

Sampling

Study sites are shown on Fig. S1 and the characteristics of each site are given in Table S1; they are part of the REPHY monitoring network by Ifremer coastal laboratories (REPHY, 2017). The mean temperature in each site mostly depended on its latitude, reflecting the climate of the region, while salinity in one site could be considered as a proxy for evaporation and terrestrial inputs from rivers.

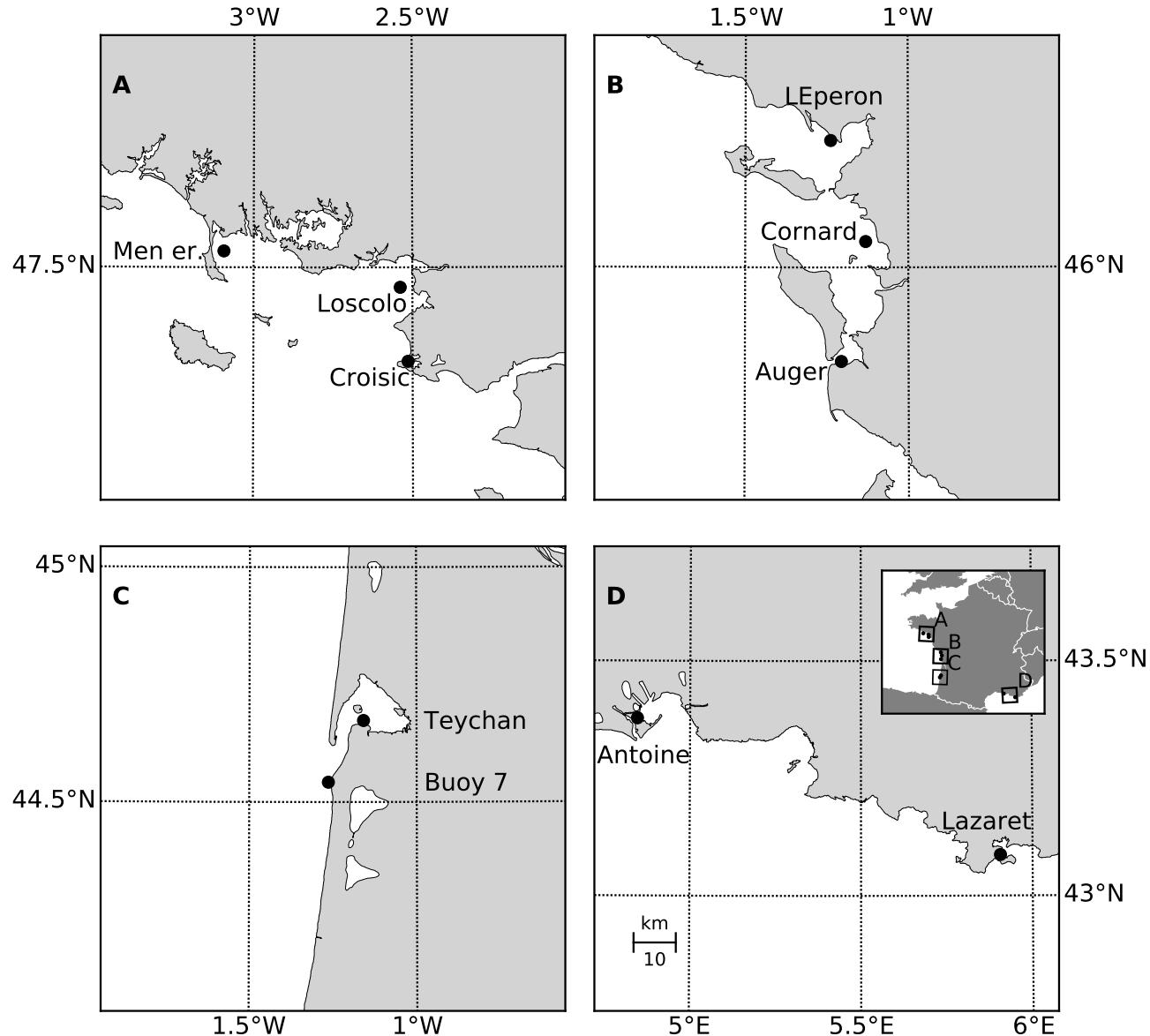


Figure S1: Location of each study site in their region: Brittany (A), Oléron (B), Arcachon (C) and the Mediterranean Sea (D). The common scale of the panels is given in the left corner of D.

At each site, water samples were collected below surface (between 0 and 1m depth) in a Niskin bottle, from which 10mL were taken for phytoplanktonic counts. We focus on phytoplanktonic taxa between 20 and 200 μm , the

so-called microphytoplankton fraction (Reynolds, 2006). The scaling between the volume sampled and the size of individual organisms means that approximately up to 1000 cells could be lined up (in a thought experiment) along one single dimension of an equivalent cubic sample. In other words, the volume sampled is approximately 1000 body sizes to the power three. We therefore consider samples to be representative of local community competition, if not of the spatial structure of the community.

Name of site	Location	Region	N. samples	Temperature (°C)	Salinity (g/L)
Men Er Roue	47°32' N / 3°5' W	Brittany	503	14.4 +/- 3.7	33.5 +/- 1.9
Loscolo	47°27' N / 2°32' W	Brittany	463	14.9 +/- 4.0	32.0 +/- 3.0
Croisic	47°18' N / 2°30' W	Brittany	500	14.7 +/- 3.9	31.8 +/- 3.1
L'Eperon	46°16' N / 1°14' W	Oléron	460	15.3 +/- 4.8	32.1 +/- 3.2
Cornard	46°3' N / 1°7' W	Oléron	491	15.6 +/- 4.8	32.7 +/- 2.4
Auger	45°47' N / 1°12' W	Oléron	524	15.4 +/- 4.4	32.7 +/- 1.8
Buoy 7	44°32' N / 1°15' W	Arcachon	311	15.2 +/- 3.8	34.7 +/- 0.7
Teychan	44°40' N / 1°9' W	Arcachon	494	15.5 +/- 4.6	32.5 +/- 1.9
Antoine	43°22' N / 4°50' E	Mediterranean Sea	539	16.8 +/- 5.1	32.3 +/- 3.9
Lazaret	43°5' N / 5°54' E	Mediterranean Sea	512	17.4 +/- 4.2	35.9 +/- 2.4

Table S1: **Summary of the study site characteristics**, including the mean and standard deviation of the two main environmental parameters (temperature and salinity).

