Supplementary Information
for

Both local stability and dispersal contribute to metacommunity sensitivity to asynchronous habitat availability (depending on landscape structure and foodweb complexity)

Landscape Ecology

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1 *DETAILED METHODS AND ADDITIONAL RESULTS*

1.1 Detailed methods

Landscape generation and dynamics: We represent dynamic landscapes as dynamic graphs, i.e. time-varying graphs with node-dynamics (Harary and Gupta, 1997). Vertices represent sites where local communities can be assembled, edges represent a non-zero probability of species dispersal between sites, and edge weights represent the Euclidean distance between two adjacent sites. Our algorithm creates connected modular landscapes by laying sites at random on a square, creating a minimum spanning tree, and then adding edges at random to reach a desired connectance. The process uses five parameters, namely n_P, n_E, n_C, F, and x. They represent the number of sites, the number of edges, the number of modules, the excess factor, and the distance exponent. The first three are self-explanatory. We fixed n_E to $2n_P$ and n_C to 5. Real parameter $F \geq 1$ regulates how tight the modules are. A value of 1 results in no discernible clustering of sites, i.e. they are distributed uniformly at random, while a high value will produce tight modules. Real parameter $x \geq 0$ controls how the distances among sites determine the probability of edges being added to the landscape. A value of zero indicates that distances between sites do not affect the probability of edges being added. A larger value favors adding shorter edges over longer ones. Thus, spatial modularity increases with both F and x. See Figure SI1 for an example. We set $x = 2$ for all our simulations. A site of a randomly chosen module is designated as *the mainland*.

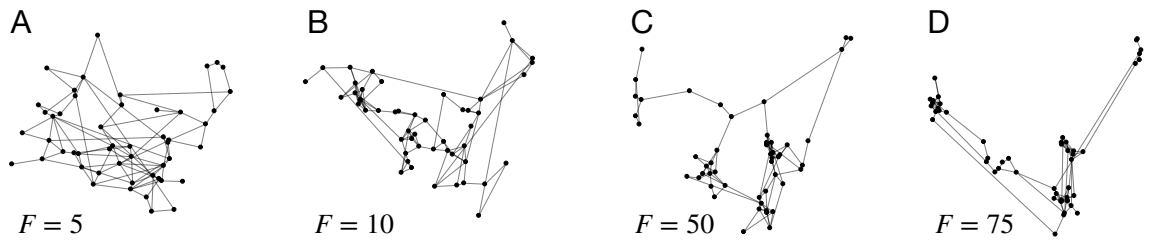

Fig. SI1. Examples of landscapes with different degrees of spatial modularity generated by our algorithm through varying excess factor F. We used 50 sites, 100 edges, 5 modules, and a distance exponent of 2.

At a given time, each site p is in either of two states: "active" or "inactive." Species can be present in p only when the site is "active." The mainland is always "active", and all species in the regional pool are present therein. All the other sites transition stochastically between the two states. For a site p, the nominal length of the "active" period is randomly drawn from a uniform distribution $w_p \sim U(0.2, 0.3)$. Assuming no overlapping "active" periods from consecutive years, the start of the "active" period for the year k is $start_{p,k} = k + z_{p,k}$, where $z_{p,k} \sim U(-A, +A)$, and parameter $A > 0$ is the magnitude of asynchrony among the sites' activation times. The end of the period will be $end_{p,k} = start_{p,k} + w_p$. To account for overlaps, we define $ACTIVE_p = \cup_k [start_{p,k}, end_{p,k}]$ and we say site p is "active" at time t if and only if $t \in ACTIVE_p$.

Modular landscape generation algorithm

```
function modular_landscape(n_P, n_E, F, n_C, x)
   // Choose potential locations for sites.
   // Locations are points on the real (x,y) plane.
   Let L be an array of ⌊n_S · F⌋ points in a 512 × 512 square randomly drawn
      from a uniform distribution.

   // Select the first n_C of these locations as cluster centers
   Let C = {1, 2, ..., n_C}.

   // Compute all pairwise distances, and the distances to the closest center
   Let d_{i,j} be the euclidean distance between points L_i and L_j
   Let δ_i = min_{j∈C} d(i, j)

   // Randomly select the non−center sites and combine with centers, yielding
   // the final set of sites S.
   Let V be a set of n_S − n_C integers from {n_C + 1, n_C + 2, ..., ⌊n_S · F⌋} chosen with
      probabilities inversely proportional to δ_i
   Let P = C ∪ V // These vertices will be the landscape sites
```

// Compute a minimum spanning tree of the clique of all final sites
Let $K = (P, P \times P)$ // A complete graph with all the vertices
Let $Tree = MST(K)$ using distances $d_{i,j}$
Let $E_T = edges(Tree)$

// Randomly choose the remaining edges
Let E be a set of $n_E - n_P + 1$, randomly chosen undirected edges from $P \times P - E_T$
The probability to choose (i, j) is inversely proportional to $d^x_{i,j}$

Return $G = (P, E + E_T)$ and the weights $d_{i,j}$ for all the edges in G
end

Local community dynamics: The regional pool of species and interactions is modeled as a foodweb following Klaise and Johnson (2016), which extends the Preferential Prey Model (Johnson et al., 2014). Unlike the niche or the cascade models, the algorithm in Klaise and Johnson (2016) creates foodwebs with varying degrees of trophic coherence, a structural property that strongly determines stability in empirical and quasi-empirical foodwebs (Johnson et al., 2014). The algorithm creates foodweb topologies from target values of species richness n_S, number of basal species n_B, number of predation links n_L, and foodweb temperature T (a surrogate for trophic coherence). We fixed the number of basal species to 20% of the species richness. We define foodweb connectance C as $n_L/(n_S \cdot (n_S - n_B - 1) + n_B)$, i.e. the ratio between the number of present links n_L and the maximum possible number of edges in a foodweb with n_B basal species and no cannibals.

We assume that the dynamics of $x_{i,p}$, the biomass of species i at site p, is governed by Lotka-Volterra type equations and reaches equilibrium instantaneously. The ODEs describing local community dynamics are:

$$\frac{dx_{i,p}}{dt} = \left(r_i + \sum_j M_{ij} x_{j,p} \right) x_{i,p}, \tag{SI1}$$

where i and j range over all species in the pool. Elements $M_{i,j}$ of the *community matrix* M represent the effect of increasing population biomass of species j on the per unit biomass growth rate of species i. Parameters r_i's are the intrinsic growth rates.

To define M, we first assign $M_{ii} = -\lambda$, where the self-regulation parameter λ is a positive real. If there are no trophic interactions between species i and j, then $M_{ij} = 0$. If j feeds on i, then $M_{ij} = -\mathcal{X}$, where $\mathcal{X}$ is drawn from a lognormal distribution, with mean 1 and a standard deviation of 0.25. Following Johnson et al. (2014), we set $M_{ji} = 0.4\mathcal{X}$. To choose the values for the r_i's, we solve the linear program:

$$
\begin{aligned}
&\max y^* \\
r_i^* + \sum_j M_{ij} x_j^* &= 0 \\
x_i^* &\geq y^* \\
y^* &\geq 0 \\
r_i^* &\leq \rho && \text{for basal species } i \\
r_i^* &\leq -\mu && \text{for non-basal species } i.
\end{aligned}
$$

We set $\rho = 1$ to limit the intrinsic growth rate for basals. Parameter $\mu = 0.01$ is the smallest possible mortality rate value for non-basal species. The decision variables are y^*, all the r_i^*'s, and all the x_i^*'s. Maximizing y^* means maximizing the smallest species abundance at equilibrium. If the program is not feasible, then it is impossible to choose r_i^*'s in such a way that all the x_i^*'s are positive. If this happens, the foodweb is discarded and the process is repeated. If the program is feasible, we check that, at equilibrium (the values obtained for the x_i^*'s), the Jacobian matrix of Eq. (SI1) has only eigenvalues with negative real parts. If this is not the case, then the system is unstable and it is discarded to start the process again.

Metacommunity dynamics: Dispersal is modeled as a continuous time Markov chain. The dispersal events, i.e. individuals moving from one site to another one, are coupled with events representing the activation and deactivation of landscape sites, and with the local community dynamics. A dispersal event of a species s from site p to site q is only possible if sites p and q are active, s is present in p but not in q, and s is either a basal species or a consumer with at least one of its prey species present in q. The biomasses of all species present in q are recomputed as the equilibrium of Eq. SI1 and set to zero for all species whose value is below an extinction threshold of 0.001. If at least one species goes extinct, equilibrium is recalculated until no further secondary extinctions occur. The set of species in p is not altered by dispersal events originating from p. The *effective rate* of dispersal events between sites p and q is the ratio between the dispersal ability $a \in \mathbb{R}^+$ and the Euclidean distance between p and q. However, if this ratio is less than 0.1, we set the rate to zero. Site deactivation drives all species' biomasses in that site to zero. To perform our simulations, we use a variant of the first-reaction method (Gillespie, 1976), in the framework of dynamic Monte Carlo methods.

Metacommunity simulation algorithm

There are three types of events:

1. Site activation events, described as triples $\langle t, p, \text{`}activate\text{'} \rangle$, meaning at time t site p becomes active.

2. Site deactivation events, described as triples $\langle t, p, \text{`}deactivate\text{'} \rangle$, meaning at time t site p becomes inactive.

