Supplementary: Community structure determines the predictability of population collapse

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1. Mutualistic interaction

For the mutualism community module, we assume that competition is trait-independent but mutualistic interaction is trait-dependent. For mutualistic interactions, individual of trait $z$ of species $i$ (say plants) will interact strongly and have fitness gains from another species $j$ (say animals) in the community if their traits were similar. One could write the per-capita growth rate for a species in either of the two groups of species in the mutualism community as:

$$r_i^m(z,t,N) = \int \left( b_i^m(z) - \sum_{j=1}^{S} N_j(t) a_{ij}^m(t) + \sum_{k=1}^{A} A_k(t) \int g(z,z') p_k(z',t)(t) \right) p_i(z,t) dz$$  \hspace{1cm} (1)

Where, $S$ is the number of species in the one of the groups (species 1, 2, 3, 4) and $A$ is the number of species in other guild (species 5, 6); $g(z, z')$ is the Gaussian trait-matching function given as $g(z, z') = \exp\left(-\frac{(z-z')^2}{\sigma^2}\right)$.

where, $b_i^m(z)$ is a rectangular fitness function given as :

$$b_i^m(z) = \begin{cases} 1, & \text{if } \theta \geq z \geq -\theta \\ 0, & \text{otherwise}, \end{cases}$$

Thus, population dynamics of a species $i$ in either of the two trophic levels in the mutualism only community could be written as:

$$\frac{dN_i}{dt} = \frac{N_i}{A} \left( b_i^m(z) - \sum_{j=1}^{S} N_j(t) a_{ij}^m(t) + \sum_{k=1}^{A} A_k(t) \int g(z,z') p_k(z',t)(t) \right) p_i(z,t) dz$$  \hspace{1cm} (2)

$$\gamma_{ik}(u_i, u_k) = \int \left( \int g(z,z') p_k(z',t)(t) \right) dz' p_i(z,t) dz = \frac{\gamma}{\sqrt{2\sigma_i^2 + 2\sigma_k^2 + \gamma^2}} \exp \left( -\frac{(u_i - u_k)^2}{(2\sigma_i^2 + 2\sigma_k^2 + \gamma^2)} \right)$$  \hspace{1cm} (3)

The mean growth rate of a species in the trait axis i.e., $b_i^m(z)$ could be written as from above :

$$\int b_i^m(z) p_i(z,t) dz = \frac{1}{2} \left[ \text{erf} \left( \frac{\theta - \mu_i}{\sqrt{2}\sigma_i} \right) + \text{erf} \left( \frac{\theta + \mu_i}{\sqrt{2}\sigma_i} \right) \right]$$

where $\theta$ goes from -1 to 1 defining the boundary of the trait axis. Within this trait boundary, species will have a growth rate of 1 in the absence of mutualistic and competitive interaction.

For the dynamics of the mean trait we can write:

$$\frac{du_i}{dt} = \sigma_i^2 h_i^2 \frac{\partial}{\partial u_i} \left( r_i^m(z,t,N) \right)$$  \hspace{1cm} (4)

$$= \sigma_i^2 h_i^2 \frac{\partial}{\partial u_i} \left( b_i^m(u_i,\theta) - \sum_{j=1}^{S} N_j(t) a_{ij}^m(t) + \sum_{k=1}^{A} A_k(t) \gamma_{ik}(u_i, u_k) \right)$$  \hspace{1cm} (5)
Figure S1: Time series of all six species with the parameter values mentioned in the appendix for the mutualistic interaction community.

In this case,\[ \frac{\partial}{\partial u_i} \gamma_{ik}(u_i, u_k) = \frac{-2\gamma \sigma_i^2 (u_i - u_k)}{(2\sigma_i^2 + 2\sigma_k^2 + \gamma^2)^2} \exp \left(-\frac{(u_i - u_k)^2}{2\sigma_i^2 + 2\sigma_k^2 + \gamma^2} \right) \] (6)

And,\[ \frac{\partial}{\partial u_i} b_m(u_i) = \frac{\sigma_i}{\sqrt{2\pi}} \exp\left(-\frac{(\theta + u_i)^2}{2\sigma_i^2}\right)(1 - \exp\left(2\theta u_i / \sigma_i^2\right)) \] (7)

Since competition is trait-independent, thus\[ \frac{\partial}{\partial u_i} \alpha_{ij} = 0 \]

$A_k$ is the density of the mutualistic counterparts. In the mutualistic community module (fig. 1 main-text), $A_k$ could represent either species 1 or 2 or species 3,4,5, or 6. If, for instance, $N_i$ represents any one of the two basal species (1 or 2), then $A_k$ would be the density of any species $k$ belonging to the other guild i.e., either species 3,4,5, or 6.

