Regional connectivity, local environmental conditions, and biotic interactions jointly structure a temperate seagrass epifaunal metacommunity

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Appendix S1: Supporting Information

Equation S1. Equations for D^2_{adj} calculations

Explained deviance or D² (Guisan and Zimmerman 2000) was calculated by the equation:

 $D^2 = 1$ - Residual deviance / Null deviance

Where the residual deviance refers to the deviance in predicted species occurrences, and the null deviance refers to deviance in observed species occurrences.

Adjusted D^2 (Guisan and Zimmerman 2000) was calculated by the equation:

 $D^{2}_{adj} = 1 - (((n-1)/(n-p-1)*(D^{2}-1)))$

Where n is the number of sites (13) in our study, and p is the number of parameters the model estimated (4, Ovaskainen et al. 2017, Supporting Information). Negative D^2_{adj} values (those which had greater residual deviance than null deviance) were set to 0.

Equation S2. Calculation for type III variation partitioning result

m1 = the fraction of variation explained by all environmental variables in the HMSC model estimated with only environmental variables; m2 = the fraction of variation by spatial distances in the version of the HMSC model estimated with only spatial distances; m3 = the global model including both;

Fraction *ab* (pure environment + shared fraction) = $D^2_{adj} m l$ Fraction *bc* (pure space + shared fraction) = $D^2_{adj} m 2$ Fraction *abc* (pure environment + shared fraction + pure space) = $D^2_{adj} m 3$

Fraction *a* (pure environment) = abc - bcFraction *c* (pure space) = abc - abFraction *b* (shared fraction) = ab + bc - abcFraction *d* (residuals) = 1 - abc

Fractions *a* ("Environmental conditions"), *c* ("Spatial distance"), *b* (shared fraction), and *d* ("Residuals") are shown in the Venn diagram in Fig. S3.



Figure S2. Site-by-species presence-absence matrix of all 58 invertebrate species in the study listed in alphabetical order. Black cells indicate species presences.

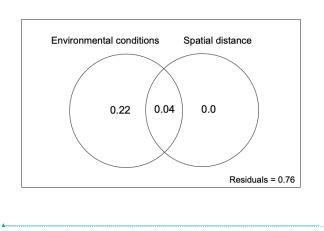


Figure S3. Venn diagram summarizing the fractions of variation explained by environmental covariates only (9 water quality and 5 biotic variables), spatial distance only, and the shared fraction explained by environment and space.

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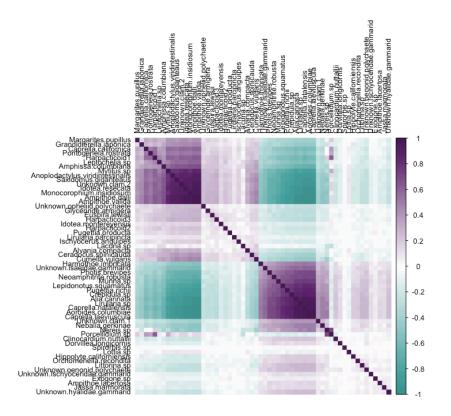


Figure S4. A correlation plot showing modelled site-level co-occurrence of species pairs across all species. Purple cells represent positively co-occurring species pairs, and turquoise cells represent negatively co-occurring species pairs. Species names along both axes are ordered according to the output of hierarchical clustering with Ward's criterion (Ward 1963) on pairwise co-occurrence values. This figure is a supplement to Fig. 4a in the main text.

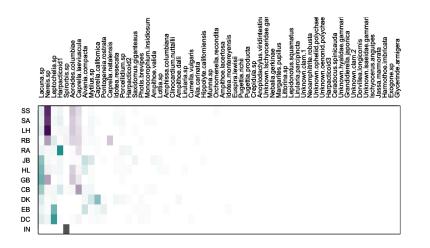


Figure S5. Heat map depicting abundance patterns in all 58 species in the study. Species names are ordered from highest to lowest predicted mean proportional abundance. Cell colours correspond to the co-occurrence groups in Fig. 4b, with turquoise cells representing members of the turquoise assemblage, purple cells indicating members of the purple assemblage, and grey cells indicating species that did not significantly co-occur negatively or positively with other species. Cell shade strength represents proportional abundance at a given site (darker means higher abundance). Most species outside the top twenty most abundant had extremely low predicted proportional abundances owing to their low raw abundances. This figure is a supplement to Fig. 4b in the main text.

Literature Cited

- Guisan, A., and N. E. Zimmermann. 2000. Predictive habitat distribution models in ecology. Ecological Modelling 145:147–186.
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- Ward, J. H. 1963. Hierarchical Grouping to Optimize an Objective Function. Journal of the American Statistical Association 58:236-244.