SUPPORTING INFORMATION Bi-trophic interactions shape biodiversity in space

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¹ SI MATERIALS AND METHODS

² S1 Model Description

As described in the main text, simulations are stochastic, in a lottery manner (1). This means that at each generation (=time step), N_p plants (N_a animals) are drawn at random to replace the N_p plants (N_a animals) of the previous generation. A detailed scheme of the spatial organization of the metacommunity can be found in Fig. S1.

The probabilities of this lottery are detailed in the main text. We here provide addi-7 tional explanations for the choice of seed (egg) production equations. In the mutualistic 8 case, we consider that there is a base seed (egg) production equal to $1 - c_p (1 - c_a)$ for 9 plants (animals). For the plants, this base fecundity corresponds to selfing, that we here 10 assume constant among species for simplicity. For the animals, assuming that fecundity is 11 proportional to diet, the base fecundity corresponds to the diet part which is not achieved 12 during the mutualistic interaction with the plants. The additional term corresponds to 13 the part of seed (egg) production which depends on the mutualistic interaction. For the 14 plants, we consider that each animal of species j effectively pollinates a flower of species i15 at a rate I_{ij} . Hence a flower of species *i* is pollimated at a total rate equal to $\sum_{j=1}^{S_a} n_j^a I_{ij}$. We 16 further assume that flowers compete to attract animals, so that the pollinator-mediated 17 fecundity of a flower of species i depends on the rate at which the flower is pollinated 18 compared to the rate at which other flowers are pollinated. This leads to the expres-19 sion: $c_p \frac{\sum_{j=1}^{S_a} n_j^a I_{ij}}{\sum_{k=1}^{S_p} \left(\frac{n_p^p}{N_p} \sum_{l=1}^{S_a} n_l^a I_{kl}\right)}$. Our formulation implies that a flower will have a fecundity 20 above (below) 1 if it is more (less) pollinated than an average flower. For the animals, 21 we consider that animals gather resources from the plant at the same rate I_{ij} that they 22 pollinate the plant, and that the plants provide a fixed amount of resources. We assume 23

that animals compete for these resources, so that an animal of species j gathers from a plant of species i an amount of resources equal to $\frac{I_{ij}}{\sum_{k=1}^{S_a} \frac{n_k^a}{N_a} I_{ik}}$. When summing over the relative frequency of the plants, we recover Equation 2. We additionally studied another way to model animal fecundity, and obtained similar results (see *SI Section S2.11.2*). In the antagonistic case, the reasoning is the same, except that plants are negatively affected by the interaction.

This model formulation presents several advantages. First, it corresponds to a purely 7 neutral model when removing between groups interactions. Consequently, this model 8 enables to explore the deterministic effect of ecological interactions in a background of 9 demographic and environmental stochasticity as is often the case in nature (2). Second, 10 this model can be quickly simulated by coalescence, so that it is possible to fit this model 11 to real data by Approximate Bayesian Computation (see Methods). Third, by fixing con-12 stant community sizes, it focuses on community composition by removing the potential 13 confounding influence of variations in community sizes. This constant community size 14 assumption is a good first approximation for plants in many terrestrial systems. Indeed, 15 herbivores generally have a limited feeding effect on plant biomass for various reasons in-16 cluding the low food quality of many plant parts, and the control of insect herbivores by 17 natural enemies (3). Although it is not the case for insects, their population fluctuations 18 are likely to be mainly driven by factors not related to plants like climate (4). Conse-19 quently, our fixed community size assumption is a good simplifying assumption which 20 is unlikely to make us miss any retroactions taking place between the plant and insect 21 groups. An alternative approach would have been to use Lotka-Volterra type equations 22 to model the coupled dynamics of plants and animals (5). A drawback of this approach 23 is that it requires a large number of species-specific parameters like intrinsic growth rates 24 and carrying capacities. Such an increase in the number of parameters would prevent 25

- 1 the model from being fitted to available data, in that we would need much additional
- ² information on each species or community dynamics.



Fig. S1: Model representation. Circles stand for patches, horizontal and vertical arrows represent dispersal between neighboring patches, and oblique arrows indicate dispersal from the species pool. N_p (N_a) is the number of plant (animal) individuals in each patch. m_p (m_a) is the plant (animal) dispersal rate between neighboring patches. μ_p (μ_a) is the plant (animal) dispersal rate from the species pool to each patch.

¹ S2 Model results - impact on the plant set

$_{2}$ S2.1 α diversity of plants

In this section, we detail the results obtained in Fig. 2 of the main text. Let us start by 3 considering nested mutualistic networks produced with a threshold rule (Fig. 2A). For 4 the limiting case of low dispersal rates and weak mutualism (low m_p and c_p), we recover 5 Bastolla et al.'s result (5), namely, that nested networks tend to increase plant local 6 richness (bottom left of Fig. 2A). In this case, bi-trophic interactions have a stabilizing effect (6) induced by the heterogeneity among animals in their plant preferences. Thus, communities tend to gain species with over-dispersed traits during the coupled dynamics 9 (see "Variance Test" in SI Section S2.5). This limiting case without dispersal corresponds 10 to the standard network approach. 11

When dispersal rates increase and/or mutualistic interactions become stronger (larger 12 c_p), the positive effect of mutualistic interactions on plant richness decreases and even 13 becomes negative (Fig. 2A). The stabilizing effect of the mutualistic interactions is now 14 counterbalanced by their filtering effect: plants survive only if they encounter a corre-15 sponding mutualist. We detect this filtering effect by computing the average interaction 16 strength between plant and animal individuals. When mutualistic interactions have a 17 negative impact on plant species richness, the average interaction strength increases com-18 pared to the neutral case (see "Coupling Test" in SI Section S2.4). The surviving plants 19 are those which encounter more mutualists. 20

Similar results are obtained with antagonistic networks (Fig. 2B). In this case, when bi-trophic interactions have a negative impact on plant species richness, the average interaction strength decreases compared to the neutral case (see "Coupling Test" in *SI Section S2.4*). The surviving plants are those which encounter fewer antagonists. Once we have considered nested networks, we now turn our attention to highly specialized networks. We obtained similar results for this type of networks (Fig. 2C-D). The common feature of both nested and specialized networks is their low average degree (i.e., species interact on average with a low number of species), although the variance in degree distribution is larger in nested networks. This average degree hence appears to play a major role in how network architecture determines the impact of bi-trophic interactions on plant richness.