3. Dispersal events, described as triples $\langle t, s, dest \rangle$, meaning at time t individuals of species s move to site *dest*.

The algorithm begins by initializing the event queue with site activation/deactivation events. Let $\mathcal{S}$ be the set of all species and let $\mathcal{P}$ be the set of all landscape sites. For every site p, define the pulse train function $f_p(t) = 1$ if $t \in ACTIVE_p$ and zero otherwise. Let $t^{on}_{p,k}$ be the rising time of the k-th pulse in f_p. Event $\langle t^{on}_{p,k}, p, \text{'activate'} \rangle$ is added to the queue. Similarly, define $t^{off}_{p,k}$ as the falling time of the k-th pulse in f_p and add $\langle t^{off}_{p,k}, p, \text{'deactivate'} \rangle$ to the queue.

Conceptually, the algorithm to simulate the metacommunity dynamics is as follows:

```
Init queue Q with site activation/deactivation events

// Set initial state of the systems
for all sites p
    // C[p] is the set of species present at site p
    C[p] = S if p is the mainland
    C[p] = {} if p is insular
    A[p] = 'inactive' // A[p] is the state ('active' or 'inactive') of site p
end


time = 0

while Q ≠ {} //Main simulation loop
    ⟨t_m, s, dest⟩ = next_migration_event()
    ⟨t, p, type⟩ = earliest(Q)
    if t < t_m
        if type='activate'
            A[p] = 'active'
        else
            C[p] = {}
            A[p] = 'inactive'
        end
        Q = Q − ⟨t, p, type⟩
        time = t
    else
        migration_process(s, dest)
        time = t_m
    end
end

function next_migration_event()
    C1 = {⟨s, dest, orig⟩ such that
            s ∉ C[dest]
            s ∈ C[orig]
            A[dest] = 'active'
            s is basal or preys(s)∩C[dest] ≠ {}}
    C2 = {⟨τ, s, dest, orig⟩ such that
```

```
            ⟨s, dest, orig⟩ ∈ C1  and
            τ ∼ exp(distance(orig, dest)/a))}
    ⟨τ, s, dest, orig⟩ = earliest(C2)
    return ⟨τ + time, s, dest⟩
end

function migration_process(s, dest)
   C[dest] = C[dest] ∪ {s}
   repeat
      solve
         r_i + Σ_j CM_ij x_j = 0  for  i, j ∈ C[dest]
      C[dest] = C[dest] − {s'|x_s' < 0.001}
   until for all k ∈ C[dest],  x_k ≥ 0.001
end
```

1.2 Power mean

Let ρ be a real parameter, let t_0 and t_1 be reals and let $y(t)$ be an integrable function in (t_0, t_1). The average value of y on (t_0, t_1) is

$$\left(\frac{1}{t_1 - t_0}\int_{t_0}^{t_1} y(t)^\rho dt\right)^{\frac{1}{\rho}}. \tag{SI2}$$

This reduces to the arithmetic mean when $\rho = 1$ and is biased toward the time series maxima for larger values of ρ. We chose $\rho = 4$ to reduce the effect of zero abundances during the "inactive" periods. However, our results were robust to changes in ρ values. In our case, $t_0 = 0$, and t_1 is the end of the simulation.

1.3 Local species persistence and biomass in single communities

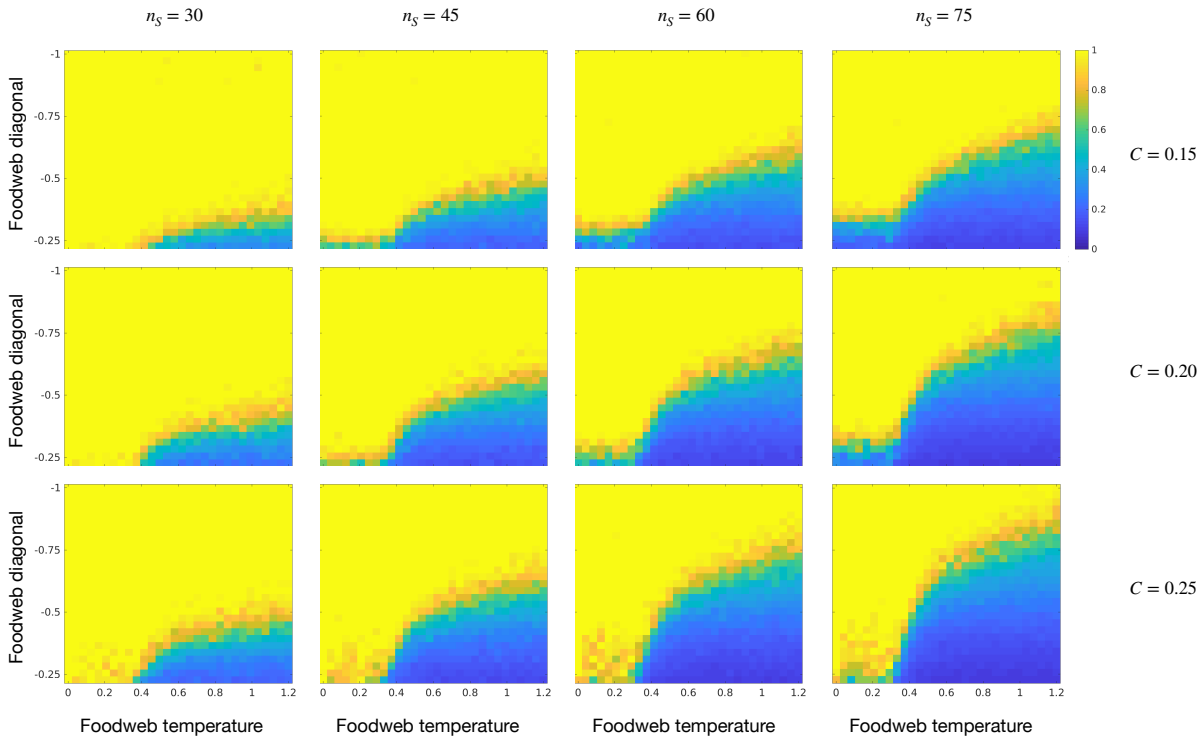

Fig. SI2. Species persistence $\mathcal{P}$ in a single local community with colonization from a regional pool, as a function of foodweb diagonal values (opposite of intensity of self-regulation) and foodweb temperature values (inverse of trophic coherence) for a gradient of richness n_S and connectance C of the species pool. Each cell value shows the mean of 50 replicates.

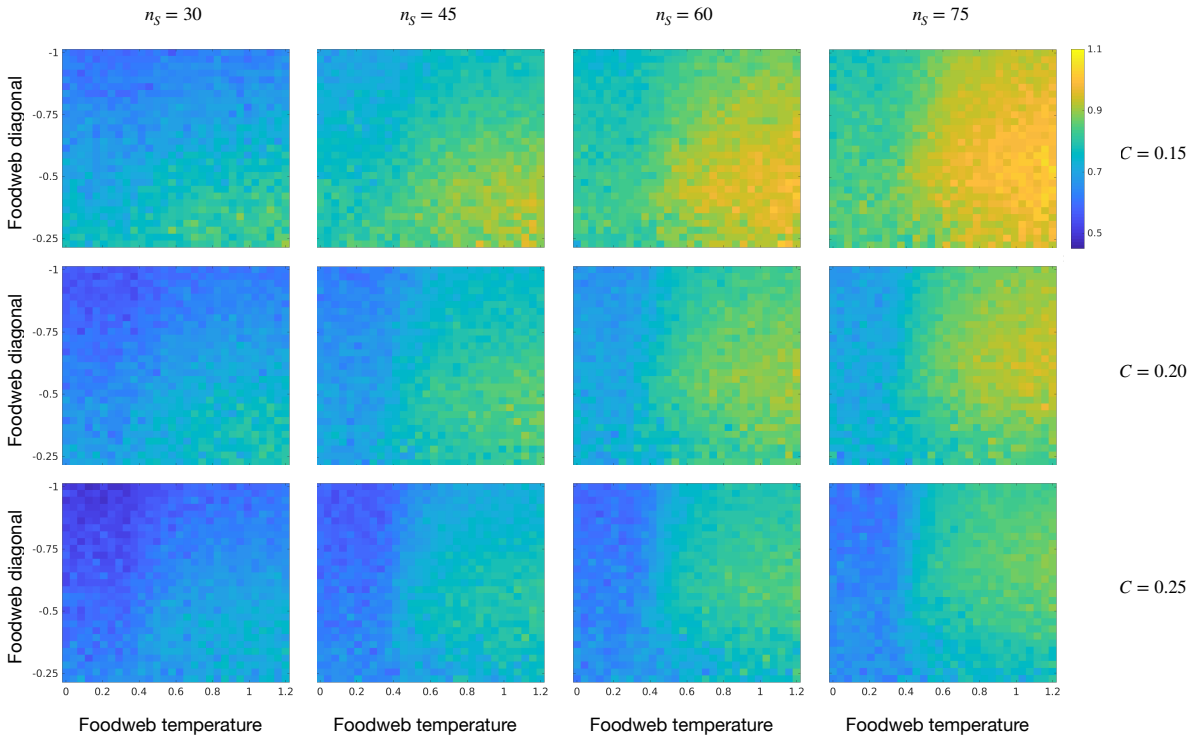

Fig. SI3. Species biomass $\mathcal{B}$ (in $\log_{10}$) in a single local community with colonization from a regional pool, as a function of foodweb diagonal values (opposite of intensity of self-regulation) and foodweb temperature values (inverse of trophic coherence) for a gradient of richness n_S and connectance C of the species pool. Each cell value shows the mean of 50 replicates.