Intraspecific competition for all the species was kept at 0.5 and interspecific competition was randomly assigned during each simulation from a random uniform distribution [0.001, 0.005]. Species density at the start of the simulation was kept at 1. Initial mean trait values were randomly assigned to each species until from a uniform distribution $U[-1, 1]$ until we found a set of mean trait values $u_i$ that led to feasible species densities.
We used these mean trait values to start the simulations for species collapses. Species’ trait variances for this community was randomly assigned for each replicate simulation of population collapse from a random uniform distribution [0.005, 0.06]. At each time step of population dynamics we added Gaussian white noise with mean zero and variance of 0.1.

Mean trait dynamics $u_i$ of a species $i$ followed from equation 2 of the main-text.

Example time series of species collapse in mutualistic community are shown in figure S2.

### 2. Predator-prey interactions

In the community of predator-prey interactions, competition was trait-independent but predator-prey interactions were trait-mediated. Growth rate of species $i$ for the basal species can be written as:

$$r_i^\rho(z, t, N) = \int \left( b_k(z) - \sum_{j \text{ basal sp.}} \alpha_{ij}^b(t) N_j(t) - \sum_{k \text{ consumers}} C_k(t) \int (b(z, z') p_k(z', t) dz') \right) p_k(z, t) dz$$  \hspace{1cm} (8)

Here, $b_k$ is the growth rate independent of competitive interactions and predation pressure; $\alpha_{ij}^b(t)$ captures the competitive effect of basal species $j$ on basal species $b$; $b(z, z')$ is the Gaussian predation function that captures the likelihood of an individual with trait $z$ of basal species being predated by an individual with trait $z'$ from the consumers with trait distribution given by $p_k(z', t)$. The more similar the traits are the more likely is a consumer able to successfully predate on an individual from basal species with trait $z$. Thus population dynamics can be written by integrating and substituting the above equation in equation 1 of the main-text:

$$\frac{dN_j}{dt} = N_j(t) \left( b_k(u_k) - \sum_{j \text{ basal sp.}} \alpha_{ij}^b(t) N_j(t) - \sum_{k \text{ consumers}} C_k(t)\beta_{jk}(u_i, u_k) \right)$$  \hspace{1cm} (9)

And the evolutionary trait dynamics can be written as:

$$\frac{du_i}{dt} = \sigma_i^2 h_i^2 \frac{\partial}{\partial u_i} (r_i^\rho(z, t, N)) = \sigma_i^2 h_i^2 \frac{\partial}{\partial u_i} \left( b_k \sum_{j \text{ basal sp.}} \alpha_{ij}^b(t) N_j(t) - \sum_{k \text{ consumers}} C_k(t)\beta_{jk}(u_i, u_k) \right)$$  \hspace{1cm} (10)
Figure S3: Time series of abundance and trait of all six species with the parameter values mentioned in the appendix for the predator-prey community.
Here, the function from partial derivative of the $b_k$ and $\beta_{lk}$ will look similar to what is derived in equation 6 and equation 7; $h_k^2$ is the broad sense heritability of the mean trait of the basal species $b$ and $\sigma_k^2$ is the trait variance.

$C_k$ is the density of a consumer species $k$, $\beta_{lk}$ captures the trait-mediated predation by consumer species $k$ on basal species $b$; $\sigma_k^2$ captures both intra and interspecific competition among the basal species that is independent of mean trait values. $\beta_{lk}(u_k, u_k) = \int \int b(z, z') p_k(z', t)dz' p_k(z, t)dz = \frac{b}{\sqrt{2\pi \sigma_k^2 + 2\sigma_{lk}^2 + b^2}} \exp \left( -\frac{(z - z')^2}{2(2\sigma_k^2 + 2\sigma_{lk}^2 + b^2)} \right)$; where $b$ captures the strength of predator-prey interaction between the basal species and the consumers.

