APPENDIX A: EXPANDING CAPS TO MORE THAN TWO PROCESSES

In the model presented in the main article, both neutral and niche processes are represented by a single axis for simplification, corresponding to two community attributes: the dispersal limitation and the niche width, which are two parameters of the model. However, these processes may not be limited to a single parameter. For example, neutral models often consider constant immigration of individuals speciation into the community from a regional species pool to avoid monodominance of a single species [1-3]. This has been shown to influence the structure of the community [4, 5]. Implementing immigration (or speciation) plus dispersal limitation within the local community, as well as niche selection, means that three corresponding axes will be needed in CAPS (Figure A1). Any model with parameters lying on the niche axis is therefore a niche process, whereas any model with parameters lying on the plane defined by the dispersal and immigration (or speciation) axes is a neutral process (Figure A1). We therefore have a neutral plane instead of a neutral axis. Nonetheless, it is still possible to assess a composite process with respect to its neutral and niche components, like for the two-dimensional case, by using the distance from the neutral plane and the distance from the niche axis, respectively, and by comparing the values of the corresponding patterns (Figure A1). Similarly, niche axes such as distance between niche optima can also be added to the CAPS, and the measures of distance can simply be generalised to more complex dimensions.

Although beyond the scope of this paper, more processes (or additional complexity in the neutral and niche processes) and environmental configurations, can therefore be included as additional dimensions, to test not only if, but under which community and environmental attributes the continuum hypothesis is true or not. As shown by previous studies [4, 5], factors such as the immigration rate from a regional pool of species, the ratio between niche separation and number of species, the spatial configuration of the environment (such as environmental heterogeneity and distribution – or rather the ratio between dispersal limitation and these factors), are particularly likely to be important to understand when the neutral-niche continuum holds or not, because they affect how the environment can act as a dispersal barrier, and therefore change the potential for mass-effect to occur. To this end, different dispersal kernels would be important to consider, especially those with fat tails allowing for long-range dispersal events. Adding other processes to CAPS, such as density dependence [6, 7], non-neutral dispersal kernels [8], variable niche optima [9], trade-off between dispersal limitation and niche separation (corresponding to patch-dynamics, the last of the four meta-community paradigms) [10], or R* relative competitive ability [11], is likely to further improve understanding of when the continuum holds and when it does not.

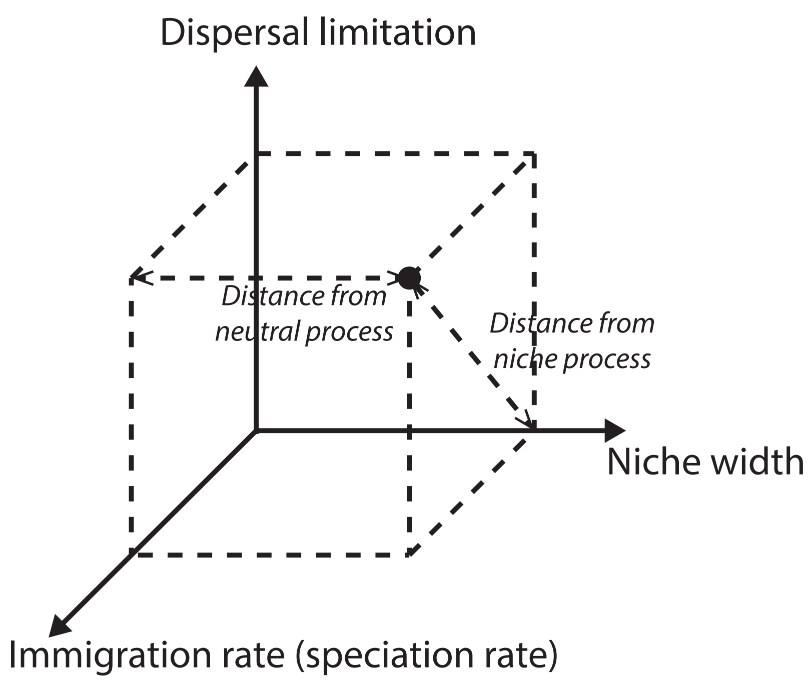

Figure A1. A three dimensional Community Assembly Phase Space. The neutral plane, representing a neutral process, is defined by the dispersal limitation and the immigration (or speciation) rate axes, whereas a niche process is represented by the niche axis. Processes are characterised by their position in the space as shown by the black circles, and the value of the patterns can be computed, as shown by the different diameters of the circles. A composite process can therefore be compared to the corresponding neutral and niche processes.

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APPENDIX B: NEUTRAL, NICHE AND COMPOSITE MODEL IMPLEMENTATION AND SIMULATION PARAMETERS

(a) Model Implementation

Neutral model:

The neutral model only accounts for the neutral filter. In the neutral model, each species has a probability of reaching a cell, corresponding to the probability of at least one individual of this species reaching the cell.

The probability of 1 individual i_l from species i reaching the cell is given by the following dispersal function:

$$^{ne}S_i(i_j) = \exp\left(\frac{\ln(0.01)}{d^2}r^2\right), \qquad \text{(B1)}$$

where r is the distance from the source to the focal cell, and d the distance for which $^{ne}S_i(i_j) = 0.01$ (d is the dispersal ability, i.e. the inverse of dispersal limitation). Given two individuals i_j and i_k of species i, considering that the events of i_j and i_k reaching the cell are independent of each other, the probability of at least one of them reaching the empty cell can thus be calculated using the classic probability of the union:

$$^{ne}S_i(i_j \cup i_k) = {}^{ne}S_i(i_j) + {}^{ne}S_i(i_k) - {}^{ne}S_i(i_j \cap i_k)$$

$$^{ne}S_i(i_j) + {}^{ne}S_i(i_k) - {}^{ne}S_i(i_j) \times {}^{ne}S_i(i_k \vee i_j)$$

$$^{ne}S_i(i_j) + {}^{ne}S_i(i_k) - {}^{ne}S_i(i_j) \times {}^{ne}S_i(i_k), \qquad \text{(B2)}$$

By extension, given a third individual i_l:

$$^{ne}S_i(i_j \cup i_k \cup i_l) = {}^{ne}S_i(i_j \cup i_k) + {}^{ne}S_i(i_l) - {}^{ne}S_i(i_j \cup i_k) \times {}^{ne}S_i(i_l), \qquad \text{(B3)}$$

This is applied iteratively until all individuals from species i are considered. The result is ${}^{ne}S_i = {}^{ne}S_i(\cup\, i_j)$, the probability of at least one individual i_j of species i reaching the focal cell.

In practice, computing ${}^{ne}S_i$ over all individuals is too computationally intensive. To overcome this problem, we only applied the iterative process to the individuals closer than d, *i.e.* at the local scale. We therefore compute an approximation ${}^{ne}S_{i.}'$ of ${}^{ne}S_{i.}$, corresponding to the probability of an individual from the local community or from the regional community reaching a cell, and based on Eqn B2:

$$ {}^{ne}S_i' = {}^{ne}S_i(\cup\, i_j for r < d) + m \cdot \frac{n_i}{\sum_j n_j} - {}^{ne}S_i(\cup\, i_j for r < d) \times m \cdot \frac{n_i}{\sum_j n_j} \quad \text{(B4)} $$

where m is the proportion with which the regional community influences the neutral process with respect to the local community, i.e. represents long distance dispersal, and n_i is the abundance of species i. Since our purpose is to model Gaussian-like dispersal with no long distance dispersal, we kept it low and used m=0.1 in the simulations. The probability of species i colonizing a cell in the neutral model therefore becomes:

$$ {}^{ne}R_i = \frac{{}^{ne}S_i'}{\sum_j {}^{ne}S_j'}, \quad \text{(B5)} $$

<u>Niche model:</u>

The niche model only accounts for the niche filter. In the niche model, we consider that there is no dispersal limitation, and that any species can reach any cell. Each species then has a survival probability ${}^{ni}S_i$, which equals to its fundamental niche $\lambda_i(E)$ (Eqn B6) [1, 2], and the probability of having species i colonizing a cell is given by Eqn B7.

$$ S_i = \lambda_i(E) = \exp\left(\frac{-(E-\mu_i)^2}{2\sigma^2}\right), \quad \text{(B6)} $$

$$R_i = \frac{S_i}{\sum_j \; S_j}, \qquad \text{(B7)}$$

where μ_i is the niche optimum of species i, and σ its niche width (equal for all species). For infinite niche width, we have λ_i=1 for all E values, i.e. complete niche overlap.

<u>Composite model:</u>

The composite model accounts for both filters, and therefore has to consider the probability of a species reaching an empty cell, and surviving in this cell. Here, these two probabilities are independent, so the joint probability can be simply computed as the product of the two. We thus get:

$$^{m}S_i = {}^{ne}S_i' \times {}^{ni}S_i, \qquad \text{(B8)}$$

And the probability of species i colonizing a cell therefore becomes:

$$^{m}R_i = \frac{^{ne}S_i' \times \; S_i}{\sum_j {}^{ne}S_j' \times \; S_j}, \qquad \text{(B9)}$$

<u>Equivalence between species vs. between individuals:</u>

Note that to allow for a smooth transition from the neutral-model to the species-sorting paradigm in the two-dimensional CAPS considered here (Figures 1b, C1), we released the strict assumption of equivalence between individuals as implemented by previous models [1, 2]: ($^{ne}S_i = {}^{ne}S_i(i_1) + {}^{ne}S_i(i_2) + \cdots + {}^{ne}S_i(i_n)$. This equation is <1 and correspond to a probability only if two different propagules cannot arrive in the focal cell, in which case $^{ne}S_i(i_j \cap i_k) = 0$. This is obviously not the case in our model, and this equation produces a score rather than a probability. We assumed instead equivalence between species ($^{ne}S_i =$

${}^{ne}S_i(i_1 \cup i_2 \ldots \cup i_n)$). Doing so ensures that for S species under infinite dispersal, each species will have a probability ${}^{ne}R_i=1/S$ of colonising any location in the neutral model, and that the composite model then becomes equivalent to a niche model. Individuals from different species are therefore not strictly equal, because there is a density-dependence effect, but species remain equal [3]. By contrast, using the simple sum instead of equation B3 would correspond to strict equivalence between individuals, but would make the composite process sensitive to the relative abundance of the species for infinite dispersal rather than representing pure species-sorting, as assumed by the niche process.

Equation B3 implies that as dispersal and the number of individuals of a species increase, ${}^{ne}S_i$ will converge towards 1. In other words, ${}^{ne}S_i$ will saturate as the abundance of a species increases, and saturation will occur faster for wide dispersal kernels. We can compute an estimate of the relationship between ${}^{ne}S_i$, d, r and the species abundance n_i by considering that all individuals in a species are equidistant from the focal cell. In that case, ${}^{ne}S_i(i_j) = {}^{ne}S_i(i_k) = \exp(\ln(0.01)\times r^2/d^2)$ in Eqn B1, and we get the following equation.

$$ {}^{ne}S_i = \sum_{k=1}^{n}(-1)^{k-1}\times C_n^k\, {}^{ne}S_i\ (i_k)^k, \qquad \text{(B10)} $$

By contrast, using the simple sum [1,2] provides the score ${}^{ne}S_i = \text{n} \times {}^{ne}S_i(i_j)$. The outputs of the two equations (Figures B1 and B2) shows that the saturation effect occurs when individuals are close to the focal cell, but that using equation B3 gives a higher chance of reaching the focal cell to species whose individuals are at intermediate distance than when using the simple sum.