When interactions are generalized both mutualistic and antagonistic networks increase 8 species richness at low dispersal rates and decrease it at high dispersal rates (Fig. 2E-F). 9 At low dispersal rates, local species richness is mainly controlled by local interactions. 10 When they are generalized, the filtering effect of the interactions is low, and the sta-11 bilizing effect predominates. Equitability in plant abundance is low without bi-trophic 12 interactions and increases in the presence of such interactions. This increase in plant 13 equitability is positively correlated with the variation in plant richness in the presence 14 of interactions (see "Equitability Test" in SI Section S2.6). At higher dispersal rates, 15 local species richness increases and becomes more dependent on the recurrent dispersal of 16 locally rare species. When disrupting the fitness equivalence among individuals, interac-17 tions tend to destabilize this dynamic equilibrium (7). This disruption leads to a reduced 18 equitability in species abundances and, ultimately, in species loss (see "Equitability Test" 19 in SI Section S2.6). This result is in agreement with a recent meta-analysis of herbi-20 vore exclusion experiments showing that herbivory reduced plant species richness when 21 equitability in plant abundances was high, and vice versa (8). 22

Along the second axis of variation, we find that mutualistic interactions have an increased negative effect on plant richness for stronger values of coupling c_p (Fig. 2E). This is due to an increase of the filtering effect of the interaction, as encountered earlier for specialized interactions. In contrast, we find the reverse relationship for antagonistic interactions: stronger coupling leads to an increased positive effect on plant richness,
especially at low dispersal rates (Fig. 2F). Here the stabilizing effect of herbivores exceeds their filtering effect, so that the resulting effect of herbivores on plants is positive.
Stronger coupling between plants and herbivores thus increase the magnitude of this positive effect, especially at low dispersal rates for which local interactions have the strongest
impact on community dynamics.

The balance between the filtering and the stabilizing effects also depends on the species 8 richness of the plant set, both at the local and regional scales. In metacommunities with 9 larger regional species richness, we find a stronger positive effect of both mutualistic and 10 antagonistic interactions on local plant species richness. In contrast, in communities with 11 larger local richness, we observe a stronger negative effect of both interaction types on 12 plant richness, this contrast being stronger for antagonistic interactions (see SI Section 13 2.7). These results differ from those of Thébault and Fontaine (9) who studied network 14 dynamics in closed communities and found that higher diversity promotes persistence 15 in mutualistic networks and destabilizes it in antagonistic ones. Our current results, 16 therefore, show that local and regional diversity may be associated with different effects 17 of bi-trophic interactions in spatially-extended systems. Another difference is that, as 18 reported here, local and regional richness have a very small correlation with the effect of 19 bi-trophic interactions on plant richness in this spatially extended model $(R^2 = 0.01)$. 20

²¹ S2.2 β diversity of plants

²² Up to here, we have described patterns of local species richness, namely, plant richness ²³ at each lattice site. Our framework also enabled us to study the effect of bi-trophic inter-²⁴ actions on plant richness at the regional scale, i.e., considering the regional abundances

across the entire lattice. When interactions have a negative effect on plant local richness, 1 β diversity simultaneously increases (Fig. S2). In 91% (89 %) of the cases for mutual-2 istic (antagonistic) interactions, the decrease in metacommunity richness is smaller than 3 the decrease in local richness. For the small system size used in the simulations (5×5) 4 patches), this increase in β diversity is not always sufficient to make up for decreases in 5 local richness; consequently metacommunity richness can also decrease due to both mutu-6 alistic and antagonistic interactions. However, as system size increases in the simulations, 7 metacommunity richness becomes less affected by bi-trophic interactions (Fig. S3A). This 8 means that animals do not act to filter the same plant species in every patch, thereby 9 increasing the spatial structure of plant diversity. Indeed, when computing the relative 10 fecundity of plant species in each patch, we find that 63% (56%) of the plant species are 11 positively filtered in at least one patch by the mutualistic (antagonistic) animal group 12 (see SI Section S2.10). These results suggest that bi-trophic interactions tend to strongly 13 impact the spatial heterogeneity of plant diversity. 14



Fig. S2: Relative variation (in %) of plant β diversity between trophically coupled and uncoupled communities. β diversity is measured as the ratio of metacommunity over local plant richness S_p^m/S_p . Panels A and D display a threshold model of interaction with one trait; panels B and E show results for the matching model with one trait and $\sigma = 0.015$; panels C and F are based on a matching model with one trait and $\sigma = 1$. Panels A-C correspond to mutualistic interactions. Panels D-F correspond to antagonistic interactions. Parameter values are $\mu_p = \mu_a = 0.004$, $m_a = 0.625$, $c_a = 0.16$.

¹ S2.3 Effects of the model parameters on the impact of bi-trophic ² interactions

As mentioned in the main text, mutualistic and antagonistic interactions can have both positive and negative effects on plant richness S_p , but also on Shannon's diversity H_p . We explore the effects of each model parameter and interaction type by multiple regressions (Tables S1-4). In these regressions, the dependent variable is the relative variation in species richness due to the bi-trophic interactions: $\Delta S_p = \left(S_p^i - S_p^n\right)/S_p^n$, and $\Delta H_p = \left(H_p^i - H_p^n\right)/H_p^n$, where the superscript *i* means with interaction, and *n* without interaction.

Less diverse, more dispersal-limited, and more strongly impacted plant sets are experiencing a stronger filter from both mutualistic and antagonistic interactions: plant dispersal rates m_p and μ_p are positively correlated with variations in plant Shannon's index ΔH_p , while the interaction impact on plants c_p is negatively correlated with ΔH_p (Tables S3-4). Parameter effects are less straightforward when looking at variation in plant species richness ΔS_p (Tables S1-2), probably because they impact plant diversity patterns at both local and metacommunity scales, and these patterns have contradictory effects on local plant persistence (see below). Parameters of the animal set have overall a lower effect on plant composition.

