "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
```

```
925             }
926             mod.Z014<<-jags(inits=init.funZ014,model.file = "modelZ014_code.txt",data =
927     list("visit","ab_P","dim1","dim2"),parameters.to.save =
928     c("mu","effet_I","effet_P","tau_I","tau_P","delta","beta","theta0","loglik"),n.chains = 1,
929     n.iter=1000000, n.burnin = 250000, n.thin = 250)
930             mod.Z014.mcmc<-as.mcmc(mod.Z014)
931             mZ014<-mod.Z014$BUGSoutput$sims.list
932             mZ014.deviance<-mZ014$deviance
933             mZ014.loglik<-mZ014$loglik
934             dimSEM<-dim(mZ014.loglik)[1]
935             list.mZ014<-sapply(1:dimSEM,function(x) matrix(mZ014.loglik[x,,],nrow=dim1*dim2))
936             list.tmZ014<-(t(list.mZ014))
937             mZ014.loo<-loo(list.tmZ014)
938             mZ014.loo
939             loo_file<-paste(dossier, "/", site, "_Z014_loo.txt", sep="")
940             write_values("mZ014", app=T, loo_file)
941             mZ014_loo_pointwise<-mZ014.loo$pointwise
942             mZ014_loo_pareto_k<-mZ014.loo$pareto_k
943             mZ014.loo$pareto_k<-NULL
944             mZ014.loo$pointwise<-NULL
945             write_values(as.matrix(mZ014.loo), app=T, loo_file)
946             save.image(paste(dossier, "/", site, "_Z014.RData", sep=""))
947     }
948     ### MODEL Z013
949     mZ013<-function(){
950             init.funZ013 <-function(){
```

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```
951         list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =

952    rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),

953    "inter"=inter0)

954         }

955         mod.Z013<<-jags(inits=init.funZ013,model.file = "modelZ013_code.txt",data =

956    list("visit","ab_I","dim1","dim2"),parameters.to.save =

957    c("mu","effet_I","effet_P","tau_I","tau_P","gamma","beta","theta0","loglik"),n.chains = 1,

958    n.iter=1000000, n.burnin = 250000, n.thin = 250)

959         mod.Z013.mcmc<-as.mcmc(mod.Z013)

960         mZ013<-mod.Z013$BUGSoutput$sims.list

961         mZ013.deviance<-mZ013$deviance

962         mZ013.loglik<-mZ013$loglik

963         dimSEM<-dim(mZ013.loglik)[1]

964         list.mZ013<-sapply(1:dimSEM,function(x) matrix(mZ013.loglik[x,,],nrow=dim1*dim2))

965         list.tmZ013<-(t(list.mZ013))

966         mZ013.loo<-loo(list.tmZ013)

967         mZ013.loo

968         loo_file<-paste(dossier, "/", site, "_Z013_loo.txt", sep="")

969         write_values("mZ013", app=T, loo_file)

970         mZ013_loo_pointwise<-mZ013.loo$pointwise

971         mZ013_loo_pareto_k<-mZ013.loo$pareto_k

972         mZ013.loo$pareto_k<-NULL

973         mZ013.loo$pointwise<-NULL

974         write_values(as.matrix(mZ013.loo), app=T, loo_file)

975         save.image(paste(dossier, "/", site, "_Z013.RData", sep=""))

976    }
```

```r
977     ### MODEL Z012
978     mZ012<-function(){
979             init.funZ012 <-function(){
980              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "theta0" =
981     rnorm(1,0,1), "epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
982     "inter"=inter0)
983             }
984             mod.Z012<<-jags(inits=init.funZ012,model.file = "modelZ012_code.txt",data =
985     list("cooc","visit","dim1","dim2"),parameters.to.save =
986     c("mu","effet_I","effet_P","tau_I","tau_P","beta","theta0","epsilon","loglik"),n.chains = 1,
987     n.iter=1000000, n.burnin = 250000, n.thin = 250)
988             mod.Z012.mcmc<-as.mcmc(mod.Z012)
989             mZ012<-mod.Z012$BUGSoutput$sims.list
990             mZ012.deviance<-mZ012$deviance
991             mZ012.loglik<-mZ012$loglik
992             dimSEM<-dim(mZ012.loglik)[1]
993             list.mZ012<-sapply(1:dimSEM,function(x) matrix(mZ012.loglik[x,,],nrow=dim1*dim2))
994             list.tmZ012<-(t(list.mZ012))
995             mZ012.loo<-loo(list.tmZ012)
996             mZ012.loo
997             loo_file<-paste(dossier, "/", site, "_Z012_loo.txt", sep="")
998             write_values("mZ012", app=T, loo_file)
999             mZ012_loo_pointwise<-mZ012.loo$pointwise
1000            mZ012_loo_pareto_k<-mZ012.loo$pareto_k
1001            mZ012.loo$pareto_k<-NULL
1002            mZ012.loo$pointwise<-NULL
```

