

# Figures

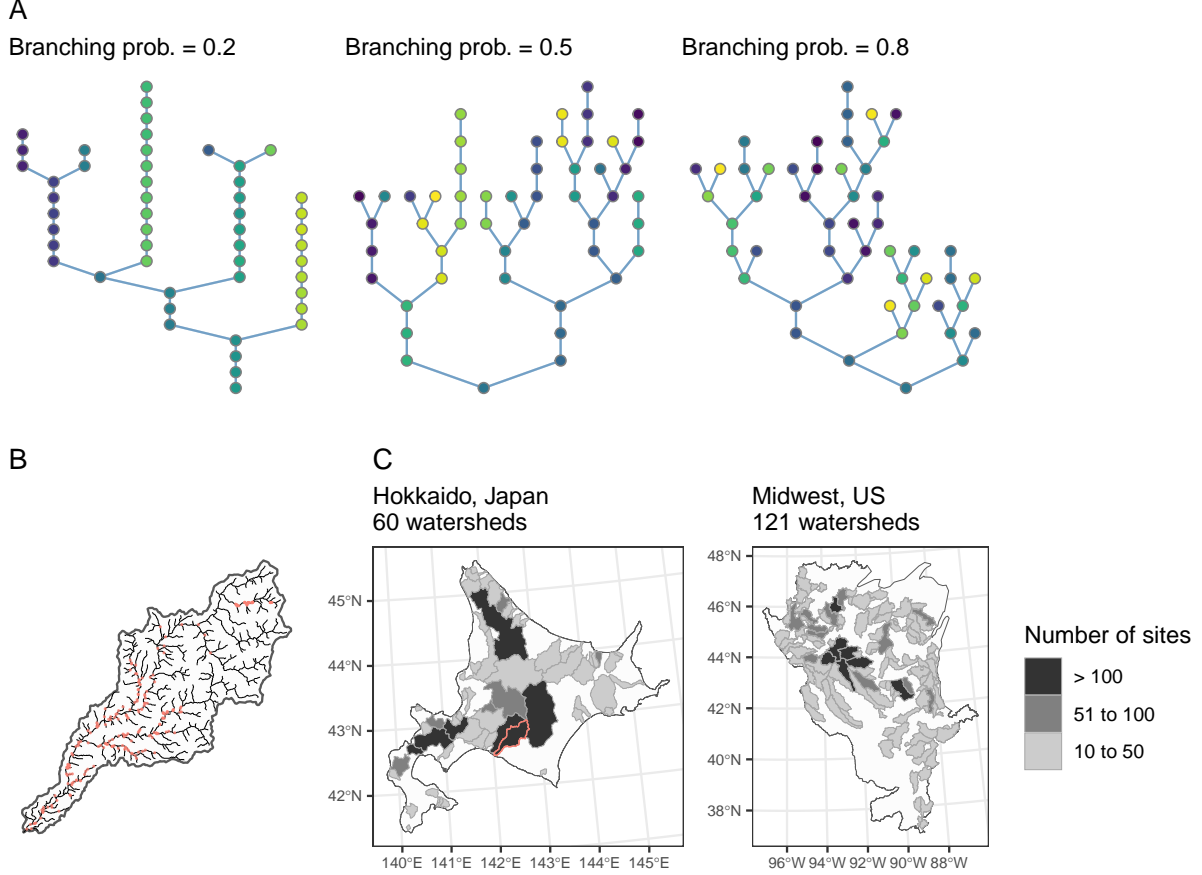


Figure 1: (A) Framework for generating theoretical branching river networks. Branching river networks are depicted as a network of connected habitat patches, in which the number of habitat patches  $N$  and branching probability  $P_b$  dictate the ecosystem size and complexity ( $N = 50$  and  $P_b = \{0.2, 0.5, 0.8\}$  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). (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, Midwest, US; right, Hokkaido, Japan). Watersheds (i.e., metacommunities) are gray-shaded in proportion to the number of sampling sites.