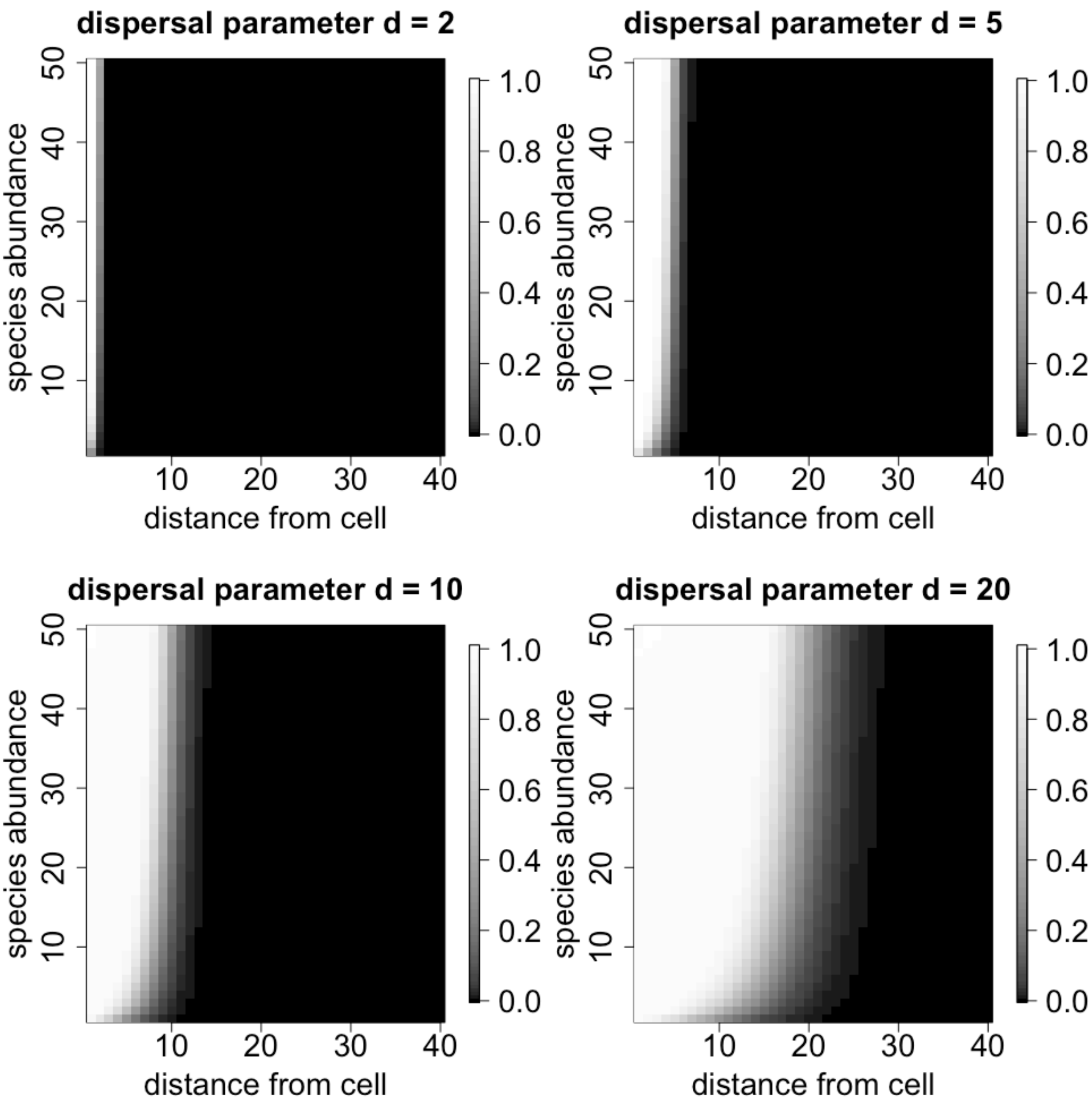

Figure B1. Probability of at least an individual of a particular species to arrive in a focal cell with respect to the species abundance and the distance between the focal cell and other individuals from the same species (assuming all individuals are at the same distance), based on Eqn B3.

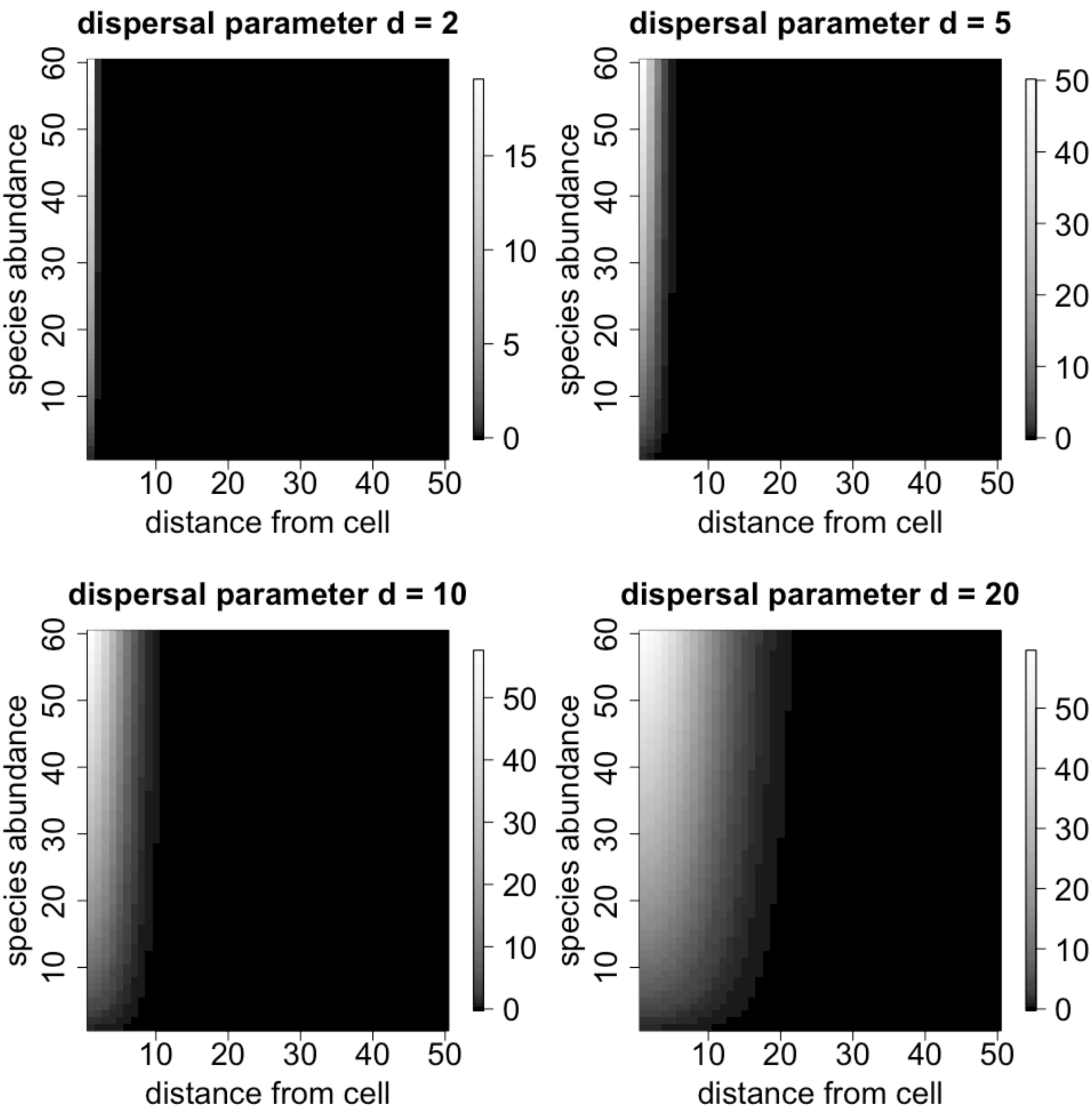

Figure B2. Score obtained by summing the probability of all individuals of a particular species to arrive in a focal cell with respect to the species abundance and the distance between the focal cell and other individuals from the same species (assuming all individuals are at the same distance).

To control for the saturation effect, one should use ${}^{ne}S_i(i_j \cup i_k) = {}^{ne}S_i(i_j) + {}^{ne}S_i(i_k) - sat \times {}^{ne}S_i(i_j) \times {}^{ne}S_i(i_k)$ instead of equation B3, with $0 \leq sat \leq 1$ as an extra axis (see Appendix A). Note that ${}^{ne}S_i$ is then not a probability anymore since it can be > 1, but is a score. Varying *sat* therefore allows for transiting from individual equivalence (but departure from pure species-sorting for infinite dispersal) to species equivalence (complying with species-sorting for infinite dispersal). Here, we used *sat* = 1 to keep the complexity of the model low and more clearly analyse the results with species-sorting being a limiting case of the composite model.

(b) Simulation parameters

We modelled 100 species, whose niche means were regularly spaced from 0.5 to 99.5 by an increment of 1. We varied the strengths of the neutral and niche filters by modifying the dispersal limitation (varying d, from 20,10, 5 to 2 cells) and the degree of niche separation (varying σ, from 200, 100, 50, 25, 10 to 5). The spatial distribution of the environmental variable E was generated using a Gaussian random field (Package *gstat* version 1.0-19 in R 3.0.2) [4, 5] with the range parameter of spatial autocorrelation set at 5 (large values result in high spatial autocorrelation). Since E follows a normal distribution, it was then transformed using its cumulative distribution function to obtain a uniform distribution, and rescaled between 0 and 100 (Figure C3). Note that we also performed simulations for 60 species in an environment generated with a range parameter of 10, but results were similar and thus not presented here. We initialised simulations by filling cells with randomly assigned individuals, with all species equally abundant. Initialising individuals based on their niche preference (i.e. using the niche process) led to the same results in the model. During each iteration 25% of individuals were randomly removed to represent ecological drift and the level of drift only affected the rate of convergence. We ran 1000 iterations for all simulations, replicating simulations 50 times for each parameter combination. Real convergence cannot be achieved in the model due to ecological drift except for strict niche separation. However, preliminary simulations with 5000 iterations have led to similar results, and 1000 iterations were thus kept here for consistency. As immigration from a species pool was not implemented in the model to reduce complexity, we prevented monodominance by randomly assigning one individual of each extinct species to an empty location before each iteration.