Phytoplankton dynamics

Code	Taxa
AST	<i>Asterionella+Asterionellopsis+Asteroplanus</i>
CHA	<i>Chaetoceros</i>
CRY	<i>Cryptophytes</i>
DIT	<i>Ditylum</i>
EUG	<i>Euglenophytes</i>
GUI	<i>Guinardia</i>
GYM	<i>Gymnodinium+Gyrodinium</i>
LEP	<i>Leptocylindrus</i>
NIT	<i>Nitzschia+Hantzschia</i>
PLE	<i>Pleurosigma+Gyrosigma</i>
PRO	<i>Prorocentrum</i>
PRP	<i>Protoperidinium+Archaeoperidinium+Peridinium</i>
PSE	<i>Pseudo-nitzschia</i>
RHI	<i>Rhizosolenia+Neocalyptrella</i>
SCR	<i>Scrippsiella+Ensicalifera+Pentapharsodinium+Bysmatrum</i>
SKE	<i>Skeletonema</i>
THL	<i>Thalassionema+Lioloma</i>
THP	<i>Thalassiosira+Porosira</i>

Table S2: **Name and composition of the phytoplanktonic groups used in main text**, based on the work by Hernández Fariñas *et al.* (2015)

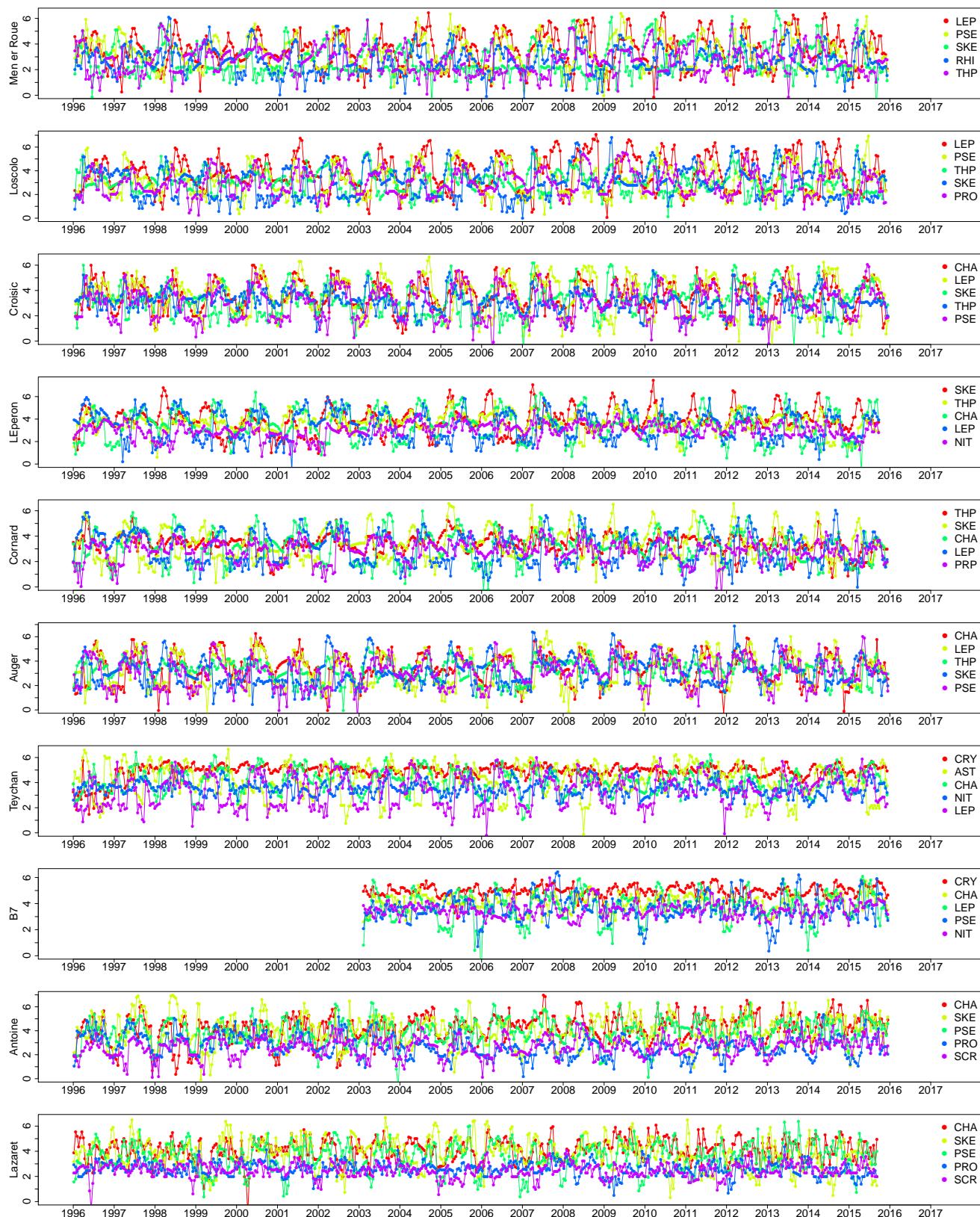


Figure S2: Time series of the 5 most abundant phytoplanktonic genera in each site.

MAR(1) models

We selected the most parsimonious interaction matrices using BIC. Not only the best-ranking model, but also the overall ranking of interaction scenarios were similar for most sites (Fig. S3). Based on these results, we considered the model selection to be quite robust, and focused on the pennate-centric scenario to analyze interaction matrices, as this scenario corresponded to the best fitted models that still allowed interactions between groups.

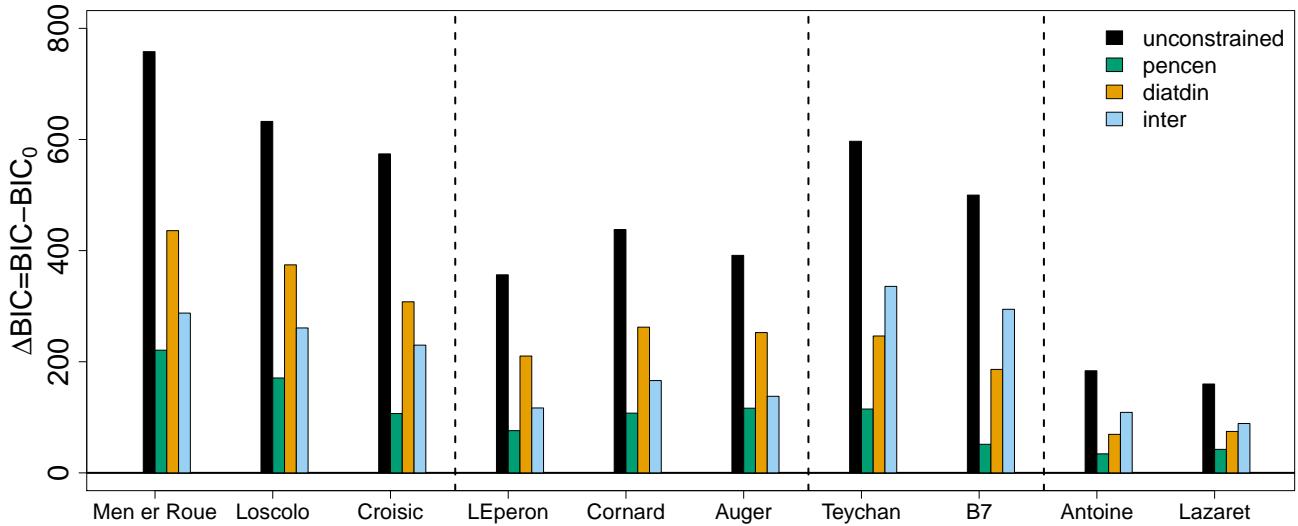


Figure S3: **Comparison of the BIC of different interaction scenarios**, compared to the null scenario (diagonal interaction matrix, allowing only intragroup interactions), for 10 sites in 4 different regions, separated by dashed lines (Brittany, Oléron, Arcachon and the Mediterranean Sea). Different interaction matrices may allow interactions between all taxa (unconstrained), only interactions within pennate diatoms, centric diatoms, dinoflagellates, or other phytoplanktonic taxa (pencent), only interactions within diatoms, dinoflagellates or other taxa (diatdin), or only interactions between taxa belonging to these different groups (inter). As data structures (length of the times series) are different between sites and regions, groups of bars should not be compared.