Similarly, for the consumer species population dynamics can be written as:

$$\frac{dC_p}{dt} = C_p \left( d_C - \sum_{j \neq \text{consumers}} C_j(t) a_{pj}(t) + \sum_{k \in \text{basal sp.}} \int b(z, z') p_k N_k(t)(z', t)dz' - \int b(z, z'') p_l N_l(t)(z'', t)dz'' \right) p_p(z, t) dz (11)$$

Here, $b(z, z)$ is the gaussian interaction kernel for consumers and basal species with $p_k(z', t)$ being the trait distribution for the basal species $k$; $b(z, z'')$ is the gaussian interaction kernel for the top predator $l$ predating on consumer species $p$. Expanding equation 11 we get:

$$\frac{dC_p}{dt} = C_p \left( d_C - \sum_{j \neq \text{consumers}} C_j(t) a_{pj}(t) + \sum_{k \in \text{basal sp.}} \beta_{lk}(u_k, u_k) N_k(t) - E_{pl} P_l(t) \right)$$

and evolutionary trait dynamics can be written as

$$\frac{d\alpha_p}{dt} = \alpha_p \frac{\partial}{\partial u_p} \left( d_C - \sum_{j \neq \text{consumers} \ sp.} a_{pj} C_j(t) + \sum_{k \in \text{basal sp.}} \beta_{lk}(u_k, u_k) N_k(t) - E_{pl} P_l(t) \right)$$

where, $d_C$ is the mortality rate of the consumer species; $\beta_{lk}(u_k, u_k)$ captures fitness gain from trait-mediated predation of basal species $k$; $E_{pl}$ captures the predation from the top predator on the consumers (species 4, 5) in the predator-prey foodweb community. $E_{pl} = \frac{b}{\sqrt{2\sigma_k^2 + 2\sigma_{lk}^2 + b^2}} \exp \left( -\frac{(z - z')^2}{2(2\sigma_k^2 + 2\sigma_{lk}^2 + b^2)} \right)$ is also a Gaussian function.
Here, \( u_p \) is the mean trait of the consumer, \( u_k \) is the mean trait of the basal species \( k \), \( \sigma_p \) and \( \sigma_k \) are the trait variances of consumer \( p \) and basal species \( k \) respectively. And for

\[
\frac{\partial}{\partial u_p} \beta_p(u_p, u_l)(t) = \frac{-2b_p\sigma_p^2(u_p - u_l)\exp{-\frac{(u_p - u_l)^2}{2\sigma_p^2 + 2\sigma_k^2 + b^2}}}{(2\sigma_p^2 + 2\sigma_k^2 + b^2)^2}
\]

Here, \( u_l \) is the mean trait of the top predator, and \( u_p \) is the mean trait of the consumer and \( \sigma_p \) and \( \sigma_l \) are the trait variances of top predator mean trait and consumer \( l \) respectively.

And finally the dynamics of the top predator can be written as:

\[
\frac{dP_p}{dt} = P_p \left( d_p - a_{pp} P_p + \sum_{l \in \text{consumers}} E_p(l) C_l(t) \right)
\]  

(14)

and evolutionary dynamics of the top predator can be written as:

\[
\frac{dp_p}{dt} = \sigma_p^2 b_p \frac{\partial}{\partial p_p} \left( d_p - a_{pp} P_p + \sum_{l \in \text{consumers sp.}} E_p(u_p, u_l(t)) C_p(l) \right)
\]  

(15)

here, \( d_p \) is constant, \( a_{pp} \) is the density dependence term which was fixed at 0.005 for the top predator, \( u_l \) is the mean trait of the consumer \( l \) and \( u_p \) is the mean trait of the top predator.

For all the basal species, \( b_p \) was kept at 1; for the consumers and the top predators, \( d_C \) and \( d_p \) were mortality rates drawn in accordance with Petchey et al. 2008. Predator-prey interaction strength of consumers on the basal was kept at \( b = 0.005 \) and for top-predators on consumers was also kept at \( b = 0.005 \).

We ran simulations for 5000 time points with varying mean traits values for each species in the community from random uniform distribution \([-1, 1]\) until we found a set of mean trait values that led to feasible species densities. We used these mean trait values as the starting point of our simulations for population collapses in the mixed interaction community. Initial abundances of the all the species were kept at 1. Strength of predator-prey interaction both between the basal species and the consumers, and between the consumers and the top predator were kept at 0.005. Species trait variances for the competition community were randomly assigned for each replicate simulation of population collapse from a random uniform distribution \([0.007, 0.02]\). At each time step of population dynamics we added Gaussian white noise with mean zero and variance of 0.1. Mean trait dynamics \( u_i \) of a species \( i \) followed from equation 6.2 of the main-text.