1.4 Effects of local and regional stabilizing factors depending on landscape structure

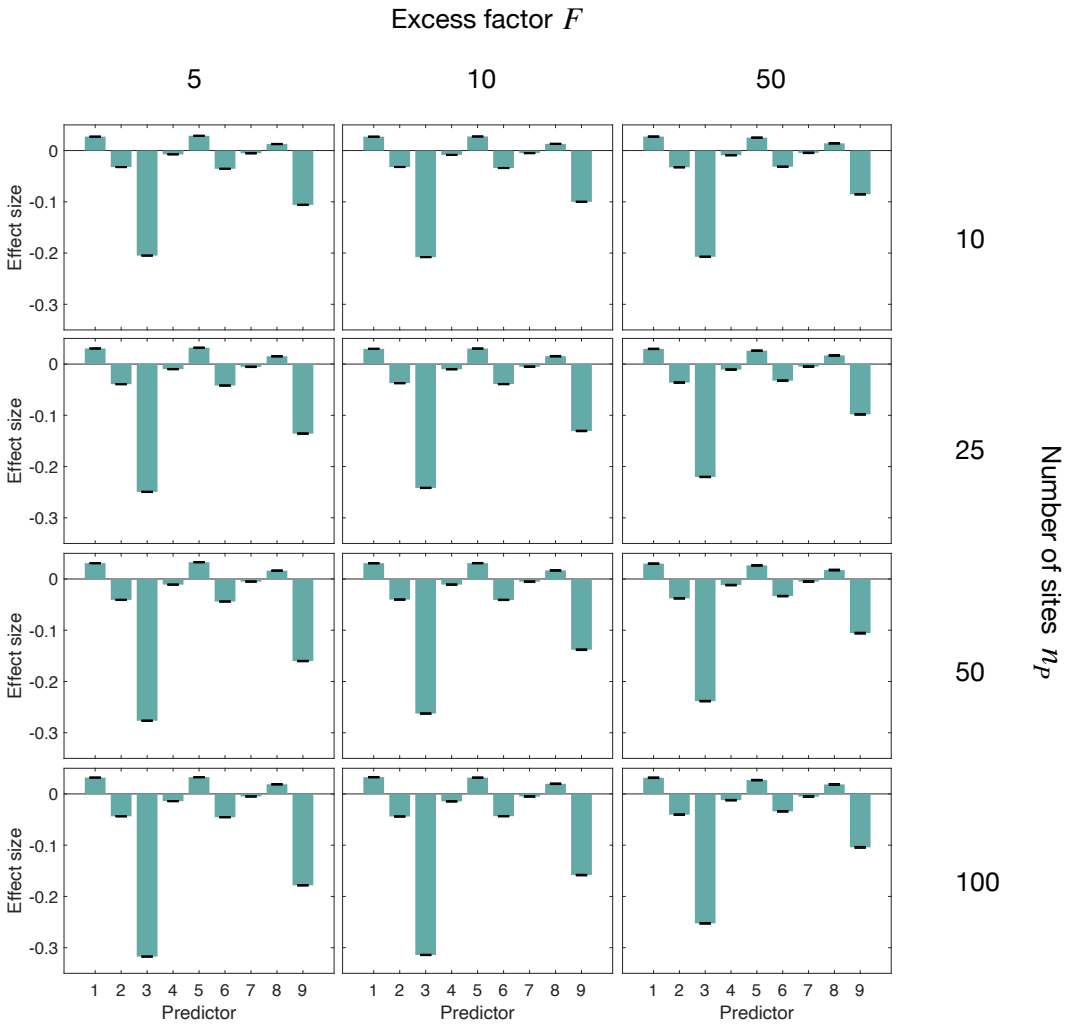

Fig. SI4. Effect sizes on A-sensitivities of local species persistence $\mathcal{S}[\mathcal{P}_\alpha]$ in a gradient of number of sites n_P and excess factor F. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Foodweb parameters are $n_S = 45$ and $C = 0.2$

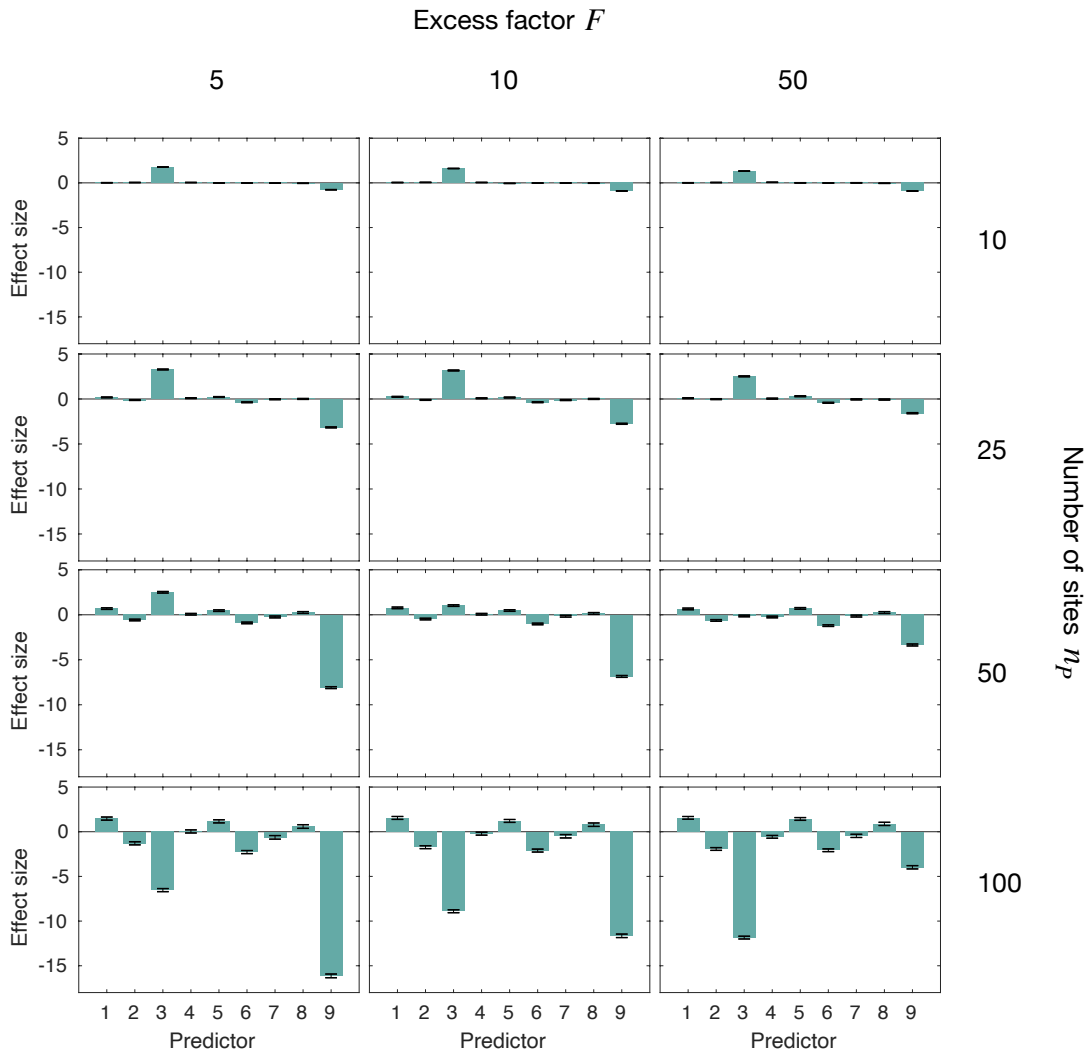

Fig. SI5. Effect sizes on A-sensitivities of among-site dissimilarity in species persistence $\mathcal{S}[\mathcal{P}_\beta]$ in a gradient of number of sites n_P and excess factor F. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Foodweb parameters are $n_S = 45$ and $C = 0.2$