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```
1003        write_values(as.matrix(mZ012.loo), app=T, loo_file)

1004        save.image(paste(dossier, "/", site, "_Z012.RData", sep=""))

1005    }

1006    ### MODEL Z011

1007    mZ011<-function(){

1008        init.funZ011 <-function(){

1009            list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "theta0"

1010    = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

1011        }

1012        mod.Z011<<-jags(inits=init.funZ011,model.file = "modelZ011_code.txt",data =

1013    list("cooc","visit","dim1","dim2"),parameters.to.save =

1014    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","beta","theta0","loglik"),n.chains = 1,

1015    n.iter=1000000, n.burnin = 250000, n.thin = 250)

1016        mod.Z011.mcmc<-as.mcmc(mod.Z011)

1017        mZ011<-mod.Z011$BUGSoutput$sims.list

1018        mZ011.deviance<-mZ011$deviance

1019        mZ011.loglik<-mZ011$loglik

1020        dimSEM<-dim(mZ011.loglik)[1]

1021        list.mZ011<-sapply(1:dimSEM,function(x) matrix(mZ011.loglik[x,,],nrow=dim1*dim2))

1022        list.tmZ011<-(t(list.mZ011))

1023        mZ011.loo<-loo(list.tmZ011)

1024        mZ011.loo

1025        loo_file<-paste(dossier, "/", site, "_Z011_loo.txt", sep="")

1026        write_values("mZ011", app=T, loo_file)

1027        mZ011_loo_pointwise<-mZ011.loo$pointwise

1028        mZ011_loo_pareto_k<-mZ011.loo$pareto_k
```

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```r
1029        mZ011.loo$pareto_k<-NULL

1030        mZ011.loo$pointwise<-NULL

1031        write_values(as.matrix(mZ011.loo), app=T, loo_file)

1032        save.image(paste(dossier, "/", site, "_Z011.RData", sep=""))

1033    }

1034    ### MODEL Z010

1035    mZ010<-function(){

1036        init.funZ010 <-function(){

1037            list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =

1038    rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1),

1039    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

1040            }

1041        mod.Z010<<-jags(inits=init.funZ010,model.file = "modelZ010_code.txt",data =

1042    list("visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =

1043    c("mu","effet_I","effet_P","tau_I","tau_P","gamma","delta","beta","theta0","loglik"),n.chains = 1,

1044    n.iter=1000000, n.burnin = 250000, n.thin = 250)

1045        mod.Z010.mcmc<-as.mcmc(mod.Z010)

1046        mZ010<-mod.Z010$BUGSoutput$sims.list

1047        mZ010.deviance<-mZ010$deviance

1048        mZ010.loglik<-mZ010$loglik

1049        dimSEM<-dim(mZ010.loglik)[1]

1050        list.mZ010<-sapply(1:dimSEM,function(x) matrix(mZ010.loglik[x,,],nrow=dim1*dim2))

1051        list.tmZ010<-(t(list.mZ010))

1052        mZ010.loo<-loo(list.tmZ010)

1053        mZ010.loo

1054        loo_file<-paste(dossier, "/", site, "_Z010_loo.txt", sep="")
```

```
1055        write_values("mZO10", app=T, loo_file)

1056        mZO10_loo_pointwise<-mZO10.loo$pointwise

1057        mZO10_loo_pareto_k<-mZO10.loo$pareto_k

1058        mZO10.loo$pareto_k<-NULL

1059        mZO10.loo$pointwise<-NULL

1060        write_values(as.matrix(mZO10.loo), app=T, loo_file)

1061        save.image(paste(dossier, "/", site, "_ZO10.RData", sep=""))

1062    }

1063    ### MODEL Z09

1064    mZ09<-function(){

1065        init.funZ09 <-function(){

1066         list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "delta" = rnorm(1,0,1),

1067    "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),

1068    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

1069        }

1070        mod.Z09<<-jags(inits=init.funZ09,model.file = "modelZ09_code.txt",data =

1071    list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =

1072    c("mu","effet_I","effet_P","tau_I","tau_P","delta","beta","theta0","epsilon","loglik"),n.chains = 1,

1073    n.iter=1000000, n.burnin = 250000, n.thin = 250)

1074        mod.Z09.mcmc<-as.mcmc(mod.Z09)

1075        mZ09<-mod.Z09$BUGSoutput$sims.list

1076        mZ09.deviance<-mZ09$deviance

1077        mZ09.loglik<-mZ09$loglik

1078        dimSEM<-dim(mZ09.loglik)[1]

1079        list.mZ09<-sapply(1:dimSEM,function(x) matrix(mZ09.loglik[x,,],nrow=dim1*dim2))

1080        list.tmZ09<-(t(list.mZ09))
```

```
1081          mZ09.loo<-loo(list.tmZ09)

1082          mZ09.loo

1083          loo_file<-paste(dossier, "/", site, "_Z09_loo.txt", sep="")

1084          write_values("mZ09", app=T, loo_file)

1085          mZ09_loo_pointwise<-mZ09.loo$pointwise

1086          mZ09_loo_pareto_k<-mZ09.loo$pareto_k

1087          mZ09.loo$pareto_k<-NULL

1088          mZ09.loo$pointwise<-NULL

1089          write_values(as.matrix(mZ09.loo), app=T, loo_file)

1090          save.image(paste(dossier, "/", site, "_Z09.RData", sep=""))

1091   }

1092   ### MODEL Z08

1093   mZ08<-function(){

1094          init.funZ08 <-function(){

1095          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =

1096   rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),

1097   "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

1098          }

1099          mod.Z08<<-jags(inits=init.funZ08,model.file = "modelZ08_code.txt",data =

1100   list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =

1101   c("mu","effet_I","effet_P","tau_I","tau_P","gamma","beta","theta0","epsilon","loglik"),n.chains = 1,

1102   n.iter=1000000, n.burnin = 250000, n.thin = 250)

1103          mod.Z08.mcmc<-as.mcmc(mod.Z08)

1104          mZ08<-mod.Z08$BUGSoutput$sims.list

1105          mZ08.deviance<-mZ08$deviance

1106          mZ08.loglik<-mZ08$loglik
```