3. Effective potential curves

3.1. Mutualistic interaction

For a mutualistic community, the effective potential for a species embedded in the six species community can be written as:

\[
V_m(N_i) = - \int \left( \bar{b}_i^m(u_i) - \sum_{j=1}^{N} \alpha_{ij}^m N_j + \sum_{K=1}^{A} \bar{A}_k \gamma_{ik} \right) N_i dN_i
\]

which gives:

\[
V_m(N_i) = -\bar{b}_i^m(u_i) N_i^2/2 - \alpha_{ii}^m N_i^3/3 - \sum_{i \neq j}^{N} \alpha_{ij}^m N_j N_i^2/2 + \sum_{K=1}^{A} \bar{A}_k \gamma_{ik} N_i^3/3
\]  

(16)

Here, the effective potential is evaluated for a single species in the community with the assumption that all the other species in the community are at their positive equilibrium. Here, \( \bar{A}_k \) and \( \bar{N}_i \) are equilibrium densities which means they are fixed points. Next, we estimate \( V_m(N_i) \) just before environmental forcing starts i.e., at \( t = 800 \) time point. At that time point, we estimated three quantities that accurately characterize the potential curves: a) slope of the potential curve which quantifies how stable the one-dimensional system is; b) depth of the potential curve given as: \( \min(V_m(N_i)) - \max(V_m(N_i)) \), which quantifies how resilient the system is; and c) scaled potential width, which is the distance between the tipping point and the lowest point of the
potential. Potential width quantifies the amount of perturbation a one-dimensional system such as a population can withstand before transitioning to another state [2]. We quantify these three metrics just before the start of environmental forcing for each replicate population collapses (n=100) and for each of the community modules, and try to evaluate whether different interaction types modify these stability-resilience metrics and in turn influence the utility of EWS of population collapses.

3.2. Predator-prey interactions

Similarly, for the predator-prey food-web we evaluate the effective potential of a species embedded in the community and not the entire community. This means that we restrict the evaluation of the potential to a one-dimensional system of a single species with the assumption that all the other species are at their positive equilibria. For the basal species, the effective potential can be written as at time point \(t\) as:

\[
V_b(N_p) = - \int \left( b_p(u_p) - \sum_{j \in \text{basal sp}} a_{pj} \bar{N}_j - \sum_{k \in \text{consumers}} \bar{C}_k \beta_{pk} \right) N_p dN_p
\]

which gives:

\[
V_b(N_p) = - \left( b_p(u_p) \frac{N_p^2}{2} - a_{pp} N_p^3/3 - \sum_{ppj} a_{pj} \bar{N}_j \frac{N_p^2}{2} - \sum_{k \in \text{consumers}} C_k \beta_{pk} \frac{N_p^2}{2} \right)
\]

(17)

And for the consumer species 4 and 5,

\[
V_c(C_i) = -(d_i C_i^2/2 - a_{ic} C_i^3/3 - \sum_{pqk} a_{ik} C_k \frac{C_i^2}{2} + \sum_{k \in \text{basal exp.}} N_k \beta_{ik} \frac{C_i^2}{2} - E_d \bar{P}_i \frac{C_i^2}{2})
\]

(18)

And finally for the top predator (species 6):

\[
V_p = -(d_p P_p^2/2 - a_{ip} P_p^3/3 + \sum_{k \in \text{consumers}} C_k \frac{P_p^2}{2})
\]

(19)

Here, \(\bar{N}_j\), \(\bar{C}_k\), \(\bar{P}_i\) in equation 17, 18 and 19 are considered to be at their positive equilibrium hence are considered to be fixed points. Specifically, we estimate the effective potentials of the basal species, \(V_b(N_p)\) consumers \(V_c(C_i)\) and the top predators \(V_p\) just before environmental forcing started. At that time point, we estimated three quantities that accurately characterize the potential curves: a) slope of the potential curve which quantifies how stable the one-dimensional system is; b) depth of the potential curve, which quantifies how resilient the system is; and c) scaled potential width, which is the distance between the tipping point and the lowest point of the potential. Potential width quantifies the amount of perturbation a one-dimensional system such as a population can withstand before transitioning to another state [2]. We quantify these three metrics (see Fig. 1) just before the start of environmental forcing for each replicate population collapses (n=100) and for each of the community modules, and try to evaluate whether different interaction types modify these stability-resilience metrics and in turn influence the utility of EWS of population collapses.

3.3. Quasi-potential function: Friedlin-Wentzell action potential

We numerically calculate/estimate a quasi-potential (Wentzell Potential function to be precise in our case) of the entire 6-dimensional ecological networks. Following the methods of [4, 3, 1], we now calculate the quasi-potential of the entire community modules. We would, however, like to reiterate that our motivation in this paper was to evaluate the effects of community type and interaction on the predictability of population collapse and not on the predictability of community collapse.

