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de Manincor, N., Hautekeete, N., Piquot, Y., Schatz, B., Vanappelghem, C. and Massol, F. 2020. Does phenology explain plant–pollinator interactions at different latitudes? An assessment of its explanatory power in plant–hoverfly networks in French calcareous grasslands. – Oikos doi: 10.1111/oik.07259

Appendix 1

The following Supplementary material is available for this article:

Figure A1. Sites location in France.

Figure A2. Block clustering provided by LBM in the site of Falaises (FAL, Normandie), overlaid on a heatmap of species phenology overlap.

Figure A3. Block clustering provided by LBM in the site of Bois de Fontaret (BF, Occitanie), overlaid on a heatmap of species phenology overlap.

Figure A4. Block clustering provided by LBM in the site of Larris (LAR, Hauts-de-France), overlaid on a heatmap of species phenology overlap.

Figure A5. Block clustering provided by LBM in the site of Riez (R, Hauts-de-France), overlaid on a heatmap of species phenology overlap.

Table A1. Table of transformed plant abundances.

Table A2. Table of hoverfly and plant species names and abbreviations used in the LBM Figures.

Table A3. Table of model accuracy.

Appendix 2

Appendix 2.1. Script modularity and latent block model analysis (LBM).

Appendix 2.2. Model code.

Appendix 2.3. Model script for the 16 models.

Appendix 1

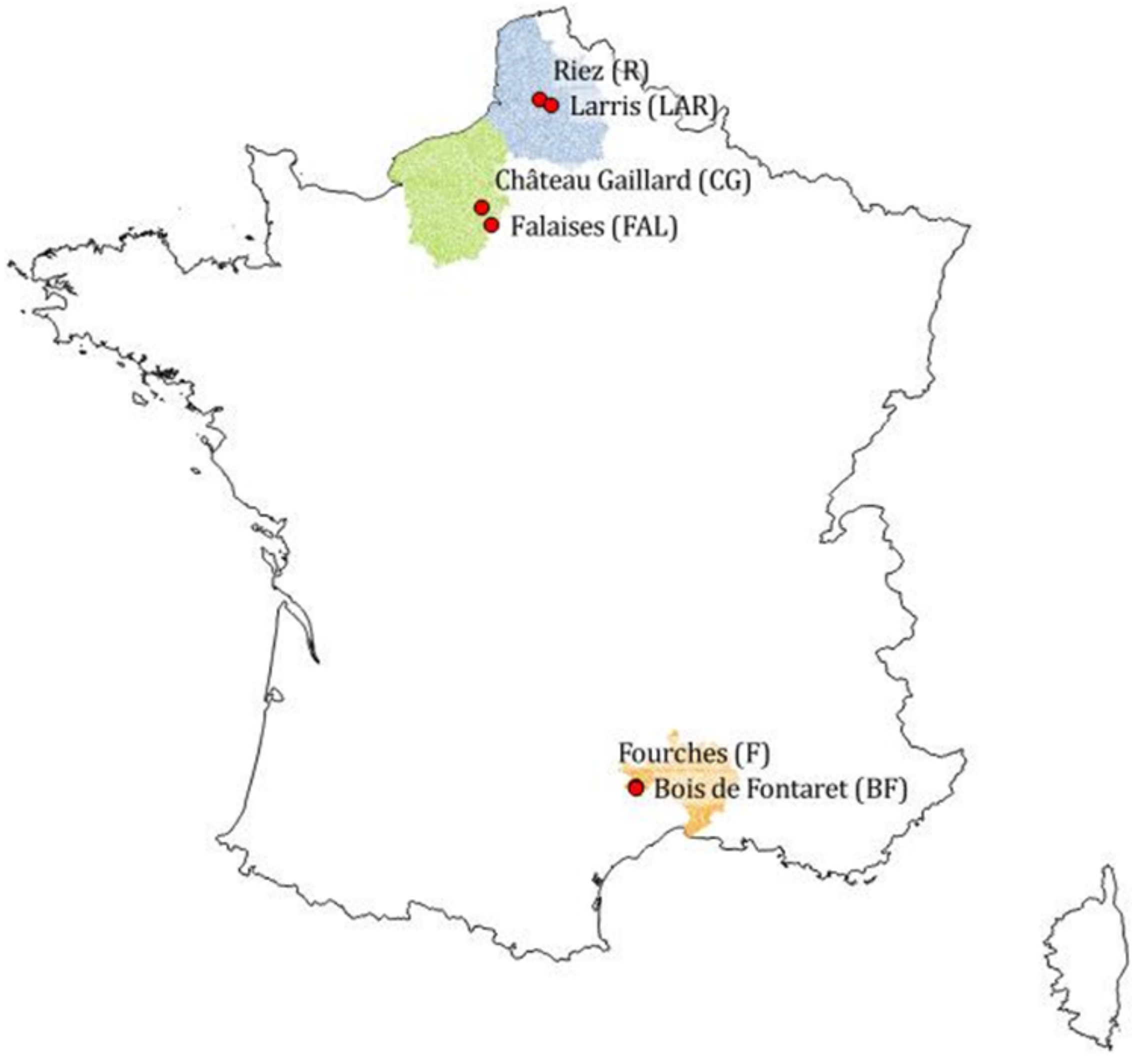

Figure A1. Site location in France: in blue the French départements Pas-de-Calais and Somme (Hauts-de-France region), in green the départements Eure and Seine Maritime (Normandie region), in orange the départment Gard (Occitanie region). The six sites correspond to the red dots (with the sites of Fourches and Bois de Fontaret represented by the same dot due to their closeness).