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APPENDIX C: SUPPORTING FIGURES

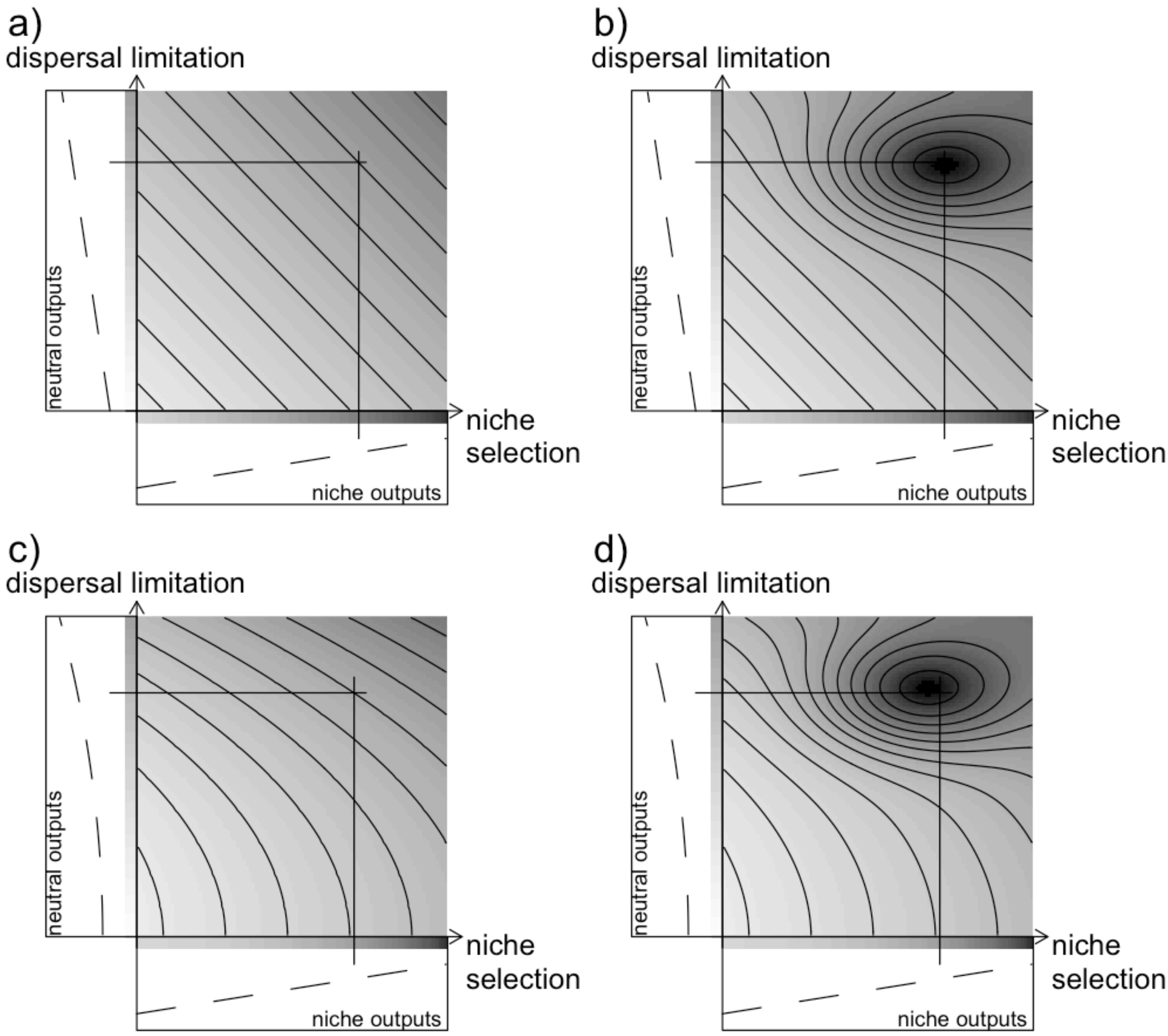

Figure C1. Theoretical representations of a pattern in the phase space delimited by neutral and niche model outputs. The grey scale represents the hypothetical value of a pattern, for example the AUC of the rank-abundance distributions. The x-axis, when niche selection is null, corresponds to a neutral model outputs. The y-axis, when dispersal limitation is null, corresponds to a niche model outputs. Each point of the space therefore corresponds to a combination of neutral and niche processes, i.e. to a composite model. a) Neutral and niche model outputs increase linearly with niche selection and dispersal limitation, and the composite model outputs lie between the neutral and niche model outputs for the same dispersal limitation and niche selection, i.e. corresponds to the neutral-niche continuum, and the isolines go from one axis to the other. b) in some part of the space, the composite model outputs lie outside of the neutral and niche model outputs for the same dispersal limitation and niche selection, and some isolines do not go from one axis to the other anymore. c,d) same example when the niche model outputs do not increase linearly with niche selection: the isolines are not linear.

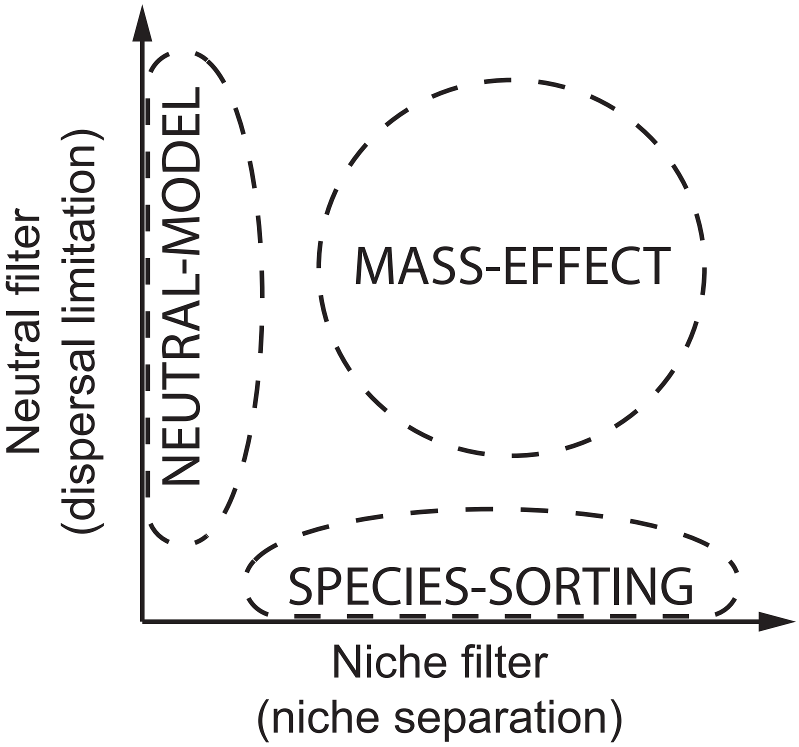

Figure C2. Three metacommunity paradigms qualitatively positioned in the community assembly phase space for the simulations performed in this study. Each axis represents the value of a parameter for the neutral and niche filters: dispersal limitation and niche separation. CAPS is not restricted to two axes, but is versatile in the number of filters it can accommodate (Appendix A). By quantifying the differences community patterns depending on the values of the parameters, it will be possible to determine the boundaries between the three paradigms. This representation is similar to Figure 1 in Logue *et al*. (2011). However, here the axes refer to community attributes, rather than characteristics of the environment, such as heterogeneity, as in Logue *et al.* (2011), because we did not explore the effect of varying the environment in this study. Axes representing characteristics of the environment can nonetheless be represented in CAPS.

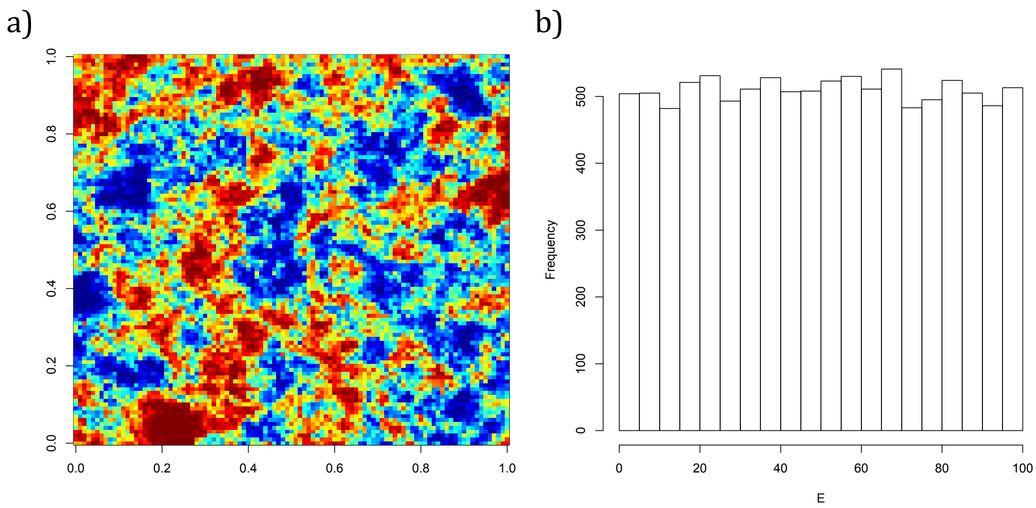

Figure C3. a) The configuration of the environmental data for a range coefficient of 5. b) The corresponding histograms of the environmental variable *E*.

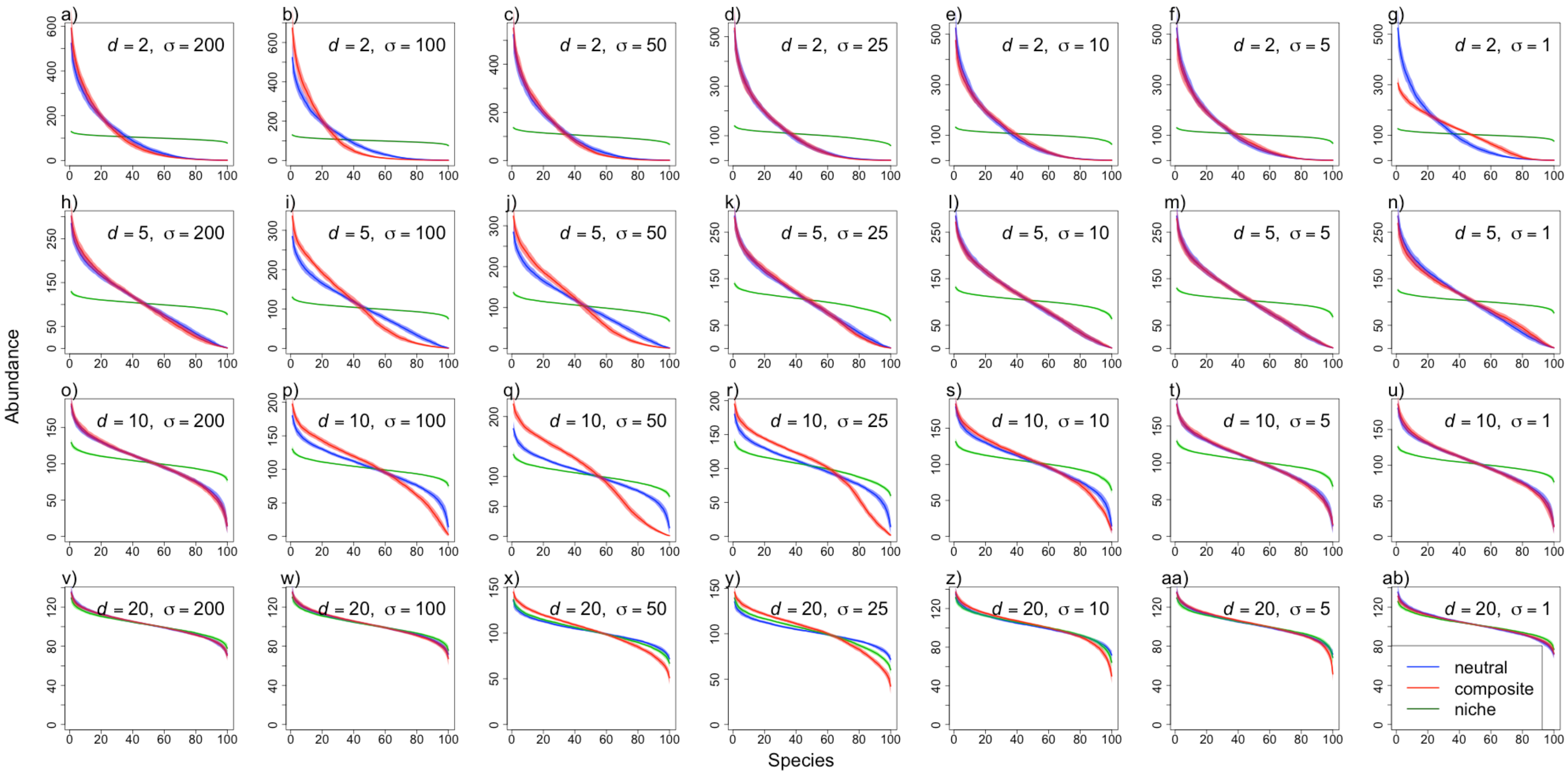

Figure C4. Rank abundance distributions for the range of neutral and niche parameters used in simulations. The shaded areas represent the area between the 25% and 75% percentiles. The bottom-left figure corresponds to low dispersal limitation and niche separation (large *d* and σ) and is close to spatially random.