- ¹ Table S1: Effect of mutualistic interactions on the variation in plant species richness
- ² ΔS_p .
- ³ *the first (second) number is the number of matching (threshold) rules.
- $_{\textbf{4}} \quad R^{\textbf{2}}=0.52$

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Parameter	Estimate	Standard Error	<i>p</i> -value
Intercept	-0.08	0.002	$<\!2e-16$
μ_p	5.06	0.18	<2e-16
μ_a	3.11	0.18	<2e-16
m_p	-0.09	0.001	<2e-16
m_a	-0.03	0.001	<2e-16
c_p	-0.53	0.001	<2e-16
c_a	0.09	0.001	<2e-16
$Model_{1-0*}$	-0.12	0.002	$<\!2e-16$
$Model_{0-2^*}$	-0.13	0.002	$<\!2e-16$
Model_1-1*	-0.25	0.002	<2e-16
$Model_{2-0*}$	-0.19	0.002	$<\!2e-16$
$Model_{1-2^*}$	-0.33	0.002	$<\!2e-16$
$Model_{2-1*}$	-0.30	0.002	$<\!2e-16$
$Model_{2-2*}$	-0.37	0.002	$<\!2e-16$
σ	0.04	0.0001	<2e-16

- ¹ Table S2: Effect of antagonistic interactions on the variation in plant species richness
- ² ΔS_p .
- *the first (second) number is the number of matching (threshold) rules.
- $_{4}$ $\mathrm{R}^{\mathbf{2}}=0.12$

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Parameter	Estimate	Standard Error	p-value
Intercept	-0.17	0.007	< 2e-16
μ_p	-17.87	0.73	< 2e-16
μ_a	9.01	0.73	
m_p	-0.38	0.005	< 2e-16
m_a	-0.04	0.005	6e-13
c_p	0.09	0.09 0.003	
C_a	0.14	0.003	< 2e-16
$Model_{1-0*}$	0.27	0.007	< 2e-16
$Model_{0-2^*}$	-0.43	0.009	< 2e-16
$Model_{1-1*}$	-0.39	0.007	< 2e-16
$Model_{2-0*}$	0.14	0.007	< 2e-16
$Model_{1-2^*}$	-0.56	0.007	< 2e-16
$Model_{2-1*}$	-0.37	0.007	<2e-16
$Model_{2-2*}$	-0.51	0.007	<2e-16
σ	0.06	0.0004	<2e-16

Table S3: Effect of mutualistic interactions on the variation in plant equitability ΔH_p .

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- ² *the first (second) number is the number of matching (threshold) rules.
- $\mathbf{R^2}=0.49$
- 4

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Parameter Estimate Standard Error *p*-value Intercept -0.070.002 <2e-16 <2e-16 14.150.19 μ_p < 2e-161.960.19 μ_a $\overline{<2e}$ -16 0.0010.06 m_p <2e-16 -0.03 0.001 m_a -0.470.001 <2e-16 c_p 0.08 0.001< 2e-16 c_a Model 1-0*-0.19 0.002 <2e-16 Model $0-2^{*}$ -0.13 0.002 <2e-16 Model 1-1* -0.30 <2e-16 0.002Model 2-0*-0.290.002 <2e-16 Model $1-2^*$ -0.390.002< 2e-16-0.38 Model 2-1* 0.002< 2e-16 $2-2^*$ Model -0.450.002< 2e-16<2e-16 0.05 0.0001 σ

- Table S4: Effect of antagonistic interactions on the variation in plant equitability ΔH_p .
- ² *the first (second) number is the number of matching (threshold) rules.
- $\mathbf{R^2}=0.33$
- 4

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Parameter Estimate Standard Error *p*-value Intercept -0.36 0.002 <2e-16 18.71 0.23 $<\!2e-16$ μ_p 0.31-0.240.23 μ_a $\overline{<2e}$ -16 0.0020.03 m_p <2e-16 -0.03 0.002 m_a -0.400.001 <2e-16 c_p 0.070.001< 2e-16 c_a Model 1-0*0.32 0.002 <2e-16 Model $0-2^{*}$ -0.08 0.003 <2e-16 Model 1-1* -0.07<2e-16 0.002Model 2-0*0.26 0.002 <2e-16 Model $1 - 2^*$ -0.080.002 $<\!2e-16$ Model 2-1* -0.040.002< 2e-16 $2-2^*$ Model -0.04 0.002< 2e-16<2e-16 0.01 0.0001 σ

¹ S2.4 Coupling Test

Animals have two opposite effects on plant assemblages. Individually, they have a filtering
effect by introducing fitness differences among species. But collectively, they have a stabilizing effect by introducing some kind of heterogeneity in resources (6). The emergent
effect of the interactions thus depends on the relative importance of these two counteracting effects.

We introduce a statistic (IS) that measures the average interaction strength between
plants and animals:

$$IS = \frac{\sum_{i,j} I_{ij}}{S_p S_a},\tag{S1}$$

where I_{ij} indicates the interaction strength between plant *i* and animal *j*. Before starting 9 the dynamics with bi-trophic interactions, we compute the initial interaction strength IS^n 10 between plants and animals. To do this, we use plant and animal abundances obtained 11 with neutral assembly and I_{ij} values subsequently used in the dynamics with interactions. 12 At the end of the dynamics with interactions (100 generations forward), we compute the 13 final interaction strength IS^i between plants and animals, using final abundances of plants 14 and animals. We record the variation of the interaction strength $\Delta IS = IS^i - IS^n$ due 15 to the dynamics with bi-trophic interactions. When interactions are mutualistic and 16 their impact on plants is dominated by the filtering effect, plants survive only if they 17 encounter some well-adapted mutualists. Interactions should thus produce an increase of 18 the statistics IS. For antagonistic interactions, on the contrary, plants survive only if they 19 do not encounter well-adapted antagonists, and the statistics IS should then decrease. If 20 our interpretation is correct, then ΔS_p should be negatively (positively) correlated with 21 ΔIS when interactions are mutualistic (resp. antagonistic). This is what we observed 22

1 (R² = 0.02 and 0.03 respectively, p < 0.001). Note that IS is not correlated with S_p and 2 H_p , hence the correlation observed here is not spurious.