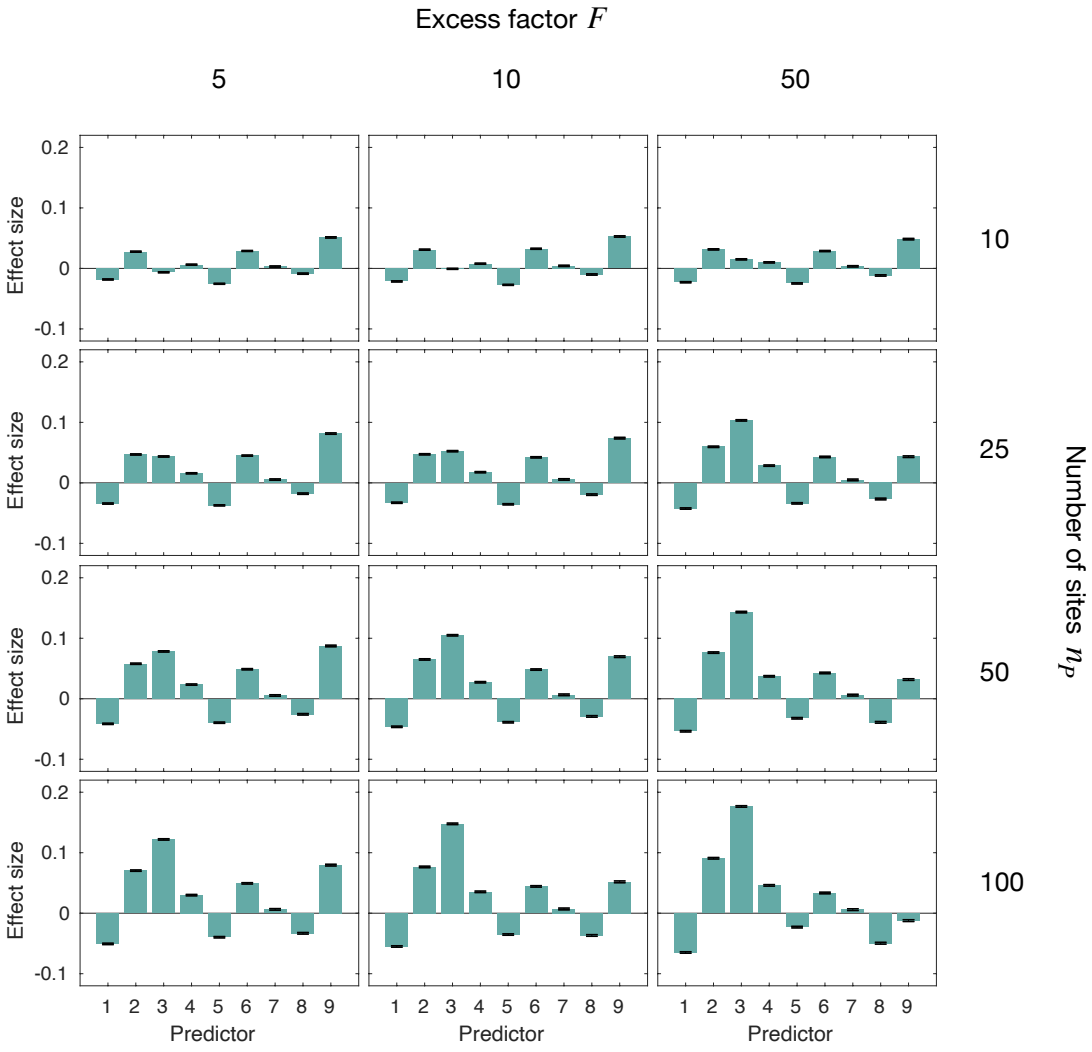

Fig. SI6. Effect sizes on A-sensitivities of regional species persistence $\mathcal{S}[\mathcal{P}_\gamma]$ in a gradient of number of sites n_P and excess factor F. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Foodweb parameters are $n_S = 45$ and $C = 0.2$

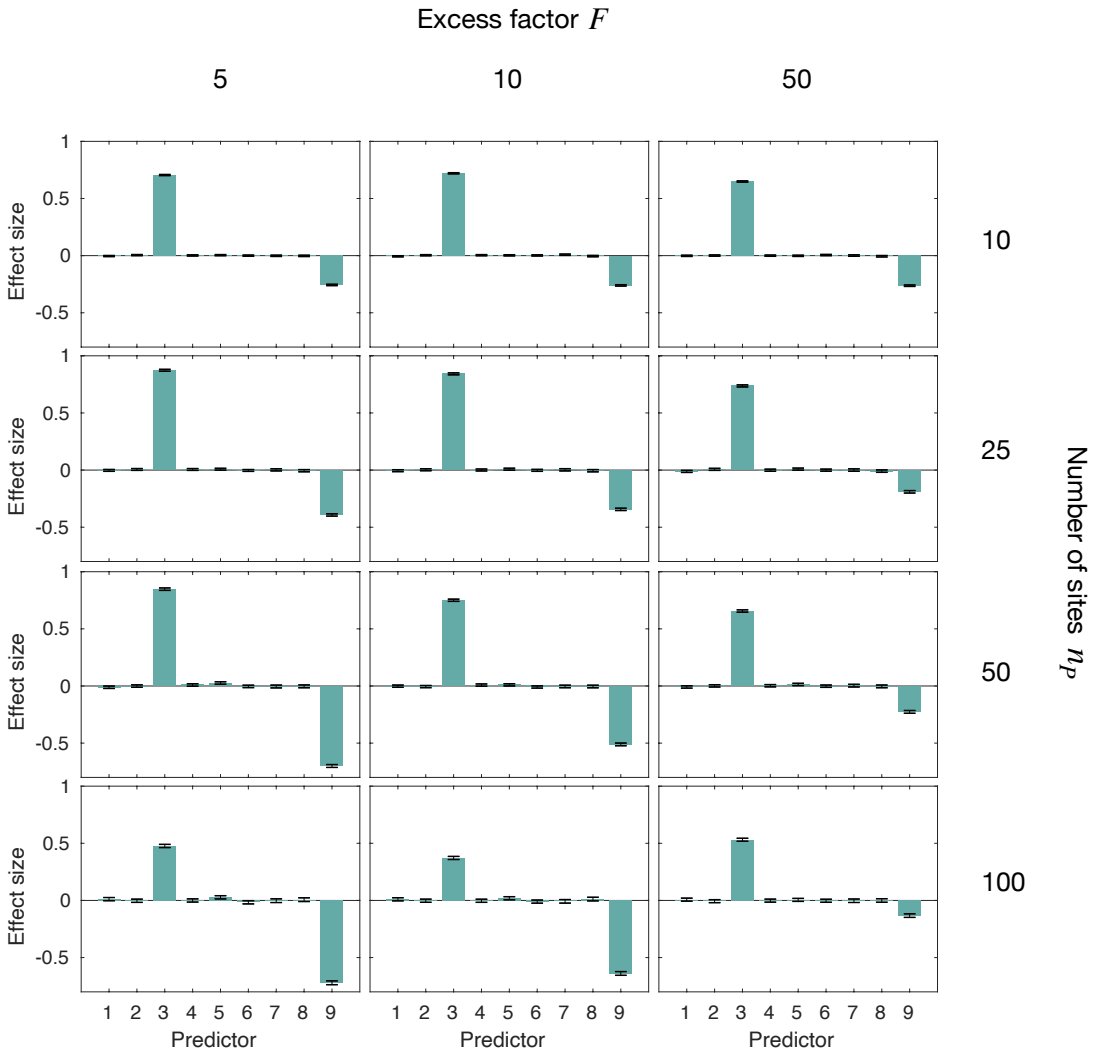

Fig. SI7. Effect sizes on A-sensitivities of among-site dissimilarity in community biomass $\mathcal{S}[\mathcal{B}_\beta]$ in a gradient of number of sites n_P and excess factor F. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Foodweb parameters are $n_S = 45$ and $C = 0.2$