Supplementary Information: Phenology and plant-hoverfly interactions

```
1107          dimSEM<-dim(mZ08.loglik)[1]

1108          list.mZ08<-sapply(1:dimSEM,function(x) matrix(mZ08.loglik[x,,],nrow=dim1*dim2))

1109          list.tmZ08<-(t(list.mZ08))

1110          mZ08.loo<-loo(list.tmZ08)

1111          mZ08.loo

1112          loo_file<-paste(dossier, "/", site, "_Z08_loo.txt", sep="")

1113          write_values("mZ08", app=T, loo_file)

1114          mZ08_loo_pointwise<-mZ08.loo$pointwise

1115          mZ08_loo_pareto_k<-mZ08.loo$pareto_k

1116          mZ08.loo$pareto_k<-NULL

1117          mZ08.loo$pointwise<-NULL

1118          write_values(as.matrix(mZ08.loo), app=T, loo_file)

1119          save.image(paste(dossier, "/", site, "_Z08.RData", sep=""))

1120  }

1121  ### MODEL Z07

1122  mZ07<-function(){

1123          init.funZ07 <-function(){

1124           list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "delta" =

1125  rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),

1126  "inter"=inter0)

1127          }

1128          mod.Z07<<-jags(inits=init.funZ07,model.file = "modelZ07_code.txt",data =

1129  list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =

1130  c("mu","effet_I","effet_P","tau_I","tau_P","alpha","delta","beta","theta0","loglik"),n.chains = 1,

1131  n.iter=1000000, n.burnin = 250000, n.thin = 250)

1132          mod.Z07.mcmc<-as.mcmc(mod.Z07)
```

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```
1133        mZ07<-mod.Z07$BUGSoutput$sims.list

1134        mZ07.deviance<-mZ07$deviance

1135        mZ07.loglik<-mZ07$loglik

1136        dimSEM<-dim(mZ07.loglik)[1]

1137        list.mZ07<-sapply(1:dimSEM,function(x) matrix(mZ07.loglik[x,,],nrow=dim1*dim2))

1138        list.tmZ07<-(t(list.mZ07))

1139        mZ07.loo<-loo(list.tmZ07)

1140        mZ07.loo

1141        loo_file<-paste(dossier, "/", site, "_Z07_loo.txt", sep="")

1142        write_values("mZ07", app=T, loo_file)

1143        mZ07_loo_pointwise<-mZ07.loo$pointwise

1144        mZ07_loo_pareto_k<-mZ07.loo$pareto_k

1145        mZ07.loo$pareto_k<-NULL

1146        mZ07.loo$pointwise<-NULL

1147        write_values(as.matrix(mZ07.loo), app=T, loo_file)

1148        save.image(paste(dossier, "/", site, "_Z07.RData", sep=""))

1149    }

1150    ### MODEL Z06

1151    mZ06<-function(){

1152        init.funZ06 <-function(){

1153         list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"

1154    = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),

1155    "inter"=inter0)

1156        }

1157        mod.Z06<<-jags(inits=init.funZ06,model.file = "modelZ06_code.txt",data =

1158    list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
```

```r
1159    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","beta","theta0","loglik"),n.chains = 1,

1160    n.iter=1000000, n.burnin = 250000, n.thin = 250)