³ S2.5 Variance Test

To measure the stabilizing effect of the bi-trophic interactions, we use the statistic VT4 which measures the average variance in trait values among plant individuals, the average being done among the t traits involved in the interactions. The stabilizing effect should produce an increase in VT. If our interpretation is correct, then ΔS_p should be positively 7 correlated with ΔVT . A possible confounding effect, though, is that VT is positively cor-8 related with S_p and H_p . Hence, this dependence of VT should be taken into account when 9 testing for a correlation between ΔVT and ΔS_p . To do this, we fit a multiple linear regres-10 sion of VT^n against S_p^n and H_p^n using the simulated non-interacting communities. We then 11 use this fitted regression to predict VT_{fit}^i based on the values of S_p^i and H_p^i observed in the 12 interacting communities. We then define a modified $\Delta VT = \left(VT_{observed}^{i} - VT_{fit}^{i}\right)/VT_{fit}^{i}$. 13 Using this conservative statistic, we find a positive correlation between ΔVT and ΔS_p 14 $(R^2 = 0.56 \text{ and } 0.10 \text{ respectively}, p < 0.001).$ 15

¹⁶ S2.6 Equitability Test

Hillebrand et al. (8) meta-analyzed herbivore exclusion experiments, and found that herbivory was reducing (increasing) plant species richness when equitability in plant abundances (measured by H' = H/ln(S)) was high (low). We found the same negative relationship between the equitability before the interactions $H'^n = H_p^n/ln(S^n)$ and ΔS_p (R² = 0.007 and 0.019 respectively, p<0.001), and this relationship was stronger for antagonistic and generalized interactions (i.e., matching interaction rule with one or two traits, and $\sigma>1$, R² = 0.008 and 0.09 respectively, p<0.001).

¹ S2.7 Effect of network richness on the impact of bi-trophic inter-² actions

We also investigate the effect of species richness at both the local patch, and the (landscape) metacommunity on the variation in plant species richness by linear regressions. As mentioned in the main text, larger metacommunity richness is associated with stronger positive effect of both mutualistic and antagonistic interactions on plant species richness, while larger local richness is associated with stronger negative effect of both interaction types ($\mathbb{R}^2 = 0.01, p < 0.001$).

⁹ S2.8 Temporal turnover

As mentioned in the main text, two statistics of temporal turnover in species composition from one generation to the next have been computed for both plants and animals, in both uncoupled and coupled metacommunities. The first statistic is the Jaccard index of similarity J and is computed as follows:

$$J = \frac{\sum_{i} I(n_{i}^{t} > 0) I(n_{i}^{t-1} > 0)}{\sum_{i} I(n_{i}^{t} + n_{i}^{t-1} > 0)},$$
(S2)

where n_i^t is the number of individuals of species *i* at generation *t*, and I(n > 0) equals 1 if n > 0 and 0 otherwise.

The second statistic is an abundance-weighted version of the Jaccard index and is computed as follows:

$$J_q = \frac{\sum_i I(n_i^t > 0) I(n_i^{t-1} > 0) (n_i^t + n_i^{t-1})}{\sum_i (n_i^t + n_i^{t-1})},$$
(S3)

Larger J and J_q values indicate a lower temporal turnover.

¹⁹ We investigate how variations in community equitability due to bi-trophic interactions

are correlated with variations in the temporal turnover of communities due to these same 1 bi-trophic interactions. Temporal turnover is measured with the Jaccard index of similar-2 ity across time steps (J) and its abundance-weighted version (J_q) . Since these statistics 3 are correlated with H_p in non-interacting communities, variations in H_p due to the interactions could mechanically cause variations in J and J_q , without any real effect of bi-trophic interactions on the way community composition varies with time. We hence fit two linear 6 regressions of J^n and J^n_q against H^n_p using the simulated non-interacting communities. We 7 then use this fitted regression to predict J^i_{fit} and $J^i_{q_{fit}}$ based on the values of H^i_p observed 8 in the interacting communities. We then define a modified $\Delta J = \left(J_{observed}^i - J_{fit}^i\right)/J_{fit}^i$ 9 and a modified $\Delta J_q = (J^i_{q_{observed}} - J^i_{q_{fit}})/J^i_{q_{fit}}$. Using these conservative statistics, we 10 find a positive correlation between ΔJ and ΔH_p for both mutualistic and antagonistic 11 interactions (R² = 0.44 and 0.35 respectively, p < 0.001), and between ΔJ_q and ΔH_p (R² 12 = 0.72 and 0.02 respectively, p < 0.001). Since J and J_q measure temporal similarity, this 13 means that in communities experiencing a stronger filter from the bi-trophic interactions 14 (lower ΔH_p), temporal turnover will be larger than expected if bi-trophic interactions 15 were not modifying community dynamics. In such communities, a core of plant species 16 are temporally stabilized by the interactions, while a subset of species become satellites 17 which are temporally unstable (10). 18

¹⁹ S2.9 Interactions mostly affect rare species

Mutualists and antagonists principally affect the presence and abundance of rare plant species. When comparing coupled and uncoupled plant communities, the abundanceweighted measure of similarity J_q is larger than the unweighted measure J in 97% (resp. 95%) of the cases for mutualistic (resp. antagonistic) interactions.

¹ S2.10 Interactions produce a spatially heterogeneous filter

At the end of the coupled metacommunity dynamics, we test whether the filtering effect 2 of the animal set on the plant one is homogeneous across space. To do this, we compute 3 the relative fecundity of each plant species in each patch. The relative fecundity of plant 4 species i equals $f_i^p / \sum_k \frac{n_k^p}{N_p} f_k^p$. For each plant species, we count the number of patches where 5 its relative fecundity is above 1, meaning that it obtains a local competitive advantage 6 due to bi-trophic interactions. We find that 63% (56%) of the plant species are positively 7 filtered in at least one patch due to mutualistic (antagonistic) interactions. To perform 8 this analysis, we used a large grid of 20×20 patches, and a subset of parameter values: μ_p 9 and μ_a in {0.0005; 0.004}, m_p and m_a in {0.005; 0.625}, c_p and c_a in {0.04; 0.64}. We only 10 considered interaction rules with one trait, using either a threshold rule or a matching rule 11 with σ in {0.015;1}. We performed 10 replicates per combination of parameters values. 12