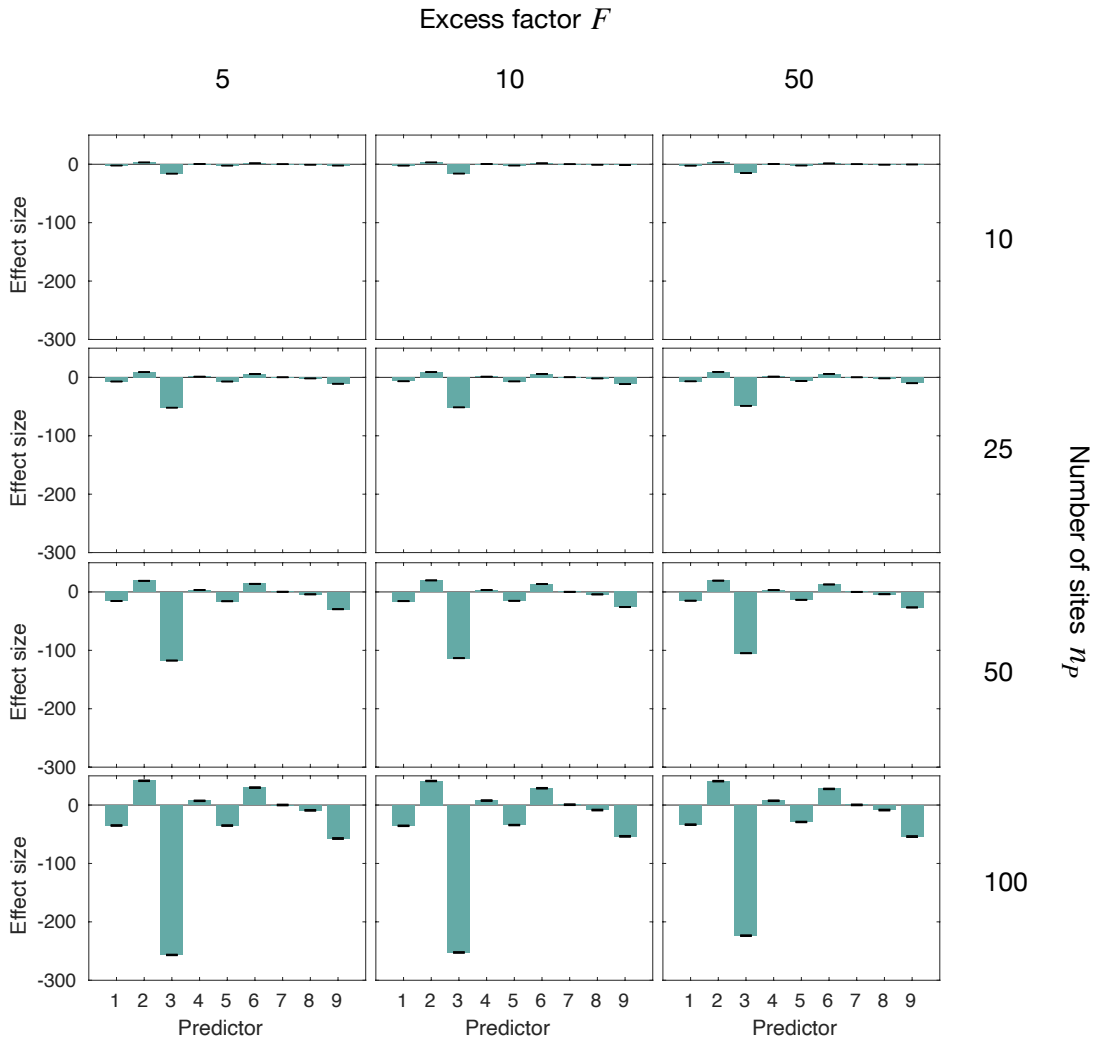

Fig. SI8. Effect sizes on A-sensitivities of regional biomass $\mathcal{S}[\mathcal{B}_\gamma]$ in a gradient of number of sites n_P and excess factor F. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Foodweb parameters are $n_S = 45$ and $C = 0.2$

1.5 Effects of local and regional stabilizing factors depending on foodweb topology

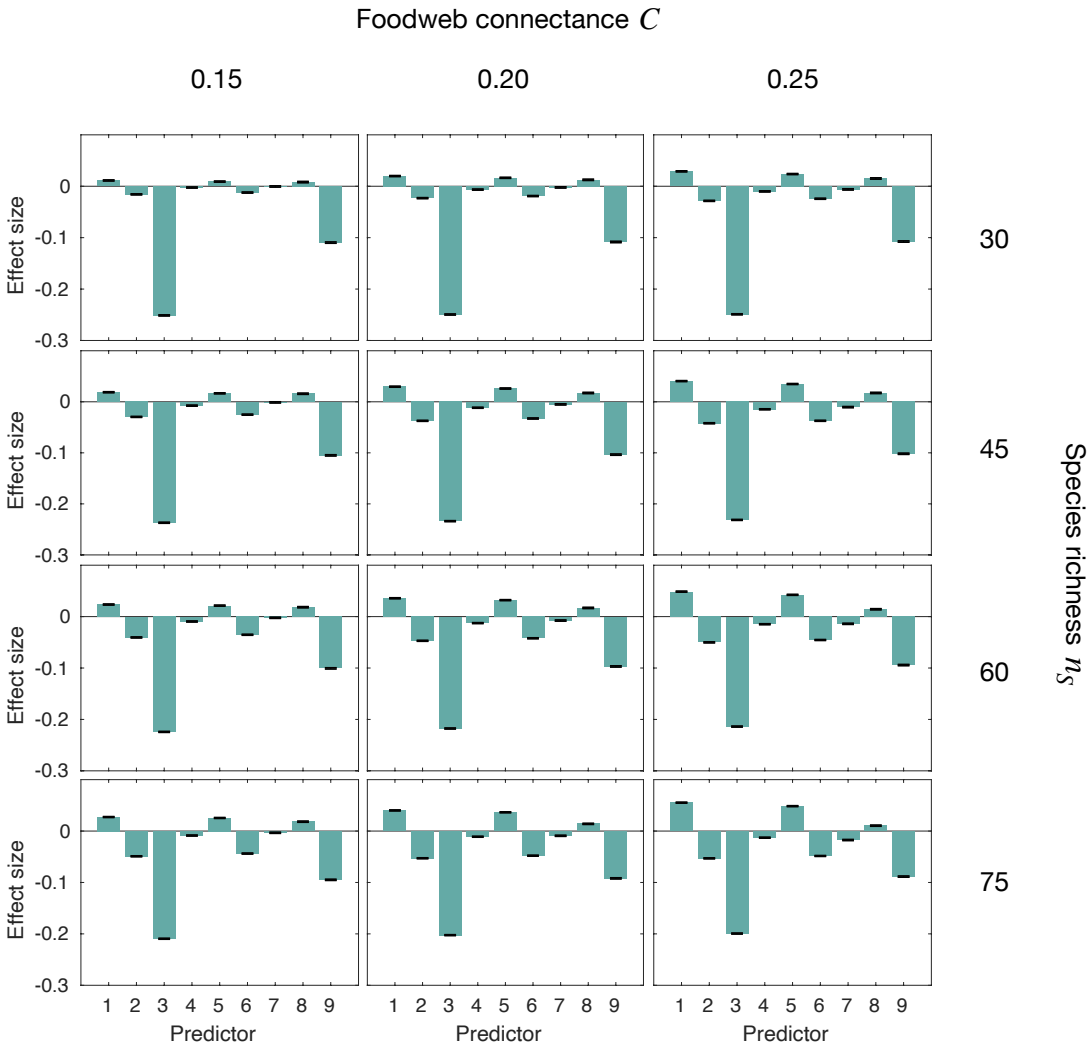

Fig. SI9. Effect sizes on A-sensitivities of local species persistence $\mathcal{S}[\mathcal{P}_\alpha]$ in a gradient of foodweb connectance C and species richness n_S in the regional pool. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Landscape parameters are $n_P = 50$ and $F = 50$

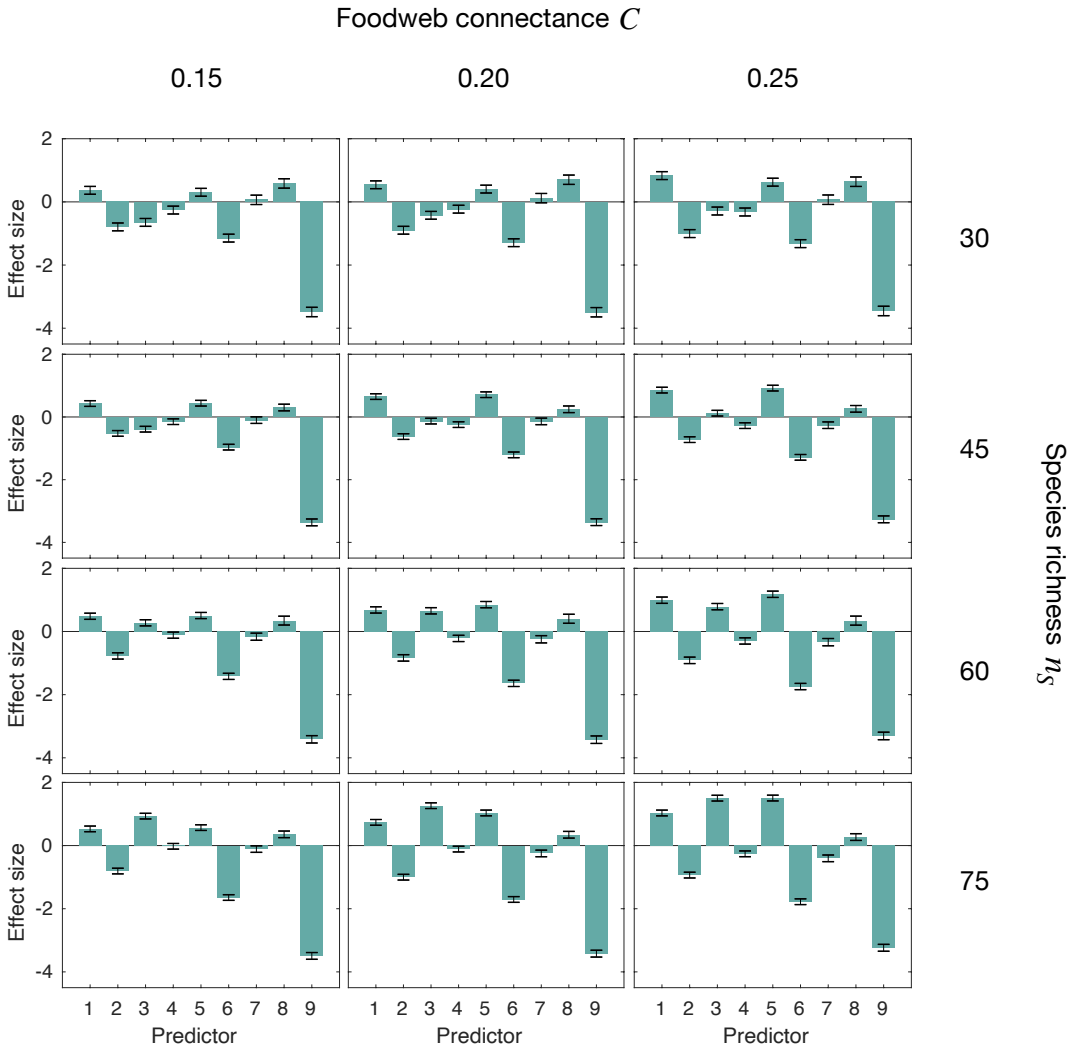

Fig. SI10. Effect sizes on A-sensitivities of among-site dissimilarity in species persistence $\mathcal{S}[\mathcal{P}_\beta]$ in a gradient of foodweb connectance C and species richness n_S in the regional pool. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Landscape parameters are $n_P = 50$ and $F = 50$

