Figures

A

Branching prob. = 0.2   Branching prob. = 0.5   Branching prob. = 0.8

B

C

Hokkaido, Japan
59 watersheds

Midwest, US
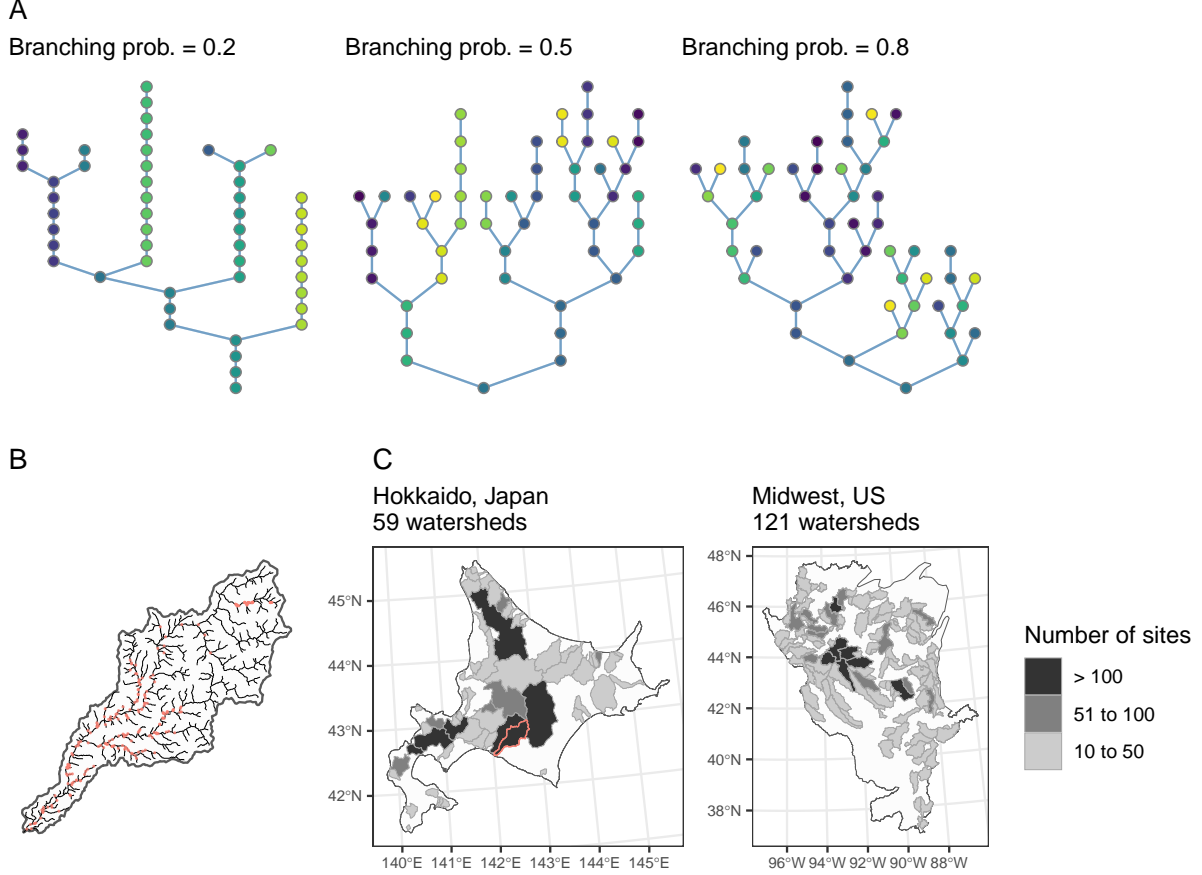121 watersheds

Number of sites

> 100

51 to 100

10 to 50

Figure 1: (A) Framework for generating theoretical branching river networks. Branching river networks are depicted as a network of connected habitat patches, in which the number of habitat patches N_p and branching probability P_b dictate the ecosystem size and complexity ($N_p = 50$ and $P_b = \{0.2, 0.5, 0.8\}$ in this example). Environmental conditions at headwaters (i.e., the most upstream patches) are drawn randomly from a normal distribution and propagate downstream with local environmental noise (a spatially autoregressive process with white noise; Methods). Habitat patches are