¹³ S2.11 Robustness of the results

¹⁴ S2.11.1 Effect of the number of patches used in the simulations

To perform this computer intensive study, we used a relatively small number of patches: 15 a grid of $l \times l$ patches, with l = 5. We performed additional simulations with l = 10, 16 and l = 20 for a subset of parameter values: $\mu_p = \mu_a = 0.005$, m_p in {0.001; 0.005; 17 $0.025; 0.125; 0.625\}, m_a \text{ in } \{0.005; 0.625\}, c_p \text{ in } \{0.01; 0.04; 0.16; 0.64; 1\}, \text{ and } c_a = 0.01.$ 18 For these simulations, we only considered interaction rules with one trait, using either 19 a threshold rule, or a matching rule with σ in {0.015; 0.125; 1; 8}. We performed 10 20 replicates per combination of parameters values, and computed in each simulation the 21 variation in plant metacommunity richness due to bi-trophic interactions ΔS_p^{met} , and the 22 variation in local plant richness ΔS_p . As the number of patches in the metacommunity 23 increases, the distribution of ΔS_p^{met} converges to zero (Fig. S3A). On the contrary, system 24

size has little impact on the variation in local plant richness due to bi-trophic interactions
(Fig. S3B). This means that for large (and realistic) system sizes, bi-trophic interactions
have a weak effect on metacommunity richness, but change local richness patterns, and
hence the spatial structure of plant diversity.

⁵ We additionally performed correlations between ΔS_p and ΔH_p in these simulations ⁶ with larger l, and the statistics ΔS_p , and ΔH_p of the main text. We computed the ⁷ correlations \mathbb{R}^2 , as well as the slopes and intercepts of reduced major axis regressions, ⁸ using the R package "smatr" (11). Correlations were high $(R \ge 0.91)$, intercepts close to ⁹ 0 ($|intercept| \le 0.062$), and slopes close to 1 ($|slope - 1| \le 0.081$).



Fig. S3: Effect of system size on bi-trophic impact. Panel A: Distribution of ΔS_p^{met} as a function of the number l * l of patches in the simulations. Panel B: Distribution of ΔS_p as a function of the number l * l of patches in the simulations.

¹ S2.11.2 Symmetric model of interaction

We evaluated the sensitivity of our results to the way we modeled the plants' impact on their interactors. We considered alternative models of mutualistic and antagonistic interactions, replacing Eq. (2) in the main text by:

$$f_i^a = (1 - c_a) + c_a \frac{\sum_{j=1}^{S_p} n_j^p I_{ji}}{\sum_{k=1}^{S_a} \left(\frac{n_k^a}{N_a} \sum_{l=1}^{S_p} n_l^p I_{lk}\right)}.$$
 (S4)

⁵ We performed the same simulation analysis of these two models on a subset of the ⁶ parameter grid: we used the same subset as for the analysis studying the variation in ⁷ number of patches. We computed the same statistics ΔS_p and ΔH_p , which summarize ⁸ the way interactions affect community composition. For these calculations, community ⁹ statistics were averaged over the 10 simulated replicates. For each of these statistics, we ¹⁰ computed the correlations R² between their values in the these symmetric models, and ¹¹ their values in the models reported in the main text, as well as the slopes and intercepts of reduced major axis regressions. Correlations were high $(R \ge 0.95)$, intercepts close to $(|intercept| \le 0.062)$, and slopes close to 1 $(|slope - 1| \le 0.051)$.

³ S2.11.3 Variation in community size

We evaluated the robustness of our results to variations in the animal group sizes N_a . 4 We considered the alternative values $N_a = 40$, and $N_a = 1000$. We performed the same 5 simulation analysis as in the main text, on a subset of the parameter grid: we used the 6 same subset as for the analysis studying the variation in number of patches. We computed 7 the same statistics ΔS_p and ΔH_p , which summarize the way interactions affect community 8 composition. For these calculations, community statistics were averaged over the 10 9 simulated replicates. For each of these statistics, we computed the correlations \mathbf{R}^2 with 10 the simulations of the main text, as well as the slopes and intercepts of reduced major axis 11 regressions. Correlations were high $(R \ge 0.89)$, intercepts close to 0 ($|intercept| \le 0.072$), 12 and slopes close to 1 ($|slope - 1| \le 0.124$). 13

¹⁴ S2.11.4 Variation in boundary conditions

We evaluated the robustness of our results to boundary conditions. We considered two 15 alternative conditions: a reflexive condition, where migrants crossing the boundary return 16 to their patch of origin; and a condition where migrants crossing the boundary are lost. We 17 performed the same simulation analysis as in the main text, on a subset of the parameter 18 grid: we used the same subset as for the analysis studying the variation in number of 19 patches. We computed the two statistics ΔS_p and ΔH_p . For each of these statistics, we 20 computed the correlations \mathbb{R}^2 with the simulations of the main text, as well as the slopes 21 and intercepts of reduced major axis regressions. Correlations were high $(R \ge 0.95)$, 22 intercepts close to 0 ($|intercept| \le 0.024$), and slopes close to 1 ($|slope - 1| \le 0.046$). 23

¹ S3 Model results - impact on the animal set

We performed similar analyses, focusing this time on the effect of bi-trophic interactions 2 on the animal set. Overvall, we found very similar results. The analogue of Fig. 2 for 3 animals is reported in Fig. S4, while the analogue of Fig. S2 is reported in Fig. S5. By 4 comparing Fig. 2 and Fig. S4, one can note that the main differences is that herbivores are 5 more positively impacted than plants by bi-trophic interactions when they are specialized 6 (Panel D in Fig.2, panel E in Fig. S4), while this is the opposite when interactions are 7 generalized (Panels F in the two figures). Indeed, when they are specialized, herbivores 8 feed on different plant species and thereby easily coexist (12), while for plants, another 9 effect is at stake: although herbivore feeding have a stabilizing effect (13), specialized 10 herbivores also induce fitness differences among species, while generalized herbivores have 11 a more equalized effect. 12