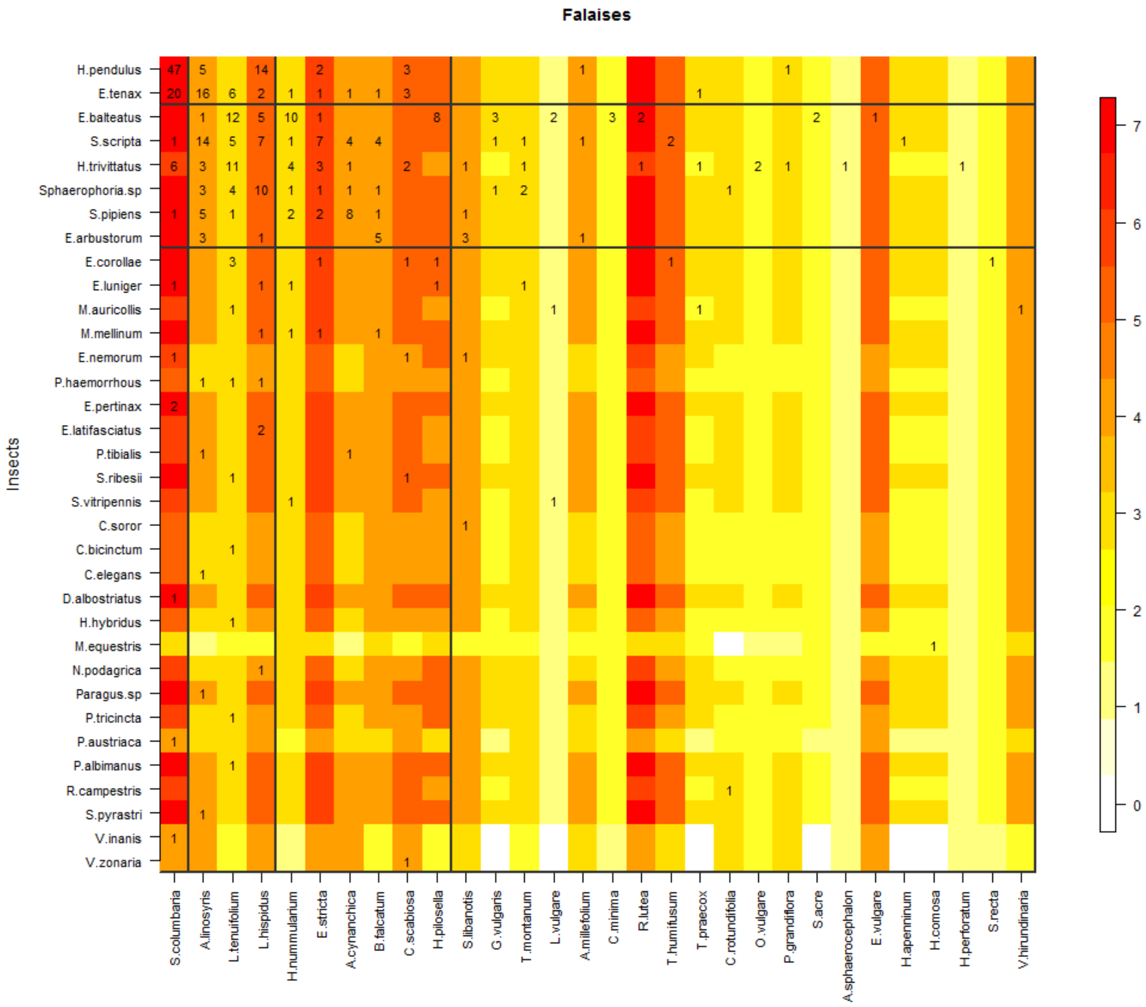

Figure A2. Block clustering provided by LBM in the site of Falaises (FAL, Normandie), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are 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 Supplementary material Appendix 1 Table A2.

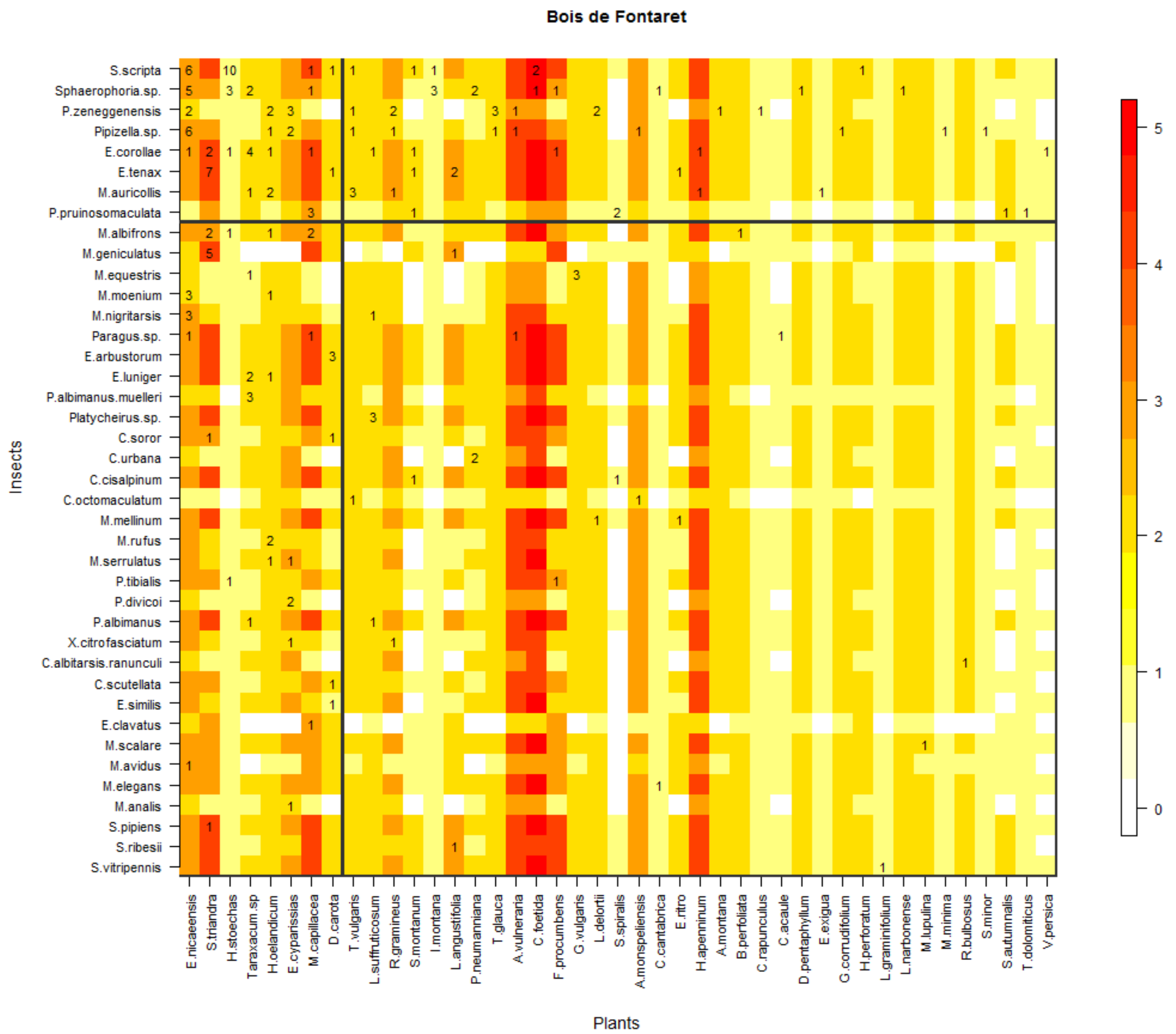

Figure A3. Block clustering provided by LBM in the site of Bois de Fontaret (BF, Occitanie), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are separated by solid black lines. Colours correspond to the number of months that are shared by each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker colours. Numbers are the number of visits observed in the field for a given plant–insect pair. Complete species names are reported in Supplementary material Appendix 1 Table A2.