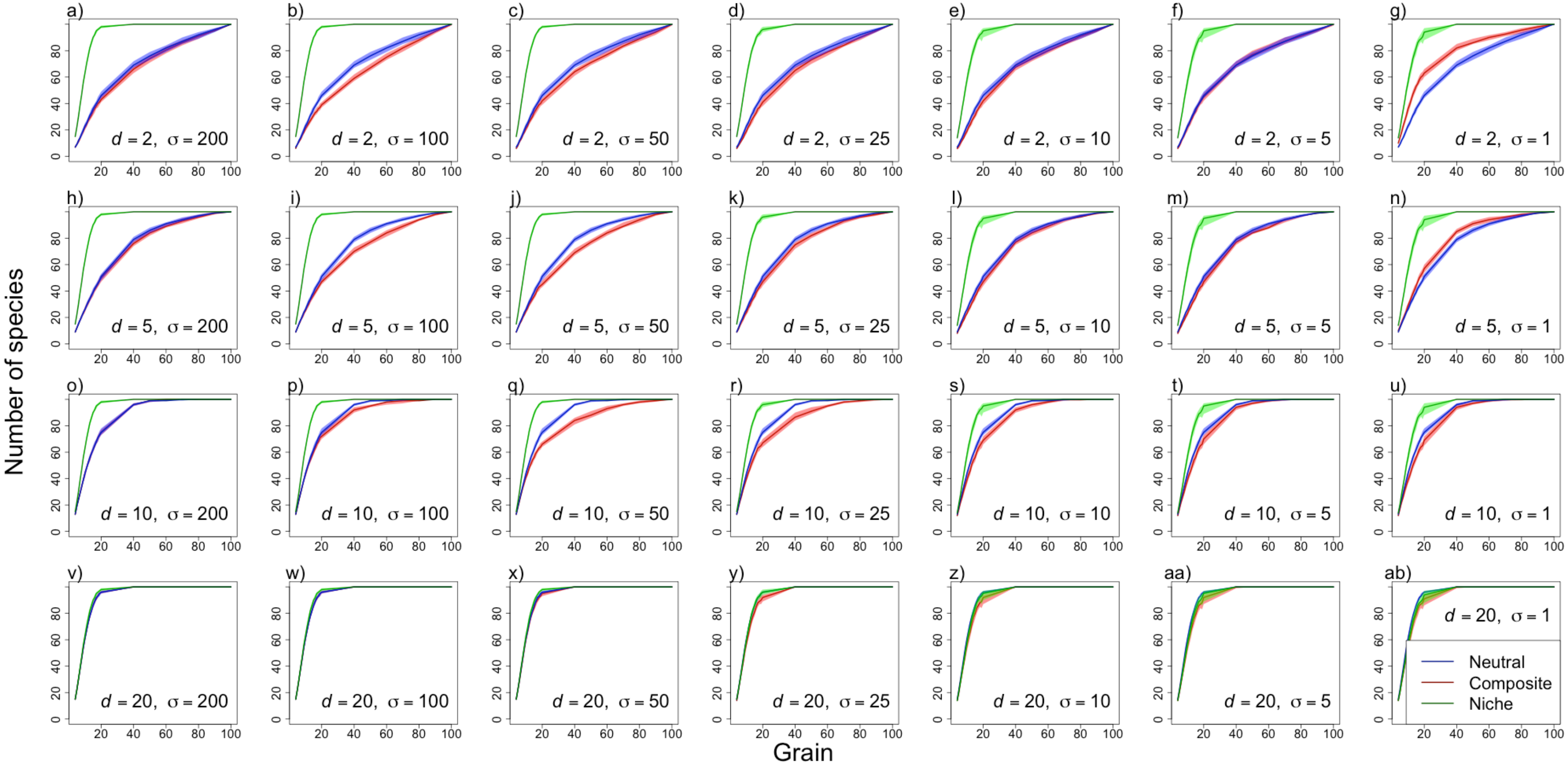

Figure C5. Species-area curves for the range of neutral and niche parameters used in simulations. The shaded areas represent the area between the 25% and 75% percentiles. The bottom-left figure corresponds to low dispersal limitation and niche separation (large *d* and σ) and is close to spatially random.

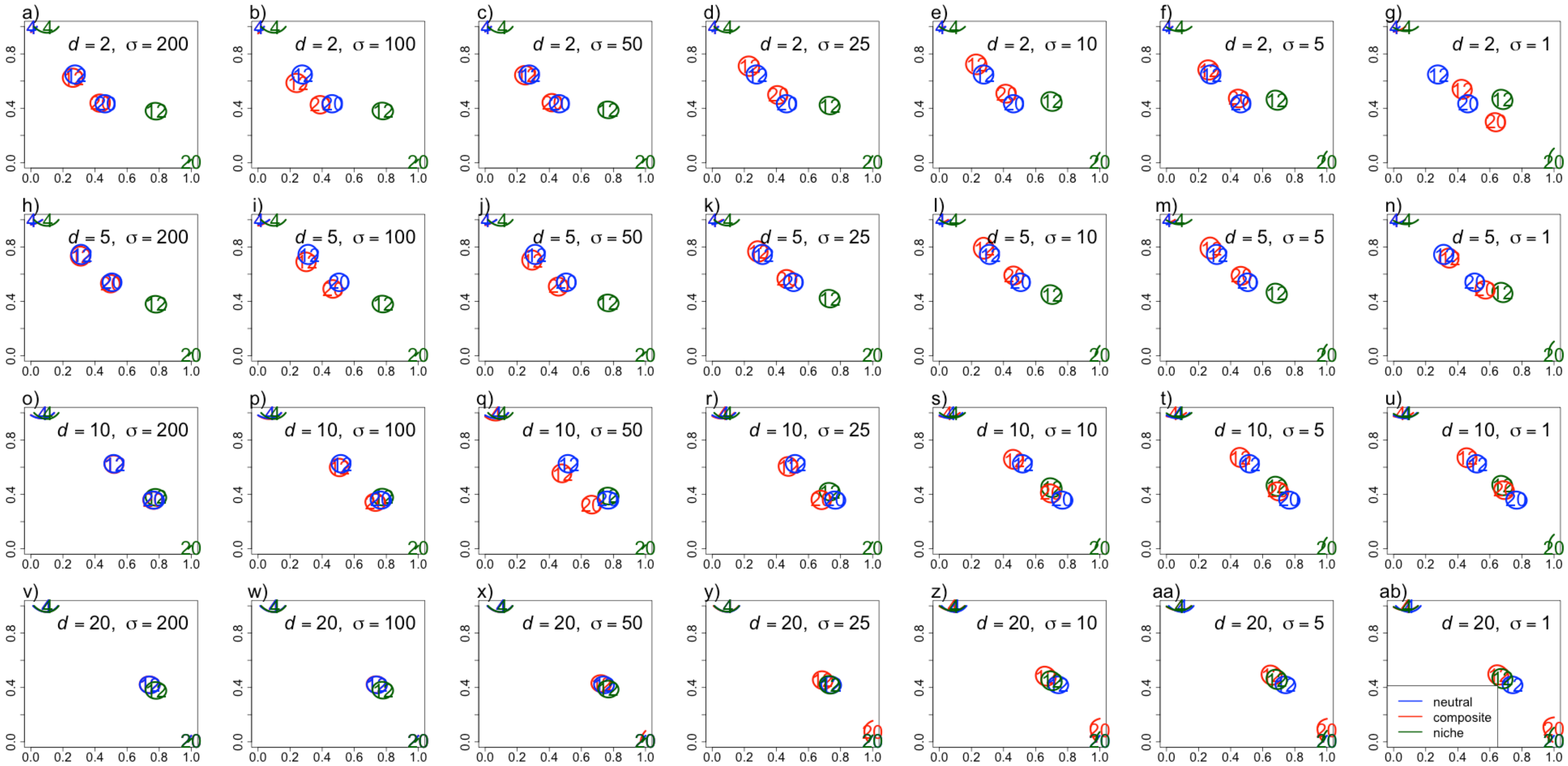

Figure C6. Density signatures for the range of neutral and niche parameters used in simulations. The numbers are placed on the modes locations for each grain and the circles represent the 90% thresholds of the surface densities computed over all simulations. The bottom-left figure corresponds to low dispersal limitation and niche separation (large *d* and σ) and is close to spatially random.

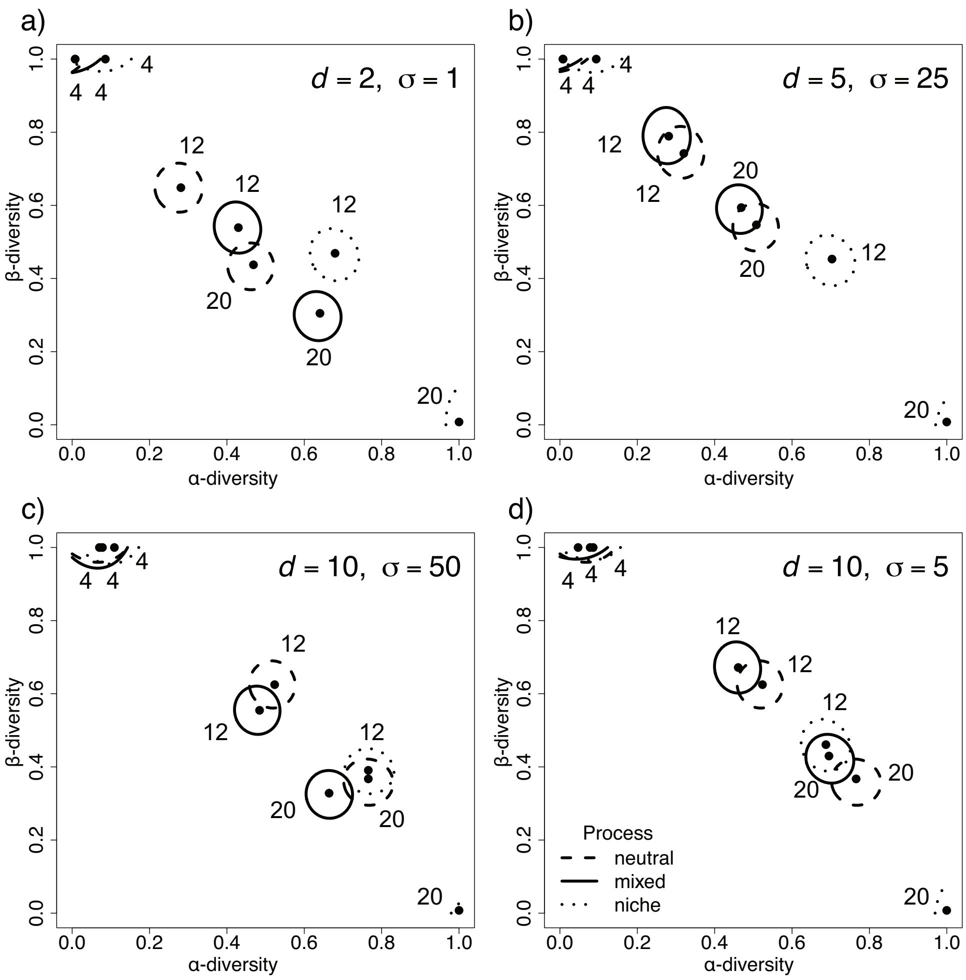

Figure C7. Snapshots of diversity signatures produced for niche, neutral and composite model processes for different combinations (a-d) of dispersal ability *d* and niche width *σ*, at three different grains (4, 12 and 20). The points represent the modes for each grain and the circles represent the 90% thresholds of the surface densities computed over all simulations. a) The composite outputs lie between the neutral and niche model outputs and the modes of the diversity signatures are located between those of the neutral and niche models; b) the composite outputs are equivalent to the expected neutral diversity signature; c) the composite model diversity signature lies outside of the neutral and niche model outputs and the β-diversity values are between neutral and niche, whereas α-diversity values are lower than both; d) the composite model diversity signature lies outside of the neutral and niche model outputs and the β-diversity values are higher than both neutral and niche ones, whereas α-diversity values are lower than both.