1161            mod.Z06.mcmc<-as.mcmc(mod.Z06)

1162            mZ06<-mod.Z06$BUGSoutput$sims.list

1163            mZ06.deviance<-mZ06$deviance

1164            mZ06.loglik<-mZ06$loglik

1165            dimSEM<-dim(mZ06.loglik)[1]

1166            list.mZ06<-sapply(1:dimSEM,function(x) matrix(mZ06.loglik[x,,],nrow=dim1*dim2))

1167            list.tmZ06<-(t(list.mZ06))

1168            mZ06.loo<-loo(list.tmZ06)

1169            mZ06.loo

1170            loo_file<-paste(dossier, "/", site, "_Z06_loo.txt", sep="")

1171            write_values("mZ06", app=T, loo_file)

1172            mZ06_loo_pointwise<-mZ06.loo$pointwise

1173            mZ06_loo_pareto_k<-mZ06.loo$pareto_k

1174            mZ06.loo$pareto_k<-NULL

1175            mZ06.loo$pointwise<-NULL

1176            write_values(as.matrix(mZ06.loo), app=T, loo_file)

1177            save.image(paste(dossier, "/", site, "_Z06.RData", sep=""))

1178    }

1179    ### MODEL Z05

1180    mZ05<-function(){

1181            init.funZ05 <-function(){

1182                list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "theta0"

1183    = rnorm(1,0,1), "epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),

1184    "inter"=inter0)
```

```
1185            }
1186            mod.Z05<<-jags(inits=init.funZ05,model.file = "modelZ05_code.txt",data =
1187    list("cooc","visit","dim1","dim2"),parameters.to.save =
1188    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","beta","theta0","epsilon","loglik"),n.chains = 1,
1189    n.iter=1000000, n.burnin = 250000, n.thin = 250)
1190            mod.Z05.mcmc<-as.mcmc(mod.Z05)
1191            mZ05<-mod.Z05$BUGSoutput$sims.list
1192            mZ05.deviance<-mZ05$deviance
1193            mZ05.loglik<-mZ05$loglik
1194            dimSEM<-dim(mZ05.loglik)[1]
1195            list.mZ05<-sapply(1:dimSEM,function(x) matrix(mZ05.loglik[x,,],nrow=dim1*dim2))
1196            list.tmZ05<-(t(list.mZ05))
1197            mZ05.loo<-loo(list.tmZ05)
1198            mZ05.loo
1199            loo_file<-paste(dossier, "/", site, "_Z05_loo.txt", sep="")
1200            write_values("mZ05", app=T, loo_file)
1201            mZ05_loo_pointwise<-mZ05.loo$pointwise
1202            mZ05_loo_pareto_k<-mZ05.loo$pareto_k
1203            mZ05.loo$pareto_k<-NULL
1204            mZ05.loo$pointwise<-NULL
1205            write_values(as.matrix(mZ05.loo), app=T, loo_file)
1206            save.image(paste(dossier, "/", site, "_Z05.RData", sep=""))
1207    }
1208    ### MODEL Z04
1209    mZ04<-function(){
1210            init.funZ04 <-function(){
```

Supplementary Information: Phenology and plant-hoverfly interactions

```
1211        list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" =

1212   rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),

1213   "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

1214        }

1215        mod.Z04<<-jags(inits=init.funZ04,model.file = "modelZ04_code.txt",data =

1216   list("cooc","visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =

1217   c("mu","effet_I","effet_P","tau_I","tau_P","gamma","delta","beta","theta0","epsilon","loglik"),n.chai

1218   ns = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)

1219        mod.Z04.mcmc<-as.mcmc(mod.Z04)

1220        mZ04<-mod.Z04$BUGSoutput$sims.list

1221        mZ04.deviance<-mZ04$deviance

1222        mZ04.loglik<-mZ04$loglik

1223        dimSEM<-dim(mZ04.loglik)[1]

1224        list.mZ04<-sapply(1:dimSEM,function(x) matrix(mZ04.loglik[x,,],nrow=dim1*dim2))

1225        list.tmZ04<-(t(list.mZ04))

1226        mZ04.loo<-loo(list.tmZ04)

1227        mZ04.loo

1228        loo_file<-paste(dossier, "/", site, "_Z04_loo.txt", sep="")

1229        write_values("mZ04", app=T, loo_file)

1230        mZ04_loo_pointwise<-mZ04.loo$pointwise

1231        mZ04_loo_pareto_k<-mZ04.loo$pareto_k

1232        mZ04.loo$pareto_k<-NULL

1233        mZ04.loo$pointwise<-NULL

1234        write_values(as.matrix(mZ04.loo), app=T, loo_file)

1235        save.image(paste(dossier, "/", site, "_Z04.RData", sep=""))

1236   }
```

Supplementary Information: Phenology and plant-hoverfly interactions