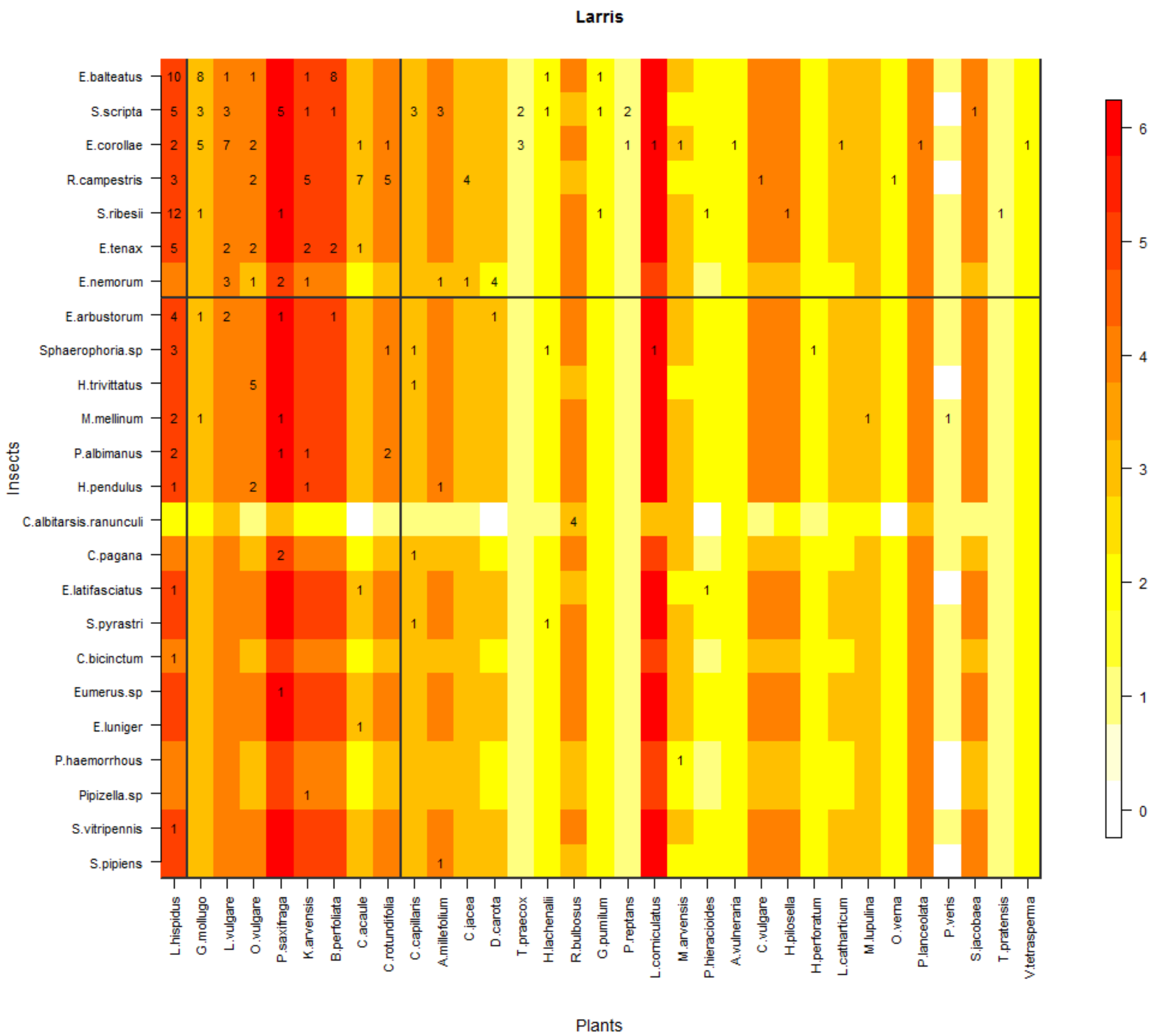

Figure A4. Block clustering provided by LBM in the site of Larris (LAR, Hauts-de-France), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are separated by solid black lines. Colours correspond to the number of months that are shared by each pair of plant and insect species (PO, phenology overlap), with higher PO corresponding to darker colours. Numbers are the number of visits observed in the field for a given plant–insect pair. Complete species names are reported in Supplementary material Appendix 1 Table A2.

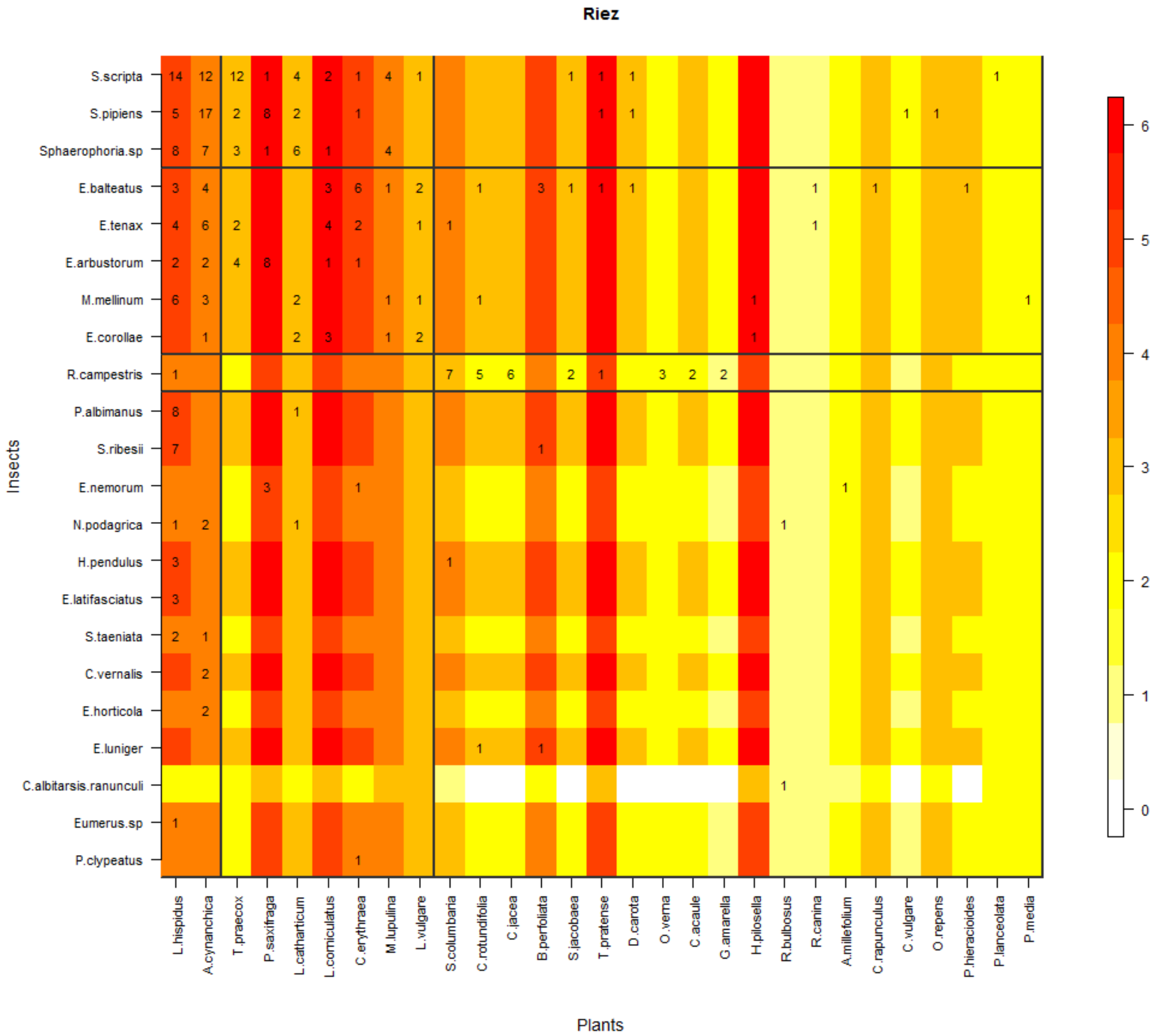

Figure A5. Block clustering provided by LBM in the site of Riez (R, Hauts-de-France), overlaid on a heatmap of species phenology overlap. Insect species are displayed in rows and plant species in columns, following their degree (number of partners). The blocks of insects and the blocks of plants are 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 Supplementary material Appendix 1 Table A2.

