Controlling biodiversity loss via spatial management

Spatial structure mediates the balance between local and regional biodiversity

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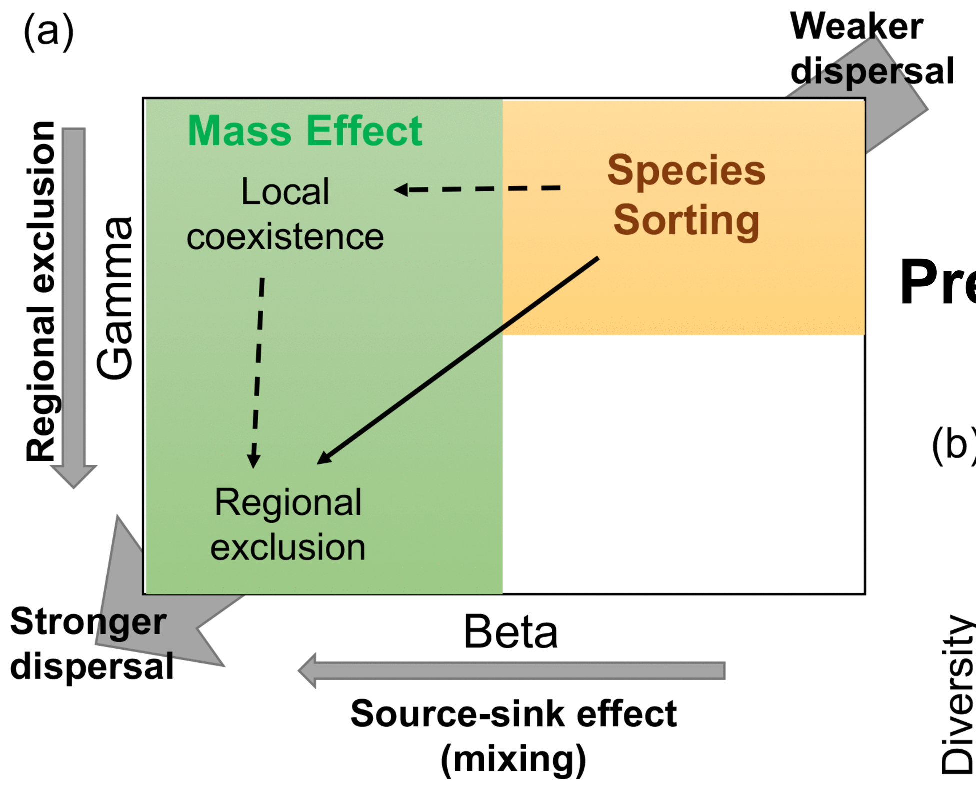
Previous studies that used models with simple spatial structure have predicted that intermediate dispersal rate increases local diversity, resulting in the maintainance of regional diversity (Fig. 1). However, we found this is an extreme case when a wider variety of spatial structures (Fig. 2) are considered. We determined that more complex linear and tree-like spatial structures maintain higher regional biodiversity (Fig. 3). Finally, we show that these theoretical results are applicable to more realistic and complex spatial structure in marine metacommunities (Fig. 4, 5).