```
1237    ### MODEL Z03
1238    mZ03<-function(){
1239            init.funZ03 <-function(){
1240              list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"
1241    = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
1242    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
1243            }
1244            mod.Z03<<-jags(inits=init.funZ03,model.file = "modelZ03_code.txt",data =
1245    list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
1246    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","beta","theta0","epsilon","loglik"),n.cha
1247    ins = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
1248            mod.Z03.mcmc<-as.mcmc(mod.Z03)
1249            mZ03<-mod.Z03$BUGSoutput$sims.list
1250            mZ03.deviance<-mZ03$deviance
1251            mZ03.loglik<-mZ03$loglik
1252            dimSEM<-dim(mZ03.loglik)[1]
1253            list.mZ03<-sapply(1:dimSEM,function(x) matrix(mZ03.loglik[x,,],nrow=dim1*dim2))
1254            list.tmZ03<-(t(list.mZ03))
1255            mZ03.loo<-loo(list.tmZ03)
1256            mZ03.loo
1257            loo_file<-paste(dossier, "/", site, "_Z03_loo.txt", sep="")
1258            write_values("mZ03", app=T, loo_file)
1259            mZ03_loo_pointwise<-mZ03.loo$pointwise
1260            mZ03_loo_pareto_k<-mZ03.loo$pareto_k
1261            mZ03.loo$pareto_k<-NULL
1262            mZ03.loo$pointwise<-NULL
```

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```
1263        write_values(as.matrix(mZ03.loo), app=T, loo_file)

1264        save.image(paste(dossier, "/", site, "_Z03.RData", sep=""))

1265    }

1266    ### MODEL Z02

1267    mZ02<-function(){

1268        init.funZ02 <-function(){

1269          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1, "beta" = rnorm(1,0,1), "delta" =

1270    rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),

1271    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

1272        }

1273        mod.Z02<<-jags(inits=init.funZ02,model.file = "modelZ02_code.txt",data =

1274    list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =

1275    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","delta","beta","theta0","epsilon","loglik"),n.chain

1276    s = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)

1277        mod.Z02.mcmc<-as.mcmc(mod.Z02)

1278        mZ02<-mod.Z02$BUGSoutput$sims.list

1279        mZ02.deviance<-mZ02$deviance

1280        mZ02.loglik<-mZ02$loglik

1281        dimSEM<-dim(mZ02.loglik)[1]

1282        list.mZ02<-sapply(1:dimSEM,function(x) matrix(mZ02.loglik[x,,],nrow=dim1*dim2))

1283        list.tmZ02<-(t(list.mZ02))

1284        mZ02.loo<-loo(list.tmZ02)

1285        mZ02.loo

1286        loo_file<-paste(dossier, "/", site, "_Z02_loo.txt", sep="")

1287        write_values("mZ02", app=T, loo_file)

1288        mZ02_loo_pointwise<-mZ02.loo$pointwise
```

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```
1289        mZ02_loo_pareto_k<-mZ02.loo$pareto_k

1290        mZ02.loo$pareto_k<-NULL

1291        mZ02.loo$pointwise<-NULL

1292        write_values(as.matrix(mZ02.loo), app=T, loo_file)

1293        save.image(paste(dossier, "/", site, "_Z02.RData", sep=""))

1294   }

1295   ### MODEL Z01

1296   mZ01<-function(){

1297        init.funZ01 <-function(){

1298          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"

1299   = rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1),

1300   "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

1301        }

1302        mod.Z01<<-jags(inits=init.funZ01,model.file = "modelZ01_code.txt",data =

1303   list("cooc","visit","ab_I","ab_P", "dim1", "dim2"),parameters.to.save =

1304   c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","delta","beta","theta0","loglik"),n.chain

1305   s = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)

1306        mod.Z01.mcmc<-as.mcmc(mod.Z01)

1307        mZ01<-mod.Z01$BUGSoutput$sims.list

1308        mZ01.deviance<-mZ01$deviance

1309        mZ01.loglik<-mZ01$loglik

1310        dimSEM<-dim(mZ01.loglik)[1]

1311        list.mZ01<-sapply(1:dimSEM,function(x) matrix(mZ01.loglik[x,,],nrow=dim1*dim2))

1312        list.tmZ01<-(t(list.mZ01))

1313        mZ01.loo<-loo(list.tmZ01)