The coupling test (see Section S2.4) provides coherent results. When animals are neg-13 atively filtered by bi-trophic interactions, the average interaction strength IS increases 14 for both mutualists and antagonists ($R^2 = 0.07$ and 0.02 respectively, p < 0.001): only 15 the more interacting animals are surviving. The variance test (see Section S2.5) is also 16 providing coherent results: when animals are positively impacted by bi-trophic interac-17 tions, their trait variance increase in both mutualistic and antagonistic cases ($R^2 = 0.11$ 18 and 0.005 respectively, p < 0.001). As for plants, larger animal metacommunity richness is 19 associated with more positive bi-trophic effect, while we observe the opposite correlation 20 with animal local richness in both mutualistic and antagonistic cases ($R^2 = 0.08$ and 0.0321 respectively, p < 0.001, see Section S2.7). Temporal similarity in animal composition (mea-22 sured by J and J_q) is also positively correlated with animal equitability H_a , as we had 23 observed for plants ($\mathbf{R}^2 = 0.0001$ and 0.0001 respectively for J and $\mathbf{R}^2 = 0.001$ and 0.000124

1 for J_q , p<0.001, see Section S2.8). Finally, bi-trophic interactions are also mostly impact-2 ing rare animal species: when comparing coupled and uncoupled animal communities, the 3 abundance-weighted measure of similarity J_q is larger than the unweighted measure J in 4 97% (92%) of the cases for mutualistic (antagonistic) interactions (see Section S2.9).



Fig. S4: Relative variation (in %) of animal α diversity between trophically coupled and uncoupled communities. α diversity is measured as the local animal species richness S_a . A positive value means that trophically coupled communities are species-richer than uncoupled ones. Different panels show results for the threshold model with one trait (A and D), the matching model with one trait and $\sigma = 0.015$ (B and E), and the matching model with one trait and $\sigma = 1$ (C and F). Panels A-C correspond to mutualistic interactions, while panels D-F correspond to antagonistic interactions. Parameter values are $\mu_p = \mu_a = 0.004, m_p = 0.625, c_p = 0.16$.



Fig. S5: Relative variation (in %) of animal β diversity between trophically coupled and uncoupled communities. β diversity is measured as the ratio of metacommunity over local animal richness S_a^m/S_a . Panels A and D display a threshold model of interaction with one trait; panels B and E show results for the matching model with one trait and $\sigma = 0.015$; panels C and F are based on a matching model with one trait and $\sigma = 1$. Panels A-C correspond to mutualistic interactions. Panels D-F correspond to antagonistic interactions. Parameter values are $\mu_p = \mu_a = 0.004, m_p = 0.625, c_p = 0.16$.

¹ S4 Application to real datasets

² S4.1 Approximate Bayesian Computation (ABC) procedure

Since the effects of the interactions depend on the interaction rules used (Tables S1-4),
and given that not all interaction rules lead to realistic ecological networks (14), we want
to constrain our simulation results so that they use realistic network structure. To fit
observed networks, we use Approximate Bayesian Computation (15). It consists here in
six steps (see Fig. 1 in the main text).

First, we simulate a neutral uncoupled metacommunity of plants and animals to serve
as a benchmark to quantify bi-trophic impact on the plant set, drawing at random all
the model parameters in uniform prior distributions. Prior distributions express our

¹ uncertainty on the parameters values before confronting them to real data.

Second, starting from this neutral metacommunity, we simulate a coupled dynamics of
plants and animals using Eqs. (1) and (2) of main text, choosing one of the 8 interaction
rules in turn, and drawing at random all the additional model parameters (linked to the
interaction) in uniform prior distributions. The prior distributions were tailored to each
dataset so as to reduce computing time. Indeed, only some areas of the parameter space
are likely to produce networks similar to the observed ones. The priors used for each
dataset are reported in Table S5.

⁹ Third, at the end of the dynamics, a network of interactions is simulated with the ¹⁰ same total number of interactions N_n^{obs} as in the real dataset. N_n^{obs} animals are drawn ¹¹ at random proportionally to their local abundance, and they are simulated to interact ¹² with one of the plant species. An animal *j* interacts with a plant *i* proportionally to $n_i^p I_{ij}$ ¹³ where I_{ij} is computed with the model parameters used in the simulation.

Fourth, four summary statistics of the simulated networks are computed: the plant species richness in the network S_p^s , the animal species richness in the network S_a^s , the nestedness index Ne_p , and the specialization index ϕ .

Fifth, the computed network statistics of the simulations are used to select the best-fit simulations. The simulations are retained if both $|S_p^s - S_p^{obs}| \leq 5$ and $|S_a^s - S_a^{obs}| \leq 5$, and the simulation procedure goes on until a total of 2000 such simulations are produced. Out of these 2000 simulations, 200 are retained which statistics ϕ , and Ne_p lead to the smallest Euclidean distance to the observed values (ϕ^{obs}, Ne_p^{obs}) . Each statistic is normalized before performing this selection (15).

Sixth, these retained simulations are used to compute the approximate posterior distribution of the statistics ΔS_p , ΔH_p , ΔJ , and ΔJ_q , which describe the impact of the interactions on plant composition and dynamics. A large part of the variation in the posterior distribution of these statistics is explained by the variation among the simulations of the two model parameters m_p and c_p . Therefore, approximate posterior distributions are plotted as a function of these two parameters (see the section "Predicted effect of the interactions in real networks based on best-fit simulations" below). ¹ Table S5: Priors used for the Approximate Bayesian Computation.

² $ln(m_p)$ is always drawn in $[\ln(0.001); \ln(0.2)]$. $ln(c_p)$ is always drawn in $[\ln(0.01); \ln(1)]$.