Transition between species sorting and mass effect archetypes



Prediction by previous theories with complete network

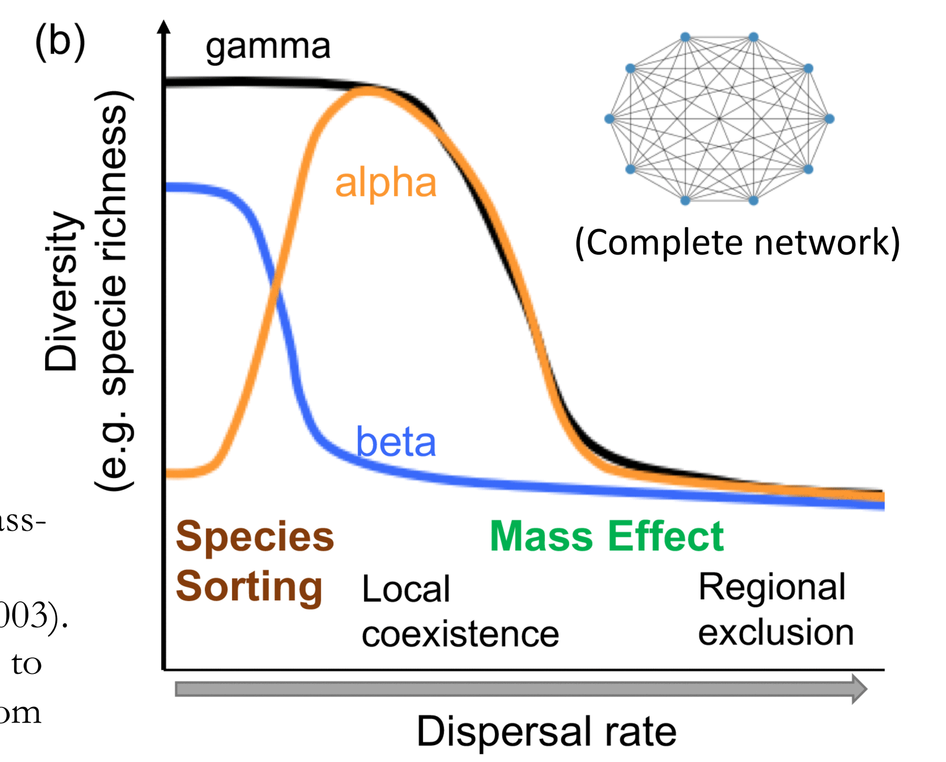
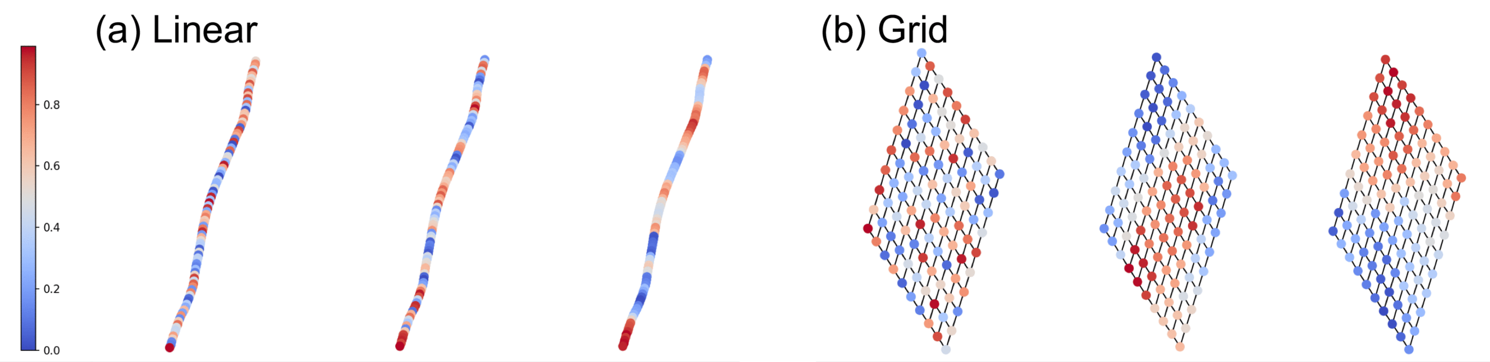
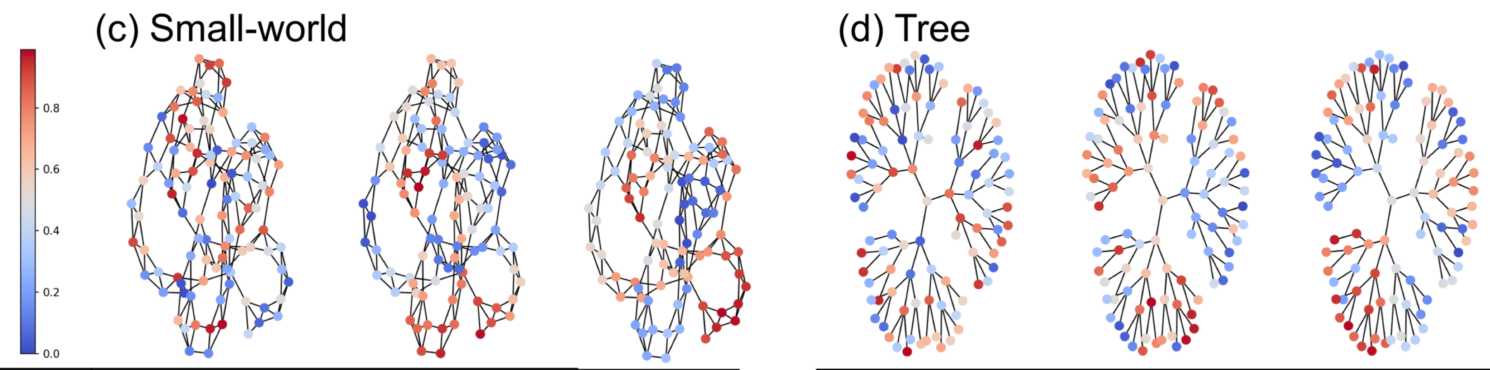