1314        mZ01.loo
```

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```
1315    loo_file<-paste(dossier, "/", site, "_Z01_loo.txt", sep="")

1316    write_values("mZ01", app=T, loo_file)

1317    mZ01_loo_pointwise<-mZ01.loo$pointwise

1318    mZ01_loo_pareto_k<-mZ01.loo$pareto_k

1319    mZ01.loo$pareto_k<-NULL

1320    mZ01.loo$pointwise<-NULL

1321    write_values(as.matrix(mZ01.loo), app=T, loo_file)

1322    save.image(paste(dossier, "/", site, "_Z01.RData", sep=""))

1323    }

1324    ### MODEL Z00

1325    mZ00<-function(){

1326            init.funZ00 <-function(){

1327             list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma"

1328    = rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),

1329    "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)

1330            }

1331            mod.Z00<<-jags(inits=init.funZ00,model.file = "modelZ00_code.txt",data =

1332    list("cooc","visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =

1333    c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","delta","beta","theta0","epsilon","loglik

1334    "),n.chains = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)

1335            mod.Z00.mcmc<-as.mcmc(mod.Z00)

1336            mZ00<-mod.Z00$BUGSoutput$sims.list

1337            mZ00.deviance<-mZ00$deviance

1338            mZ00.loglik<-mZ00$loglik

1339            dimSEM<-dim(mZ00.loglik)[1]

1340            list.mZ00<-sapply(1:dimSEM,function(x) matrix(mZ00.loglik[x,,],nrow=dim1*dim2))
```

Supplementary Information: Phenology and plant-hoverfly interactions

```
1341        list.tmZ00<-(t(list.mZ00))

1342        mZ00.loo<-loo(list.tmZ00)

1343        mZ00.loo

1344        loo_file<-paste(dossier, "/", site, "_Z00_loo.txt", sep="")

1345        write_values("mZ00", app=T, loo_file)

1346        mZ00_loo_pointwise<-mZ00.loo$pointwise

1347        mZ00_loo_pareto_k<-mZ00.loo$pareto_k

1348        mZ00.loo$pareto_k<-NULL

1349        mZ00.loo$pointwise<-NULL

1350        write_values(as.matrix(mZ00.loo), app=T, loo_file)

1351        save.image(paste(dossier, "/", site, "_Z00.RData", sep=""))

1352    }

1353    ###### end model functions

1354    print("JOB DONE")

1355    ###################################################

1356    ###      Network information (do not change)   ###

1357    ###################################################

1358    ###########################BLOCK 3 – MODEL EXECUTION #######################

1359    #launch_modele<-function(){

1360        ntw<-read.table(paste(dossier, "/", site, "_ntw.txt", sep=""),

1361 sep="\t",header=T,row.names=1)

1362        dim1<-dim(ntw)[1]

1363        dim2<-dim(ntw)[2]

1364        web<-as.matrix(ntw,dim1,dim2)

1365        inter0<-dget(paste(dossier, "/", site, "_web_i.txt", sep=""))

1366        cooc<-dget(paste(dossier, "/", site, "_co.txt", sep=""))
```

Supplementary Information: Phenology and plant-hoverfly interactions

```
1367        visit<-read.table(paste(dossier, "/", site, "_ntw.txt", sep=""),sep="\t",header=T)

1368        visit<-as.matrix(visit)

1369        abundanceI<-read.table(paste(dossier, "/", site, "_abI.txt", sep=""), sep="\t", header=T)

1370        ab_I <- log(abundanceI[,2])

1371        abundanceP<-read.table(paste(dossier, "/", site, "_abP.txt", sep=""), sep="\t", header=T)

1372        ab_P <- log(abundanceP[,2])

1373        if(opt$modele == "all")

1374        {

1375                print("modele: all")

1376                for(i in 0:15)

1377                {

1378                        print(paste("COMPUTING MODELE ", i, "\n", sep=""))

1379                        mod<-eval(parse(text=paste("mZ0", i, sep="")))

1380                        mod()

1381

1382                }

1383        }else{

1384                print(paste("modele: ", opt$modele), sep="")

1385                mod<-eval(parse(text=paste("m", opt$modele, sep="")))          #recupération de la

1386    fonction du modele

1387                mod()

1388        }

1389    #### end model execution

1390    #launch_modele()

1391

1392    #############################PARAMETER VALUES#############################
```

```r
1393    library(optparse)
1394    option_list = list(
1395            make_option(c("-d", "--dir"), type="character", default=NULL, help="model directory",
1396    metavar="character"),
1397            make_option(c("-s", "--site"), type="character", default=NULL, help="site name",
1398    metavar="character"))
1399    opt_parser = OptionParser(option_list=option_list);
1400    opt = parse_args(opt_parser);
1401    rdata<-list.files(opt$dir, pattern="*_Z015.RData")
1402    load(paste(opt$dir, "/", rdata, sep=""))  #chargement du RData qui contient tous les modèles pour un
1403    site donné
1404    print(paste("RData ", rdata, " loaded", sep=""))
1405    for(mod in ls(pattern="mod.Z0*"))
1406    {
1407            print(paste("getting values from ", mod, sep=""))
1408            model<-eval(parse(text=mod))
1409            if(is.null(model$BUGSoutput$mean$alpha)){model$BUGSoutput$mean$alpha<-NA}
1410            if(is.null(model$BUGSoutput$mean$beta)){model$BUGSoutput$mean$beta<-NA}
1411            if(is.null(model$BUGSoutput$mean$delta)){model$BUGSoutput$mean$delta<-NA}
1412            if(is.null(model$BUGSoutput$mean$epsilon)){model$BUGSoutput$mean$epsilon<-NA}
1413            if(is.null(model$BUGSoutput$mean$gamma)){model$BUGSoutput$mean$gamma<-NA}
1414            val<-matrix(c(model$BUGSoutput$mean$alpha, model$BUGSoutput$mean$beta,
1415    model$BUGSoutput$mean$delta, model$BUGSoutput$mean$epsilon,
1416    model$BUGSoutput$mean$gamma), 1, 5, dimnames=list("values", c("alpha", "beta", "delta",
1417    "epsilon", "gamma")))
```