We inspected the Hessian matrices (i.e., Hessians of the negative log-likelihood which is the observed Fisher Information Matrix) for interaction parameters in order to check that results presented in Fig. 3 of the main text could not be due to statistical constraints. Correlation matrices (derived from the Hessian matrices) showed that the mean absolute value of the correlation was 0.02 (hence on average there were no correlations), few of those were noticeable (75% were below 0.1 in only 1 site, even lower in the 9 other sites) and even the very few large ones were never above 0.5 in absolute value.

In addition to the coefficients of the interaction matrix, MAR(1) models allowed us to estimate the effect of environmental variables. The regression coefficients reveal abiotic effects such as phenology (temperature, related to insolation) or responses to hydrological changes such as salinity variation (Fig. S4). Overall, temperature tended to have more effect on phytoplankton dynamics than salinity, which was logical since it integrates seasonal variation in received solar energy. The absolute effect of temperature was on average 3.5 times higher than salinity effects and temperature coefficients were significant at the 95% threshold for 68% of all estimates, as opposed to 16% for salinity effects. Temperature had a positive effect in 80% of the cases while salinity had a negative effect for 66% of all estimates. The sign of significant temperature effects on a given species remained the same between regions, except for SKE, which was negatively affected by temperature in Brittany and Oléron but positively affected by temperature in the Mediterranean Sea.



Figure S4: Effect of environmental variables (temperature, TEMP or salinity, SAL) on phytoplankton genera in Brittany (a, b), Oléron (c, d), Arcachon (e, f) and in the Mediterranean Sea (g, h). Each color corresponds to a different site. Error bars correspond to the 95% confidence interval around the estimated coefficient. All variables were normalized before estimation.

Network analysis

Interaction types

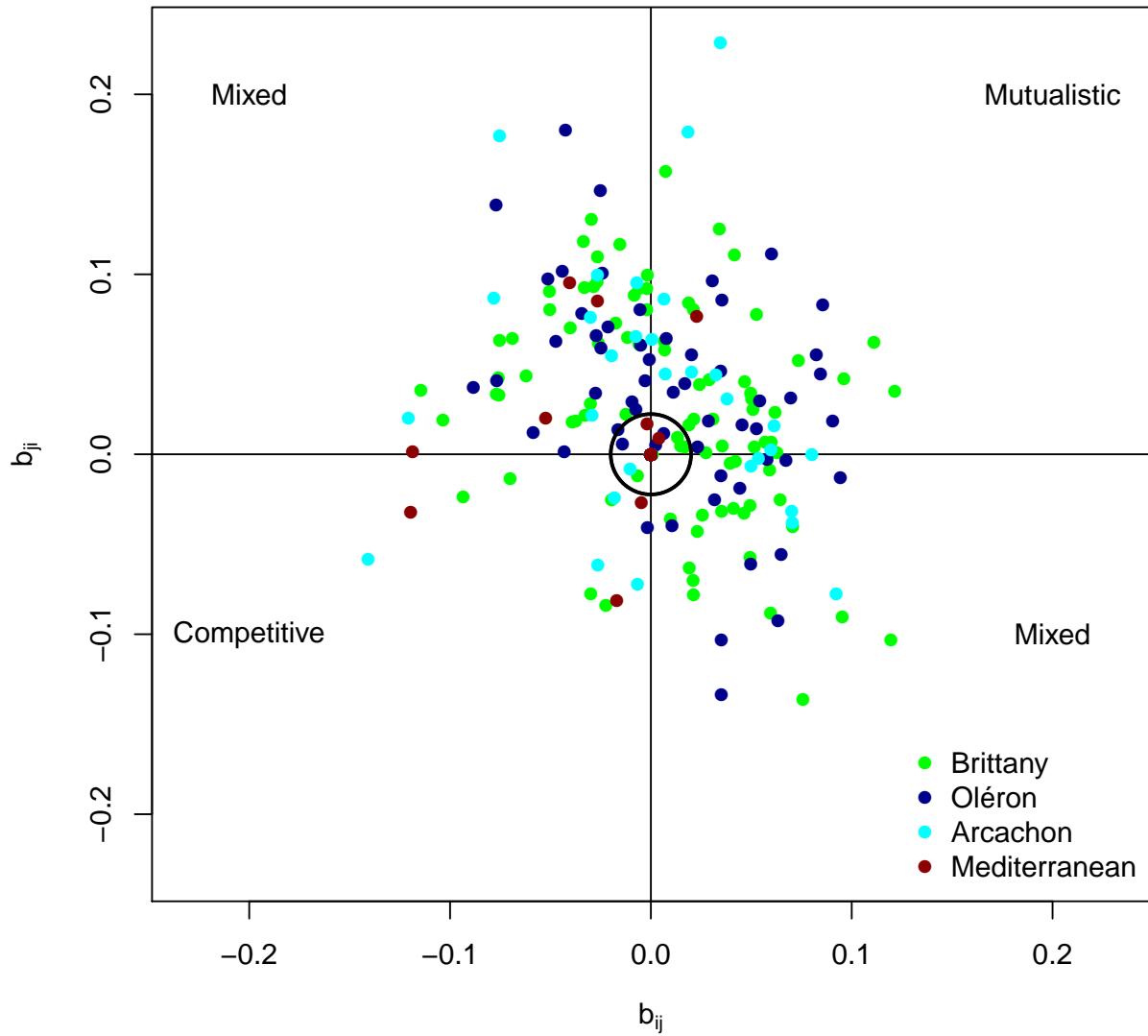


Figure S5: Pairs of coefficients for each study site. The effect of species i on j is given as a function of the effect of species j on species i . The black circle indicates the first quartile of the interaction values, under which we can assume that the effect is weak or null. Below this limit, $(+/+)$, $(+/-)$ or $(-/+)$ interactions can translate into commensalism or amensalism. Above, they can be respectively mutualistic or mixed $(+/-)$ links.

Metrics

We characterised each interaction network with 4 quantitative descriptors: the mean and variance of the intra- and intergenus coefficients (i.e., on and off the matrix diagonal) and the linkage density and weighted connectance of **B-I**. The mean of absolute values of intragenus coefficients was approximately 8 times higher than the mean of the absolute values of the effect of intergenus interactions. The intragenus interactions' variance was about 4 times higher than the variance of intergenus interactions (Fig. S6).

