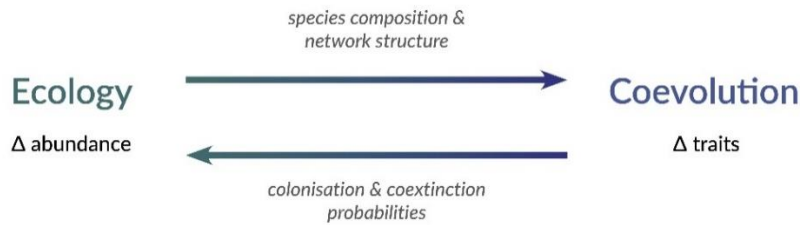


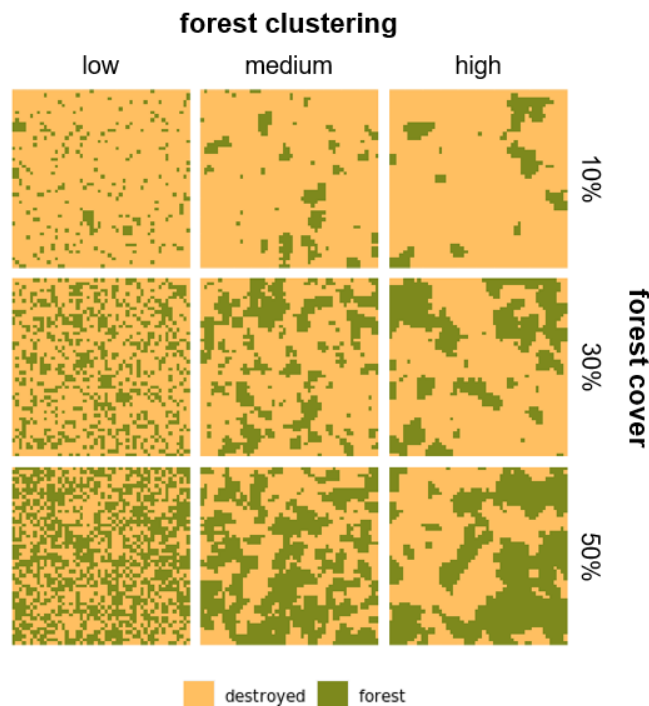
Eco-evo model

We combine a cellular-automaton-based model for spatial metacommunity dynamics with a coevolutionary model for ecological networks to simulate the coupled eco-evolutionary (eco ↔ evo) dynamics in landscapes.



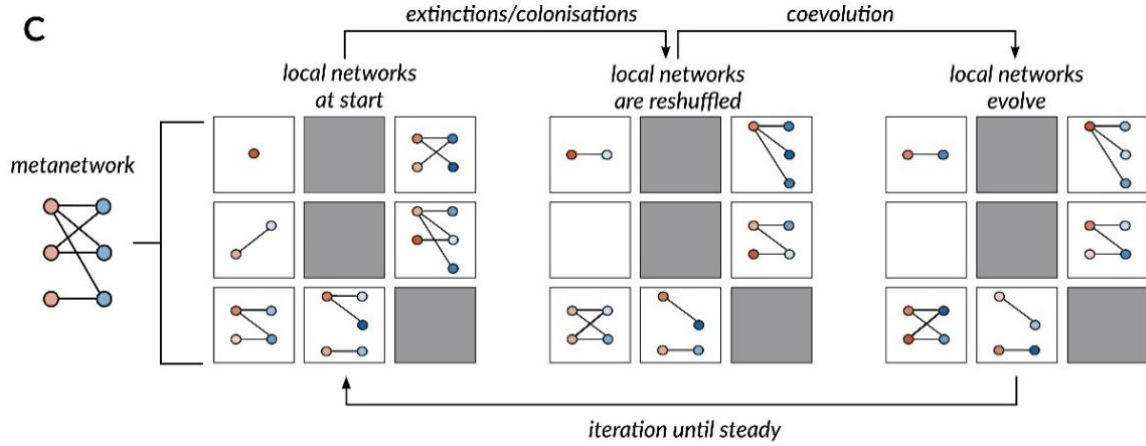
Our model includes a feedback loop whereby (1) ecological processes affect coevolutionary dynamics through species composition and local network structure, and (2) the outcome of coevolution (i.e., changes in species' traits) affects species' abundance through colonisation and extinction probabilities.

The landscapes have a dimension of 50×50 square patches. The patches are classified as “forest” or “destroyed”. We generate landscapes with varying forest cover and clustering.



Examples of generated landscapes with varying forest cover and clustering.

We perform simulations adopting an empirical host-parasite network as the metanetwork (i.e. the network of all species and interactions across the entire landscape). The network includes 45 host species and 266 parasite species. Each host species is classified as “forest specialist” or “disturbance-adapted”. We assume that forest specialists can only occur in forest patches, whereas disturbance-adapted can persist in any patch.



We used an empirical network as the metanetworks in the simulations. Each patch can contain a local network which is a subset of the metanetwork. We simulate metacommunity dynamics (extinctions and colonisations) followed by coevolution within each local network, repeating this sequence until we reach a steady state at the global scale. Extinction and/or colonisation events lead to the reshuffling of the local networks. The subsequent coevolution results in changes in trait values associated with each species in each patch (here, indicated by a change of colour of a node).

Spatial ecological dynamics

We adopted a patch dynamics perspective (Leibold et al., 2004) whereby the patches can be occupied or empty by a species. The spatial metacommunity dynamics are governed by local extinction and colonisation events which depend on the local species composition, and the degree of trait matching arising from coevolution (eco \leftarrow evo coupling). We defined trait matching at between species i and j as:

$$T_{ij} = \exp\left(-\alpha(Z_j - Z_i)^2\right)$$

where Z_i is the mean trait value of the population of species i , and α is a constant controlling the sensitivity of the differences between species' traits (hereafter "sensitivity to trait matching").

