Detection of eco-evolutionary dynamics in metacommunities using Joint Species Distribution Models

Jelena H. Pantel, Ruben J. Hermann

Ecological Modelling, Faculty of Biology, University of Duisburg-Essen, Universitätsstraße 5, 45141 Essen, Germany

1 Title

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2 Abstract

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3 Introduction

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4 Methods

4.1 Simulation model

We simulated growth and competition dynamics for a multi-species assemblage in a patchy landscape, with site variation in one environmental property (Figure 1).

4.1.1 Environmental variation

Population growth for species in the metacommunity simulation follows a Leslie-Gower model (a discrete-time version of a Lotka-Volterra model (Beverton and Holt 1957) (Leslie and Gower 1958)). We consider the impact of trait evolution for growth using a discrete time quantitative genetic model of evolutionary rescue (**?**). The model for population size is as follows:

$$N_{i,t+1} = \frac{\hat{W} e^{\frac{-[(\frac{w+(1-h^2)P}{P+w})(E-x_{i,t})]^2}{2(P+w)}} N_{i,t}}{1 + \alpha_{ii} N_{i,t} + \sum_{j \neq i}^{S} \alpha_{ij} N_{j,t}}$$
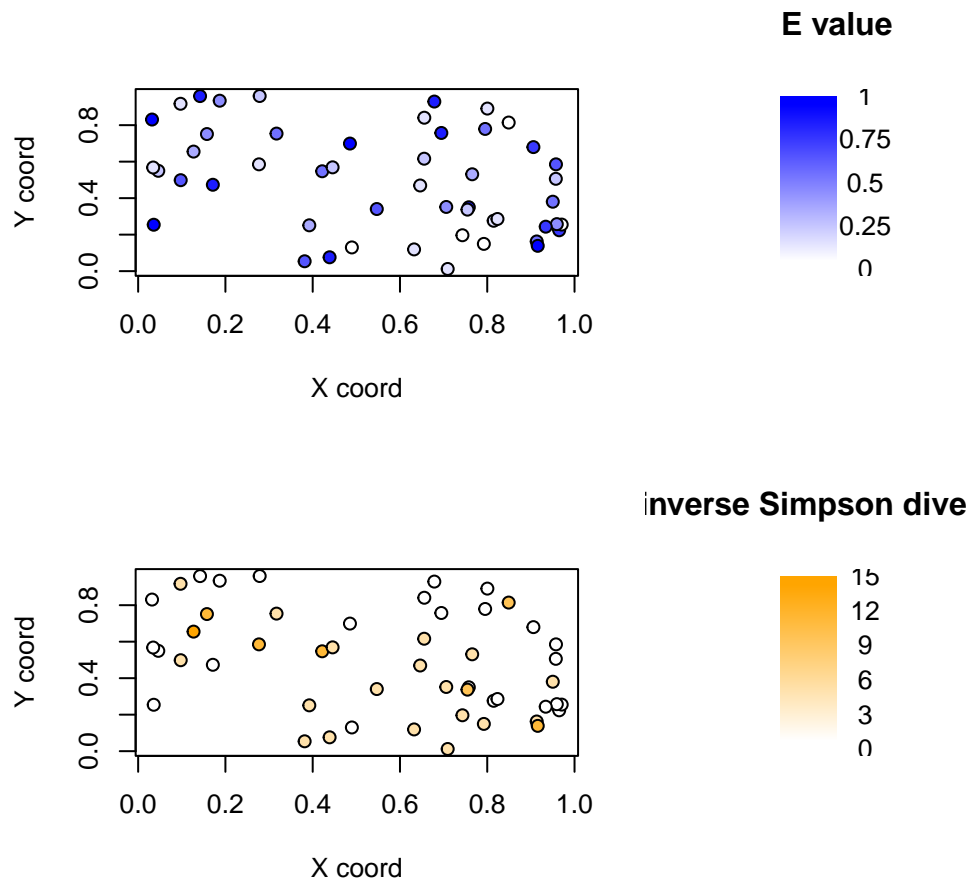
Figure 1: 1. Spatial maps showing position of all 50 sites in the simulation, their value for the single environmental variable E, and their value for initial Simpson's diversity at the beginning of the simulation.

21 where N_i, t is the population size of species i at time t, $\hat{W}$ is calculated as $\hat{W} = W_{max}\sqrt{(\frac{w}{P+w})}$, W_{max}

22 is the species' maximum per-capita growth rate, w is the width of the Gaussian fitness function (which

23 determines the strength of selection, as increasing values indicate a weaker reduction in fitness with distance

24 from optimum trait value), P is the width of the distribution of the phenotype x, h^2 is the heritability of

25 the trait x, E is the local environmental optimum trait value, $x_{i,t}$ is the trait value of species i at time t,

26 α_{ii} is the intraspecific competition coefficient (the per capita impact of species i on itself) and α_{ij} is the

27 interspecific competition coefficient. Populations have a critical density N_c, below which the population is

28 subject to extinction due to demographic stochasticity at a probability of p (**?**).