Table A1. Table of transformed plant abundances. The first column shows the Braun-Blanquet coefficients of, the second column, their percentages, and the third column, the transformed abundances used as the plant abundances in the model.

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

Table A2. 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	
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	*Platycheirus.sp*	*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	*Sphaerophoria.sp.*	*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*	
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*	
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*

Table A3. Table of model accuracy. The upper part of the table shows the results of the self-validation: in the region Occitanie the self-validation was tested for the site Bois de Fontaret (BF ~ BF) and the site of Fourches (F ~ F); in the region Normandie for the site of Château Gaillard (CG ~ CG) and the sites of Falaises (FAL ~ FAL) ; and in the region Hauts-de-France for the site of Larris (LAR ~ LAR) and for the site of Riez (R ~ R). The lower part of the table shows the results of the cross-validation only between each site of the same region: in the region Occitanie between Bois de Fontaret et Fourches (BF ~ F and vice versa F ~ BF); in the region Normandie between the site of Château Gaillard and Falaises (CG ~ FAL and vice versa FAL ~ CG); and in the region Hauts-de-France between the site of Larris and Riez (LAR ~ R and vice versa R ~ LAR).

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

Appendix 2

Appendix 2.1: Modularity and latent block model analysis

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

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

#site data (ex: Bois de Fontaret, BFs)
BFs<-read.table("ntwBFs.txt",header=T,sep="\t")
webBFs <- as.matrix(BFs)

###### Modularity analysis, binary data ################
BFs.graph.bin<-graph_from_incidence_matrix(webBFs,multiple=F) #binary
BFs.bin.cle<-cluster_leading_eigen(BFs.graph.bin)
BFs.bin.cle
#get phenology overlap matrix
coBF<-dget("coBFs.txt")

########### LBM code: LBM analysis following Poisson ################
bmi_BFs<-BM_poisson('LBM', webBFs)
bmi_BFs$estimate()
numi_BFs<-which.max(bmi_BFs$ICL)
densi_BFs<-sum(webBFs)/(nrow(webBFs)*ncol(webBFs))
probi_BFs<-bmi_BFs$model_parameters[[numi_BFs]]$lambda
row.nb.gpi<-nrow(probi_BFs)
col.nb.gpi<-ncol(probi_BFs)
prob.rowi<-bmi_BFs$memberships[[numi_BFs]]$Z1
hh.namei<-rownames(webBFs)
mbrshp.hhi<-apply(prob.rowi,1,which.max)
```

```
ls.freq.rowi<-rowSums(webBFs)
res.hhi<-cbind.data.frame(hh.namei=hh.namei, mbrshp.hhi=mbrshp.hhi, freq.hhi=ls.freq.rowi)
res.hh.ordi<-res.hhi[order(res.hhi$freq.hhi),]
cpt=0
for(k in 1: (nrow(res.hh.ordi)-1))
{
  if (res.hh.ordi$mbrshp.hhi[k] !=res.hh.ordi$mbrshp.hhi[k+1]) cpt=cpt+1
}
nb.diff.hhi=cpt-(length(levels(as.factor(res.hh.ordi$mbrshp.hhi)))-1)
#write tables
write.table(res.hh.ordi,sep="\t",row.names=FALSE)
prob.coli<-bmi_BFs$memberships[[numi_BFs]]$Z2
sp.namei<-colnames(webBFs)
mbrshp.spi<-apply(prob.coli,1,which.max)
ls.freq.coli<-colSums(webBFs)
res.spi<-cbind.data.frame(sp.namei=sp.namei, mbrshp.spi=mbrshp.spi, freq.spi=ls.freq.coli)
res.sp.ordi<-res.spi[order(res.spi$freq.spi),]
cpt=0
for (k in 1: (nrow(res.sp.ordi)-1))
{
  if(res.sp.ordi$mbrshp.spi[k] !=res.sp.ordi$mbrshp.spi[k+1]) cpt=cpt+1
}
nb.diff.spi=cpt-(length(levels(as.factor(res.sp.ordi$mbrshp.spi)))-1)
res.sp.ord2i=res.spi[order(res.spi$mbrshp.spi),]
write.table(res.sp.ordi,sep="\t",row.names=FALSE)
write.table(probi_BFs,file="_prob_BFs",sep="\t",row.names=FALSE)

##################Matrix organization ###############
par(mfrow=c(1,1))
webBFs2<-webBFs
webBFs[which(webBFs>1)]=1
nb.row=nrow(webBFs)
nb.col=ncol(webBFs)
nds=webBFs
nps=coBF
res.prob=read.table("_prob_BFs",sep="\t",h=TRUE)
ls.ord.col.prob=order(colSums(res.prob),decreasing=TRUE)
ls.ord.row.prob=order(rowSums(res.prob),decreasing=TRUE)
ls.ord.hhi=sapply(res.hhi$mbrshp.hhi,function(x) which (x==ls.ord.row.prob))
res.hh.ord2i=res.hhi[order(ls.ord.hhi),]
row.nb.gpi=length(levels(as.factor(res.hhi$mbrshp.hhi)))
res.hh.ord3i=NULL
for (h in ls.ord.row.prob)
{
  part=res.hh.ord2i[res.hh.ord2i$mbrshp.hhi==h,]
  part.ord=part[order(part$freq.hhi,decreasing=TRUE),]
```

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

######## Plot matrix with heatcolors and the number of visits #######
visits<-matrix(webBFs2,nrow=dim(webBFs2)[1]*dim(webBFs2)[2],ncol=1)
visits<-visits[which(visits>0)] #without the zeros
coord.function<-function(x,nI,nP){
  c(((x-1)%%nI)+1,((x-1)%/%nI)+1)
}
func.plot.matrix<-function(x,y){
  indices<-which(x==1)
  min<-min(y)
  max<-max(y)
  yLabels<-rownames(x)
  xLabels<-colnames(x)
  title<-c("Bois de Fontaret")
  if(is.null(xLabels)){
    xLabels<-c(1:ncol(x))
  }
  if(is.null(yLabels)){
    yLabels<-c(1:nrow(x))
  }
  reverse<-nrow(x):1
  yLabels<-yLabels[reverse]
  y<-y[reverse,]
  image.plot(1:length(xLabels),1:length(yLabels),t(y),col=c("white",heat.colors(12)[12:1]), xlab="",
ylab="",axes=FALSE,zlim=c(min,max))
  if(!is.null(title)){
    title(ylab="Insects", line=8, cex.lab=1)
    title(xlab="Plants", line=6, cex.lab=1.2)
    title("Bois de Fontaret")
  }
  axis(BELOW<-1,at=1:length(xLabels),labels=as.factor(as.character(xLabels)),las =2, cex.axis=0.6)
```

```
 axis(LEFT<-2,at=1:length(yLabels), labels=as.factor(as.character(yLabels)),las= 2,cex.axis=0.6)
 axis(BELOW<-1,at=1:length(xLabels),labels=rep("",length(xLabels)),las =2,cex.axis=0.6)
 axis(LEFT<-2,at=1:length(yLabels),labels=rep("",length(yLabels)),las=2,cex.axis<-0.6)
 coo<-t(rbind(sapply(indices,function(xx) coord.function(xx,nrow(x),ncol(x)))))
 text(coo[,2],nrow(webBFs)+1-coo[,1],labels=visits, cex=0.6)
}
func.plot.matrix(nds,nps)

####### Black lines to delimit blocks in the plot ######
if (row.nb.gpi>1)
{
 ls.class=as.numeric(as.data.frame(table(res.hh.ord2i$mbrshp.hhi))[ls.ord.row.prob,2])
 ls.cum=sum(ls.class)-cumsum(ls.class)
 abline(h=ls.cum+0.5,col="grey20", lwd=2)
}
if (col.nb.gpi>1)
{
 ls.class=as.numeric(as.data.frame(table(res.sp.ord2i$mbrshp.spi))[ls.ord.col.prob,2])
 ls.cum=cumsum(ls.class)
 abline(v=ls.cum+0.5,col="grey20", lwd=2)
```