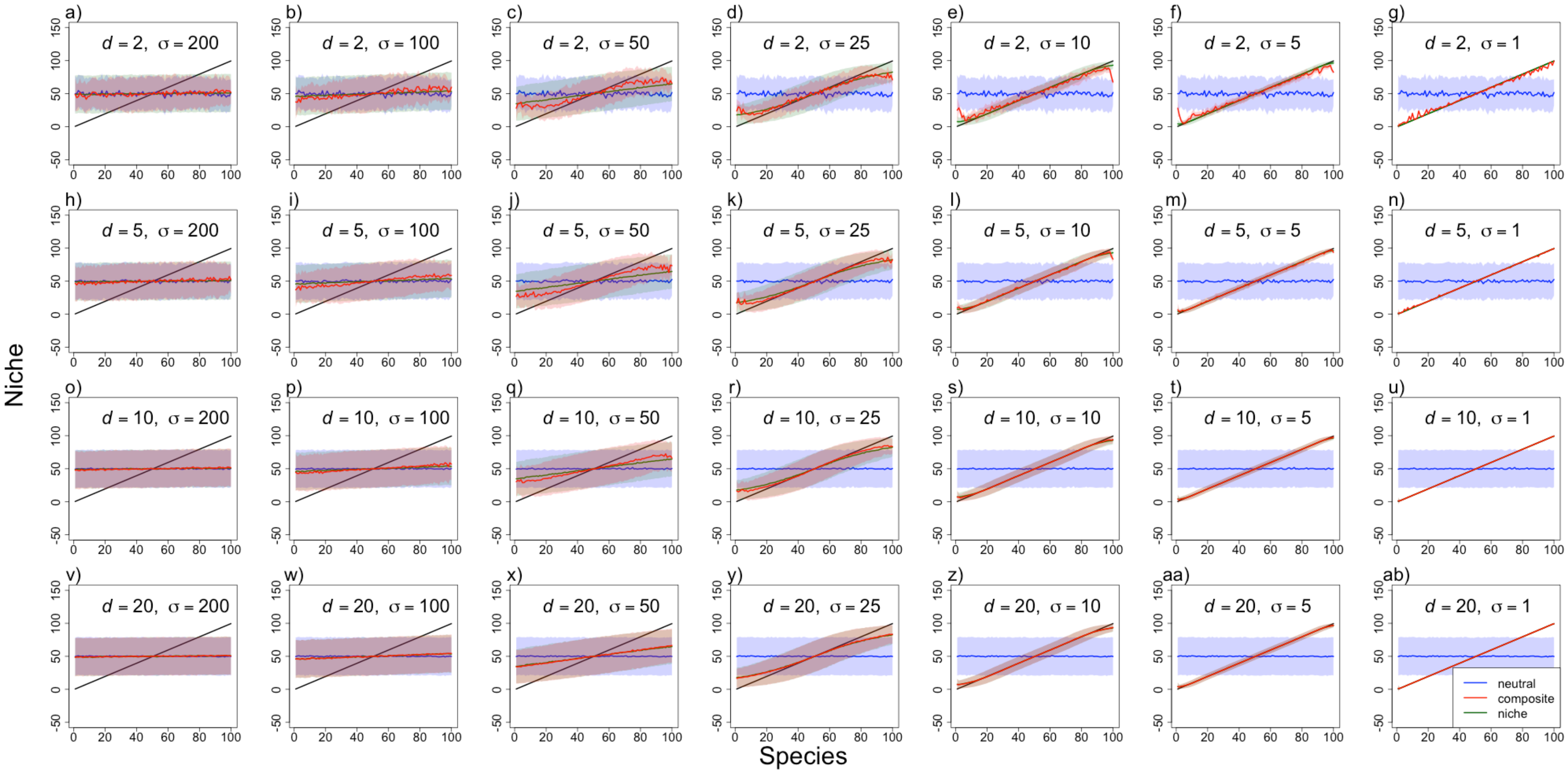

Figure C8. Realized niche per species when species are not sorted according to their realized niche, for the range of neutral and niche parameters used in simulations. Lines represent the mean of the realized niche. The shaded areas represent the niche width. The black line represents the fundamental niche optimum. The bottom-left figure corresponds to low dispersal limitation and niche separation (large *d* and σ) and is close to spatially random.

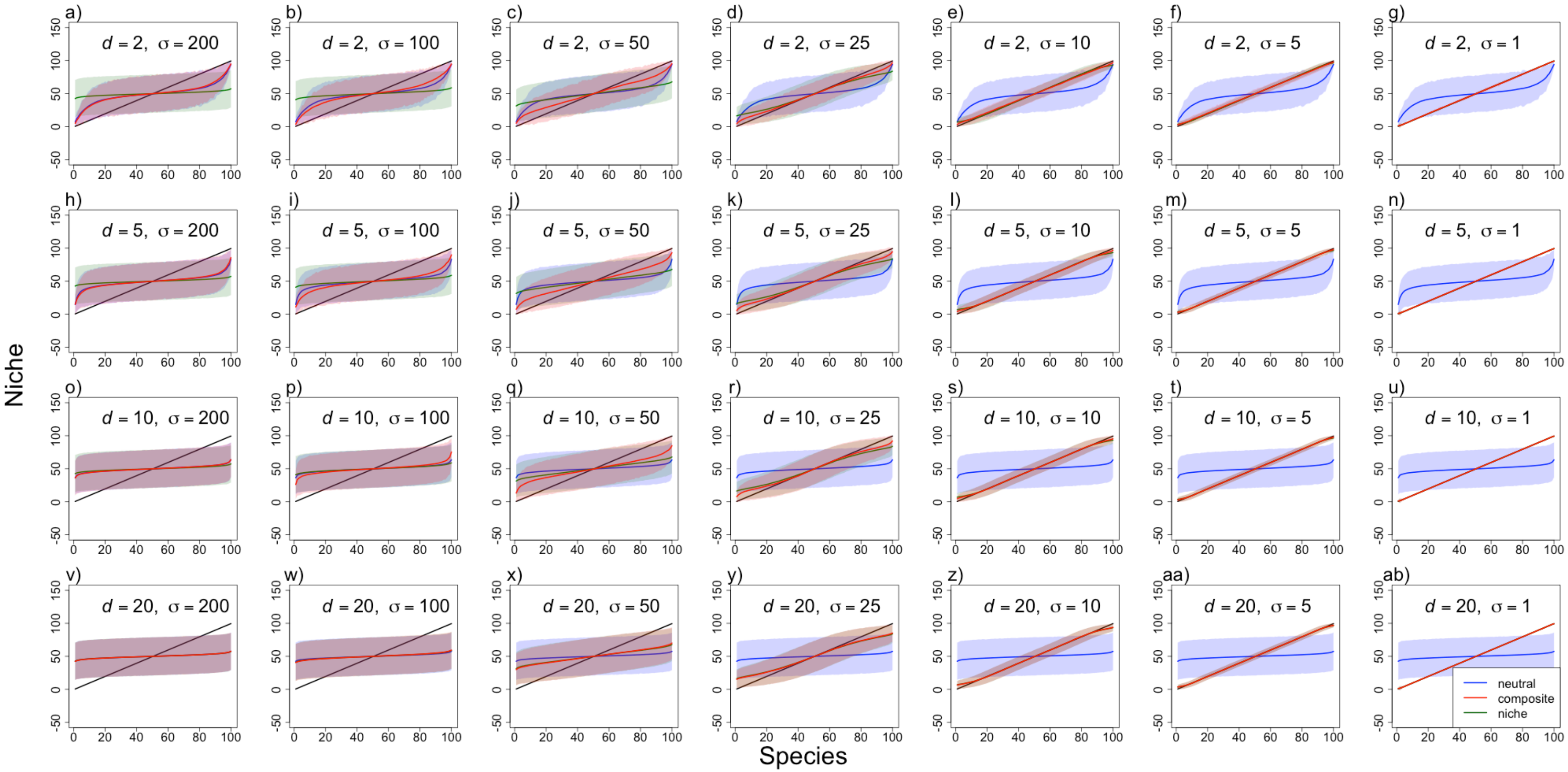

Figure C9. Realized niche per species when species are sorted according to their realized niche, for the range of neutral and niche parameters used in simulations. Lines represent the mean of the realized niche. The shaded areas represent the niche width. The black line represents the fundamental niche optimum. The bottom-left figure corresponds to low dispersal limitation and niche separation (large *d* and σ) and is close to spatially random.