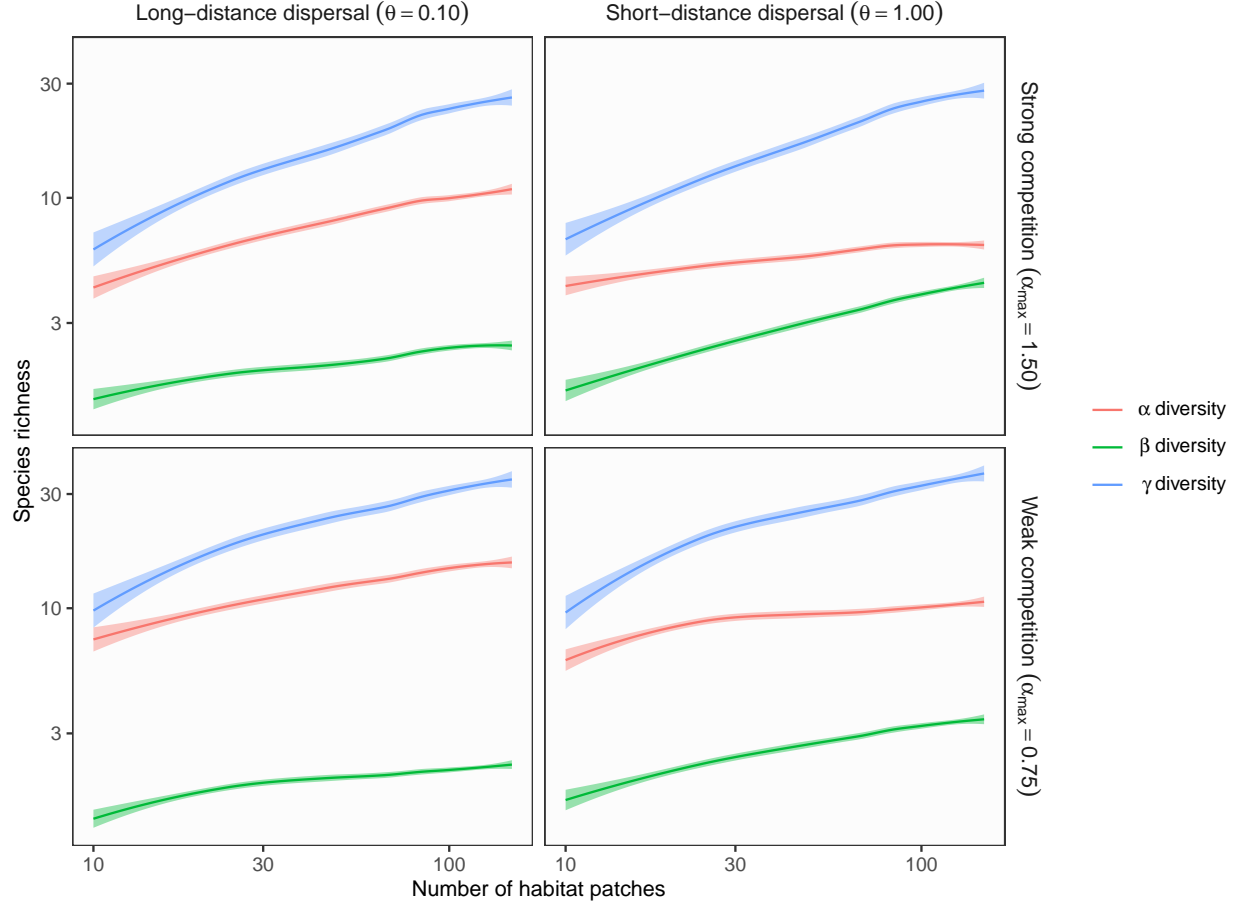


Figure 2: Theoretical predictions for ecosystem size influences (the number of habitat patches) on  $\alpha$ ,  $\beta$ , and  $\gamma$  diversity in branching networks. Lines and shades are loess curves fitted to simulated data and its 95% confidence intervals. Each panel represents different ecological scenarios under which metacommunity dynamics were simulated. Rows represent different competition strength. Competitive coefficients ( $\alpha_c$ ) 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.