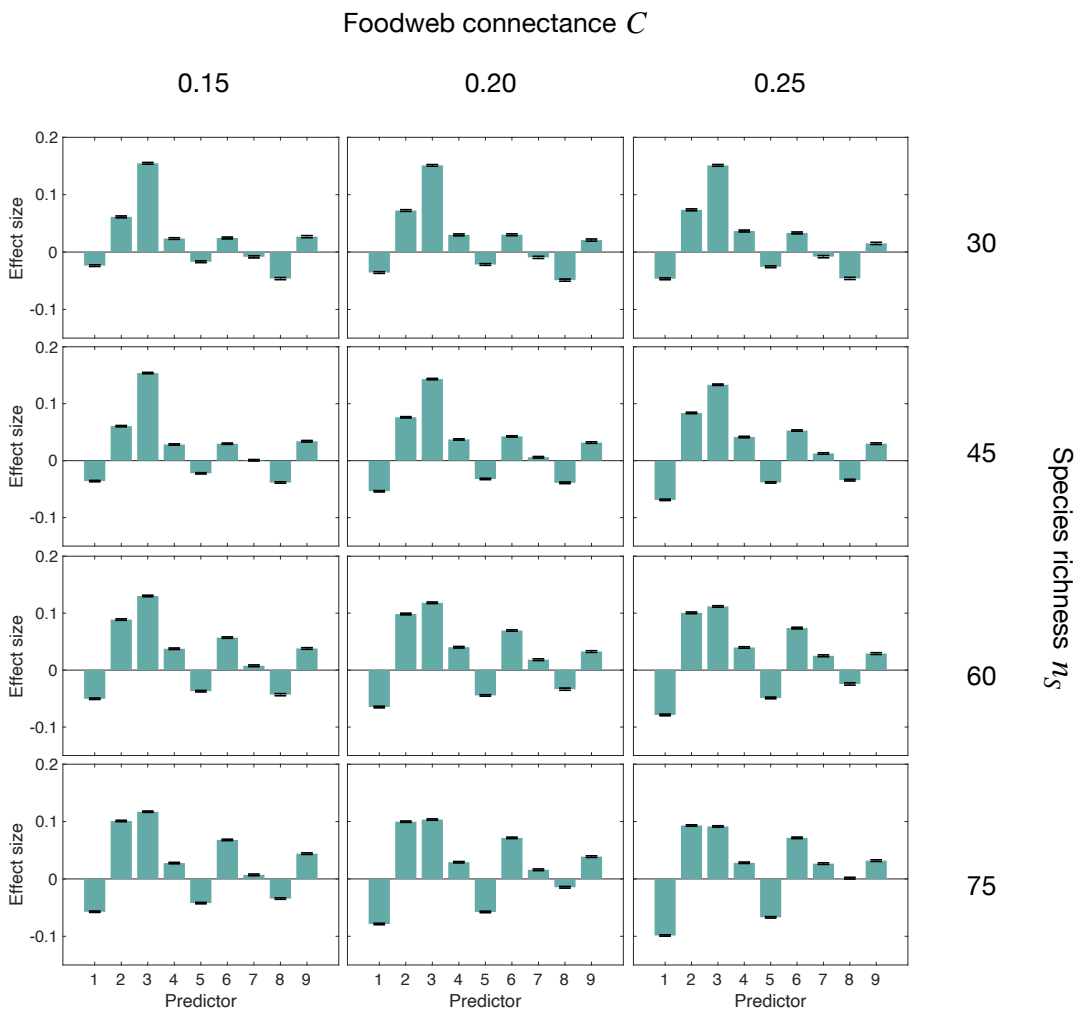

Fig. SI11. Effect sizes on A-sensitivities of regional species persistence $\mathcal{S}[\mathcal{P}_\gamma]$ in a gradient of foodweb connectance C and species richness n_S in the regional pool. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Landscape parameters are $n_P = 50$ and $F = 50$

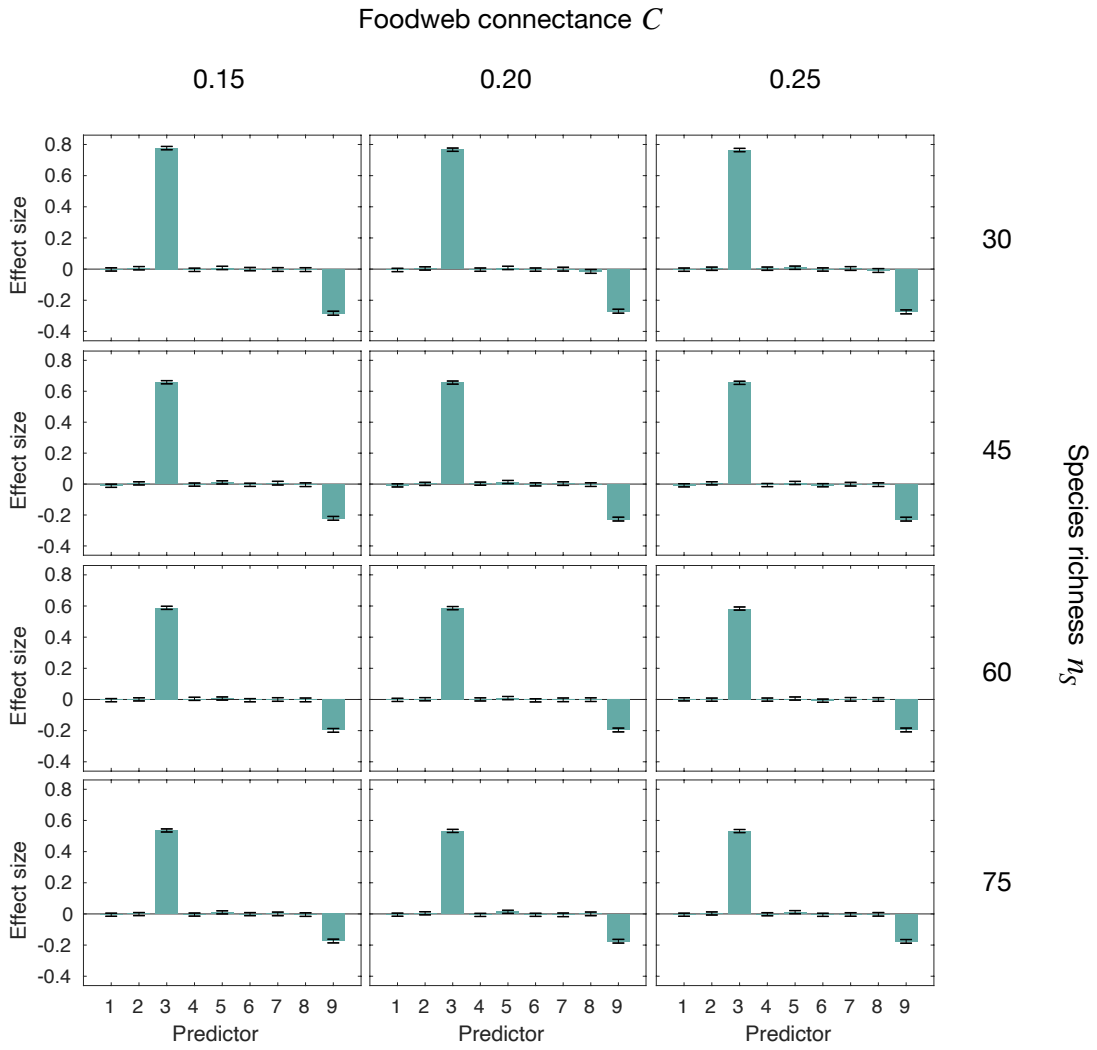

Fig. SI12. Effect sizes on A-sensitivities of among-site dissimilarity in community biomass $\mathcal{S}[\mathcal{B}_\beta]$ in a gradient of foodweb connectance C and species richness n_S in the regional pool. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Landscape parameters are $n_P = 50$ and $F = 50$