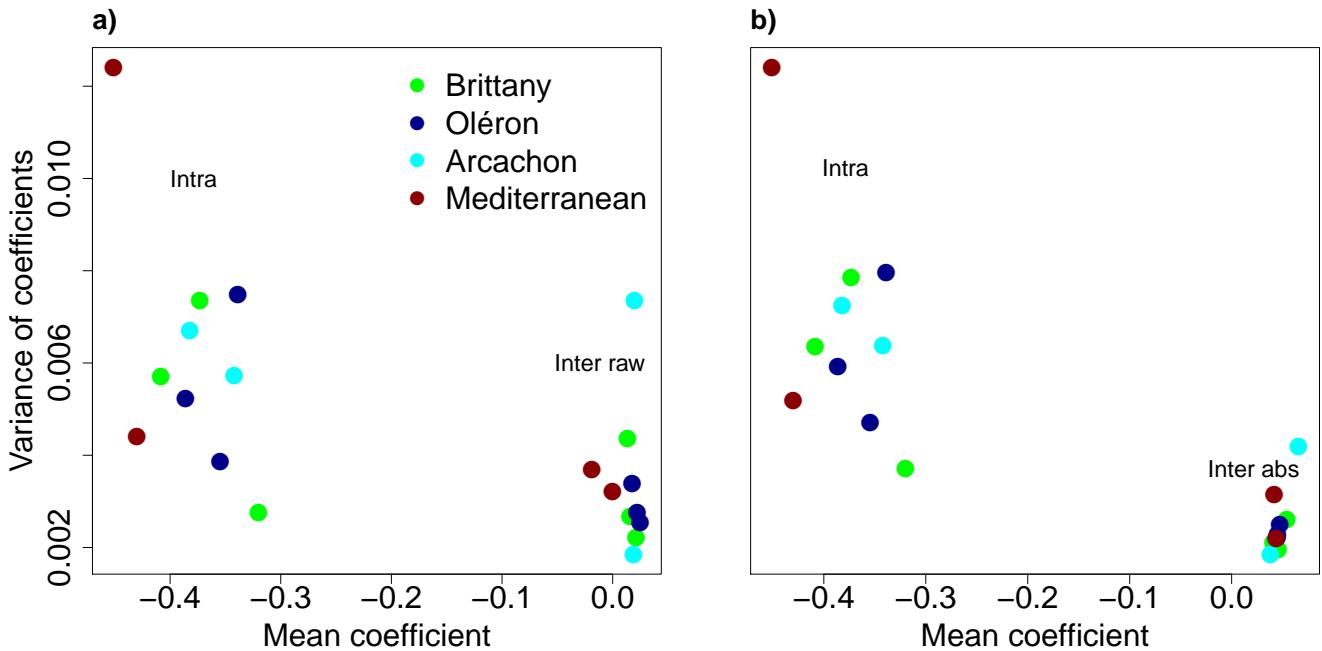


Figure S6: Relation between mean and variance of the intra- and intergenus interaction coefficients. The variance of the coefficients in the interaction matrix ($\mathbf{B}-\mathbf{I}$) increases with the mean, for 10 sites in 4 regions, with a model allowing interactions only within clads (within centric or pennate diatoms, dinoflagellates, or other taxa). The mean-variance relation was either computed with raw values of intergroup interactions (a) or absolute values of the intergroup coefficients (b). We did not take the absolute value of intragroup coefficients since they were all negative.

The intragenus interaction strength could be related to the mean abundance of each genus as the most self-regulated genera were also the least abundant (Fig. S7).

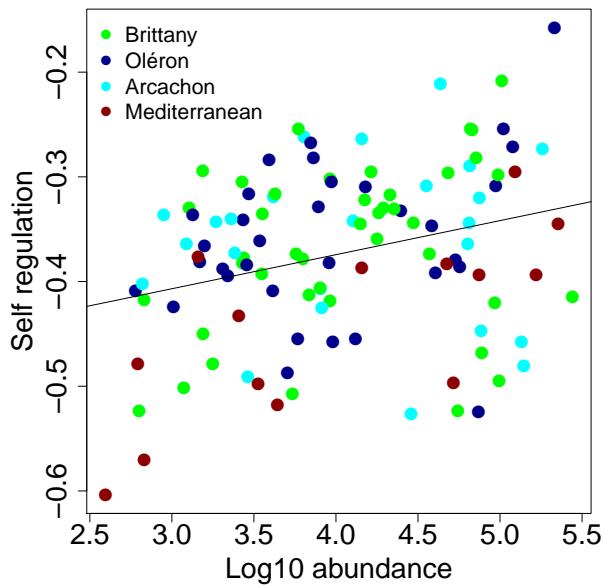


Figure S7: Relation between abundance and self-regulation (intragenus interaction coefficients). Mean abundance is computed for each genus in each site and intragenus interaction strengths are the diagonal coefficients of the interaction matrix ($\mathbf{B}-\mathbf{I}$).

Weighted connectance is described in [Bersier et al. \(2002\)](#). It is based on the average of vulnerability and

generality in the network. More precisely, diversity measures of the interactions from ($H_{P,k}$) and to ($H_{N,k}$) the phytoplanktonic group k can be computed as:

$$H_{N,k} = - \sum_{i=1}^S \frac{b_{ik}}{b_{\cdot k}} \log_2 \left(\frac{b_{ik}}{b_{\cdot k}} \right) \quad (\text{S1})$$

$$H_{P,k} = - \sum_{i=1}^S \frac{b_{ki}}{b_{k\cdot}} \log_2 \left(\frac{b_{ki}}{b_{k\cdot}} \right) \quad (\text{S2})$$

where b_{ik} is a coefficient of the interaction matrix ($\mathbf{B-I}$), $b_{k\cdot} = \sum_{i=1}^S b_{ki}$ is the sum of all coefficients over row k and S is the number of species in the network. These indices are then averaged for the whole network as the linkage density LD (eq. S3).

$$LD = \frac{1}{2} \left(\sum_{k=1}^S \frac{b_{\cdot k}}{b_{\cdot\cdot}} 2^{H_{N,k}} + \sum_{k=1}^S \frac{b_{k\cdot}}{b_{\cdot\cdot}} 2^{H_{P,k}} \right) \quad (\text{S3})$$

where $b_{\cdot\cdot} = \sum_{j=1}^S \sum_{i=1}^S b_{ji}$ is the sum of all coefficients of the interaction matrix ($\mathbf{B-I}$). Weighted connectance C is then defined as:

$$C = \frac{LD}{S} \quad (\text{S4})$$

Contrary to linkage density, weighted connectance accounts for the dimension of the interaction matrix and can be used to compare network in different regions, with different dimensions.

In addition to this network-level metric, we also considered metrics for each phytoplanktonic group. We measured both its vulnerability (mean strength of the interactions that are applied to a group, eq. S5) and its impact (mean strength of the interactions the group applies to other groups, eq. S6) in each network.

$$v_k = \frac{1}{\mathbf{1}_{b_{ki} \neq 0}} \sum_{i=1}^S b_{ki} \quad (\text{S5})$$

$$e_k = \frac{1}{\mathbf{1}_{b_{ik} \neq 0}} \sum_{i=1}^S b_{ik} \quad (\text{S6})$$

where $\mathbf{1}_{b_{ki} \neq 0}$ is the number of interactions which are different from 0 in row k .