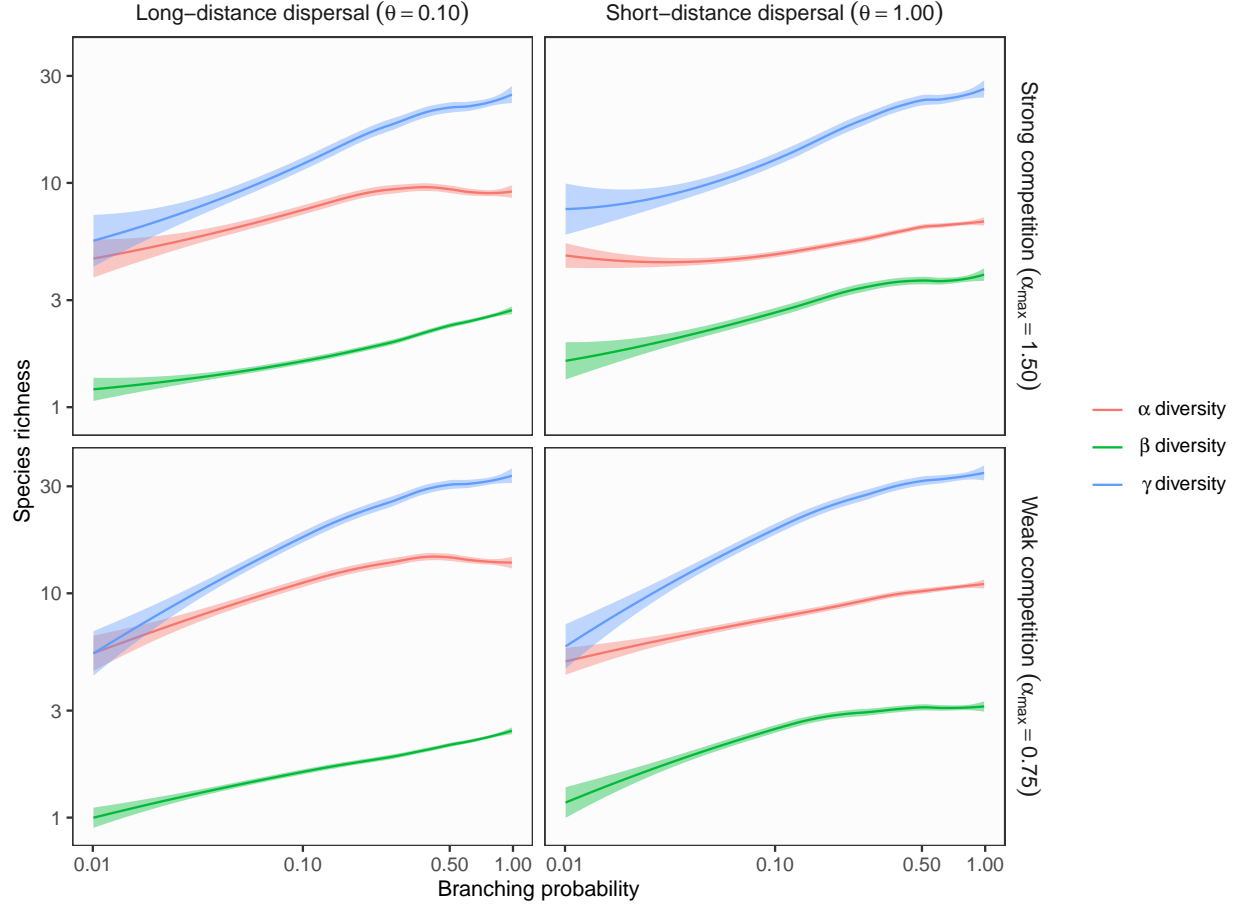


Figure 3: Theoretical predictions for ecosystem complexity influences (branching probability) on  $\alpha$ ,  $\beta$ , and  $\gamma$  diversity in branching networks. Lines and shades are loess curves fitted to simulated data and its 95% confidence intervals. Each panel represents different ecological scenarios under which metacommunity dynamics were simulated. See Figure 2 for details.