APPENDIX D: SUPPORTING TABLES

Table D1. α-diversity of the modes for the different models for grains 4 to 20 for the range of neutral and niche parameters used in simulations.

d	σ	model	Grain																
			4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
d=2	*σ*=1	neutral	0.01	0.01	0.04	0.09	0.14	0.18	0.22	0.25	0.28	0.31	0.34	0.36	0.38	0.41	0.43	0.45	0.47
		niche1	0.01	0.08	0.15	0.21	0.27	0.31	0.36	0.4	0.43	0.47	0.5	0.53	0.56	0.59	0.6	0.62	0.64
		niche	0.09	0.18	0.27	0.34	0.42	0.5	0.56	0.62	0.68	0.75	0.8	0.85	0.91	0.97	1	1	1
	σ=5	neutral	0.01	0.01	0.04	0.09	0.14	0.18	0.22	0.25	0.28	0.31	0.34	0.36	0.38	0.41	0.43	0.45	0.47
		niche1	0.01	0.01	0.02	0.08	0.12	0.17	0.2	0.23	0.27	0.3	0.32	0.34	0.38	0.4	0.41	0.43	0.45
		niche	0.09	0.19	0.27	0.35	0.43	0.5	0.57	0.63	0.69	0.76	0.81	0.87	0.92	0.99	1	1	1
	σ=10	neutral	0.01	0.01	0.04	0.09	0.14	0.18	0.22	0.25	0.28	0.31	0.34	0.36	0.38	0.41	0.43	0.45	0.47
		niche1	0.01	0.01	0.01	0.05	0.1	0.14	0.17	0.2	0.23	0.27	0.29	0.31	0.34	0.37	0.38	0.4	0.42
		niche	0.09	0.2	0.28	0.36	0.44	0.52	0.58	0.65	0.7	0.77	0.83	0.88	0.95	1	1	1	1
	σ=25	neutral	0.01	0.01	0.04	0.09	0.14	0.18	0.22	0.25	0.28	0.31	0.34	0.36	0.38	0.41	0.43	0.45	0.47
		niche1	0.01	0.01	0.01	0.05	0.1	0.14	0.17	0.2	0.23	0.27	0.29	0.31	0.34	0.36	0.38	0.4	0.41
		niche	0.1	0.2	0.29	0.38	0.45	0.53	0.61	0.67	0.73	0.8	0.86	0.92	1	1	1	1	1
	σ=50	neutral	0.01	0.01	0.04	0.09	0.14	0.18	0.22	0.25	0.28	0.31	0.34	0.36	0.38	0.41	0.43	0.45	0.47
		niche1	0.01	0.01	0.02	0.08	0.12	0.16	0.2	0.23	0.26	0.28	0.3	0.33	0.35	0.38	0.39	0.41	0.42

		niche	0.11	0.21	0.3	0.39	0.48	0.55	0.63	0.7	0.77	0.84	0.9	0.98	1	1	1	1	1
		neutral	0.01	0.01	0.04	0.09	0.14	0.18	0.22	0.25	0.28	0.31	0.34	0.36	0.38	0.41	0.43	0.45	0.47
	σ=100	niche1	0.01	0.01	0.03	0.08	0.12	0.16	0.2	0.22	0.25	0.27	0.29	0.31	0.33	0.34	0.36	0.38	0.39
		niche	0.11	0.21	0.3	0.39	0.48	0.56	0.64	0.71	0.78	0.84	0.91	1	1	1	1	1	1
		neutral	0.01	0.01	0.04	0.09	0.14	0.18	0.22	0.25	0.28	0.31	0.34	0.36	0.38	0.41	0.43	0.45	0.47
	σ=200	niche1	0.01	0.01	0.04	0.09	0.13	0.17	0.21	0.24	0.27	0.3	0.32	0.34	0.36	0.38	0.4	0.41	0.44
		niche	0.11	0.21	0.3	0.39	0.48	0.56	0.64	0.71	0.78	0.84	0.92	1	1	1	1	1	1
		neutral	0.01	0.05	0.11	0.16	0.2	0.23	0.26	0.29	0.32	0.34	0.37	0.4	0.42	0.45	0.47	0.48	0.51
	σ=1	niche1	0.01	0.06	0.12	0.16	0.21	0.25	0.29	0.32	0.35	0.39	0.41	0.45	0.48	0.51	0.52	0.55	0.57
		niche	0.09	0.18	0.27	0.34	0.42	0.5	0.56	0.62	0.68	0.75	0.8	0.85	0.91	0.97	1	1	1
		neutral	0.01	0.05	0.11	0.16	0.2	0.23	0.26	0.29	0.32	0.34	0.37	0.4	0.42	0.45	0.47	0.48	0.51
	σ=5	niche1	0.01	0.02	0.08	0.12	0.16	0.2	0.23	0.25	0.28	0.31	0.34	0.36	0.39	0.41	0.43	0.45	0.47
		niche	0.09	0.19	0.27	0.35	0.43	0.5	0.57	0.63	0.69	0.76	0.81	0.87	0.92	0.99	1	1	1
		neutral	0.01	0.05	0.11	0.16	0.2	0.23	0.26	0.29	0.32	0.34	0.37	0.4	0.42	0.45	0.47	0.48	0.51
d=5	*σ*=10	niche1	0.01	0.02	0.08	0.12	0.16	0.2	0.23	0.26	0.28	0.31	0.34	0.36	0.39	0.41	0.44	0.45	0.47
		niche	0.09	0.2	0.28	0.36	0.44	0.52	0.58	0.65	0.7	0.77	0.83	0.88	0.95	1	1	1	1
		neutral	0.01	0.05	0.11	0.16	0.2	0.23	0.26	0.29	0.32	0.34	0.37	0.4	0.42	0.45	0.47	0.48	0.51
	σ=25	niche1	0.01	0.04	0.09	0.13	0.17	0.2	0.23	0.27	0.29	0.32	0.34	0.37	0.39	0.42	0.44	0.45	0.47
		niche	0.1	0.2	0.29	0.38	0.45	0.53	0.61	0.67	0.73	0.8	0.86	0.92	1	1	1	1	1
	σ=50	neutral	0.01	0.05	0.11	0.16	0.2	0.23	0.26	0.29	0.32	0.34	0.37	0.4	0.42	0.45	0.47	0.48	0.51
		niche1	0.01	0.05	0.1	0.15	0.18	0.22	0.24	0.27	0.3	0.32	0.34	0.37	0.39	0.41	0.43	0.45	0.46

		niche	0.11	0.21	0.3	0.39	0.48	0.55	0.63	0.7	0.77	0.84	0.9	0.98	1	1	1	1	1
		neutral	0.01	0.05	0.11	0.16	0.2	0.23	0.26	0.29	0.32	0.34	0.37	0.4	0.42	0.45	0.47	0.48	0.51
	σ=100	niche1	0.01	0.05	0.11	0.15	0.19	0.22	0.25	0.28	0.3	0.33	0.35	0.38	0.4	0.41	0.44	0.45	0.47
		niche	0.11	0.21	0.3	0.39	0.48	0.56	0.64	0.71	0.78	0.84	0.91	1	1	1	1	1	1
		neutral	0.01	0.05	0.11	0.16	0.2	0.23	0.26	0.29	0.32	0.34	0.37	0.4	0.42	0.45	0.47	0.48	0.51
	σ=200	niche1	0.01	0.05	0.11	0.16	0.2	0.23	0.26	0.29	0.31	0.34	0.37	0.39	0.41	0.44	0.46	0.48	0.5
		niche	0.11	0.21	0.3	0.39	0.48	0.56	0.64	0.71	0.78	0.84	0.92	1	1	1	1	1	1
		neutral	0.08	0.16	0.23	0.29	0.34	0.39	0.44	0.48	0.52	0.56	0.59	0.62	0.66	0.69	0.71	0.74	0.77
	σ=1	niche1	0.05	0.13	0.2	0.26	0.3	0.35	0.39	0.43	0.46	0.5	0.53	0.56	0.6	0.62	0.65	0.66	0.69
		niche	0.09	0.18	0.27	0.34	0.42	0.5	0.56	0.62	0.68	0.75	0.8	0.85	0.91	0.97	1	1	1
		neutral	0.08	0.16	0.23	0.29	0.34	0.39	0.44	0.48	0.52	0.56	0.59	0.62	0.66	0.69	0.71	0.74	0.77
	σ=5	niche1	0.05	0.13	0.2	0.25	0.3	0.35	0.39	0.43	0.46	0.51	0.54	0.57	0.6	0.63	0.66	0.67	0.7
		niche	0.09	0.19	0.27	0.35	0.43	0.5	0.57	0.63	0.69	0.76	0.81	0.87	0.92	0.99	1	1	1
		neutral	0.08	0.16	0.23	0.29	0.34	0.39	0.44	0.48	0.52	0.56	0.59	0.62	0.66	0.69	0.71	0.74	0.77
d=10	*σ*=10	niche1	0.05	0.14	0.2	0.26	0.3	0.35	0.4	0.43	0.47	0.51	0.54	0.57	0.6	0.63	0.66	0.67	0.7
		niche	0.09	0.2	0.28	0.36	0.44	0.52	0.58	0.65	0.7	0.77	0.83	0.88	0.95	1	1	1	1
		neutral	0.08	0.16	0.23	0.29	0.34	0.39	0.44	0.48	0.52	0.56	0.59	0.62	0.66	0.69	0.71	0.74	0.77
	σ=25	niche1	0.07	0.15	0.22	0.27	0.32	0.37	0.41	0.44	0.48	0.52	0.54	0.57	0.6	0.63	0.65	0.66	0.68
		niche	0.1	0.2	0.29	0.38	0.45	0.53	0.61	0.67	0.73	0.8	0.86	0.92	1	1	1	1	1
	σ=50	neutral	0.08	0.16	0.23	0.29	0.34	0.39	0.44	0.48	0.52	0.56	0.59	0.62	0.66	0.69	0.71	0.74	0.77
		niche1	0.07	0.16	0.23	0.28	0.33	0.38	0.41	0.45	0.48	0.52	0.54	0.57	0.59	0.62	0.63	0.65	0.66

		niche	0.11	0.21	0.3	0.39	0.48	0.55	0.63	0.7	0.77	0.84	0.9	0.98	1	1	1	1	1
	σ=100	neutral	0.08	0.16	0.23	0.29	0.34	0.39	0.44	0.48	0.52	0.56	0.59	0.62	0.66	0.69	0.71	0.74	0.77
		niche1	0.08	0.16	0.23	0.29	0.34	0.39	0.43	0.47	0.51	0.55	0.58	0.61	0.63	0.66	0.69	0.71	0.73
		niche	0.11	0.21	0.3	0.39	0.48	0.56	0.64	0.71	0.78	0.84	0.91	1	1	1	1	1	1
	σ=200	neutral	0.08	0.16	0.23	0.29	0.34	0.39	0.44	0.48	0.52	0.56	0.59	0.62	0.66	0.69	0.71	0.74	0.77
		niche1	0.08	0.16	0.23	0.29	0.34	0.39	0.44	0.48	0.52	0.55	0.59	0.62	0.66	0.69	0.71	0.74	0.77
		niche	0.11	0.21	0.3	0.39	0.48	0.56	0.64	0.71	0.78	0.84	0.92	1	1	1	1	1	1
d=20	*σ*=1	neutral	0.1	0.21	0.3	0.38	0.46	0.54	0.62	0.68	0.74	0.8	0.86	0.92	0.98	1	1	1	1
		niche1	0.08	0.18	0.26	0.34	0.41	0.48	0.55	0.6	0.66	0.72	0.77	0.8	0.85	0.91	0.94	0.97	1
		niche	0.09	0.18	0.27	0.34	0.42	0.5	0.56	0.62	0.68	0.75	0.8	0.85	0.91	0.97	1	1	1
	σ=5	neutral	0.1	0.21	0.3	0.38	0.46	0.54	0.62	0.68	0.74	0.8	0.86	0.92	0.98	1	1	1	1
		niche1	0.09	0.18	0.27	0.34	0.41	0.48	0.55	0.61	0.66	0.72	0.77	0.81	0.86	0.91	0.95	0.98	1
		niche	0.09	0.19	0.27	0.35	0.43	0.5	0.57	0.63	0.69	0.76	0.81	0.87	0.92	0.99	1	1	1
	σ=10	neutral	0.1	0.21	0.3	0.38	0.46	0.54	0.62	0.68	0.74	0.8	0.86	0.92	0.98	1	1	1	1
		niche1	0.09	0.19	0.27	0.34	0.42	0.49	0.55	0.62	0.66	0.73	0.77	0.82	0.87	0.92	0.96	0.98	1
		niche	0.09	0.2	0.28	0.36	0.44	0.52	0.58	0.65	0.7	0.77	0.83	0.88	0.95	1	1	1	1
	σ=25	neutral	0.1	0.21	0.3	0.38	0.46	0.54	0.62	0.68	0.74	0.8	0.86	0.92	0.98	1	1	1	1
		niche1	0.1	0.2	0.28	0.36	0.44	0.51	0.58	0.63	0.69	0.75	0.8	0.84	0.89	0.95	0.98	1	1
		niche	0.1	0.2	0.29	0.38	0.45	0.53	0.61	0.67	0.73	0.8	0.86	0.92	1	1	1	1	1
	σ=50	neutral	0.1	0.21	0.3	0.38	0.46	0.54	0.62	0.68	0.74	0.8	0.86	0.92	0.98	1	1	1	1
		niche1	0.1	0.2	0.3	0.38	0.45	0.53	0.6	0.66	0.73	0.78	0.84	0.89	0.95	1	1	1	1