Figure 1. (a) Relationship between species-sorting and mass-effect archetypes and metacommunity processes. (b) Biodiversity patterns suggested by Mouquet & Loreau (2003). This biodiversity patterns predicted by them corresponds to the trajectory shown with dashed arrows in panel (a). (From Suzuki & Economo 2021)

Spatial structures used (theoretical)



Level of S.A.	Lowest	Intermediate	Highest	Lowest	Intermediate	Highest
ρ	34.99	19.89	7.700	57.91	19.940	14.660



Level of S.A.	Lowest	Intermediate	Highest	Lowest	Intermediate	Highest
ρ	65.380	20.520	17.660	34.240	19.990	6.960

Figure 2. Network topologies and spatial arrangements of environmental conditions with three different levels of spatial autocorrelation (S.A.). (a) Linear, (b) grid, (c) small-world, (d) tree networks. In the complete topology each node is connected to all the other nodes. Thus, the complete network can take only one level of spatial autocorrelation, ρ = 1666.5, which is the sum of the difference of environmental conditions between every pair of connected patches. (From Suzuki & Economo 2021)

Resulting biodiversity patterns (with theoretical connectivity)

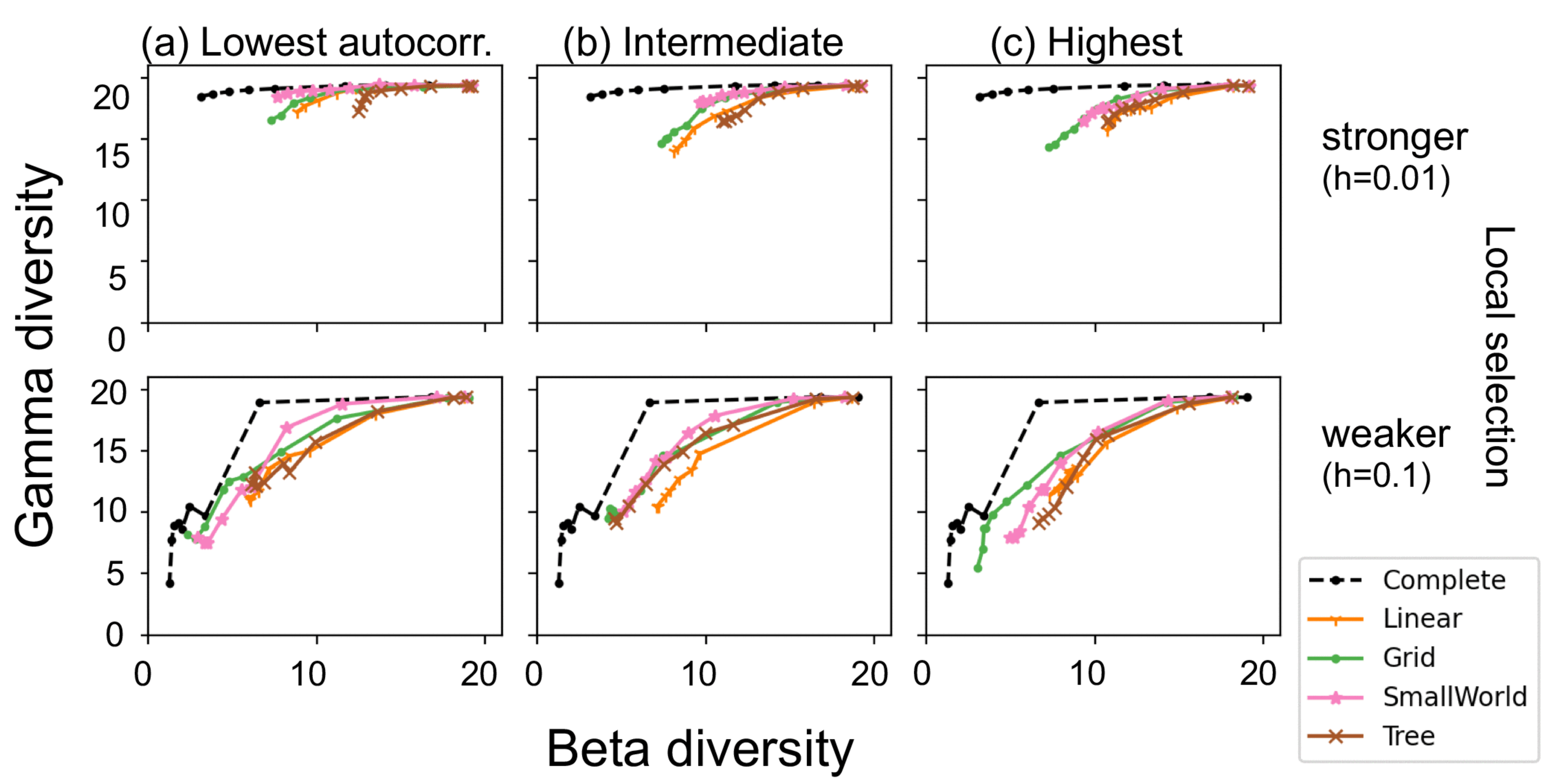
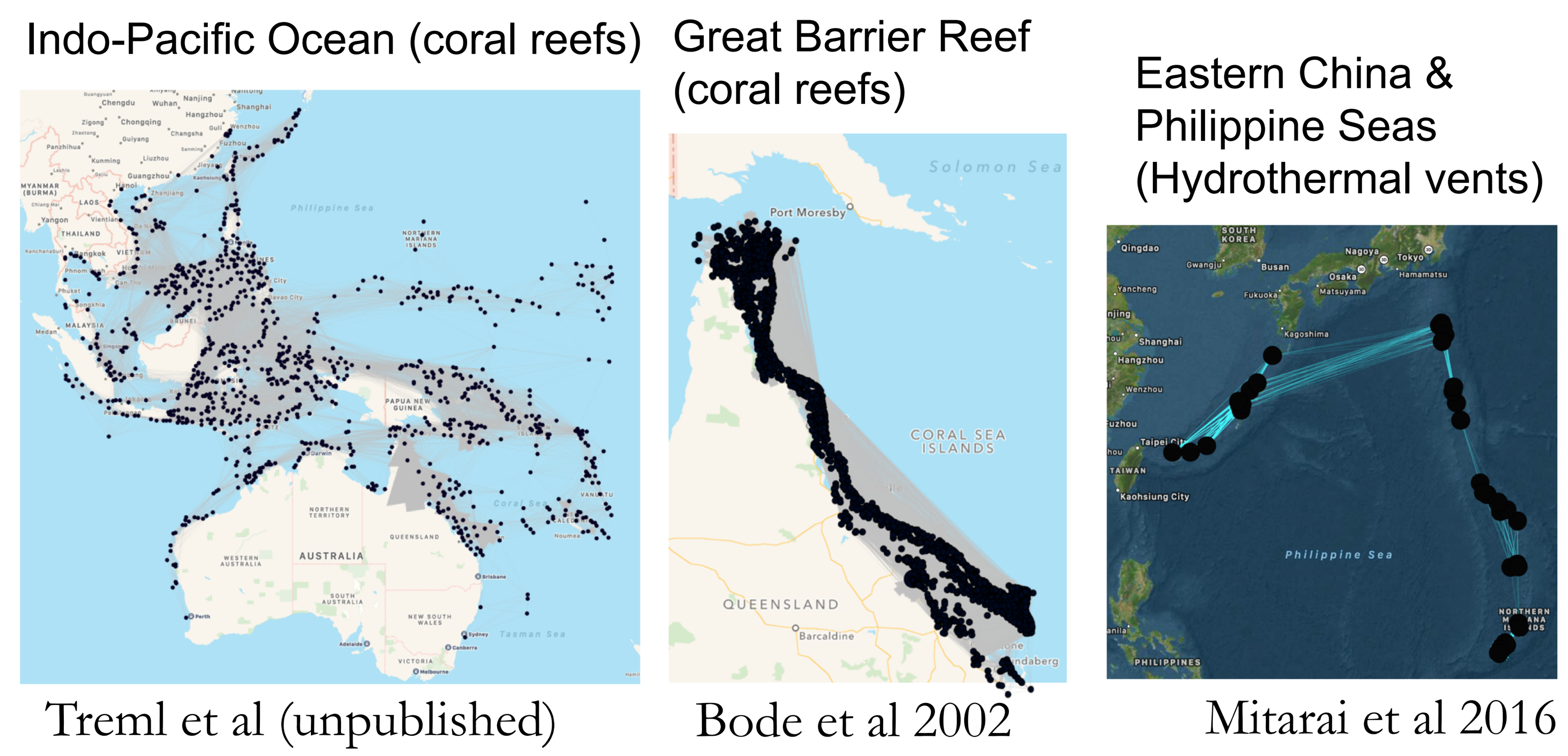