29 This model was used in Pantel & Becks (**?**) to evaluate the consequences of adaptive evolution for coexistence

30 in a three-species system. To expand this model to a metacommunity, we consider the evolution of multiple

31 species ($S = 15$) in a landscape of patches ($k = 50$). The patches have values of an environmental property E

32 (drawn from a uniform distribution ranging from 0 to 1) that determines the local optimum phenotype $E =$

33 x_{opt}, i.e. where species experience their absolute fitness W_{max}, and patches also have spatial locations X and

34 Y (both drawn from U(0, 1)). The patches thus have a connectivity matrix $\mathbf{D}$ (here given by their Euclidean

35 distance), as well as a connectivity matrix $\mathbf{C}$ that is a Gaussian function of $\mathbf{D}$ and species dispersal rate d_i.

36 To simulate trait evolution together with species growth and competition in the landscape, we used parameter

37 values of $W_{max} = 2$, $P = 1$, $w = 10$, $N_c = 100$, and $p = 0.001$. The simulated metacommunity was initialized

38 in a way that mimics community assembly in small vernal pools that periodically flood (and thus are reset

39 seasonally). In the simulated pool system, local communities are drawn at random from the regional species

40 pool, and thus their initial degree of maladaptation in the pool is random as well. The initial species richness

41 of each site s_{0k} was drawn from a random Poisson distribution, $s_{0k} \sim Pois(0.75)$, the initial population size

42 for all species $N_{0i} \sim Pois(10)$, and the initial degree of maladaptation $\beta_{i0} \sim Gamma(0.75, 1)$. From this

43 β_{i0}, the initial distance to the local patch's optimum phenotype was calculated as $d_{i0} = \sqrt{B_{i0}(w + P)}$ and

44 the initial trait value for each species x_{i0} was calculated by subtracting d_{i0} from the local environmental

45 optimum value E_k (Appendix S1, Figure S1.1).

46 The species interaction matrix was fixed throughout the simulation, with $\alpha_{ii} = 0.00125$ and

47 $\alpha_{ij} \sim U(0.0015, 1)$. After draws for all random parameter values, the same resulting initial com-

48   munity was used for all simulations, to allow direct comparison across dispersal and heritability

49   values. Simulations were run across a range of dispersal values (identical for all species; $d = 0$,

50   $10^{-9}, 10^{-8}, 10^{-7}, 10^{-6}, 10^{-5}, 10^{-4}, 10^{-3}, 10^{-2}$, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1) and heritability

51   values (identical for all species: $h^2 = 0$, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1). The simulations were run

52   in MATLAB (version R2023a) for 1000 time steps and produced records of N_{ikt} and x_{ikt}. To test the impacts

53   of strength of selection and environmental variability, we repeated simulations at a single, representative

54   level of heritability and dispersal ($d = 10^{-3}$, $h^2 = 0.1$) in four different scenarios: Scenario 1 (weak

55   selection, fixed environment: $P = 1, w = 10, v[E] = 0$), Scenario 2 (strong selection, fixed environment:

56   $P = 0.1, w = 0.2, v[E] = 0$), Scenario 3 (weak selection, variable environment: $P = 1, w = 10, v[E] = 0.01$),

57   and Scenario 4 (strong selection, variable environment: P = 0.1, w = 0.2, v[E] = 0.01). Environmental

58   variability was implemented by adding random noise to E_k every 10 time steps ($E_{k,t+1} \sim N(E_{k,t}, v[E])$).

59   *Statistical model*

60   To determine the relative influence of environmental and spatial properties, intra- and interspecific population

61   dynamics, and evolutionary dynamics for community structure, we applied hierarchical modelling of species

62   communities (HMSC, (**?**) (**?**)) to model the abundance at each site and year for each species N_{ikt}. The

63   abundance values were modeled as $N_{ikt} \sim N(L_{ikt}, \sigma_2)$, where the linear predictors **L** are the sum of fixed and

64   random effects $\mathbf{L^F} + \mathbf{L^R}$ (**?**). The fixed effects were (1) E_k, the value of the site's environmental parameter

65   (predictor 1), (2) the value of each species' population size the time step before $N_{ik,t-1}$ (predictors 2-16;

66   see (**?**)), (3) the absolute value of the change in each species' trait value from the previous time step to

67   the next $|\Delta x_{ik,t-1 \to t}|$ (predictors 17-31), (4) and an interaction term for population size by change in trait

68   value $N_{ik,t-1} \times |\Delta x_{ik,t-1 \to t}|$ (predictors 32-46), which led to a total of 46 predictors. The random effects

69   were modeled at the site-level ($\epsilon_{ik} \sim N(0, \Omega^S)$, where Ω^S is the site species-to-species covariance matrix)

70   and at the time step level ($\epsilon_{it} \sim N(0, \Omega^T)$, where Ω^T is the temporal species-to-species covariance matrix)

71   using a latent variable approach. In this approach, species-to-species covariance matrices are computed as

72   $\Omega = \lambda \top \lambda$, where λ are the loadings of each species with latent variables, and latent variables are modeled as

73   $\epsilon_{ik} = \sum_B \eta_{kB} \lambda_{Bi}$ (site) and $\epsilon_{it} = \sum_B \eta_{tB} \lambda_{Bi}$ (time) for B latent variables considered (**?**). The spatial latent

74   variables represent a spatial model, where species respond to some latent spatial predictor associated with

the *xy* coordinates of the sites (**?**). Analysis and was conducted in R (version 4.2.3) using packages 'Hmsc'

and 'R.matlab' ((**?**); (**?**)).

5 Results

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6 Discussion

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7 References

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8 Figures & Tables