Comparison with a full interaction matrix

We checked that, by choosing the model with the lowest BIC, we did not miss interactions which would have changed our conclusions. To do so, we examined the full (unconstrained) model results for all study sites. We present those results below (Fig. S8 and Table S3).

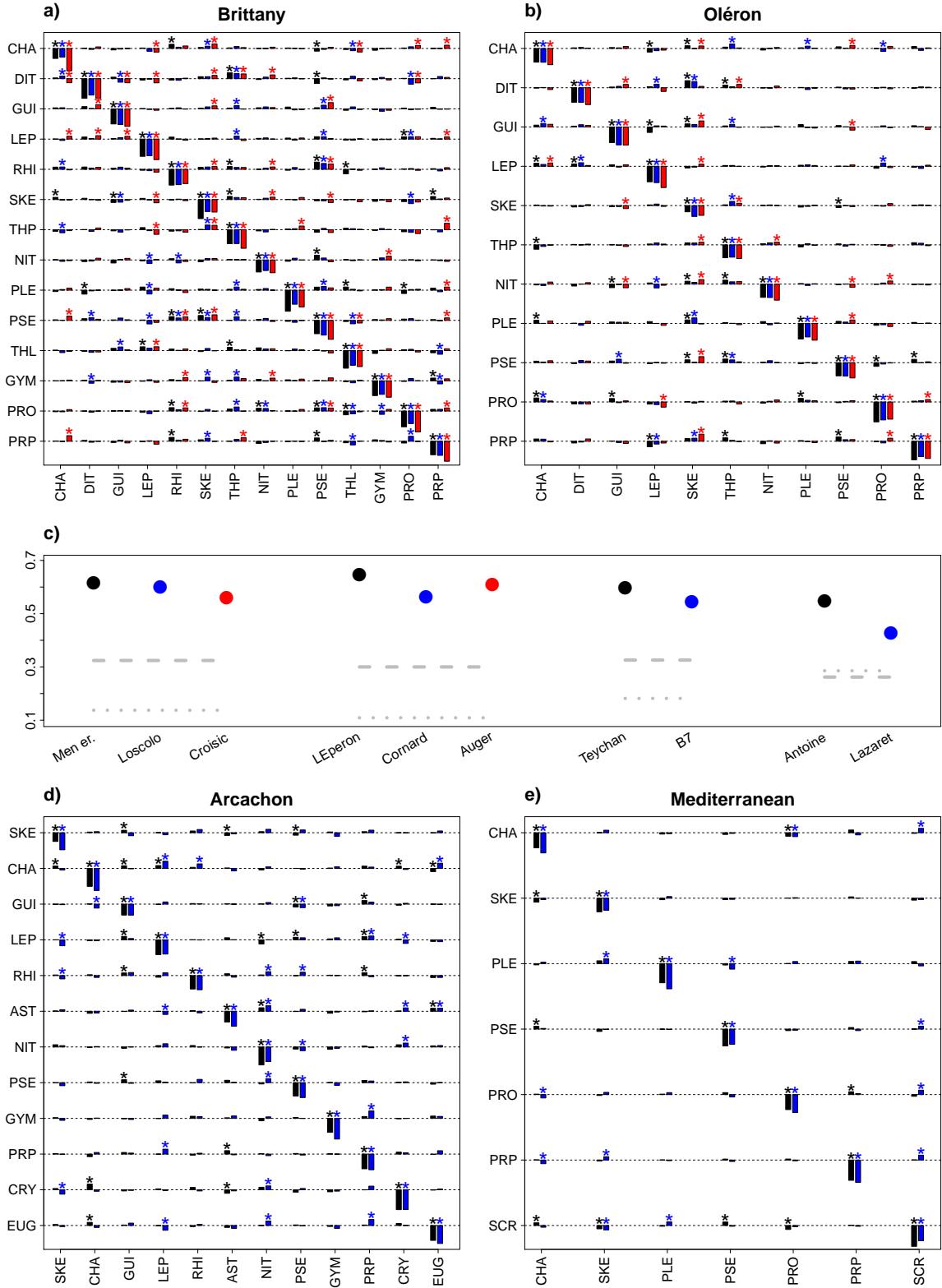


Figure S8: Interaction matrices estimated in 10 sites along the French coastline. Four regions are distinguished: Brittany (a), Oléron (b), Arcachon (d) and the Mediterranean Sea (e). There is no constraint on the structure (modularity) of the interaction matrices. The fraction of positive interactions in each matrix is given by points in c) while the dashed (resp., dotted) line represents the ratio of interactions remaining positive (resp., negative) for all sites of a given region.

	signif outside	positive	ratio intra/inter	ratio in/out block	transfo sign
Men er Roue	0.09	0.57	11.06	3.03	0.04
Loscolo	0.14	0.56	8.42	2.65	0.07
Croisic	0.13	0.52	10.15	2.89	0.09
LEperon	0.13	0.59	8.78	2.75	0.04
Cornard	0.08	0.51	10.32	3.64	0.06
Auger	0.07	0.55	9.66	3.10	0.06
Antoine	0.10	0.47	11.18	5.21	0.00
Lazaret	0.18	0.37	8.67	4.30	0.00
Teychan	0.11	0.55	10.46	3.68	0.14
B7	0.11	0.50	8.29	3.59	0.14

Table S3: Descriptors of coefficients in unconstrained interaction matrices and comparison to best-fitting pennate-centric structures: ratio of coefficients significantly different from 0 outside of the pennate-centric blocks vs total number of coefficients in the unconstrained matrix, proportion of positive interactions in the unconstrained matrix, ratio of mean intragroup interaction strength and mean intergroup interaction strength in the unconstrained matrix, ratio of mean interaction strength inside the pennate-centric modules vs outside the pennate-centric modules in the unconstrained matrix and proportion of interactions changing sign between the two structures.

Thus, even if we chose to select the full interaction model, there would be no difference in our main conclusions: intragenus interactions are much stronger than intergenus interactions and positive interactions are still the rule. There is at most 18% of interactions significantly different from zero outside of the pennate and centric blocks and those interactions are on average 3.5 times lower than the interactions inside the pennate and centric blocks (Table S3).

MAR references and analysis

We present here the MAR references we used to compare the effects of intra- and intergroup interactions (Table S4, Fig. S9). We add information on the biome and taxa used in the study as they tend to be linked to the estimated parameters (Fig. S10). We should mention two potential biases associated with this comparison across the published literature. First, low-dimensional matrices tended to be more complete (less sparse) than high-dimensional matrices, as these small interaction matrices were used to study known interaction phenomena (observed predation between organisms, for instance). In fact, we add pairs of predator and prey mainly to give a scale to the plot. Conversely, the number of parameters to estimate increases as the square of the number of interacting taxa, leading most authors to reduce this set before the estimation process for large interaction matrices. There is therefore a positive correlation between sparsity and dimensionality (Fig. S10). A second caveat is that while we informed our model selection by phylogeny, several authors have instead reduced the number of estimated parameters by an automated procedure, usually based on the comparison of hundreds of randomly chosen interaction matrices by AIC (Ives *et al.*, 1999). The latter choice is likely to bias high non-zero interactions in the literature. This is why we decided to present in the main text intra/inter ratios including interspecific (or intergroup) coefficients set to zero (see Fig. 4 in the main text), which should be less sensitive to the model selection method and therefore make comparisons across studies possible. In Fig. S9, mean interaction strengths were computed as the mean absolute value of only the set of coefficients which were deemed significant at the 95% threshold in the (**B**–**I**) matrix.