	niche	0.11	0.21	0.3	0.39	0.48	0.55	0.63	0.7	0.77	0.84	0.9	0.98	1	1	1	1	1
σ=100	neutral	0.1	0.21	0.3	0.38	0.46	0.54	0.62	0.68	0.74	0.8	0.86	0.92	0.98	1	1	1	1
	niche1	0.1	0.21	0.3	0.38	0.46	0.54	0.61	0.68	0.74	0.8	0.86	0.91	0.98	1	1	1	1
	niche	0.11	0.21	0.3	0.39	0.48	0.56	0.64	0.71	0.78	0.84	0.91	1	1	1	1	1	1
σ=200	neutral	0.1	0.21	0.3	0.38	0.46	0.54	0.62	0.68	0.74	0.8	0.86	0.92	0.98	1	1	1	1
	niche1	0.1	0.21	0.3	0.38	0.46	0.54	0.62	0.68	0.74	0.8	0.86	0.92	0.98	1	1	1	1
	niche	0.11	0.21	0.3	0.39	0.48	0.56	0.64	0.71	0.78	0.84	0.92	1	1	1	1	1	1

Table D2. β-diversity of the modes for the different models for grains 4 to 20 for the range of neutral and niche parameters used in simulations.

d	σ	model	Grain																
			4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
d=2	σ=1	neutral	1	1	0.97	0.88	0.82	0.77	0.73	0.69	0.65	0.62	0.59	0.55	0.53	0.5	0.48	0.46	0.44
		niche1	1	1	0.91	0.81	0.73	0.68	0.63	0.59	0.54	0.49	0.46	0.42	0.39	0.36	0.34	0.33	0.3
		niche	1	1	0.93	0.81	0.73	0.66	0.59	0.52	0.47	0.4	0.34	0.29	0.23	0.18	0.13	0.09	0.01
	σ=5	neutral	1	1	0.97	0.88	0.82	0.77	0.73	0.69	0.65	0.62	0.59	0.55	0.53	0.5	0.48	0.46	0.44
		niche1	1	1	1	0.94	0.85	0.8	0.76	0.72	0.68	0.65	0.62	0.59	0.56	0.54	0.52	0.5	0.48
		niche	1	1	0.91	0.81	0.73	0.66	0.59	0.52	0.46	0.39	0.33	0.27	0.22	0.16	0.12	0.07	0.01
	σ=10	neutral	1	1	0.97	0.88	0.82	0.77	0.73	0.69	0.65	0.62	0.59	0.55	0.53	0.5	0.48	0.46	0.44
		niche1	1	1	1	1	0.91	0.84	0.8	0.76	0.73	0.69	0.66	0.63	0.59	0.57	0.55	0.53	0.51
		niche	1	1	0.9	0.8	0.73	0.65	0.59	0.52	0.45	0.38	0.32	0.27	0.2	0.13	0.09	0.05	0.01
	σ=25	neutral	1	1	0.97	0.88	0.82	0.77	0.73	0.69	0.65	0.62	0.59	0.55	0.53	0.5	0.48	0.46	0.44
		niche1	1	1	1	0.98	0.88	0.83	0.78	0.75	0.71	0.68	0.65	0.62	0.59	0.56	0.54	0.52	0.5
		niche	1	0.99	0.87	0.78	0.71	0.63	0.56	0.49	0.42	0.35	0.29	0.23	0.16	0.09	0.04	0.01	0.01
	σ=50	neutral	1	1	0.97	0.88	0.82	0.77	0.73	0.69	0.65	0.62	0.59	0.55	0.53	0.5	0.48	0.46	0.44
		niche1	1	1	0.97	0.88	0.81	0.77	0.72	0.68	0.65	0.61	0.59	0.55	0.52	0.5	0.48	0.46	0.45
		niche	1	0.97	0.86	0.77	0.7	0.62	0.55	0.47	0.39	0.32	0.25	0.18	0.11	0.02	0.01	0.01	0.01
	σ=100	neutral	1	1	0.97	0.88	0.82	0.77	0.73	0.69	0.65	0.62	0.59	0.55	0.53	0.5	0.48	0.46	0.44

		niche1	1	1	0.87	0.8	0.75	0.7	0.66	0.62	0.59	0.55	0.53	0.51	0.49	0.47	0.45	0.44	0.43
		niche	1	0.97	0.86	0.77	0.7	0.62	0.54	0.46	0.38	0.31	0.24	0.16	0.09	0.01	0.01	0.01	0.01
	σ=200	neutral	1	1	0.97	0.88	0.82	0.77	0.73	0.69	0.65	0.62	0.59	0.55	0.53	0.5	0.48	0.46	0.44
		niche1	1	1	0.92	0.84	0.79	0.74	0.7	0.66	0.62	0.59	0.56	0.54	0.52	0.49	0.48	0.46	0.45
		niche	1	0.97	0.86	0.77	0.7	0.62	0.54	0.46	0.38	0.31	0.23	0.16	0.09	0.01	0.01	0.01	0.01
d=5	σ=1	neutral	1	1	1	0.95	0.89	0.84	0.8	0.77	0.74	0.72	0.69	0.66	0.64	0.61	0.59	0.57	0.55
		niche1	1	1	1	0.96	0.88	0.83	0.78	0.75	0.72	0.68	0.66	0.62	0.59	0.56	0.54	0.52	0.49
		niche	1	1	0.93	0.81	0.73	0.66	0.59	0.52	0.47	0.4	0.34	0.29	0.23	0.18	0.13	0.09	0.01
	σ=5	neutral	1	1	1	0.95	0.89	0.84	0.8	0.77	0.74	0.72	0.69	0.66	0.64	0.61	0.59	0.57	0.55
		niche1	1	1	1	1	0.97	0.9	0.86	0.82	0.79	0.75	0.73	0.7	0.68	0.65	0.63	0.61	0.59
		niche	1	1	0.91	0.81	0.73	0.66	0.59	0.52	0.46	0.39	0.33	0.27	0.22	0.16	0.12	0.07	0.01
	σ=10	neutral	1	1	1	0.95	0.89	0.84	0.8	0.77	0.74	0.72	0.69	0.66	0.64	0.61	0.59	0.57	0.55
		niche1	1	1	1	1	0.96	0.91	0.86	0.82	0.79	0.76	0.73	0.71	0.68	0.65	0.63	0.61	0.59
		niche	1	1	0.9	0.8	0.73	0.65	0.59	0.52	0.45	0.38	0.32	0.27	0.2	0.13	0.09	0.05	0.01
	σ=25	neutral	1	1	1	0.95	0.89	0.84	0.8	0.77	0.74	0.72	0.69	0.66	0.64	0.61	0.59	0.57	0.55
		niche1	1	1	1	1	0.92	0.88	0.83	0.8	0.77	0.73	0.71	0.69	0.66	0.62	0.61	0.59	0.57
		niche	1	0.99	0.87	0.78	0.71	0.63	0.56	0.49	0.42	0.35	0.29	0.23	0.16	0.09	0.04	0.01	0.01
	σ=50	neutral	1	1	1	0.95	0.89	0.84	0.8	0.77	0.74	0.72	0.69	0.66	0.64	0.61	0.59	0.57	0.55
		niche1	1	1	0.98	0.9	0.84	0.8	0.77	0.73	0.7	0.68	0.65	0.62	0.6	0.58	0.55	0.53	0.52
		niche	1	0.97	0.86	0.77	0.7	0.62	0.55	0.47	0.39	0.32	0.25	0.18	0.11	0.02	0.01	0.01	0.01
	σ=100	neutral	1	1	1	0.95	0.89	0.84	0.8	0.77	0.74	0.72	0.69	0.66	0.64	0.61	0.59	0.57	0.55

		niche1	1	1	0.95	0.88	0.83	0.79	0.76	0.72	0.7	0.66	0.63	0.61	0.59	0.55	0.54	0.52	0.49
		niche	1	0.97	0.86	0.77	0.7	0.62	0.54	0.46	0.38	0.31	0.24	0.16	0.09	0.01	0.01	0.01	0.01
		neutral	1	1	1	0.95	0.89	0.84	0.8	0.77	0.74	0.72	0.69	0.66	0.64	0.61	0.59	0.57	0.55
	σ=200	niche1	1	1	1	0.93	0.88	0.84	0.8	0.77	0.73	0.7	0.68	0.65	0.62	0.6	0.58	0.55	0.53
		niche	1	0.97	0.86	0.77	0.7	0.62	0.54	0.46	0.38	0.31	0.23	0.16	0.09	0.01	0.01	0.01	0.01
		neutral	1	1	0.92	0.85	0.8	0.75	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.45	0.42	0.39	0.37
	σ=1	niche1	1	1	1	0.9	0.83	0.78	0.74	0.7	0.67	0.63	0.6	0.57	0.54	0.51	0.48	0.47	0.44
		niche	1	1	0.93	0.81	0.73	0.66	0.59	0.52	0.47	0.4	0.34	0.29	0.23	0.18	0.13	0.09	0.01
		neutral	1	1	0.92	0.85	0.8	0.75	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.45	0.42	0.39	0.37
	σ=5	niche1	1	1	1	0.91	0.84	0.79	0.74	0.7	0.67	0.63	0.6	0.57	0.53	0.5	0.48	0.46	0.43
		niche	1	1	0.91	0.81	0.73	0.66	0.59	0.52	0.46	0.39	0.33	0.27	0.22	0.16	0.12	0.07	0.01
		neutral	1	1	0.92	0.85	0.8	0.75	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.45	0.42	0.39	0.37
	σ=10	niche1	1	1	0.99	0.89	0.83	0.77	0.73	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.46	0.44	0.41
d=10		niche	1	1	0.9	0.8	0.73	0.65	0.59	0.52	0.45	0.38	0.32	0.27	0.2	0.13	0.09	0.05	0.01
		neutral	1	1	0.92	0.85	0.8	0.75	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.45	0.42	0.39	0.37
	σ=25	niche1	1	1	0.91	0.84	0.77	0.73	0.69	0.65	0.61	0.57	0.53	0.5	0.47	0.43	0.41	0.39	0.37
		niche	1	0.99	0.87	0.78	0.71	0.63	0.56	0.49	0.42	0.35	0.29	0.23	0.16	0.09	0.04	0.01	0.01
		neutral	1	1	0.92	0.85	0.8	0.75	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.45	0.42	0.39	0.37
	σ=50	niche1	1	0.95	0.85	0.79	0.73	0.69	0.64	0.6	0.55	0.52	0.48	0.45	0.42	0.4	0.38	0.35	0.33
		niche	1	0.97	0.86	0.77	0.7	0.62	0.55	0.47	0.39	0.32	0.25	0.18	0.11	0.02	0.01	0.01	0.01
	σ=100	neutral	1	1	0.92	0.85	0.8	0.75	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.45	0.42	0.39	0.37

