Box 1. Meta-ecosystem eco-evolutionary network model.

To explore the effect of evolutionary and ecological networks on meta-ecosystem dynamics, we propose a process-based approach connecting 1) gene interaction networks to a trait distribution (Figures 1 and 2) and 2) trait distributions to predator-prey interaction strength (Figure 3). The meta-ecosystem contains P patches and S species per patch. Gene interaction networks range from traits governed by additive genetic variance to a gradient of epistasis and pleiotropy to produce a trait distribution with different variance for each species in each patch (Figure 2)[17–19,21,22,25,58].

Trait distributions obtained from additive or non-additive processes are used to obtain each predator-prey interaction strength extending previous food web models[35,59,60]. We generalize the function γ_{ixy}^t, represented as a Gaussian function describing the rate with which predator y with trait value z_y^t consumes prey x with trait value z_x^t in patch i at time t, as

$$\gamma_{ixy}^t = \frac{1}{N}\left(exp\left[-\left(z_y^t - z_x^t\right)^2\right] + 2\alpha\left[sgn(z_y^t - z_x^t)\left(1 - exp\left(-z_y^t - z_x^t\right)^2\right) + sgn(\alpha)\right]\right), \quad (1)$$

where N is a normalization constant, $sgn(X)$ is the sign function and α is the prey selection asymmetry. For $\alpha = 0$, -1, and 1, predators prefer common prey (Figure 3a, green), rare prey with more distant trait values (Figure 3a, blue), and rare prey with less distant trait values (Figure 3a, red), respectively. The interaction strength (Figure 3b-d) between prey x for a specific intraspecific niche width $(ianw)$ of the predator y in patch i at time t can then be approximated as

$$a_{ixy}^t = \int_{ianw} \gamma_{ixy}^t D(x)^t D(y)^t \mathrm{d}x\mathrm{d}y, \quad (2)$$

where $D(x)$ and $D(y)$ are the density of the prey and predator, respectively. The community matrix containing the interaction coefficients between species x and y in patch i at time t and the connectivity obtained from the species interspecific niche width $(ienw)$[59,60] is given by $A = [a_{ixy}^t]$. The phenotypes after interaction selection for each prey selection asymmetry scenario and before reproduction can be used to calculate fitness using a fitness gradient approach in the additive scenario[61] or without having to assume a particular fitness function in the non-additive scenario[62]. Fitness will then determine the ecological dynamics that is represented as a spatial network of local interaction networks.

The model can be run for many generations with each iteration containing interaction selection, mating and migration to compute the community matrix and the Jacobian for a gradient of dispersal values, following the dispersal between patches i and j, using the dispersal matrix, $D = [d_{ij}]$. The Jacobian can be used following the S-map or other stability methods to study the effect of gene interaction networks, prey selection asymmetry, intra- and inter-specific niche width, and dispersal dynamics on the stability of local food webs and the meta-ecosystem[8,63].