 $_{\texttt{3}}$ $ln\left(\sigma\right)$ is always drawn in $[\ln(0.01)\ ;\ \ln(10)].$

4

Datasets		Priors			
Code	Interaction Type	Citation	$ln\left(\mu_{p} ight)$	$ln\left(\mu_{a} ight)$	$ln\left(m_{a} ight)$
ARIZ	Pollination	Arizmendi and Ornelas (1990)	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.011)]$	$[\ln(0.001) ; \ln(0.2)]$
BAHE♣	Pollination	Barrett and Helenurm (1987)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.1002) ; \ln(0.5)]$	$[\ln(0.001) ; \ln(0.2)]$
BAUE	Pollination	Bauer (1983)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0005); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
BEZE	Pollination	Bezerra et al. (2009)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.018)]$	$[\ln(0.001) ; \ln(0.2)]$
BRIA	Pollination	Brian (1957)	$[\ln(0.0002) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.01)]$	$[\ln(0.001) ; \ln(0.2)]$
BRHO	Pollination	Brown and Hopkins (1995)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0002) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
DIHI♠	Pollination	Dicks et al. (2002)	$\left[\ln \left(0.0002 \right) \; ; \; \ln \left(0.007 \right) \right]$	$\left[\ln \left(0.01 \right) \; ; \; \ln \left(0.02 \right) \right]$	$[\ln(0.11); \ln(0.2)]$
DISH♠	Pollination	Dicks et al. (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$\left[\ln\left(0.002\right)\;;\;\ln\left(0.02\right)\right]$	$[\ln(0.11); \ln(0.2)]$
ELBE♣	Pollination	Elberling and Olesen (1999)	$[\ln(0.0015) ; \ln(0.018)]$	$[\ln(0.47); \ln(0.6)]$	$[\ln(0.001) ; \ln(0.2)]$
HARD	Pollination	Harder (1985)	$[\ln(0.0001) ; \ln(0.02)]$	$\left[\ln\left(0.0001\right)\;;\;\ln\left(0.013\right)\right]$	$[\ln(0.001) ; \ln(0.2)]$
MACI	Pollination	Macior (1978)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.015)]$	$[\ln(0.001) ; \ln(0.2)]$
MEMM♣	Pollination	Memmott (1999)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0252); \ln(0.239)]$	$[\ln(0.001); \ln(0.19)]$
OLLE♣	Pollination	Ollerton et al. (2003)	$[\ln(0.0001) ; \ln(0.013)]$	$[\ln(0.0074); \ln(0.02)]$	$[\ln(0.051) ; \ln(0.2)]$
SCHM [♣]	Pollination	Schemske (1978)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0036); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
SNOW	Pollination	Snow and Snow (1972)	$[\ln(0.0002) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.012)]$	$[\ln(0.001) ; \ln(0.2)]$
$VAZ1^{\clubsuit}$	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0011); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
VAZ2 [♣]	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.011)]$	$[\ln(0.0018); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
VAZ3 [♣]	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
VAZ4 [♣]	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0017); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
$VAZ5^{\clubsuit}$	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0007) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
VAZ6 [♣]	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
VAZ7 [♣]	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0007) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
VAZ8 [♣]	Pollination	Vazquez and Simberloff (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0009) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
HELG	Arbuscular Mycorrhizal Fungi	Helgason et al. (2002)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
OPIO	Arbuscular Mycorrhizal Fungi	Opik et al. (2008)	$[\ln(0.0001) ; \ln(0.018)]$	$[\ln(0.001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
OPIY	Arbuscular Mycorrhizal Fungi	Opik et al. (2008)	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.0008); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
WU15	Arbuscular Mycorrhizal Fungi	Wu et al. (2007)	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
WU16	Arbuscular Mycorrhizal Fungi	Wu et al. (2007)	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
JOSW	Endophytic Fungi	Joshee et al. (2009)	$[\ln(0.0001); \ln(0.01)]$	$[\ln(0.006) ; \ln(0.02)]$	$[\ln(0.01); \ln(0.2)]$
JOSS	Endophytic Fungi	Joshee et al. (2009)	$[\ln(0.0001); \ln(0.01)]$	$[\ln(0.0014); \ln(0.02)]$	$[\ln(0.018); \ln(0.2)]$
MUTD	Endophytic Fungi	Murali et al. (2007)	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.0005); \ln(0.02)]$	$[\ln(0.001); \ln(0.2)]$

MUTW	Endophytic Fungi	Murali et al. (2007)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0006) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
MUDD	Endophytic Fungi	Murali et al. (2007)	$[\ln(0.0001) ; \ln(0.019)]$	$[\ln(0.0009) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
MUDW	Endophytic Fungi	Murali et al. (2007)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0012) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
PETR	Endophytic Fungi	Petrini (1984)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0003); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
SURB	Endophytic Fungi	Suryanarayanan et al. (2005)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.019)]$	$[\ln(0.001) ; \ln(0.2)]$
SURC	Endophytic Fungi	Suryanarayanan et al. (2005)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.019)]$	$[\ln(0.001) ; \ln(0.2)]$
SURD	Endophytic Fungi	Suryanarayanan et al. (2005)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.01)]$	$[\ln(0.001) ; \ln(0.2)]$
SUTJ	Endophytic Fungi	Sutjaritvorakul et al. (2010)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
BACH*	Herbivory	Basset and Charles (2000)	$[\ln(0.0001) ; \ln(0.006)]$	$[\ln(0.4001); \ln(0.6)]$	$[\ln(0.003) ; \ln(0.2)]$
$BASA^{\diamondsuit}$	Herbivory	Basset and Samuelson (1996)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.006) ; \ln(0.02)]$	$[\ln(0.035) ; \ln(0.2)]$
BERK	Herbivory	Berkov and Tavakilian (1999)	$[\ln(0.0001) ; \ln(0.017)]$	$[\ln(0.0015); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
HANS	Herbivory	Hansen and Ueckert (1970)	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.014)]$	$[\ln(0.001) ; \ln(0.2)]$
$JANZ^{\diamondsuit}$	Herbivory	Janzen (1980)	$[\ln(0.006) ; \ln(0.199)]$	$[\ln(0.1108); \ln(0.5)]$	$[\ln(0.012) ; \ln(0.5)]$
JOEA*	Herbivory	Joern (1979)	$[\ln(0.0002) ; \ln(0.02)]$	$[\ln(0.0003); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
JOEM [♣]	Herbivory	Joern (1979)	$[\ln(0.0003); \ln(0.02)]$	$[\ln(0.0007) ; \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
JOER	Herbivory	Joern (1985)	$[\ln(0.0004); \ln(0.02)]$	$[\ln(0.0013); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
$_{NA96}$	Herbivory	Nakagawa et al. (2003)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0005); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
$_{NA98}$	Herbivory	Nakagawa et al. (2003)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0012); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
NOMI	Herbivory	Novotny et al.(2005a)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.017)]$	$[\ln(0.001) ; \ln(0.2)]$
NOVO♦	Herbivory	Novotny et al.(2005b)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0006); \ln(0.02)]$	$[\ln(0.001) ; \ln(0.2)]$
OTTE	Herbivory	Otte and Joern (1977)	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.0001); \ln(0.019)]$	$[\ln(0.001) ; \ln(0.2)]$
SHEL	Herbivory	Sheldon and Rogers (1978)	$[\ln(0.0001) ; \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.014)]$	$[\ln(0.001) ; \ln(0.2)]$
$UECK^{\diamondsuit}$	Herbivory	Ueckert and Hansen (1971)	$[\ln(0.0001); \ln(0.02)]$	$[\ln(0.0001) ; \ln(0.019)]$	$[\ln(0.001) ; \ln(0.2)]$

- ¹ Datasets found in the Interaction Web Database (http://www.nceas.ucsb.edu/interactionweb/).
- ² Datasets found in Ref. (16).
- $^{\circ}$ Datasets found in Ref. (17).
- *For this dataset, we used in the simulations $J_p=2000$, $J_a=400$ because S_p is larger
- 5 than 200.