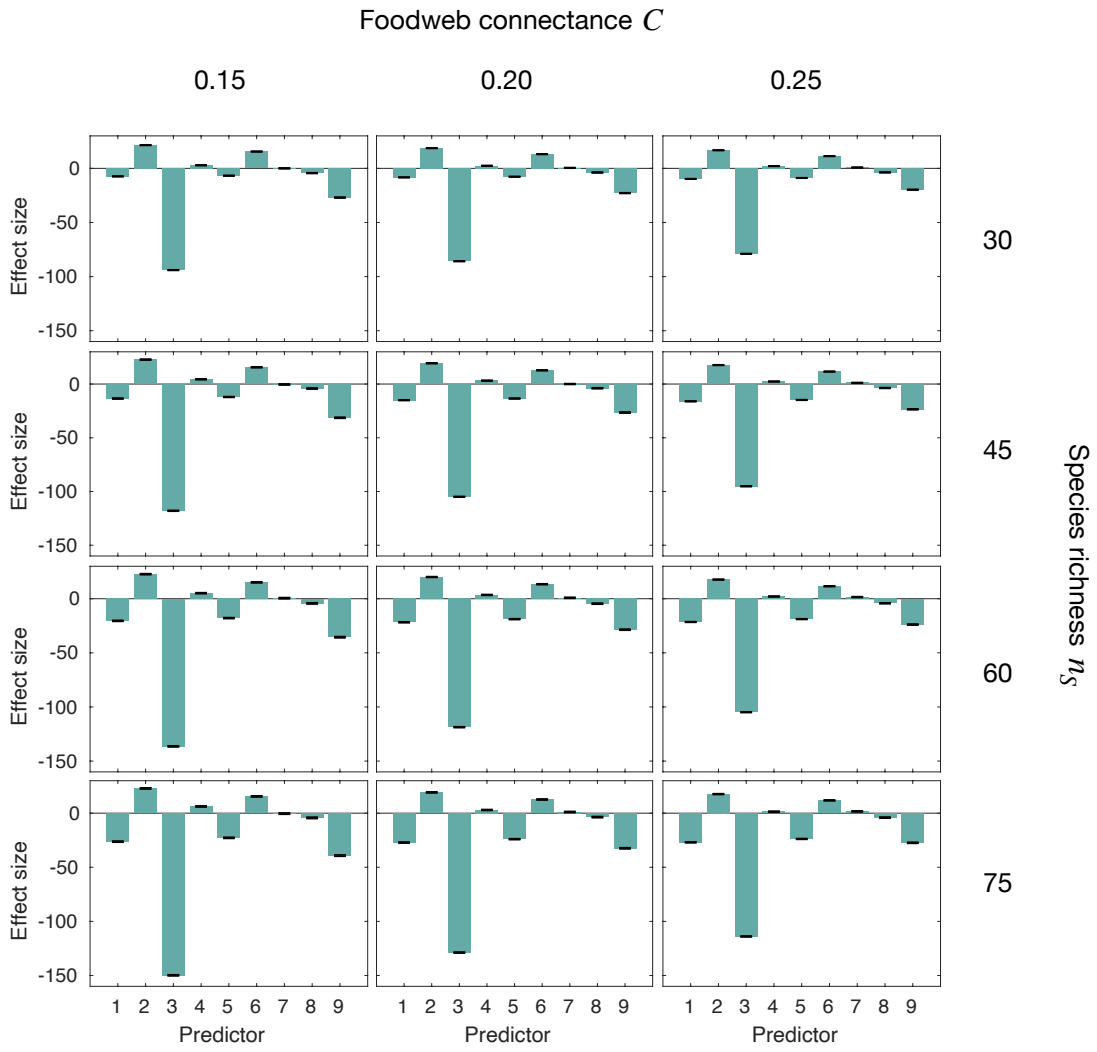

Fig. SI13. Effect sizes on A-sensitivities of regional biomass $\mathcal{S}[\mathcal{B}_\gamma]$ in a gradient of foodweb connectance C and species richness n_S in the regional pool. Predictors are foodweb temperature T (1), self limitation λ (2), dispersal ability $\hat{a} = \log_{10} a$ (3), $T \cdot \lambda$ (4), $T \times \hat{a}$ (5), $\lambda \times \hat{a}$ (6), T^2 (7), λ^2 (8), and $\hat{a}^2$ (9). Landscape parameters are $n_P = 50$ and $F = 50$

1.6 Sensitivities of $\mathcal{P}_\alpha$ and $\mathcal{P}_\gamma$

These figures depict metacommunity sensitivities as the changes in the distributions of $\mathcal{P}_\alpha$ and $\mathcal{P}_\gamma$ as sites' activation and deactivation asynchrony A increases from $A = 0$ to $A = 0.5$. For each parameter set, we run 50 replicates. However, for each data point, its coordinates represent the value of either $\mathcal{P}_\alpha$ or $\mathcal{P}_\gamma$ for the same foodweb and landscape but changing only A. The color of a dot represents the propensity to species persistence of a single local community (foodweb). The actual color depends on n_S, C, λ and T, and is looked up in Fig. SI2. Thus, yellow/blue dots represent high/low local persistence. Note that stable-prone local communities tend to produce metacommunities with high regional persistences. This is apparent by the clustering of yellow circles close to large $\mathcal{P}_\gamma$ values. By contrast, the blue circles, representing unstable-prone local communities are scattered over a larger $\mathcal{P}_\gamma$ range. All simulations were carried out for landscapes with $n_C = 5$ and $F = 50$, and for a timelapse of 5 years. The magnitudes of metacommunity sensitivities are the vertical distances between each dot and the identity line. Positive sensitivities, i.e., when the response variable increases with landscape variability, are reached when the data points lie above the identity line, and vice versa.

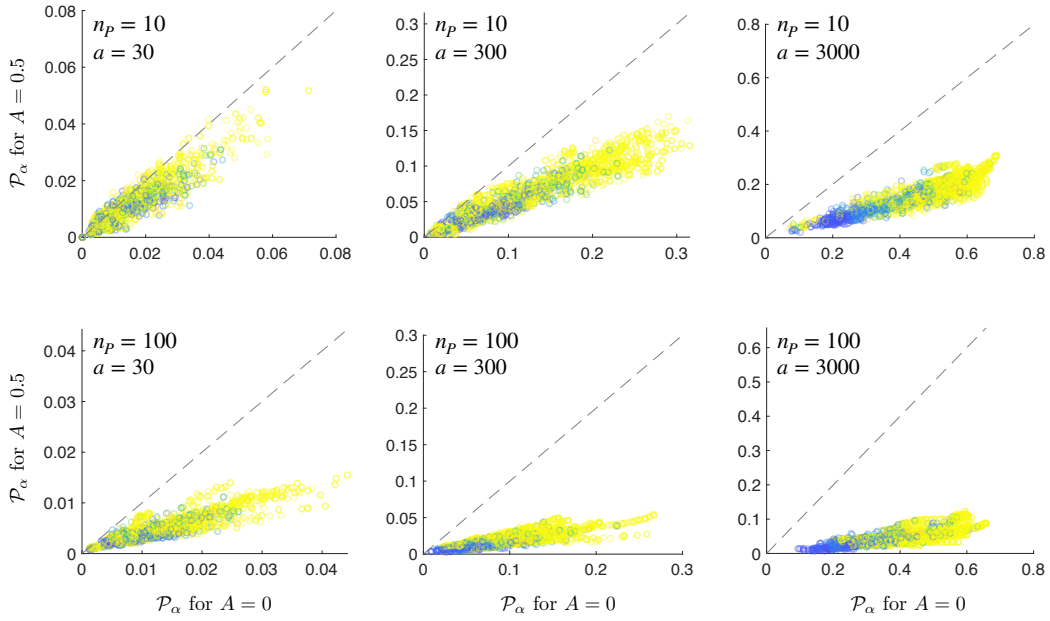

Fig. SI14. $\mathcal{P}_\alpha$ for $A = 0$ versus $A = 0.5$ and three levels of dispersal ability (a). Foodweb parameters were $n_S = 45$ and $C = 0.2$. The top and bottom rows correspond to scattered/spread and dense landscapes respectively.

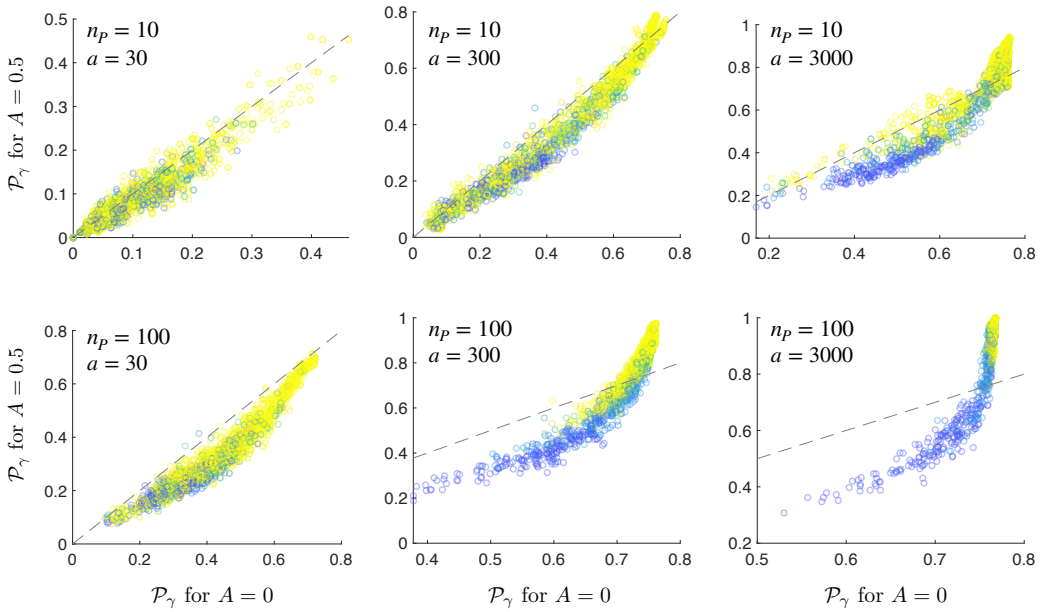

Fig. SI15. $\mathcal{P}_\gamma$ for $A = 0$ versus $A = 0.5$ and three levels of dispersal ability (a). Foodweb parameters were $n_S = 45$ and $C = 0.2$. The top and bottom rows correspond to scattered/spread and dense landscapes respectively.