Appendix 2.2. Model code

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

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

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

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

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

Appendix 2.3. Model script for the 16 models – LOO values

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

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

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

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

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

########### Librairies #########
library(bipartite)
library(vegan)
library(igraph)
library(magrittr)
library(dummies)
library(MuMIn)
library(rjags)
library(boot)
library(R2jags)
library(coda)
library(lattice)
library(ggplot2)
library(loo)
library(matrixStats)

#########Function to record the LOO values #######
write_values<-function(x, f, app)
{
           write.table(x, append=app, file=f, sep="\t", row.names=T, col.names=T, quote=F)
```

```
}
####BLOCK 2 – MODEL FUNCTIONS #####
#Model function and model initialization: one function for each model from model Z15, with 0 parameters, to
Z00 with all the parameters#
### MODEL Z015
mZ015<-function(){
	init.funZ015 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
	mod.Z015<<-jags(inits=init.funZ015,model.file = "modelZ015_code.txt",data =
list("visit","dim1","dim2"),parameters.to.save = c("mu","effet_I","effet_P","tau_I","tau_P","beta","theta0",
"loglik"),n.chains = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z015.mcmc<-as.mcmc(mod.Z015)
	mZ015<-mod.Z015$BUGSoutput$sims.list
	mZ015.deviance<-mZ015$deviance
	mZ015.loglik<-mZ015$loglik
	dimSEM<-dim(mZ015.loglik)[1]
	list.mZ015<-sapply(1:dimSEM,function(x) matrix(mZ015.loglik[x,,],nrow=dim1*dim2))
	list.tmZ015<-(t(list.mZ015))
	mZ015.loo<-loo(list.tmZ015)
	loo_file<-paste(dossier, "/", site, "_Z015_loo.txt", sep="")
	write_values("mZ015", app=F, loo_file)
	mZ015_loo_pointwise<-mZ015.loo$pointwise
	mZ015_loo_pareto_k<-mZ015.loo$pareto_k
	mZ015.loo$pareto_k<-NULL
	mZ015.loo$pointwise<-NULL
	write_values(as.matrix(mZ015.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z015.RData", sep=""))
}
### MODEL Z014
mZ014<-function(){
	init.funZ014 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0"
= rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
	mod.Z014<<-jags(inits=init.funZ014,model.file = "modelZ014_code.txt",data =
list("visit","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","delta","beta","theta0","loglik"),n.chains = 1, n.iter=1000000,
n.burnin = 250000, n.thin = 250)
	mod.Z014.mcmc<-as.mcmc(mod.Z014)
	mZ014<-mod.Z014$BUGSoutput$sims.list
	mZ014.deviance<-mZ014$deviance
	mZ014.loglik<-mZ014$loglik
	dimSEM<-dim(mZ014.loglik)[1]
	list.mZ014<-sapply(1:dimSEM,function(x) matrix(mZ014.loglik[x,,],nrow=dim1*dim2))
```

```
	list.tmZ014<-(t(list.mZ014))
	mZ014.loo<-loo(list.tmZ014)
	mZ014.loo
	loo_file<-paste(dossier, "/", site, "_Z014_loo.txt", sep="")
	write_values("mZ014", app=T, loo_file)
	mZ014_loo_pointwise<-mZ014.loo$pointwise
	mZ014_loo_pareto_k<-mZ014.loo$pareto_k
	mZ014.loo$pareto_k<-NULL
	mZ014.loo$pointwise<-NULL
	write_values(as.matrix(mZ014.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z014.RData", sep=""))
}
### MODEL Z013
mZ013<-function(){
	init.funZ013 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" = rnorm(1,0,1),
"theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
	mod.Z013<<-jags(inits=init.funZ013,model.file = "modelZ013_code.txt",data =
list("visit","ab_I","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","gamma","beta","theta0","loglik"),n.chains = 1, n.iter=1000000,
n.burnin = 250000, n.thin = 250)
	mod.Z013.mcmc<-as.mcmc(mod.Z013)
	mZ013<-mod.Z013$BUGSoutput$sims.list
	mZ013.deviance<-mZ013$deviance
	mZ013.loglik<-mZ013$loglik
	dimSEM<-dim(mZ013.loglik)[1]
	list.mZ013<-sapply(1:dimSEM,function(x) matrix(mZ013.loglik[x,,],nrow=dim1*dim2))
	list.tmZ013<-(t(list.mZ013))
	mZ013.loo<-loo(list.tmZ013)
	mZ013.loo
	loo_file<-paste(dossier, "/", site, "_Z013_loo.txt", sep="")
	write_values("mZ013", app=T, loo_file)
	mZ013_loo_pointwise<-mZ013.loo$pointwise
	mZ013_loo_pareto_k<-mZ013.loo$pareto_k
	mZ013.loo$pareto_k<-NULL
	mZ013.loo$pointwise<-NULL
	write_values(as.matrix(mZ013.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z013.RData", sep=""))
}
### MODEL Z012
mZ012<-function(){
	init.funZ012 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1),
"epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
```

