

Oikos

OIK-06785

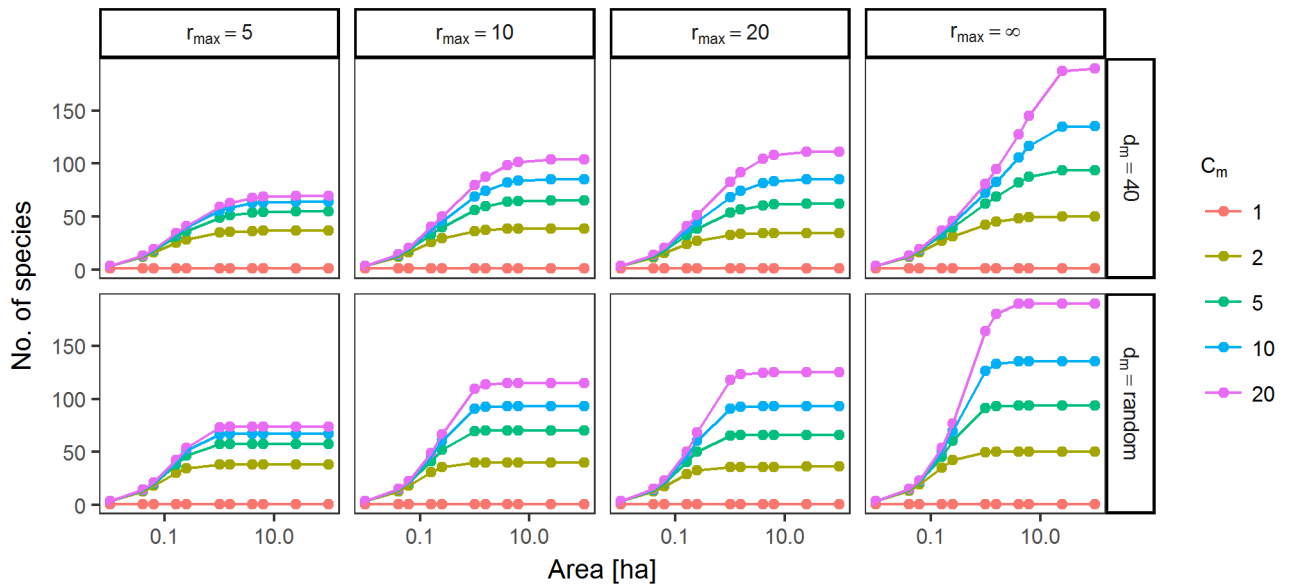
May, F., Wiegand, T., Huth, A. and Chase, J. M. 2020. Scale-dependent effects of conspecific negative density dependence and immigration on biodiversity maintenance. – Oikos doi:

10.1111/oik.06785

Appendix 1

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7 **Figure A1.** Species-area relationships (SARs) for different combinations of the strength of8 CNDD (C_m) and different neighbourhood radii of local interactions (r_{max}) in isolated

9 communities without immigration from a metacommunity. The points and lines show average

10 values of 100 replicate models runs. Note that $C_m = 1$ means that there is no CNDD and11 therefore the species number always converges to one species. The panels to the right ($r_{max} = \infty$)

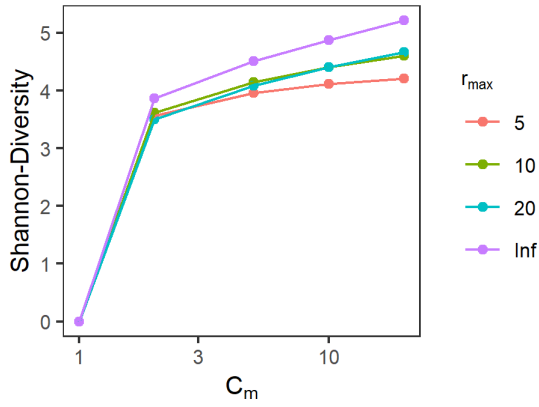
12 considers a model with spatially unlimited interactions, i.e. individuals interact with all other

13 individuals in the 100 ha plot and the distances among trees do not matter for their interactions.

14 The first row is equal to Fig. 1 in the main text and shows scenarios with spatially restricted

15 recruitment ($d_m = 40$ m), but the bottom row shows the corresponding scenarios with random16 dispersal in the local community ($d_m = \text{random}$).