If a species is present in a patch at a given time step, it has a probability of becoming extinct at the next time step. The effective extinction probabilities are summarised in the table below. For the host, they are independent of the species composition in the patch. Conversely, the effective extinction probability of the parasite decreases with increasing number of its hosts present in the patch and their trait matching with the parasite. A parasite becomes extinct if none of its hosts are present in a patch.

Similarly, a species which is absent from a patch at a given time step has a probability of colonising that patch from one of its four nearest neighbours (assuming Neumann's neighbourhood, and a reflective boundary condition) at the next time step. The colonisation events from different patches are considered independent of each other. The effective colonisation probabilities are summarised in the table below. A disturbance-adapted host can colonise any patch with a probability that is independent of the species composition in that patch. A forest specialist host can colonise only a forest patch with a probability that is independent of the species composition in that patch. The parasite can colonise a patch where at least one of its hosts is present. Its effective colonisation probability increases with the number of hosts and their trait matching according to a saturating function.

	host	parasite
effective extinction probability	$p_{ext} = e_r$	$p_{ext} = \prod_{j=1}^J \left(1 - \frac{e_c}{j}\right) (1 - e_c T_{ij})$
effective colonisation probability	$p_{col} = c_r$	$p_{col} = 1 - \prod_{j=1}^J \left(1 - \frac{c_c}{j}\right) (1 - c_c T_{ij})$

e_r – intrinsic extinction probability of host

e_c – intrinsic extinction probability of parasite

c_r – intrinsic colonisation probability of host

c_c – intrinsic colonisation probability of parasite

Coevolution

Following extinction and colonisation events at a given time step, we simulated the coevolution of the species present in each patch, thus incorporating the effect of spatial metacommunity dynamics on coevolution (eco \rightarrow evo coupling). We employed the model proposed by Andreazzi et al. (2017, 2020) for antagonistic networks. This model incorporates a selection gradient which connects the evolution of a single trait with the mean fitness consequences of interactions between species and with the environment. The mean trait evolution of species i over a time step, t , is described by:

$$Z_i^{t+1} = Z_i^t + \varphi(S_i^t + E_i^t)$$

where φ is a compound parameter that affects the slope of the selection gradient and is proportional to the additive genetic variance, whereas S_i^t and E_i^t are the partial selection differentials caused by selection imposed by interactions and environment, respectively.

We assume that the trait change driven by interactions, S_i^t , depends on the trait matching between interacting species:

$$S_i^t = m_i \sum_{j, j \neq i}^N q_{ij}^t I_{ij}^t$$

where n is the number of species in the local network, m_i is the level of coevolutionary selection and a measure of the relative importance of interactions in trait evolution (hereafter strength of coevolutionary selection), and I_{ij}^t is the phenotype selected by the interaction between species i and j (see below). q_{ij}^t describes the evolutionary effect of species j on species i and is defined as:

$$q_{ij}^t = \frac{a_{ij} \exp\left(-\alpha(Z_j^t - Z_i^t)^2\right)}{\sum_{k, i \neq k}^N a_{ik} \exp\left(-\alpha(Z_k^t - Z_i^t)^2\right)}$$

where a_{ij} is an element of the binary adjacency matrix, of the local network. Note that the local network is a subset of the metanetwork.

We assume that the phenotype selected by the interaction between two species, I_{ij}^t , depends on the guild. For both the parasite, selection favours trait matching, and thus, $I_{ij}^t = Z_j^t - Z_i^t$. Conversely, for the host, selection favours trait mismatch if the trait difference is less than or equal to the critical mismatch, ε (if $|Z_j - Z_i| \leq \varepsilon$). Note that selection can either increase or decrease the resource's trait

value. Thus, $I_{ij}^t = Z_j^t - Z_i^t + \varepsilon$ if $Z_j < Z_i$, and $I_{ij}^t = Z_j^t - Z_i^t - \varepsilon$ if $Z_j > Z_i$. Otherwise, (if $|Z_j - Z_i| > \varepsilon$), the consumer has no effect on the resource's fitness, and $I_{ij}^t = 0$.

The trait change driven by the environment, E_i^t , is defined as:

$$E_i^t = (1 - m_i)(\theta_i - Z_i^t)$$

where θ_i is the environmental optimum of species i (i.e. the phenotype favoured by the environmental selection). For we sample θ_i from normal distributions with different means for disturbance-adapted and forest specialist hosts. θ_i of a parasite is calculated as the average θ_i of all its hosts. We assume that environmental selection is the sum of the effects of all selective pressures that are not related to species interactions. Note that the relative weights of the two selective pressures (i.e. the interactions and the environment) can be controlled by parameter m_i ($0 \leq m_i \leq 1$). For example, $m_i = 0$ or $m_i = 1$ represent extreme scenarios where the trait change is driven solely by the environment or the interactions, respectively.

Finally, species which lack interaction partners in a given patch (e.g. due to their partners becoming locally extinct), evolve towards their environmental optima according to:

$$Z_i^{t+1} = Z_i^t + \varphi(\theta_i - Z_i^t)$$

Model versions

- v1 – ecological dynamics only (no coevolution, no rewiring)
- v2 – eco-evo dynamics without interaction rewiring (v1 with coevolution, described above)
- v3 – eco-evo dynamics with rewiring of local interactions at every timestep based on local trait matching (v2 with rewiring)