Figure 3. Changes in beta and gamma diversity of simulated metacommunities on the five spatial structures for dispersal rates ranging between 0.4 (top right) and 0.0005 (bottom left). Biodiversity patterns on the different spatial topologies followed different trajectories between species-sorting and mass-effect regimes (Fig. 1a). While the metacommunity with complete network (dashed line) reached the state of local coexistence (top left area) at the intermediate dispersal rate and shifted to a state of strong regional exclusion (bottom left), metacommunities with other topologies directly shifted to regional exclusion without exhibiting local coexistence. Moreover, the linear and tree topologies particularly retained relatively high gamma and beta diversity, i.e. they did not shift from species sorting to mass effects as much as other topologies at the highest dispersal rate. (From Suzuki & Economo 2021)

Spatial structures used (empirical)



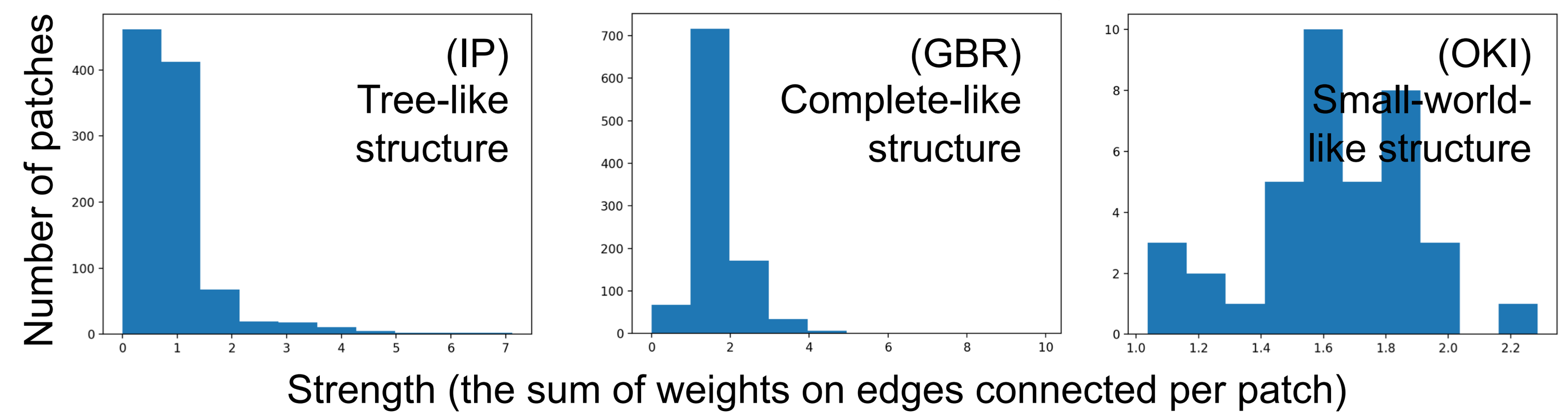


Figure 4. Spatial structures of three marine metacommunity systems. These network structures were estimated by regional-scale hydrodynamic models.

Resulting biodiversity patterns (with realistic connectivity)

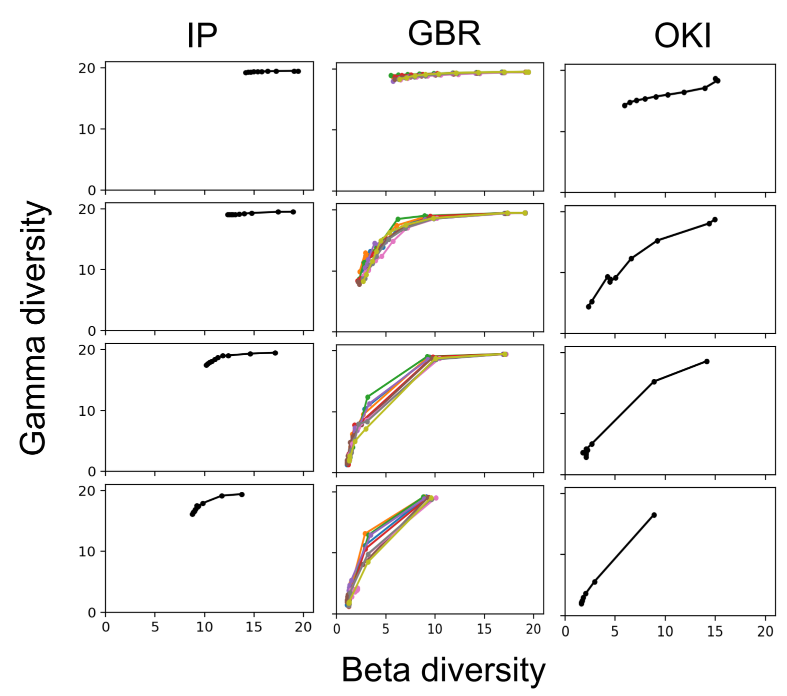


Figure 5. Changes in beta and gamma diversity of simulated metacommunities on the three marine dispersal connectivity networks for dispersal rates ranging between 0.4 (top right) and 0.0005 (bottom left) . The trajectory in the two dimensional space varied among the three networks. IP network showed species-sorting-like behavior, whereas mass effects were stronger in GBR and OKI networks. In GBR, source-sink effects acted more strongly than regional exclusion, compared with OKI network. Different colors in GBR shows results from sub-sampled networks of size about 500, 750, and 1000 patches.

References
Mouquet, N. and Loreau, M. (2003), Community patterns in source–sink metacommunities. Am. Nat. 162: 544–557.
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