```
        mod.Z012<<-jags(inits=init.funZ012,model.file = "modelZ012_code.txt",data =
list("cooc","visit","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","beta","theta0","epsilon","loglik"),n.chains = 1, n.iter=1000000,
n.burnin = 250000, n.thin = 250)
        mod.Z012.mcmc<-as.mcmc(mod.Z012)
        mZ012<-mod.Z012$BUGSoutput$sims.list
        mZ012.deviance<-mZ012$deviance
        mZ012.loglik<-mZ012$loglik
        dimSEM<-dim(mZ012.loglik)[1]
        list.mZ012<-sapply(1:dimSEM,function(x) matrix(mZ012.loglik[x,,],nrow=dim1*dim2))
        list.tmZ012<-(t(list.mZ012))
        mZ012.loo<-loo(list.tmZ012)
        mZ012.loo
        loo_file<-paste(dossier, "/", site, "_Z012_loo.txt", sep="")
        write_values("mZ012", app=T, loo_file)
        mZ012_loo_pointwise<-mZ012.loo$pointwise
        mZ012_loo_pareto_k<-mZ012.loo$pareto_k
        mZ012.loo$pareto_k<-NULL
        mZ012.loo$pointwise<-NULL
        write_values(as.matrix(mZ012.loo), app=T, loo_file)
        save.image(paste(dossier, "/", site, "_Z012.RData", sep=""))
}
### MODEL Z011
mZ011<-function(){
        init.funZ011 <-function(){
          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "theta0" =
rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
        }
        mod.Z011<<-jags(inits=init.funZ011,model.file = "modelZ011_code.txt",data =
list("cooc","visit","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","beta","theta0","loglik"),n.chains = 1, n.iter=1000000,
n.burnin = 250000, n.thin = 250)
        mod.Z011.mcmc<-as.mcmc(mod.Z011)
        mZ011<-mod.Z011$BUGSoutput$sims.list
        mZ011.deviance<-mZ011$deviance
        mZ011.loglik<-mZ011$loglik
        dimSEM<-dim(mZ011.loglik)[1]
        list.mZ011<-sapply(1:dimSEM,function(x) matrix(mZ011.loglik[x,,],nrow=dim1*dim2))
        list.tmZ011<-(t(list.mZ011))
        mZ011.loo<-loo(list.tmZ011)
        mZ011.loo
        loo_file<-paste(dossier, "/", site, "_Z011_loo.txt", sep="")
        write_values("mZ011", app=T, loo_file)
        mZ011_loo_pointwise<-mZ011.loo$pointwise
        mZ011_loo_pareto_k<-mZ011.loo$pareto_k
        mZ011.loo$pareto_k<-NULL
```

```
		mZ011.loo$pointwise<-NULL
		write_values(as.matrix(mZ011.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z011.RData", sep=""))
}
### MODEL Z010
mZ010<-function(){
		init.funZ010 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" = rnorm(1,0,1), "delta"
= rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z010<<-jags(inits=init.funZ010,model.file = "modelZ010_code.txt",data =
list("visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","gamma","delta","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z010.mcmc<-as.mcmc(mod.Z010)
		mZ010<-mod.Z010$BUGSoutput$sims.list
		mZ010.deviance<-mZ010$deviance
		mZ010.loglik<-mZ010$loglik
		dimSEM<-dim(mZ010.loglik)[1]
		list.mZ010<-sapply(1:dimSEM,function(x) matrix(mZ010.loglik[x,,],nrow=dim1*dim2))
		list.tmZ010<-(t(list.mZ010))
		mZ010.loo<-loo(list.tmZ010)
		mZ010.loo
		loo_file<-paste(dossier, "/", site, "_Z010_loo.txt", sep="")
		write_values("mZ010", app=T, loo_file)
		mZ010_loo_pointwise<-mZ010.loo$pointwise
		mZ010_loo_pareto_k<-mZ010.loo$pareto_k
		mZ010.loo$pareto_k<-NULL
		mZ010.loo$pointwise<-NULL
		write_values(as.matrix(mZ010.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z010.RData", sep=""))
}
### MODEL Z09
mZ09<-function(){
		init.funZ09 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0"
= rnorm(1,0,1), "epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
"inter"=inter0)
		}
		mod.Z09<<-jags(inits=init.funZ09,model.file = "modelZ09_code.txt",data =
list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","delta","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z09.mcmc<-as.mcmc(mod.Z09)
		mZ09<-mod.Z09$BUGSoutput$sims.list
		mZ09.deviance<-mZ09$deviance
```

```
        mZ09.loglik<-mZ09$loglik
        dimSEM<-dim(mZ09.loglik)[1]
        list.mZ09<-sapply(1:dimSEM,function(x) matrix(mZ09.loglik[x,,],nrow=dim1*dim2))
        list.tmZ09<-(t(list.mZ09))
        mZ09.loo<-loo(list.tmZ09)
        mZ09.loo
        loo_file<-paste(dossier, "/", site, "_Z09_loo.txt", sep="")
        write_values("mZ09", app=T, loo_file)
        mZ09_loo_pointwise<-mZ09.loo$pointwise
        mZ09_loo_pareto_k<-mZ09.loo$pareto_k
        mZ09.loo$pareto_k<-NULL
        mZ09.loo$pointwise<-NULL
        write_values(as.matrix(mZ09.loo), app=T, loo_file)
        save.image(paste(dossier, "/", site, "_Z09.RData", sep=""))
}
### MODEL Z08
mZ08<-function(){
        init.funZ08 <-function(){
          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" = rnorm(1,0,1),
"theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1),
"inter"=inter0)
        }
        mod.Z08<<-jags(inits=init.funZ08,model.file = "modelZ08_code.txt",data =
list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","gamma","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
        mod.Z08.mcmc<-as.mcmc(mod.Z08)
        mZ08<-mod.Z08$BUGSoutput$sims.list
        mZ08.deviance<-mZ08$deviance
        mZ08.loglik<-mZ08$loglik
        dimSEM<-dim(mZ08.loglik)[1]
        list.mZ08<-sapply(1:dimSEM,function(x) matrix(mZ08.loglik[x,,],nrow=dim1*dim2))
        list.tmZ08<-(t(list.mZ08))
        mZ08.loo<-loo(list.tmZ08)
        mZ08.loo
        loo_file<-paste(dossier, "/", site, "_Z08_loo.txt", sep="")
        write_values("mZ08", app=T, loo_file)
        mZ08_loo_pointwise<-mZ08.loo$pointwise
        mZ08_loo_pareto_k<-mZ08.loo$pareto_k
        mZ08.loo$pareto_k<-NULL
        mZ08.loo$pointwise<-NULL
        write_values(as.matrix(mZ08.loo), app=T, loo_file)
        save.image(paste(dossier, "/", site, "_Z08.RData", sep=""))
}
### MODEL Z07
mZ07<-function(){
```