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```
1418        write.table(val, file=paste(opt$dir, "/", opt$site, "_", mod, "_values.txt", sep=""), quote=F,
1419   sep="\t", row.names=F, col.names=T)
1420   }
1421
```

Supplementary Information: Phenology and plant-hoverfly interactions

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
```

```
1448    coBF<-dget("coBFs.txt")

1449    ######################### LBM code: LBM analysis following Poisson ##################

1450    bmi_BFs<-BM_poisson('LBM', webBFs)

1451    bmi_BFs$estimate()

1452    numi_BFs<-which.max(bmi_BFs$ICL)

1453    densi_BFs<-sum(webBFs)/(nrow(webBFs)*ncol(webBFs))

1454    probi_BFs<-bmi_BFs$model_parameters[[numi_BFs]]$lambda

1455    row.nb.gpi<-nrow(probi_BFs)

1456    col.nb.gpi<-ncol(probi_BFs)

1457    prob.rowi<-bmi_BFs$memberships[[numi_BFs]]$Z1

1458    hh.namei<-rownames(webBFs)

1459    mbrshp.hhi<-apply(prob.rowi,1,which.max)

1460    ls.freq.rowi<-rowSums(webBFs)

1461    res.hhi<-cbind.data.frame(hh.namei=hh.namei, mbrshp.hhi=mbrshp.hhi, freq.hhi=ls.freq.rowi)

1462    res.hh.ordi<-res.hhi[order(res.hhi$freq.hhi),]

1463    cpt=0

1464    for(k in 1: (nrow(res.hh.ordi)-1))

1465    {

1466      if (res.hh.ordi$mbrshp.hhi[k] !=res.hh.ordi$mbrshp.hhi[k+1]) cpt=cpt+1

1467    }

1468    nb.diff.hhi=cpt-(length(levels(as.factor(res.hh.ordi$mbrshp.hhi)))-1)

1469    #write tables

1470    write.table(res.hh.ordi,sep="\t",row.names=FALSE)

1471    prob.coli<-bmi_BFs$memberships[[numi_BFs]]$Z2

1472    sp.namei<-colnames(webBFs)

1473    mbrshp.spi<-apply(prob.coli,1,which.max)
```

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```
1474   ls.freq.coli<-colSums(webBFs)

1475   res.spi<-cbind.data.frame(sp.namei=sp.namei, mbrshp.spi=mbrshp.spi, freq.spi=ls.freq.coli)

1476   res.sp.ordi<-res.spi[order(res.spi$freq.spi),]

1477   cpt=0

1478   for (k in 1: (nrow(res.sp.ordi)-1))

1479   {

1480     if(res.sp.ordi$mbrshp.spi[k] !=res.sp.ordi$mbrshp.spi[k+1]) cpt=cpt+1

1481   }

1482   nb.diff.spi=cpt-(length(levels(as.factor(res.sp.ordi$mbrshp.spi)))-1)

1483   res.sp.ord2i=res.spi[order(res.spi$mbrshp.spi),]

1484   write.table(res.sp.ordi,sep="\t",row.names=FALSE)

1485   write.table(probi_BFs,file="_prob_BFs",sep="\t",row.names=FALSE)

1486

1487   ############################## Matrix organization ##############

1488   par(mfrow=c(1,1))

1489   webBFs2<-webBFs

1490   webBFs[which(webBFs>1)]=1

1491   nb.row=nrow(webBFs)

1492   nb.col=ncol(webBFs)

1493   nds=webBFs

1494   nps=coBF

1495   res.prob=read.table("_prob_BFs",sep="\t",h=TRUE)

1496   ls.ord.col.prob=order(colSums(res.prob),decreasing=TRUE)

1497   ls.ord.row.prob=order(rowSums(res.prob),decreasing=TRUE)

1498   ls.ord.hhi=sapply(res.hhi$mbrshp.hhi,function(x) which (x==ls.ord.row.prob))