Code	Ref	Dimension	Type of organisms	Taxonomic level	System	T
1a	Ives <i>et al.</i> (1999), CLS	9	Zooplankton	Species and functional groups	Lake	100
1b	Ives <i>et al.</i> (1999), TLS	9	Zooplankton	Species and functional groups	Lake	100
2a	Klug <i>et al.</i> (2000)	2	Phytoplankton	Phylum	Lake	100
2b	Klug <i>et al.</i> (2000)	3	Zooplankton	Species	Lake	50
3a	Klug & Cottingham (2001)	4	Functional groups of plankton	NA	Lake	300
3b	Klug & Cottingham (2001)	5	Taxonomic groups of plankton	Phylum/division	Lake	300
4a	Ives <i>et al.</i> (2003)	4	Plankton	Zooplankton v. phytoplankton, size classes	Lake	100
4b	Ives <i>et al.</i> (2003)	4	Plankton	Zooplankton v. phytoplankton, size classes	Lake with high planktivory	100
4c	Ives <i>et al.</i> (2003)	4	Plankton	Zooplankton v. phytoplankton, size classes	Lake with low planktivory	100
5a	Hampton & Schindler (2006)	14	Plankton	Phylum (phytoplankton), genus (zooplankton)	Lake	300
5b	Hampton & Schindler (2006)	14	Plankton, growing season	Phylum (phytoplankton), genus (zooplankton)	Lake	200
6a	Hampton <i>et al.</i> (2006)	13	Plankton	Phylum (phytoplankton), genus (zooplankton)	Lake	400
6b	Hampton <i>et al.</i> (2006)	7	Simpler web, plankton	Phylum (phytoplankton), genus (zooplankton)	Lake	400
7a	Huber & Gaedke (2006)	10	Ciliates	Genus and species	Lake	300
7b	Huber & Gaedke (2006)	10	Phytoplankton	Genus and species	Lake	300
8a	Yamamura <i>et al.</i> (2006)	3	Insects	Species	Terrestrial	50
9a	Vik <i>et al.</i> (2008)	2	Lynx/Hare	Species	Terrestrial	100
10a	Lindegren <i>et al.</i> (2009)	3	Fish	Species	Baltic Sea	30
11a	Griffiths <i>et al.</i> (2015)	7	Phytoplankton	Phylum	Coastal site	1000
11b	Griffiths <i>et al.</i> (2015)	7	Phytoplankton	Phylum	Offshore site	700
12a	Barraquand <i>et al.</i> (2018)	12	Phytoplankton	Genus	Outside a bay	300
12b	Barraquand <i>et al.</i> (2018)	12	Phytoplankton	Genus	Inside a bay	500

Table S4: Studies used when comparing $|\text{intra}|/|\text{inter}|$ ratios in Fig. 4 in main text. T is the approximate number of sampling dates in each time series.

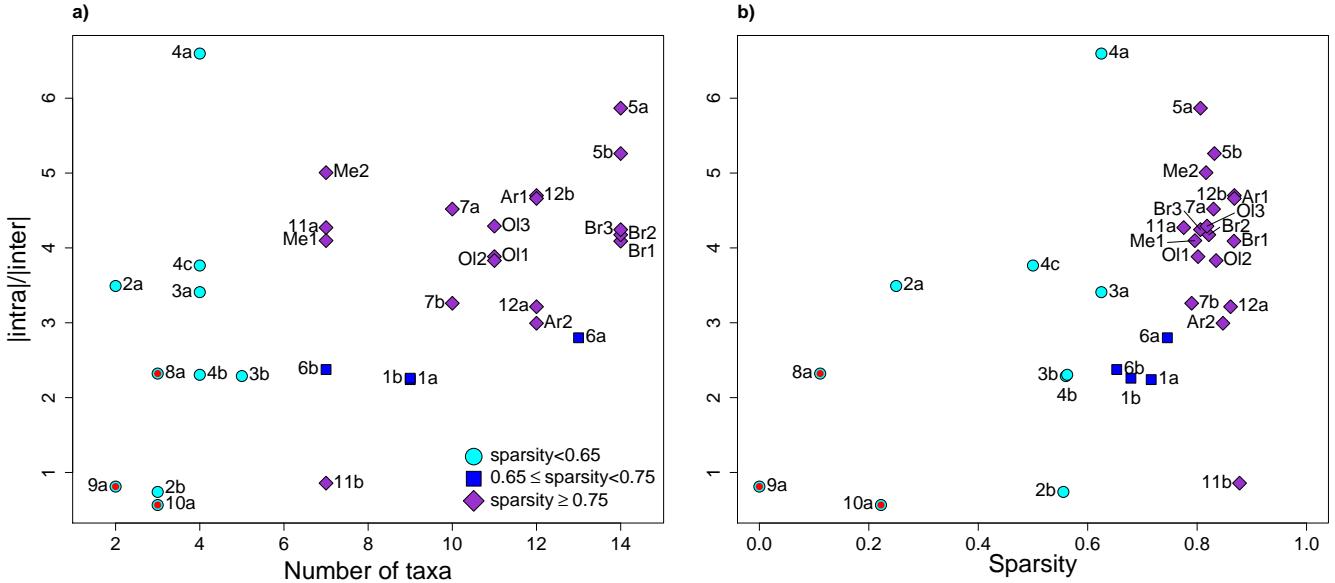


Figure S9: **Ratio of intra-to-intergroup interaction strength in MAR(1) studies.** Only significant values are taken into account and missing values in the matrix are not considered (e.g., not replaced by 0 as they are in the main text). The color and shape of each point are a function of the sparsity of the interaction matrix $\mathbf{B} - \mathbf{I}$ and the relation between the ratio and the sparsity of the matrix is given in the right panel. Red dots correspond to terrestrial and/or low dimension, predator-prey systems, giving a lower bound for the intra/inter ratio. Corresponding studies are described in Table S4.