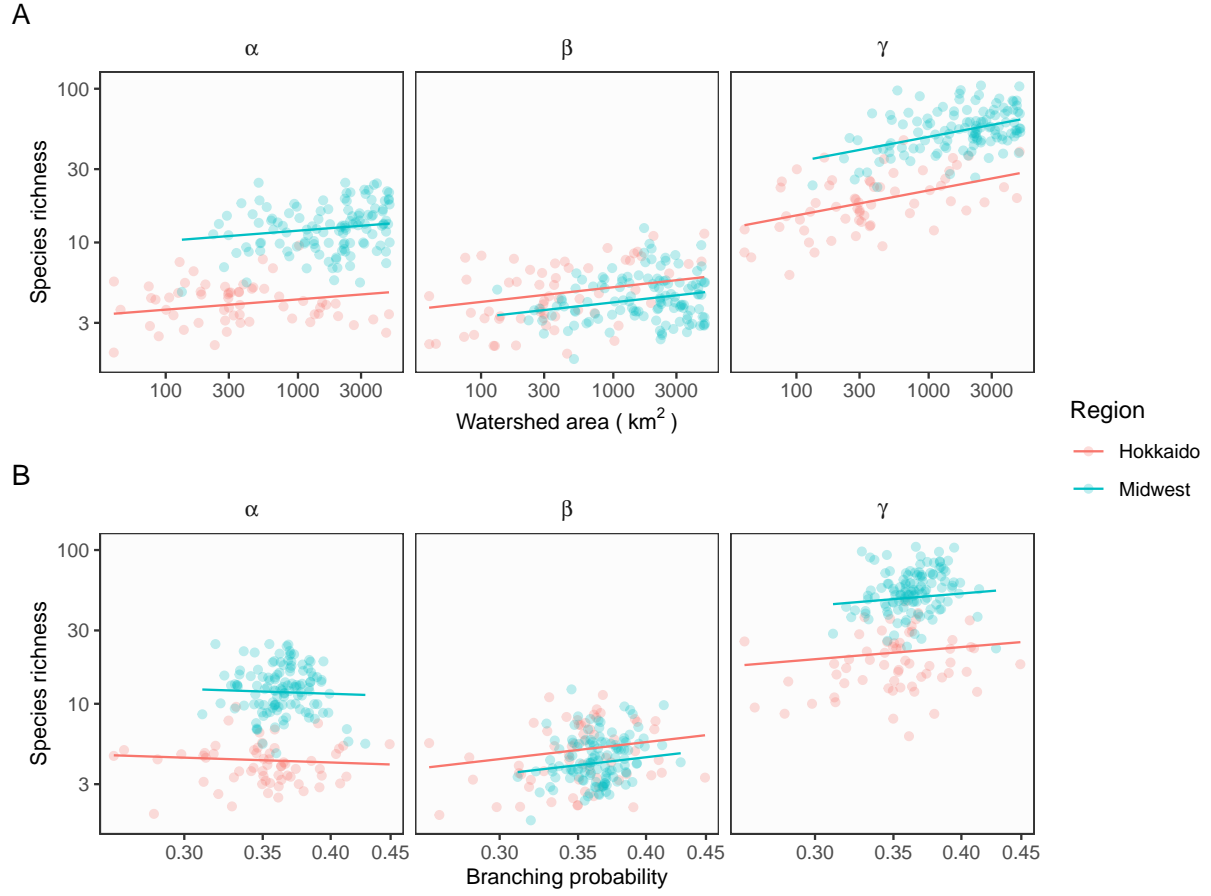


Figure 4: Influences of ecosystem size (A, watershed area) and complexity (B, branching probability) on  $\alpha$  (left),  $\beta$  (middle), and  $\gamma$  diversity (right) in Hokkaido and Midwest regions. Dots represent watershed replicates (i.e., metacommunities), and lines are predicted values from the linear regression models.