```
	init.funZ07 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "delta" =
rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
	mod.Z07<<-jags(inits=init.funZ07,model.file = "modelZ07_code.txt",data =
list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","delta","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z07.mcmc<-as.mcmc(mod.Z07)
	mZ07<-mod.Z07$BUGSoutput$sims.list
	mZ07.deviance<-mZ07$deviance
	mZ07.loglik<-mZ07$loglik
	dimSEM<-dim(mZ07.loglik)[1]
	list.mZ07<-sapply(1:dimSEM,function(x) matrix(mZ07.loglik[x,,],nrow=dim1*dim2))
	list.tmZ07<-(t(list.mZ07))
	mZ07.loo<-loo(list.tmZ07)
	mZ07.loo
	loo_file<-paste(dossier, "/", site, "_Z07_loo.txt", sep="")
	write_values("mZ07", app=T, loo_file)
	mZ07_loo_pointwise<-mZ07.loo$pointwise
	mZ07_loo_pareto_k<-mZ07.loo$pareto_k
	mZ07.loo$pareto_k<-NULL
	mZ07.loo$pointwise<-NULL
	write_values(as.matrix(mZ07.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z07.RData", sep=""))
}
### MODEL Z06
mZ06<-function(){
	init.funZ06 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma" =
rnorm(1,0,1), "theta0" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
	mod.Z06<<-jags(inits=init.funZ06,model.file = "modelZ06_code.txt",data =
list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z06.mcmc<-as.mcmc(mod.Z06)
	mZ06<-mod.Z06$BUGSoutput$sims.list
	mZ06.deviance<-mZ06$deviance
	mZ06.loglik<-mZ06$loglik
	dimSEM<-dim(mZ06.loglik)[1]
	list.mZ06<-sapply(1:dimSEM,function(x) matrix(mZ06.loglik[x,,],nrow=dim1*dim2))
	list.tmZ06<-(t(list.mZ06))
	mZ06.loo<-loo(list.tmZ06)
	mZ06.loo
	loo_file<-paste(dossier, "/", site, "_Z06_loo.txt", sep="")
```

```
		write_values("mZ06", app=T, loo_file)
		mZ06_loo_pointwise<-mZ06.loo$pointwise
		mZ06_loo_pareto_k<-mZ06.loo$pareto_k
		mZ06.loo$pareto_k<-NULL
		mZ06.loo$pointwise<-NULL
		write_values(as.matrix(mZ06.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z06.RData", sep=""))
}
### MODEL Z05
mZ05<-function(){
		init.funZ05 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "theta0" =
rnorm(1,0,1), "epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z05<<-jags(inits=init.funZ05,model.file = "modelZ05_code.txt",data =
list("cooc","visit","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z05.mcmc<-as.mcmc(mod.Z05)
		mZ05<-mod.Z05$BUGSoutput$sims.list
		mZ05.deviance<-mZ05$deviance
		mZ05.loglik<-mZ05$loglik
		dimSEM<-dim(mZ05.loglik)[1]
		list.mZ05<-sapply(1:dimSEM,function(x) matrix(mZ05.loglik[x,,],nrow=dim1*dim2))
		list.tmZ05<-(t(list.mZ05))
		mZ05.loo<-loo(list.tmZ05)
		mZ05.loo
		loo_file<-paste(dossier, "/", site, "_Z05_loo.txt", sep="")
		write_values("mZ05", app=T, loo_file)
		mZ05_loo_pointwise<-mZ05.loo$pointwise
		mZ05_loo_pareto_k<-mZ05.loo$pareto_k
		mZ05.loo$pareto_k<-NULL
		mZ05.loo$pointwise<-NULL
		write_values(as.matrix(mZ05.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z05.RData", sep=""))
}
### MODEL Z04
mZ04<-function(){
		init.funZ04 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "beta" = rnorm(1,0,1), "gamma" = rnorm(1,0,1), "delta"
= rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z04<<-jags(inits=init.funZ04,model.file = "modelZ04_code.txt",data =
list("cooc","visit","ab_I","ab_P","dim1","dim2"),parameters.to.save =
```

```
c("mu","effet_I","effet_P","tau_I","tau_P","gamma","delta","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z04.mcmc<-as.mcmc(mod.Z04)
	mZ04<-mod.Z04$BUGSoutput$sims.list
	mZ04.deviance<-mZ04$deviance
	mZ04.loglik<-mZ04$loglik
	dimSEM<-dim(mZ04.loglik)[1]
	list.mZ04<-sapply(1:dimSEM,function(x) matrix(mZ04.loglik[x,,],nrow=dim1*dim2))
	list.tmZ04<-(t(list.mZ04))
	mZ04.loo<-loo(list.tmZ04)
	mZ04.loo
	loo_file<-paste(dossier, "/", site, "_Z04_loo.txt", sep="")
	write_values("mZ04", app=T, loo_file)
	mZ04_loo_pointwise<-mZ04.loo$pointwise
	mZ04_loo_pareto_k<-mZ04.loo$pareto_k
	mZ04.loo$pareto_k<-NULL
	mZ04.loo$pointwise<-NULL
	write_values(as.matrix(mZ04.loo), app=T, loo_file)
	save.image(paste(dossier, "/", site, "_Z04.RData", sep=""))
}
### MODEL Z03
mZ03<-function(){
	init.funZ03 <-function(){
	  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma" =
rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
	}
	mod.Z03<<-jags(inits=init.funZ03,model.file = "modelZ03_code.txt",data =
list("cooc","visit","ab_I","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
	mod.Z03.mcmc<-as.mcmc(mod.Z03)
	mZ03<-mod.Z03$BUGSoutput$sims.list
	mZ03.deviance<-mZ03$deviance
	mZ03.loglik<-mZ03$loglik
	dimSEM<-dim(mZ03.loglik)[1]
	list.mZ03<-sapply(1:dimSEM,function(x) matrix(mZ03.loglik[x,,],nrow=dim1*dim2))
	list.tmZ03<-(t(list.mZ03))
	mZ03.loo<-loo(list.tmZ03)
	mZ03.loo
	loo_file<-paste(dossier, "/", site, "_Z03_loo.txt", sep="")
	write_values("mZ03", app=T, loo_file)
	mZ03_loo_pointwise<-mZ03.loo$pointwise
	mZ03_loo_pareto_k<-mZ03.loo$pareto_k
	mZ03.loo$pareto_k<-NULL
	mZ03.loo$pointwise<-NULL
```

```
        write_values(as.matrix(mZ03.loo), app=T, loo_file)
        save.image(paste(dossier, "/", site, "_Z03.RData", sep=""))
}
### MODEL Z02
mZ02<-function(){
        init.funZ02 <-function(){
          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1, "beta" = rnorm(1,0,1), "delta" =
rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
        }
        mod.Z02<<-jags(inits=init.funZ02,model.file = "modelZ02_code.txt",data =
list("cooc","visit","ab_P","dim1","dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","delta","beta","theta0","epsilon","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
        mod.Z02.mcmc<-as.mcmc(mod.Z02)
        mZ02<-mod.Z02$BUGSoutput$sims.list
        mZ02.deviance<-mZ02$deviance
        mZ02.loglik<-mZ02$loglik
        dimSEM<-dim(mZ02.loglik)[1]
        list.mZ02<-sapply(1:dimSEM,function(x) matrix(mZ02.loglik[x,,],nrow=dim1*dim2))
        list.tmZ02<-(t(list.mZ02))
        mZ02.loo<-loo(list.tmZ02)
        mZ02.loo
        loo_file<-paste(dossier, "/", site, "_Z02_loo.txt", sep="")
        write_values("mZ02", app=T, loo_file)
        mZ02_loo_pointwise<-mZ02.loo$pointwise
        mZ02_loo_pareto_k<-mZ02.loo$pareto_k
        mZ02.loo$pareto_k<-NULL
        mZ02.loo$pointwise<-NULL
        write_values(as.matrix(mZ02.loo), app=T, loo_file)
        save.image(paste(dossier, "/", site, "_Z02.RData", sep=""))
}
### MODEL Z01
mZ01<-function(){
        init.funZ01 <-function(){
          list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma" =
rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1),
"effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
        }
        mod.Z01<<-jags(inits=init.funZ01,model.file = "modelZ01_code.txt",data =
list("cooc","visit","ab_I","ab_P", "dim1", "dim2"),parameters.to.save =
c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","delta","beta","theta0","loglik"),n.chains = 1,
n.iter=1000000, n.burnin = 250000, n.thin = 250)
        mod.Z01.mcmc<-as.mcmc(mod.Z01)
        mZ01<-mod.Z01$BUGSoutput$sims.list
        mZ01.deviance<-mZ01$deviance
```