colored in proportion to environmental values (similar colors have similar environmental values). In this example, we used values of environmental variation at headwaters $\sigma_h = 1$ and the degree of local environmental noise $\sigma_l = 0.01$. (B) Example of intensively surveyed watersheds in Hokkaido, Japan (the red-colored watershed in C). Red dots indicate sampling sites for fish surveys. (C) Map of study regions (left, Hokkaido, Japan; right, Midwest, US). Watersheds (i.e., metacommunities) are gray-shaded in proportion to the number of sampling sites.
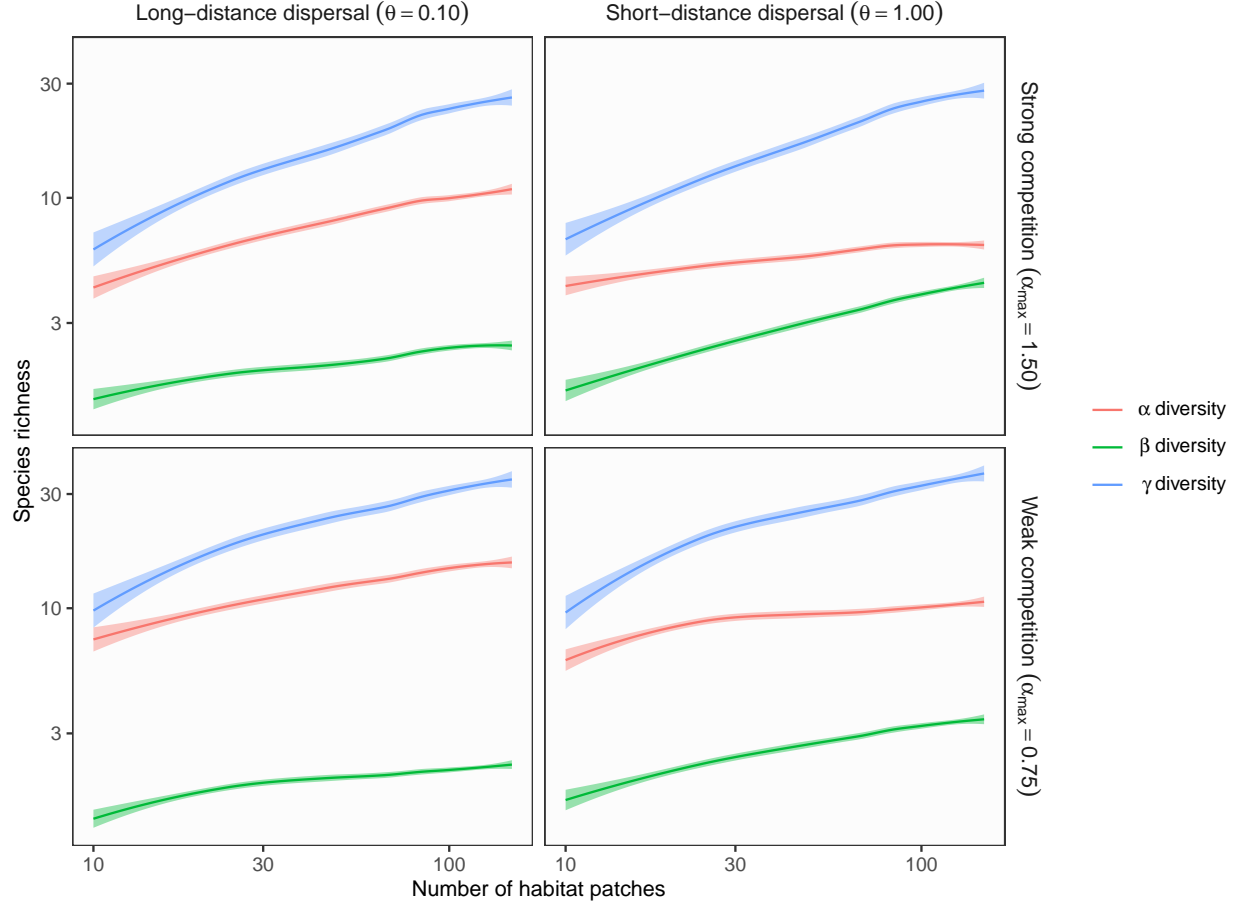
Figure 2: Theoretical predictions for ecosystem size influences (the number of habitat patches) on α, β, and γ diversity in branching networks. Lines and shades are loess curves fitted to simulated data and its 