1499   res.hh.ord2i=res.hhi[order(ls.ord.hhi),]
```

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```
1500    row.nb.gpi=length(levels(as.factor(res.hhi$mbrshp.hhi)))

1501    res.hh.ord3i=NULL

1502    for (h in ls.ord.row.prob)

1503    {

1504      part=res.hh.ord2i[res.hh.ord2i$mbrshp.hhi==h,]

1505      part.ord=part[order(part$freq.hhi,decreasing=TRUE),]

1506      res.hh.ord3i=rbind.data.frame(res.hh.ord3i,part.ord)

1507    }

1508    ls.ord.sp=sapply(res.spi$mbrshp.spi,function(x) which (x==ls.ord.col.prob))

1509    res.sp.ord2i=res.spi[order(ls.ord.sp),]

1510    col.nb.gb=length(levels(as.factor(res.spi$mbrshp.spi)))

1511    res.sp.ord3i=NULL

1512    for (h in ls.ord.col.prob)

1513    {

1514      part=res.sp.ord2i[res.sp.ord2i$mbrshp.spi==h,]

1515      part.ord=part[order(part$freq.spi,decreasing=TRUE),]

1516      res.sp.ord3i=rbind.data.frame(res.sp.ord3i,part.ord)

1517    }

1518    nds=nds[as.character(res.hh.ord3i$hh.namei),as.character(res.sp.ord3i$sp.namei)]

1519    nps=nps[as.character(res.hh.ord3i$hh.namei),as.character(res.sp.ord3i$sp.namei)]

1520    webBFs2=webBFs2[as.character(res.hh.ord3i$hh.namei),as.character(res.sp.ord3i$sp.namei)]

1521

1522    ######## Plot matrix with heatcolours and the number of visits #######

1523    visits<-matrix(webBFs2,nrow=dim(webBFs2)[1]*dim(webBFs2)[2],ncol=1)

1524    visits<-visits[which(visits>0)] #without the zeros

1525    coord.function<-function(x,nI,nP){
```

```
1526     c(((x-1)%%nI)+1,((x-1)%/%nI)+1)

1527     }

1528     func.plot.matrix<-function(x,y){

1529       indices<-which(x==1)

1530       min<-min(y)

1531       max<-max(y)

1532       yLabels<-rownames(x)

1533       xLabels<-colnames(x)

1534       title<-c("Bois de Fontaret")

1535       if(is.null(xLabels)){

1536         xLabels<-c(1:ncol(x))

1537       }

1538       if(is.null(yLabels)){

1539         yLabels<-c(1:nrow(x))

1540       }

1541       reverse<-nrow(x):1

1542       yLabels<-yLabels[reverse]

1543       y<-y[reverse,]

1544       image.plot(1:length(xLabels),1:length(yLabels),t(y),col=c("white",heat.colors(12)[12:1]), xlab="",

1545     ylab="",axes=FALSE,zlim=c(min,max))

1546       if(!is.null(title)){

1547         title(ylab="Insects", line=8, cex.lab=1)

1548         title(xlab="Plants", line=6, cex.lab=1.2)

1549         title("Bois de Fontaret")

1550       }

1551       axis(BELOW<-1,at=1:length(xLabels),labels=as.factor(as.character(xLabels)),las =2, cex.axis=0.6)
```

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```
1552    axis(LEFT<-2,at=1:length(yLabels), labels=as.factor(as.character(yLabels)),las= 2,cex.axis=0.6)

1553    axis(BELOW<-1,at=1:length(xLabels),labels=rep("",length(xLabels)),las =2,cex.axis=0.6)

1554    axis(LEFT<-2,at=1:length(yLabels),labels=rep("",length(yLabels)),las=2,cex.axis<-0.6)

1555    coo<-t(rbind(sapply(indices,function(xx) coord.function(xx,nrow(x),ncol(x)))))

1556    text(coo[,2],nrow(webBFs)+1-coo[,1],labels=visits, cex=0.6)

1557    }

1558    func.plot.matrix(nds,nps)

1559    ####### Black lines to delimit blocks in the plot ######

1560    if (row.nb.gpi>1)

1561    {

1562     ls.class=as.numeric(as.data.frame(table(res.hh.ord2i$mbrshp.hhi))[ls.ord.row.prob,2])

1563     ls.cum=sum(ls.class)-cumsum(ls.class)

1564     abline(h=ls.cum+0.5,col="grey20", lwd=3)

1565    }

1566    if (col.nb.gpi>1)

1567    {

1568     ls.class=as.numeric(as.data.frame(table(res.sp.ord2i$mbrshp.spi))[ls.ord.col.prob,2])

1569     ls.cum=cumsum(ls.class)

1570     abline(v=ls.cum+0.5,col="grey20", lwd=3)

1571    }
```

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