```
		mZ01.loglik<-mZ01$loglik
		dimSEM<-dim(mZ01.loglik)[1]
		list.mZ01<-sapply(1:dimSEM,function(x) matrix(mZ01.loglik[x,,],nrow=dim1*dim2))
		list.tmZ01<-(t(list.mZ01))
		mZ01.loo<-loo(list.tmZ01)
		mZ01.loo
		loo_file<-paste(dossier, "/", site, "_Z01_loo.txt", sep="")
		write_values("mZ01", app=T, loo_file)
		mZ01_loo_pointwise<-mZ01.loo$pointwise
		mZ01_loo_pareto_k<-mZ01.loo$pareto_k
		mZ01.loo$pareto_k<-NULL
		mZ01.loo$pointwise<-NULL
		write_values(as.matrix(mZ01.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z01.RData", sep=""))
}
### MODEL Z00
mZ00<-function(){
		init.funZ00 <-function(){
		  list("tau_I" = rexp(1,10), "tau_P" = rexp(1,10), "alpha" = 0.1,"beta" = rnorm(1,0,1), "gamma" = rnorm(1,0,1), "delta" = rnorm(1,0,1), "theta0" = rnorm(1,0,1), "epsilon" = rnorm(1,0,1), "effet_I"=rnorm(dim1,0,1),"effet_P"=rnorm(dim2,0,1), "inter"=inter0)
		}
		mod.Z00<<-jags(inits=init.funZ00,model.file = "modelZ00_code.txt",data = list("cooc","visit","ab_I","ab_P","dim1","dim2"),parameters.to.save = c("mu","effet_I","effet_P","tau_I","tau_P","alpha","gamma","delta","beta","theta0","epsilon","loglik"),n.chains = 1, n.iter=1000000, n.burnin = 250000, n.thin = 250)
		mod.Z00.mcmc<-as.mcmc(mod.Z00)
		mZ00<-mod.Z00$BUGSoutput$sims.list
		mZ00.deviance<-mZ00$deviance
		mZ00.loglik<-mZ00$loglik
		dimSEM<-dim(mZ00.loglik)[1]
		list.mZ00<-sapply(1:dimSEM,function(x) matrix(mZ00.loglik[x,,],nrow=dim1*dim2))
		list.tmZ00<-(t(list.mZ00))
		mZ00.loo<-loo(list.tmZ00)
		mZ00.loo
		loo_file<-paste(dossier, "/", site, "_Z00_loo.txt", sep="")
		write_values("mZ00", app=T, loo_file)
		mZ00_loo_pointwise<-mZ00.loo$pointwise
		mZ00_loo_pareto_k<-mZ00.loo$pareto_k
		mZ00.loo$pareto_k<-NULL
		mZ00.loo$pointwise<-NULL
		write_values(as.matrix(mZ00.loo), app=T, loo_file)
		save.image(paste(dossier, "/", site, "_Z00.RData", sep=""))
}
###### end model functions
print("JOB DONE")
```

```
#################################################
###	Network information (do not change)	###
###BLOCK 3 – MODEL EXECUTION ###
#launch_modele<-function(){
	ntw<-read.table(paste(dossier, "/", site, "_ntw.txt", sep=""), sep="\t",header=T,row.names=1)
	dim1<-dim(ntw)[1]
	dim2<-dim(ntw)[2]
	web<-as.matrix(ntw,dim1,dim2)
	inter0<-dget(paste(dossier, "/", site, "_web_i.txt", sep=""))
	cooc<-dget(paste(dossier, "/", site, "_co.txt", sep=""))
	visit<-read.table(paste(dossier, "/", site, "_ntw.txt", sep=""),sep="\t",header=T)
	visit<-as.matrix(visit)
	abundanceI<-read.table(paste(dossier, "/", site, "_abI.txt", sep=""), sep="\t", header=T)
	ab_I <- log(abundanceI[,2])
	abundanceP<-read.table(paste(dossier, "/", site, "_abP.txt", sep=""), sep="\t", header=T)
	ab_P <- log(abundanceP[,2])
	if(opt$modele == "all")
	{
		print("modele: all")
		for(i in 0:15)
		{
			print(paste("COMPUTING MODELE ", i, "\n", sep=""))
			mod<-eval(parse(text=paste("mZ0", i, sep="")))
			mod()

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

### PARAMETER VALUES ###
library(optparse)
option_list = list(
	make_option(c("-d", "--dir"), type="character", default=NULL, help="model directory", metavar="character"),
	make_option(c("-s", "--site"), type="character", default=NULL, help="site name", metavar="character"))
opt_parser = OptionParser(option_list=option_list);
opt = parse_args(opt_parser);
rdata<-list.files(opt$dir, pattern="*_Z015.RData")
```

```
load(paste(opt$dir, "/", rdata, sep=""))  #chargement du RData qui contient tous les modèles pour un site donné
print(paste("RData ", rdata, " loaded", sep=""))
for(mod in ls(pattern="mod.Z0*"))
{
	print(paste("getting values from ", mod, sep=""))
	model<-eval(parse(text=mod))
	if(is.null(model$BUGSoutput$mean$alpha)){model$BUGSoutput$mean$alpha<-NA}
	if(is.null(model$BUGSoutput$mean$beta)){model$BUGSoutput$mean$beta<-NA}
	if(is.null(model$BUGSoutput$mean$delta)){model$BUGSoutput$mean$delta<-NA}
	if(is.null(model$BUGSoutput$mean$epsilon)){model$BUGSoutput$mean$epsilon<-NA}
	if(is.null(model$BUGSoutput$mean$gamma)){model$BUGSoutput$mean$gamma<-NA}
	val<-matrix(c(model$BUGSoutput$mean$alpha, model$BUGSoutput$mean$beta, model$BUGSoutput$mean$delta, model$BUGSoutput$mean$epsilon, model$BUGSoutput$mean$gamma), 1, 5, dimnames=list("values", c("alpha", "beta", "delta", "epsilon", "gamma")))
	write.table(val, file=paste(opt$dir, "/", opt$site, "_", mod, "_values.txt", sep=""), quote=F, sep="\t", row.names=F, col.names=T)
}
```