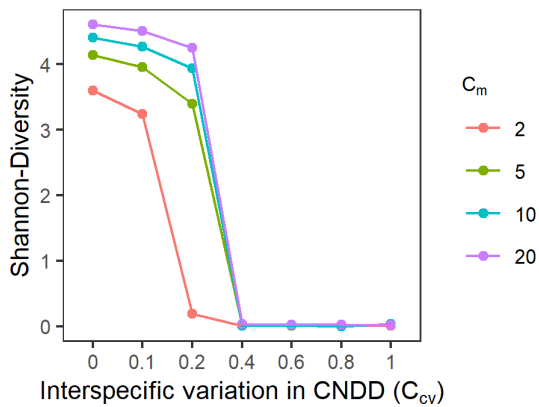
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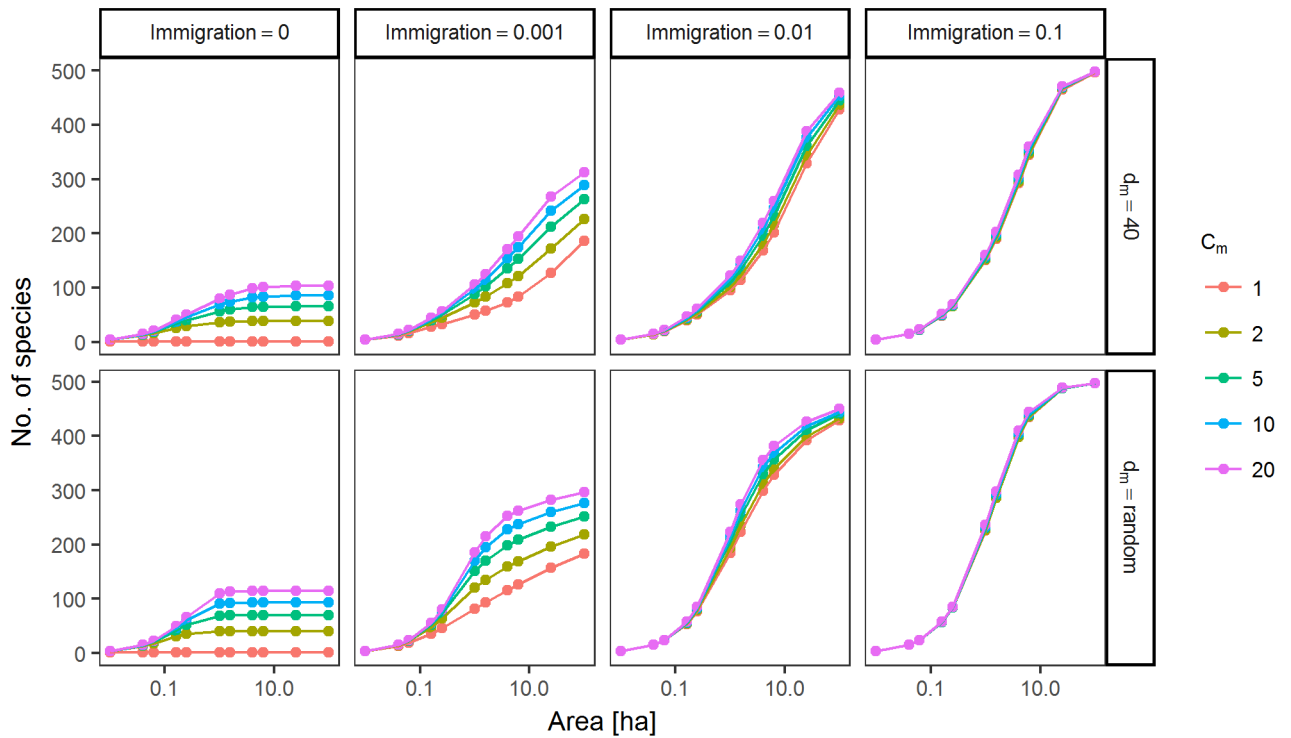
19 **Figure A2.** Shannon-diversity for different combinations of the strength of CNDD (C_m)
 20 and different neighbourhood radii of local interactions (r_{max}) in isolated communities
 21 without immigration from a metacommunity. Shannon-diversities were calculated from
 22 species relative abundances at the 100 ha scale and at the end of the simulation run. The
 23 points and lines show average values of 100 replicate models runs. The scenarios include the
 24 assumption of spatially restricted recruitment ($d_m = 40$ m).

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27 **Figure A3.** Consequences of interspecific variation in CNDD on Shannon-diversity in
 28 isolated communities. Shannon-diversities were calculated from species relative
 29 abundances at the 100 ha scale and at the end of the simulation run. The points and lines
 30 show average values of 100 replicate models runs. Interspecific variation in CNDD is
 31 measured by the coefficient of variation in CNDD among species (C_{cv}). The neighbourhood
 32 interaction radius (r_{max}) was set to be 10 m for these simulations.