		niche1	1	0.99	0.89	0.82	0.77	0.73	0.68	0.64	0.6	0.56	0.53	0.49	0.46	0.43	0.4	0.38	0.34
		niche	1	0.97	0.86	0.77	0.7	0.62	0.54	0.46	0.38	0.31	0.24	0.16	0.09	0.01	0.01	0.01	0.01
	σ=200	neutral	1	1	0.92	0.85	0.8	0.75	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.45	0.42	0.39	0.37
		niche1	1	1	0.91	0.84	0.79	0.75	0.7	0.66	0.62	0.59	0.55	0.52	0.48	0.45	0.42	0.39	0.36
		niche	1	0.97	0.86	0.77	0.7	0.62	0.54	0.46	0.38	0.31	0.23	0.16	0.09	0.01	0.01	0.01	0.01
d=20	σ=1	neutral	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.23	0.18	0.11	0.05	0.01	0.01
		niche1	1	1	0.93	0.82	0.74	0.67	0.61	0.55	0.49	0.43	0.38	0.34	0.28	0.23	0.2	0.16	0.1
		niche	1	1	0.93	0.81	0.73	0.66	0.59	0.52	0.47	0.4	0.34	0.29	0.23	0.18	0.13	0.09	0.01
	σ=5	neutral	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.23	0.18	0.11	0.05	0.01	0.01
		niche1	1	1	0.92	0.82	0.74	0.67	0.61	0.55	0.49	0.43	0.38	0.33	0.27	0.23	0.2	0.16	0.09
		niche	1	1	0.91	0.81	0.73	0.66	0.59	0.52	0.46	0.39	0.33	0.27	0.22	0.16	0.12	0.07	0.01
	σ=10	neutral	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.23	0.18	0.11	0.05	0.01	0.01
		niche1	1	1	0.91	0.81	0.73	0.66	0.6	0.54	0.48	0.42	0.37	0.32	0.27	0.22	0.18	0.15	0.09
		niche	1	1	0.9	0.8	0.73	0.65	0.59	0.52	0.45	0.38	0.32	0.27	0.2	0.13	0.09	0.05	0.01
	σ=25	neutral	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.23	0.18	0.11	0.05	0.01	0.01
		niche1	1	0.99	0.87	0.79	0.71	0.65	0.58	0.52	0.46	0.4	0.34	0.29	0.24	0.19	0.16	0.12	0.08
		niche	1	0.99	0.87	0.78	0.71	0.63	0.56	0.49	0.42	0.35	0.29	0.23	0.16	0.09	0.04	0.01	0.01
	σ=50	neutral	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.23	0.18	0.11	0.05	0.01	0.01
		niche1	1	0.97	0.86	0.78	0.7	0.63	0.57	0.5	0.43	0.37	0.31	0.25	0.2	0.15	0.1	0.05	0.01
		niche	1	0.97	0.86	0.77	0.7	0.62	0.55	0.47	0.39	0.32	0.25	0.18	0.11	0.02	0.01	0.01	0.01
	σ=100	neutral	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.23	0.18	0.11	0.05	0.01	0.01

	niche1	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.24	0.18	0.12	0.05	0.01	0.01
	niche	1	0.97	0.86	0.77	0.7	0.62	0.54	0.46	0.38	0.31	0.24	0.16	0.09	0.01	0.01	0.01	0.01
	neutral	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.23	0.18	0.11	0.05	0.01	0.01
σ=200	niche1	1	0.98	0.86	0.78	0.7	0.63	0.56	0.49	0.42	0.36	0.3	0.23	0.17	0.12	0.05	0.01	0.01
	nche	1	0.97	0.86	0.77	0.7	0.62	0.54	0.46	0.38	0.31	0.23	0.16	0.09	0.01	0.01	0.01	0.01

APPENDIX E: ANALYSIS OF RESULTS IN THE ATTRIBUTE-BASED CONTINUUM

The original attribute-based neutral-niche continuum supposes that communities composed of species with a given degree of niche separation will display patterns that will fall within the range of patterns generated when species niche are completely separated on one hand, and when species niches completely overlap on the other hand [1, 2]. It considers that any process with complete niche separation corresponds to a niche process, whereas complete niche overlap corresponds to a neutral process. The continuum is then supposed to allow for assessing the relative importance of the so-called neutral and niche processes. In the main article, we criticise two aspects of this continuum. First we show that this definition of the continuum is inadequate for this task because it equates community attributes with processes (i.e. it is an attribute-based continuum). We therefore propose the community assembly phase space (CAPS), a new approach based on mechanisms to truly assess the effect of neutral and niche processes (i.e. a process-based continuum). Second, we question the continuum hypothesis, which implies that community patterns produced by a composite model including both neutral and niche processes should fall within the range of patterns produced by pure niche and pure neutral processes. We showed that the continuum hypothesis does not hold for all attribute values in the process-based CAPS.

Here, in addition to test the continuum hypothesis using the process-based CAPS, we use three of the four community patterns presented in the article to test if the continuum hypothesis holds for the attribute-based definition (the diversity signature is more complex to analyse and is not presented here to improve the clarity of the results, which consist of the comparison of multiple models). To do so, we compared the output of the neutral and composite models for the same dispersal parameter, but varying the niche width (Figure E1). The composite model with a niche width of 1 is the closest to the complete niche segregation, i.e. the "niche model" in the attribute-based continuum, whereas the neutral model corresponds to an infinite niche width. We also compared the pure niche models for the different niche widths, which correspond to infinite dispersal. The neutral model, as it was implemented here, with infinite dispersal would correspond to a spatially random model (every empty location could be colonized by any of the 100 species with the same probability), and we did not perform simulations for the random model.

Although results are of course different from when testing the neutral-niche continuum in the process-based CAPS, since they do not compare the same simulation outputs, they nonetheless show that the continuum hypothesis does not hold for all the community patterns even for the attribute-based continuum. The continuum holds for the niche selection patterns, and realised niche optima are more similar to the fundamental ones as the niche width decrease. This is to be expected, since the decrease of overlap logically leads species to be able to colonise cells with their preferred environment through species-sorting. However, the attribute-based continuum is not verified for the RADs and only for dispersal $d \geq 20$ for the SARs. As niche width decreases, from infinity, spatial aggregation increases due to the niche selection by individuals in the spatial autocorrelation of the environment. This is the same behaviour described in the discussion of the main article. The selection of similar values of the environmental variable by individuals from the same species will cause them to be located close to each other since the environment is spatially autocorrelated. This in turn will increase the propagule pressure for this species when nearby cells become available, and therefore increases to the aggregation of the species. The processes of dispersal and niche selection therefore reinforce each other, also leading to more discrepancy between species relative abundance, i.e. steeper RADs (Figure E1).

As niche separation increases even more (*d* decreases), though, it prevents species aggregation from being higher than the spatial aggregation of the environment. This results in a non-monotonic relationship between the slopes of the RADs and SARs and the niche width. However, the reinforcement between the two processes leading to this non-monotonic relationship decreases or disappears as the dispersal limitation decreases (*d* increases), in which case the neutral model generates less aggregated species than the composite model because it tends towards spatial randomness.

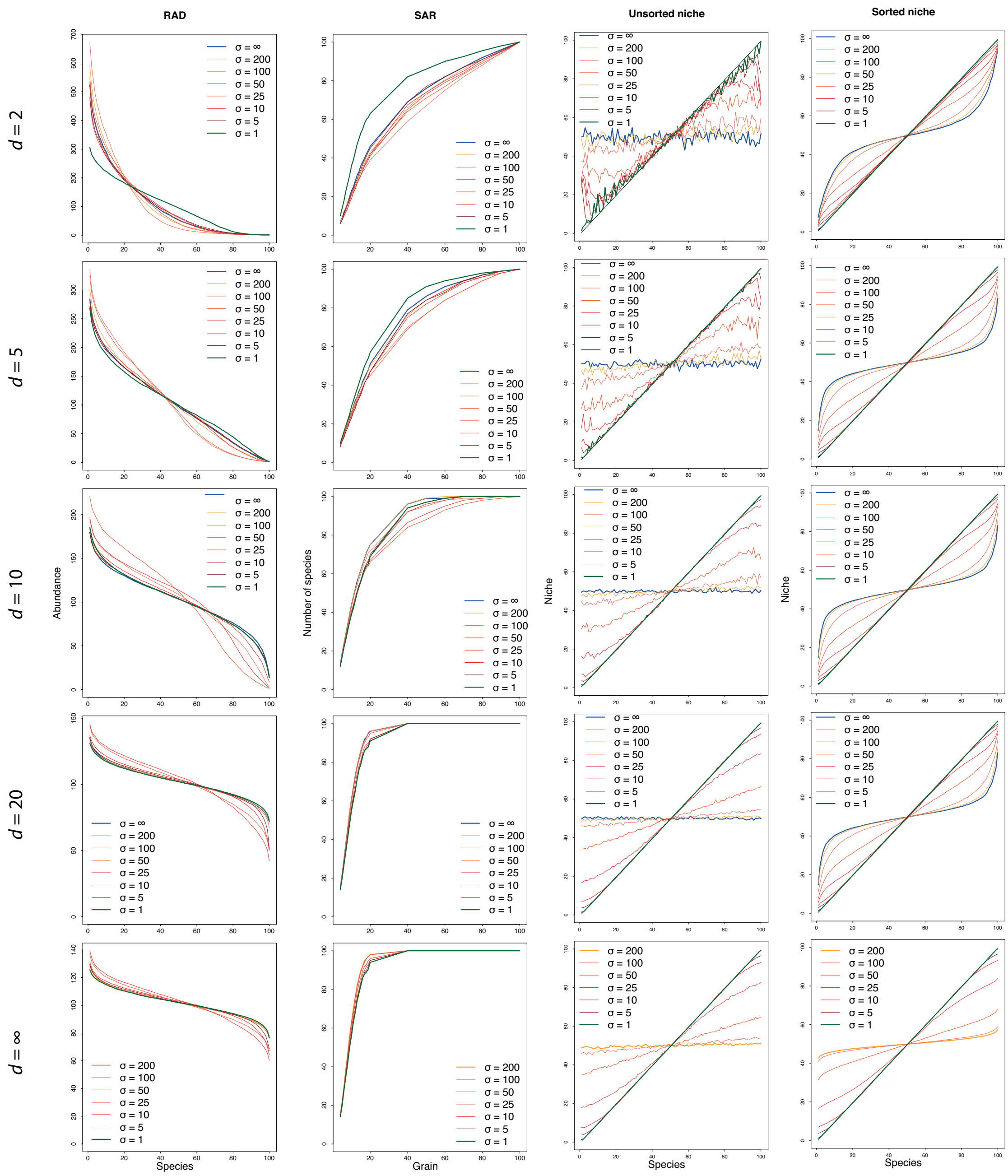

Figure E1. Results for the RAD, SAR, and niche selection patterns presented from the attribute-based continuum conceptualisation, that is by varying the niche width from σ = 1 to σ = 200. The neutral parameter corresponds to an infinite niche width σ = ∞ (no niche separation). Each row corresponds to a different value of the dispersal parameter *d* = 2, 5, 10, 20, which is inversely proportional to dispersal limitation. The last row compares pure niche models, hence corresponds to d = ∞ (no dispersal limitation). The neutral model would then correspond to a spatially random model and was not simulated.

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