95% confidence intervals. Each panel represents different ecological scenarios under which metacommunity dynamics were simulated. Rows represent different competition strength. Competitive coefficients (α_{ij}) were varied randomly from 0 to 1.5 (top, strong competition) or 0.75 (bottom, weak competition). Columns represent different dispersal scenarios. Two dispersal parameters were chosen to simulate scenarios with long-distance (the rate parameter of an exponential dispersal kernel $\theta = 0.10$) and short-distance dispersal ($\theta = 1.0$). In this simulation, environmental variability among headwaters (i.e., the most upstream patches), which is expressed as the standard deviation of a normal distribution ($\sigma_h = 1.0$), was greater than that of local environmental noise occurring at each habitat patch ($\sigma_l = 0.01$). Dispersal probability p_d was 0.01 for all the scenarios.
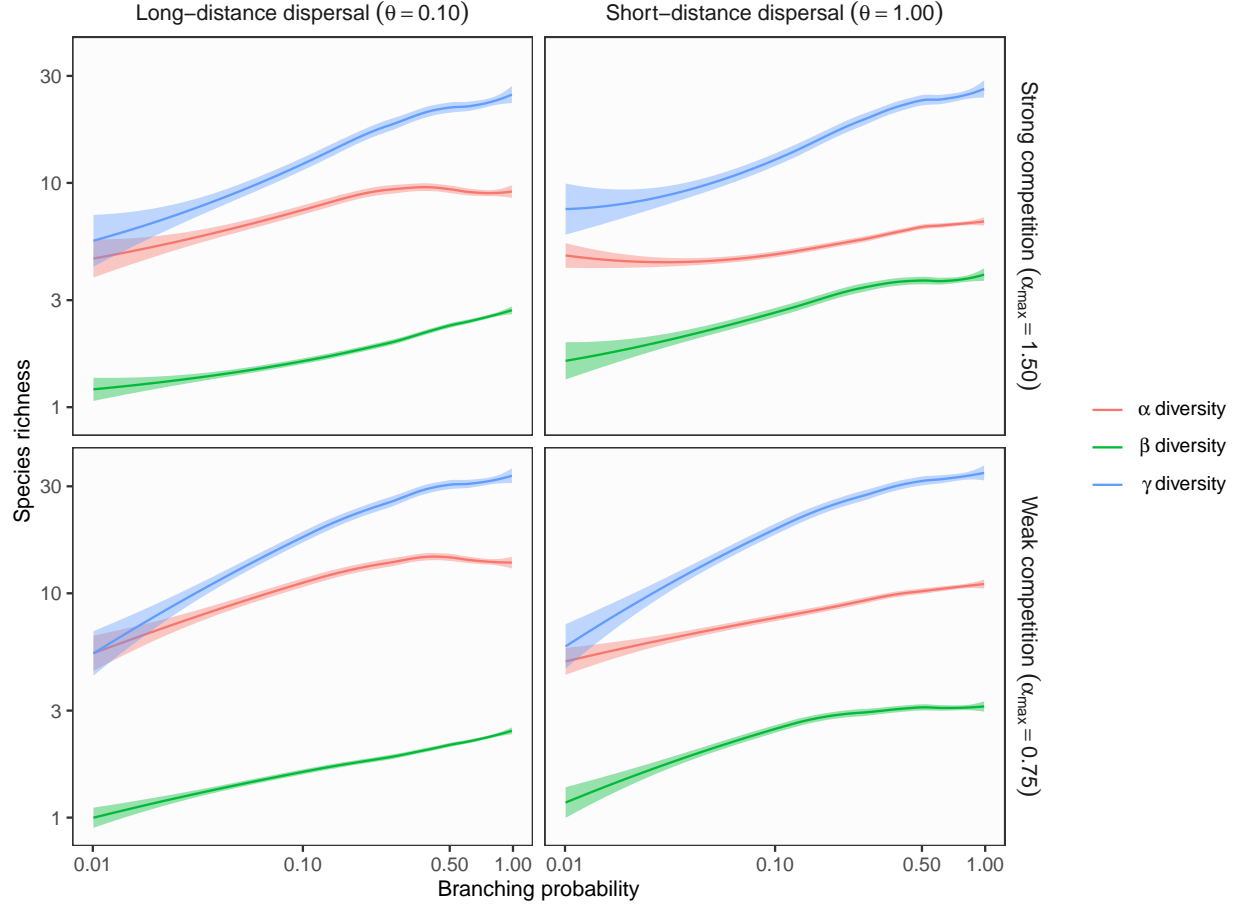
Figure 3: Theoretical predictions for ecosystem complexity influences (branching probability) on α, β, and γ diversity in branching networks. Lines and shades are loess curves fitted to simulated data and its 95% confidence intervals. Each panel represents different ecological scenarios under which metacommunity dynamics were simulated. See Figure 2 for details.
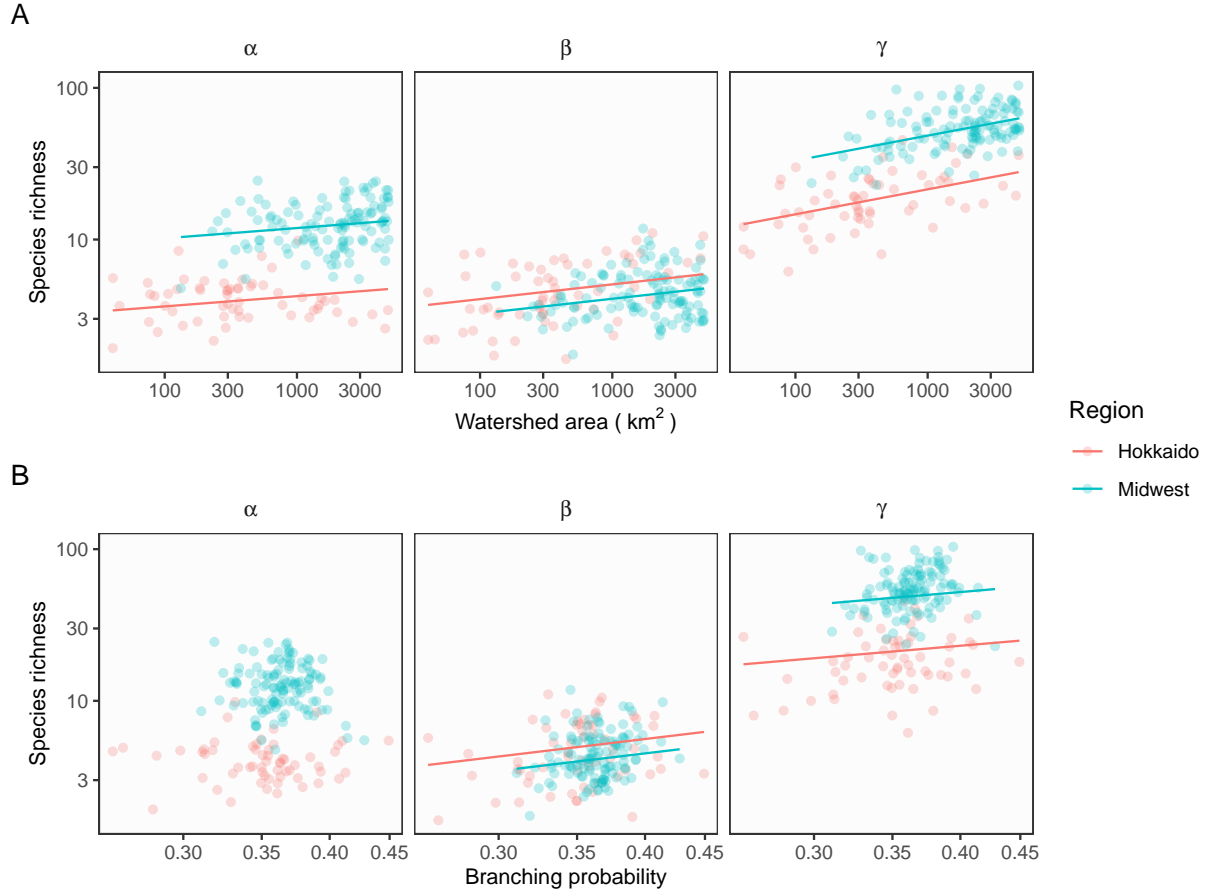
Figure 4: Influences of ecosystem size (A, watershed area) and complexity (B, branching probability) on α (left), β (middle), and γ diversity (right) in Hokkaido and Midwest regions. Dots represent watershed replicates (i.e., metacommunities), and lines are predicted values from the linear regression models.