For a gradient multispecies ecological system one could write the potential as:

\[
V(N) = - \int r_1 dx_1 + ... + r_n dx_n
\]

However, rarely such multi-species complex ecological communities could be a considered as gradient systems, as there are more than two attractors in the system making it high dimensional and almost difficult to compute a potential function. However, there are methods to estimate the quasi-potential of such multispecies communities.
from concepts derived from stochastic deviation theory. Since our dynamical system of equation can be written as:

\[ \frac{dN_i}{dt} = f_i(N_1, \ldots, N_n) + \epsilon(t) \]

where, \( \epsilon(t) \) is a stochastic perturbation, we could estimate the quasi-potential from the stochastic deviation theory of Friedlin and Wentzell [1]. Basically, assuming that under some particular stochastic perturbation the state of the entire community goes from one state, lets say, A, to another state B, out of many other multiple states (note that for some other perturbation, the community can shift to other states as well, since there are multiple transition states), one could define the action function \( V \) as the energy that is required to overcome from state A to state B of the entire community. In that regard, the quasi-potential function can be written as:

\[ V_{AB} = 0.5 \min \left( \int_t^{t+B} \left( \sum_{i=1}^n \left| \frac{dN_i}{dt} - r_i(N) \right|^2 \right) dt \right) \tag{20} \]

Since it would be impossible to find a solution of the above equation analytically, it could approximated in the discrete form as [4]:

\[ V_{AB} = \Delta t \sum_{t=1}^{M-1} \sum_{i=1}^n \left( \left| \frac{N_i(t+1) - N_i(t)}{\Delta t} - 0.5(r_i(t+1) - r_i(t)) \right|^2 \right) \tag{21} \]

Here the time trajectory is divided into discrete steps of \( \Delta t = 5 \). Now, this quasi-potential function is for the entire community and hence multidimensional when plotted w.r.t to all the species in the communities. Naively, this means that when viewed from the state-space of a particular focal species, say species \( 1 \), the quasi-potential function or the stability-landscape will look different in comparison to when viewed w.r.t say state-space of species \( 5 \) of the community. But one can still evaluate the potential function with respect to a particular species in a community. For instance, when a species, lets say species \( 1 \), in the community is forced to collapse, it has to go through the valleys of this quasi-potential function as it moves from one state to another in the state-space of species \( 1 \). Hence, we can evaluate the stability-resilience metrics of potential slope, depth and width of a species but from the purview of a particular species to make it 1-dimensional. This means that we are looking at the quasi-potential function from only one particular species’s state-space.

Next, we numerically evaluate the quasi-potential function i.e., equation 13 in this supplementary document, from time point \( t = 0 \) to the collapse of a species that is being perturbed in the community. So in terms of equation 13, \( t \) goes from 1 to the time point \( M \), at which the species collapses. Here, \( n \) is the total number of species in the community. Then, we fit a polynomial function of order 2 to this quasi-potential function w.r.t to the state space of the species being perturbed. For instance, lets say, species \( 1 \) in the predator-prey module is being forced to collapse. In that case, the state space of species \( 1 \) would be from 0 to its maximum positive density. Thus, we fit a polynomial curve of order two with the state-space of the species in question. An example is given in figure S5. Similarly, if species \( 6 \) in the predator-prey module is being forced to collapse, we evaluate the quasi-potential (equation 13 in the supplementary text) and then fit a polynomial curve of order two of the quasi-potential w.r.t to that state-space of species \( 6 \).

From the fitted polynomial curve, we estimate the stability-landscape metrics as explained in the figure 1 of the main-text, i.e., potential slope, potential width, and depth. Similarly, we do the same thing for the mutualistic community. Results of the stability-landscape metrics are shown in figure S6-S7.
Figure S5. Predicted quasi-potential function evaluated and viewed w.r.t species 1 of the predator-prey module (left) and w.r.t to species 6 of the predator-prey module. Both the quasi-potential landscape looks different. The quasi-potential function calculated from equation 13 is regressed against the state space of species 1 (left) and state-space of species 6 (right) and fit with a polynomial curve of order 2. The predicted values of the potential from their respective polynomial model is plotted in this figure.

Figure S6: Stability-landscape metrics estimated from the quasi-potential followed from equation 13 for the predator-prey food-web. The basal species (species 1, 2, and 3) had higher potential width in comparison with the consumer (species 4 and 5) and the top predator species (species 6). In terms of potential slope and depth basal species had the highest among all the species.

Figure S7: Stability-landscape metrics estimated from the quasi-potential followed from equation 13 for the mutualistic network
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