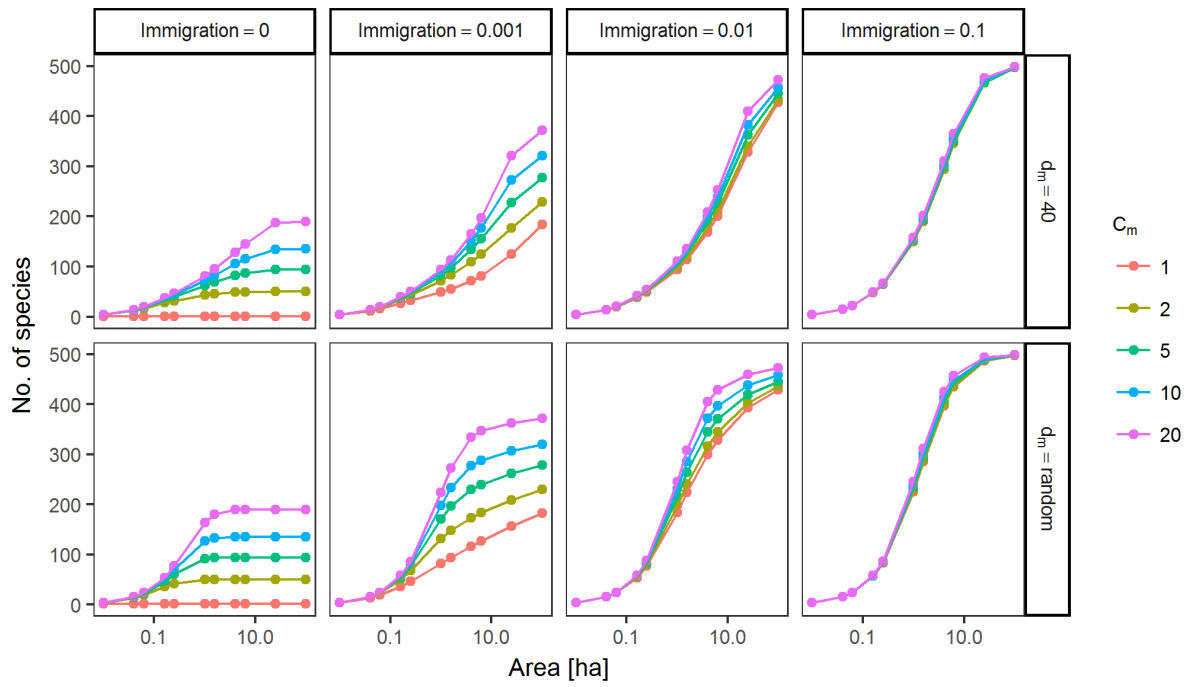


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35 **Figure A4.** Species-area relationships for different combinations of the strength of CNDD36 (C_m) and the immigration rate (in different panels). The lines show average values of 10037 replicate models runs. Note that $C_m = 1$ means that there is no CNDD. The neighbourhood38 interaction radius (r_{\max}) was set to be 10 m for these simulations. The first row is equal to39 Fig. 3 in the main text and shows scenarios with spatially restricted recruitment ($d_m = 40$ m),

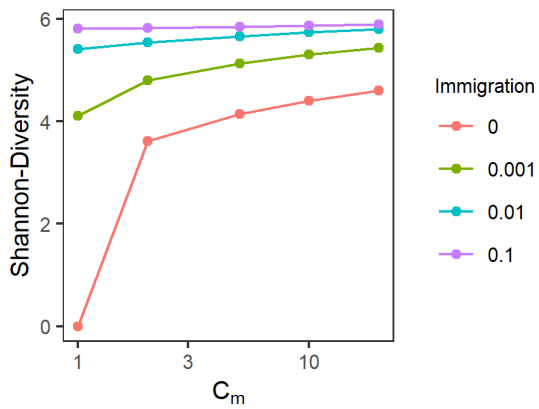
40 but the bottom row shows the corresponding scenarios with random dispersal in the local

41 community ($d_m = \text{random}$).



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43 **Figure A5.** Similar to Fig. A4, but with unlimited interaction range ($r_{\max} \rightarrow \infty$), i.e.
 44 individuals interact with all other individuals in the 100 ha plot and the distances among trees
 45 do not matter for their interactions.



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48 **Figure A6.** Shannon-diversity for different combinations of the strength of CNDD (C_m) and
 49 the immigration rate (indicated by the line colour) Shannon-diversities were calculated
 50 from species relative abundances at the 100 ha scale and at the end of the simulation run. The
 51 lines show average values of 100 replicate models runs. Note that $C_m = 1$ means that there
 52 is no CNDD. The neighbourhood interaction radius (r_{max}) was set to be 10 m for these
 53 simulations.