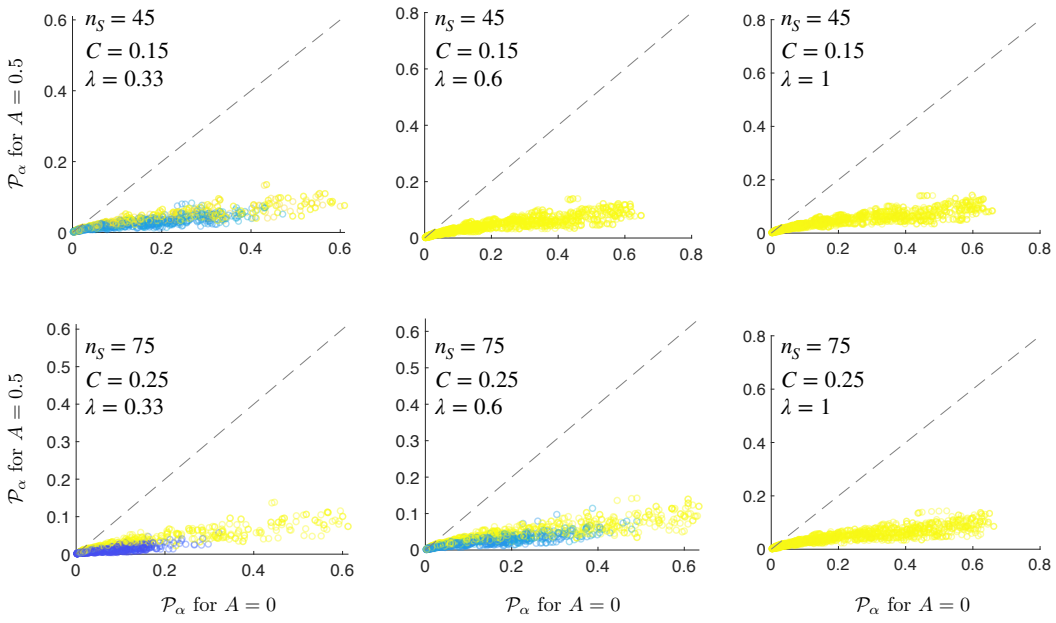

Fig. SI16. $\mathcal{P}_\alpha$ for $A = 0$ versus $A = 0.5$ with $n_P = 50$ and three levels of self limitation (λ). The top and bottom rows correspond to simpler and more complex foodwebs respectively.

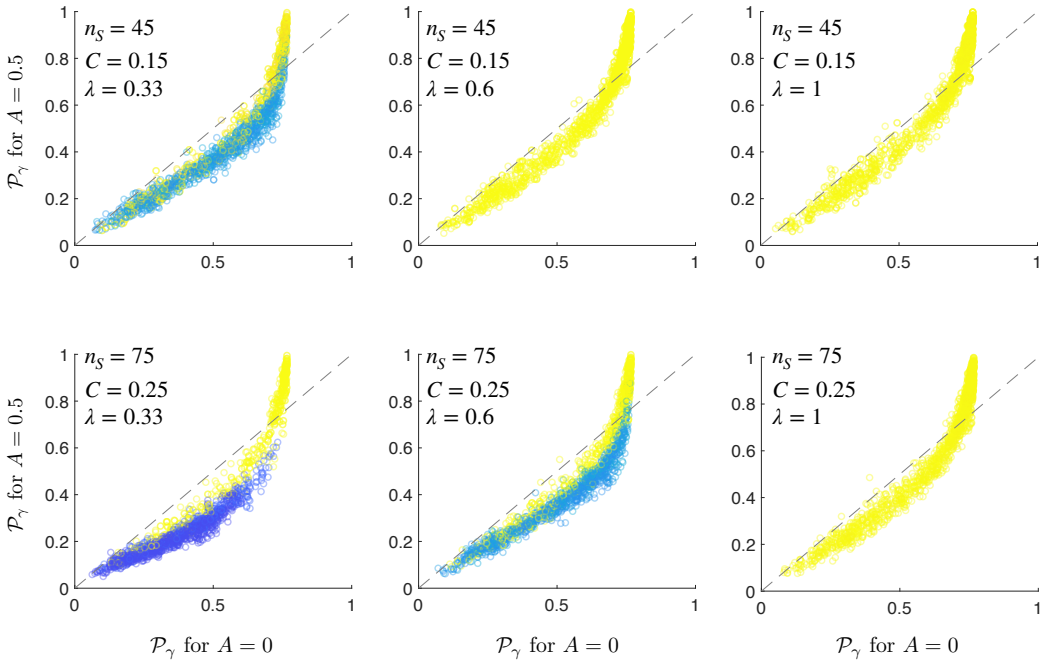

Fig. SI17. $\mathcal{P}_\gamma$ for $A = 0$ versus $A = 0.5$ with $n_P = 50$ and three levels of self limitation (λ). The top and bottom rows correspond to simpler and more complex foodwebs respectively.

1.7 Star experiment

This experiment simulated both stable-prone and unstable-prone local communities, on 10-point star landscapes. We used landscapes in which either all points or only three points can become active, mimicking low and high A values respectively. With higher A values, each temporal snapshot of the landscape graph turns sparser, thus implying fewer routes for dispersal among patches, which we approximate by allowing only three sites to be "active."

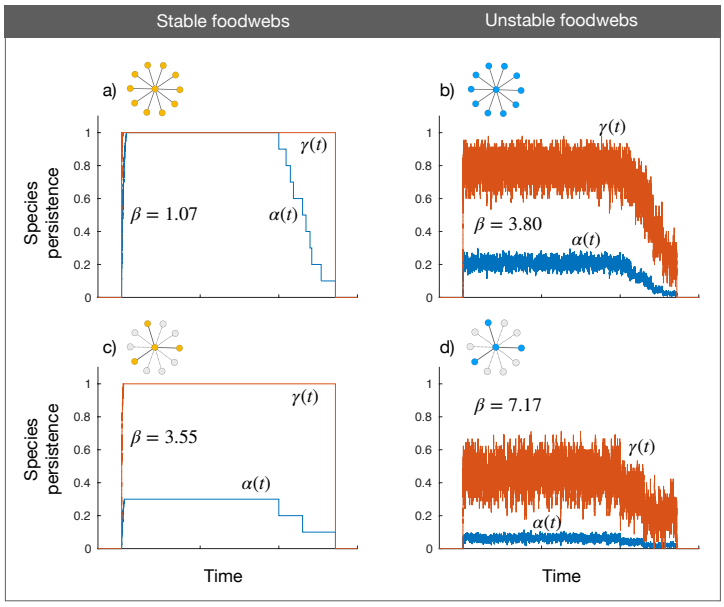

Fig. SI18. Time series of α (blue lines) and γ (red lines) diversity (species persistence) over a single simulated year, of multitrophic metacommunities on an idealized landscape of a 10-point star topology. The central site is the mainland. The time average of β diversity is shown within each plot. Parameters values are $a = 3000$, $n_S = 45$, $C = 0.2$. Plots a) and c) show the dynamics of stable communities ($T = 0$, $\lambda = 0.33$). Plots b) and d) show the dynamics of unstable communities ($T = 1$, $\lambda = 0.33$). In plots a) and b) all points (sites) are available for dispersal, representing highly synchronous landscapes. In plots c) and d) only 3 out of 10 points are available for dispersal, representing highly asynchronous landscapes.

For stable-prone local communities, all colonization attempts are successful and do not cause secondary extinctions. Thus, for sufficiently large values of a, we can assume that all active sites contain the full set of species. In this scenario, both $\mathcal{P}_\alpha$ and $\mathcal{P}_\gamma$ are maximal, while $\mathcal{P}_\beta$ is minimal. Increasing A (from Fig. SI18a to c) reduces $\mathcal{P}_\alpha$ simply by reducing the number of active sites. Conversely, if local communities are unstable-prone, two relevant competing processes

take place. The first one includes successful colonization events that do not cause secondary extinctions. This process increases $\mathcal{P}_\alpha$ due to the direct introduction of a new species in the recipient community. In the second one, colonization attempts result in secondary extinctions, leading to reductions in $\mathcal{P}_\alpha$. The temporal alternation between these two processes causes the oscillations depicted in Figs. SI18b and d and prevents $\mathcal{P}_\alpha$ and $\mathcal{P}_\gamma$ from always reaching their maximum possible values. For $A = 0$, $\mathcal{P}_\alpha$ attains low values because local instability hampers successful colonization events without secondary species extinctions. However, we do not observe a corresponding reduction in $\mathcal{P}_\gamma$, which shows there is a high among-site dissimilarity ($\mathcal{P}_\beta$). Increasing A (from Fig. SI18b to d) reduces $\mathcal{P}_\alpha$ because of reduction in active sites. However, the reduction in $\mathcal{P}_\gamma$ is relatively small because of the large values of $\mathcal{P}_\beta$. This small experiment captures the interplay between the LSFs and landscape asynchrony and how it shapes the biodiversity patterns observed in the full model.

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