¹ S4.2 Predicted effect of the interactions in real networks based ² on best-fit simulations

The information available in the data was not sufficient to fully parameterize our meta-3 community model, and hence to precisely quantify the effect of bi-trophic interactions on plant and animal richness in these datasets. It was however sufficient to greatly constrain our simulations, so that general trends could be evidenced. We illustrate this with an 6 example dataset (BEZE, see Table S5). This dataset was chosen because it contains the 7 largest number of recorded interactions. The limits of our inference approach that we are 8 pointing here are thus also happening in the other datasets. Thanks to the ABC proce-9 dure, some parameters are relatively well inferred in that they have a reasonably peaked 10 posterior distribution: μ_p , μ_a and σ (Fig. S6A,B,D). All the interaction rules are rep-11 resented in the retained simulations (Fig. S6C), which mean that the observed network 12 structure can be reproduced in multiple ways. Note that this explains the presence of two 13 peaks in the posterior distribution of parameter σ : the peak of low σ value is obtained in 14 models without threshold rules, while the other peak is obtained when one or two thresh-15 old rules are modeled on top of the matching rules. The four remaining parameters m_p , 16 m_a, c_p and c_a are less well inferred by our procedure in that they have wider posterior 17 distribution hence a large remaining uncertainty on parameters values (Fig. S6E-H). The 18 variance in these parameters values explained a large proportion of the variance of ΔS_p 19 and ΔS_a observed in the simulations. More precisely, variations in m_p and c_p were highly 20 correlated with variations in ΔS_p in the simulations, while variations in m_a and c_a were 21 highly correlated with variations in ΔS_a . This is the reason why we plot our predictions 22 regarding the bi-trophic impact on plants (animals) ΔS_p (ΔS_a) as a function of m_p and 23 c_p (m_a and c_a) in Figs. 2, S2, S4 and S5. 24

We used a kriging technique to interpolate ΔS_p as a function of m_p and c_p (R library

"fields", (18)). This interpolation explained on average 70% (64%, 45%) of the variance 1 for plants-pollinators datasets (plant-fungi, plant-insect herbivores). Similarly, the inter-2 polation of ΔS_a as a function of m_a and c_a explained on average 33% (40%, 30%) for 3 plants-pollinators datasets (plant-fungi, plant-insect herbivores). We represent in Figs. 4 11- S16 the krigged values of ΔS_p and ΔS_a predicted by the simulations fitted to each S 5 dataset. In Fig. 3, these predictions are averaged for each dataset type (plant-pollinators, 6 plants-fungi, and plants-insect herbivores). Similar results for ΔH , ΔJ , ΔJ_q , and $\Delta S^m/S$ 7 are reported in Figs. S7-S10. The temporal similarity is expected to decrease for an-8 tagonistic interactions; the same happens for mutualistic interactions only for realistically 9 strong coupling $(c_p \text{ and } c_a \geq 0.03)$ (Fig. S8). When using the abundance-weighted 10 measure of turnover J_q , the temporal similarity is predicted to be weakly affected by 11 bi-trophic interactions (Fig. S9). Overall, our results hence suggest that the temporal 12 turnover in plant and animal sets should be larger due to bi-trophic interactions, this 13 being due mainly to an increased turnover of rare species. 14

All simulations were performed in C++, and statistical analyses with the R software (R development Core Team 2009).



Fig. S6: Approximate posterior distribution of the model parameters. Panels A-B: approximate posterior distribution for parameters μ_p and μ_a . Panel C: posterior weight of the different interaction rules. The length of each square side is proportional to the number of retained simulations with the corresponding number of matching and threshold rules. Panel D: approximate posterior distribution for parameters m_p , m_a , c_p and c_a .



Fig. S7: Relative variation of plant and animal Shannon's index H between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets (n=23). Panels B and E: Plant-fungi datasets (n=16). Panels C and F: Plant-insect herbivores datasets (n=15). 41% of the variance is explained by the interpolation on average in each dataset.



Fig. S8: Relative variation of plant and animal temporal similarity J between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets (n=23). Panels B and E: Plant-fungi datasets (n=16). Panels C and F: Plant-insect herbivores datasets (n=15). 21% of the variance is explained by the interpolation on average in each dataset.



Fig. S9: Relative variation of plant and animal temporal similarity J_q between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets (n=23). Panels B and E: Plant-fungi datasets (n=16). Panels C and F: Plant-insect herbivores datasets (n=15). 33% of the variance is explained by the interpolation on average in each dataset.



Fig. S10: Relative variation of plant and animal β diversity S^m/S between coupled and uncoupled communities in simulations which best fit observed network structure in real datasets. Panels A-C: results for plants. Panels D-F: results for animals. Panels A and D: Plant-pollinators datasets (n=23). Panels B and E: Plant-fungi datasets (n=16). Panels C and F: Plant-insect herbivores datasets (n=15). 31% of the variance is explained by the interpolation on average in each dataset.



Fig. S11: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-pollinator datasets.



Fig. S12: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-fungi datasets.



Fig. S13: Relative variation of plant species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-insect herbivores datasets.



Fig. S14: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-pollinator datasets.



Fig. S15: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-fungi datasets.



Fig. S16: Relative variation of animal species richness between coupled and uncoupled communities in simulations which best fit observed network structure in real plant-insect herbivores datasets.

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