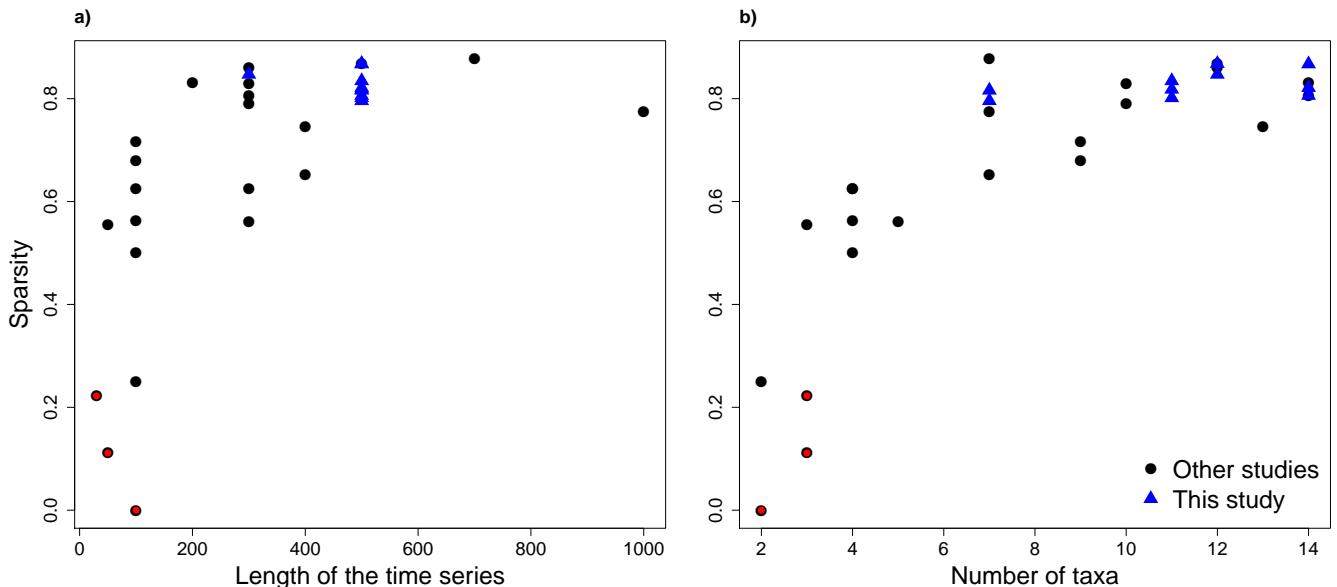


Figure S10: **Relation between interaction sparsity and study design** in studies described in Table S4. Red dots correspond to terrestrial and/or low dimension, predator-prey systems, giving a lower bound for the intra/inter ratio. Blue triangles correspond to the present study.

Connection to continuous-time models

The relation between complexity and stability in community model has been a debate in coexistence studies for decades (May, 1972). In the ecology field, the Random Matrix Theory to which we compare our data-based results has been mostly developed on continuous-time interaction models (Allesina & Tang, 2015). Here, we intend to connect discrete- and continuous-time models. The discrete log-linear model writes $\mathbf{x}_{t+1} = \mathbf{B}\mathbf{x}_t$ in the main text. This model can only approximate continuous-time dynamics (the equation $d\mathbf{x} = \mathbf{A}\mathbf{x}dt$, where \mathbf{A} is the continuous-time interaction matrix, would be closer) but there are at least two ways to relate these dynamics.

The first approach is to linearize continuous-time dynamics and integrate the system over time. In this case, the log-abundance evolution from one time-step to the other can be written $\mathbf{x}_{t+1} = e^{\mathbf{A}}\mathbf{x}_t$. In this case, the discrete-time equivalent of the community matrix \mathbf{A} is $\log(\mathbf{B})$ where \mathbf{B} is the matrix we present in the main text.

The second approach is to first integrate a continuous-time model over a time-step and then linearize the system. In this case, $\mathbf{A} \approx \mathbf{B} - \mathbf{I}$.

Moreover, the measure of resilience differs in discrete- and continuous-time models. In discrete-time models, and therefore in this study, resilience is measured as the maximum modulus of the eigenvalues of the community matrix ($\max(|\lambda_B|)$), also called the dominant eigenvalue. In continuous-time models, resilience is linked to the maximum real part of the eigenvalues ($\max(\text{Re}(\lambda_A))$), also called the leading eigenvalue. There is therefore a link to be made between these metrics. We present here the relation between resilience metrics $\max(|\lambda_B|) = f(\max(\text{Re}(\lambda_A)))$ (Fig. S11) to make sure our results are robust to the approximations described above.

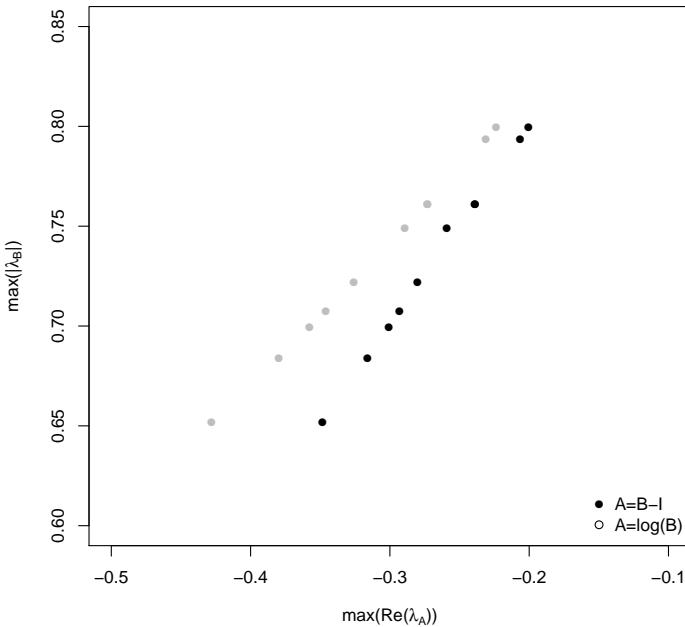


Figure S11: Relation between the dominant eigenvalue for \mathbf{B} (discrete time, on the y-axis) and leading eigenvalue for $\mathbf{A} = \mathbf{B} - \mathbf{I}$ and $\log(\mathbf{B})$ (continuous time, on the x-axis)

We see in Fig. S11 that:

- leading eigenvalues of \mathbf{A} s are similar for $\mathbf{A} = \mathbf{B} - \mathbf{I}$ and $\mathbf{A} = \log(\mathbf{B})$ (the difference is around 0.04 for values between -0.45 and -0.2)
- the dominant eigenvalue of \mathbf{B} is strongly correlated to the leading eigenvalue of $\mathbf{A} = \mathbf{B} - \mathbf{I}$ and $\mathbf{A} = \log(\mathbf{B})$ (> 0.99 in both cases)

We therefore consider our results on the absence of relation between stability and complexity to be robust to variations in model formulations.

Connection to Lotka-Volterra competition dynamics

The Beverton-Holt multispecies competition model, whose variants are widely used for modelling plant community dynamics (Levine & HilleRisLambers, 2009; Kraft *et al.*, 2015), is the closest discrete time equivalent to the continuous-time Lotka-Volterra model (see Cushing *et al.* 2004; although the mapping is not perfect for $n \geq 3$, Roeger & Allen 2004). The Beverton-Holt multispecies competition model writes

$$N_{i,t+1} = \frac{e^{r_i} N_{i,t}}{1 + \sum_j \alpha_{ij} N_{j,t}} \quad (\text{S7})$$

where $N_{i,t}$ is the abundance of species i at time t , r_i is its growth rate and α_{ij} is the effect of species j on species i . Here, we show how the interaction strengths α_{ij} map to those of the MAR(1) models used in the main text.

We start with a 2 species model for simplicity, and we note the equilibrium values of species 1 and 2 as N_1 and N_2 (without time subscript). We re-write the model at equilibrium.

$$\begin{cases} R_1 = \alpha_{11}N_1 + \alpha_{12}N_2 \\ R_2 = \alpha_{21}N_1 + \alpha_{22}N_2 \end{cases}, \text{with} \quad \begin{cases} R_1 = e^{r_1} - 1 \\ R_2 = e^{r_2} - 1 \end{cases} \quad (\text{S8})$$

$$\Leftrightarrow \begin{cases} \alpha_{21}R_1 = \alpha_{21}\alpha_{11}N_1 + \alpha_{21}\alpha_{12}N_2 \\ \alpha_{11}R_2 = \alpha_{11}\alpha_{21}N_1 + \alpha_{11}\alpha_{22}N_2 \end{cases} \quad (\text{S9})$$

$$\Leftrightarrow \begin{cases} N_1 = \frac{\alpha_{12}R_2 - \alpha_{22}R_1}{\alpha_{12}\alpha_{21} - \alpha_{22}\alpha_{11}} \\ N_2 = \frac{\alpha_{21}R_1 - \alpha_{11}R_2}{\alpha_{12}\alpha_{21} - \alpha_{22}\alpha_{11}} \end{cases} \quad (\text{S10})$$

Setting $n = \log(N)$, eq. S7 is equivalent to

$$\begin{cases} n_{1,t+1} = r_1 + n_{1,t} - \ln(1 + \alpha_{11}N_{1,t} + \alpha_{12}N_{2,t}) \\ n_{2,t+1} = r_2 + n_{2,t} - \ln(1 + \alpha_{21}N_{1,t} + \alpha_{22}N_{2,t}) \end{cases} \quad (\text{S11})$$

We want to compute J , the log-scale Jacobian matrix of the model. Let us note $X = \ln(1 + \alpha_{11}N_1 + \alpha_{12}N_2)$ and $Y = \ln(1 + \alpha_{21}N_1 + \alpha_{22}N_2)$.

$$J = \begin{pmatrix} 1 - \frac{\partial X}{\partial n_1} & -\frac{\partial X}{\partial n_2} \\ -\frac{\partial Y}{\partial n_1} & 1 - \frac{\partial Y}{\partial n_2} \end{pmatrix} \quad (\text{S12})$$

We have $\frac{\partial X}{\partial n_1} = \frac{\partial X}{\partial N_1} \frac{\partial N_1}{\partial n_1} = \frac{\alpha_{11}}{1 + \alpha_{11}N_1 + \alpha_{12}N_2} e^{n_1} = \frac{\alpha_{11}}{1 + \alpha_{11}N_1 + \alpha_{12}N_2} N_1$, which leads to

$$J - I = \begin{pmatrix} -\frac{\alpha_{11}N_1}{1 + \alpha_{11}N_1 + \alpha_{12}N_2} & -\frac{\alpha_{12}N_2}{1 + \alpha_{11}N_1 + \alpha_{12}N_2} \\ -\frac{\alpha_{21}N_1}{1 + \alpha_{21}N_1 + \alpha_{22}N_2} & -\frac{\alpha_{22}N_2}{1 + \alpha_{21}N_1 + \alpha_{22}N_2} \end{pmatrix} \quad (\text{S13})$$

For this demonstration, we consider diffuse competition, that is

$$\begin{cases} \alpha_{ii} = k\alpha \\ \alpha_{ij} = \alpha, \forall i \neq j \end{cases} \quad (\text{S14})$$

If we combine eq. S10 and eq. S14, we have

$$\begin{cases} N_1 = \frac{\alpha R_2 - k\alpha R_1}{\alpha^2 - k^2\alpha^2} \\ N_2 = \frac{\alpha R_1 - k\alpha R_2}{\alpha^2 - k^2\alpha^2} \end{cases} \quad (\text{S15})$$

and

$$J - I = \begin{pmatrix} -\frac{k\alpha N_1}{1 + k\alpha N_1 + \alpha N_2} & -\frac{\alpha N_2}{1 + k\alpha N_1 + \alpha N_2} \\ -\frac{\alpha N_1}{1 + \alpha N_1 + k\alpha N_2} & -\frac{k\alpha N_2}{1 + \alpha N_1 + k\alpha N_2} \end{pmatrix} \quad (\text{S16})$$

$$\Rightarrow \begin{cases} (J - I)_{11} = \frac{-\frac{k}{1-k^2}(R_2 - kR_1)}{1 + \frac{k}{1-k^2}(R_2 - kR_1) + \frac{1}{1-k^2}(R_1 - kR_2)} \\ (J - I)_{12} = \frac{-\frac{1}{1-k^2}(R_1 - kR_2)}{1 + \frac{k}{1-k^2}(R_2 - kR_1) + \frac{1}{1-k^2}(R_1 - kR_2)} \end{cases} \Rightarrow (J - I)_{11} = k \frac{R_2 - kR_1}{R_1 - kR_2} (J - I)_{12} \quad (\text{S17})$$

By symmetry, we can also write

$$(J - I)_{22} = k \frac{R_1 - kR_2}{R_2 - kR_1} (J - I)_{21} \quad (\text{S18})$$

Therefore, unless the growth rates and the resulting abundances differ over several orders of magnitude, the strength of the competition ratio k should be roughly comparable between MAR(1) and Lotka-Volterra or Beverton-Holt models. The same reasoning can actually be applied with n species as the Jacobian has a similar form.

$$\begin{aligned} (J - I)_{ii} &= \frac{-\alpha_{ii}N_i}{1 + \sum_j \alpha_{ij}N_j} \\ &= \frac{-k\alpha N_i}{1 + k\alpha N_i + \sum_{j,j \neq i} \alpha N_j} \end{aligned} \quad (\text{S19})$$

and

$$\begin{aligned} (J - I)_{ij} &= \frac{-\alpha_{ij}N_j}{1 + \sum_l \alpha_{il}N_l} \\ &= \frac{-\alpha N_j}{1 + k\alpha N_i + \sum_{l,l \neq i} \alpha N_l} \\ &= (J - I)_{ii} \frac{\alpha N_j}{k\alpha N_i} \\ &= \frac{1}{k} (J - I)_{ii} \frac{N_j}{N_i} \end{aligned} \quad (\text{S20})$$

Therefore, as long as the intrinsic growth rates and the resulting equilibrium abundances do not differ too much, the order of magnitude of competition should be the same in MAR(1), Lotka-Volterra and multispecies Beverton-Holt models.

In this paper, the maximum ratio between pairs of abundances vary between 1.01 and 439.5, with a right-skewed distribution and median/mean values around 6/24. Thus, the order of magnitude between interaction strengths might change, depending on the species in presence. Moreover, competition is not completely diffuse: α_{ij} and k vary between species and sites. We can only say that the ratio between intraspecific and interspecific interactions vary on average between 1 and 2 orders of magnitude.

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