

Functional traits contribute in opposite directions to taxonomic turnover in northeastern US forests over time

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APPENDIX S3. Null models

TEXT

Methods for calculating the null model:

The exclusion of sets of species from the plots alters the species richness and this may affect similarity metrics. To account for this potential bias, we implemented a null model analysis. We shuffled the species names 999 times in the trait data before doing the binning. For each iteration, we used this null distribution of values to exclude species from the plots (e.g., removing null small-seeded species). Next, we calculated taxonomic dissimilarity using Sørensen, Horn and Morisita-Horn in the same way described in the main text. As a result, we obtained 999 null sets of temporal comparisons across all FIA plots, per trait exclusion category (i.e., small seeded/low wood density species, medium seeded/ wood density species, large seeded/high wood density species) and metric (i.e., Sørensen, Horn, Morisita-Horn). Next, we compared trajectories between the whole community and each of the null communities (bin-3, bin-2, for wood density and seed mass) using a Kruskal-Wallis test. At the end, we obtained 999 Chi^2 values from each iteration and compared the distribution of these Chi^2 null values with our observed Chi^2 value (Figs S3.1-S3.2). If the position of observed Chi^2 value (vertical dashed line in the figures) is > 0.975 , then we considered that the observed value is significantly different than the null distribution and the observed differences in turnover are driven by species differences in traits and not due to a random removal of species.

FIGURES

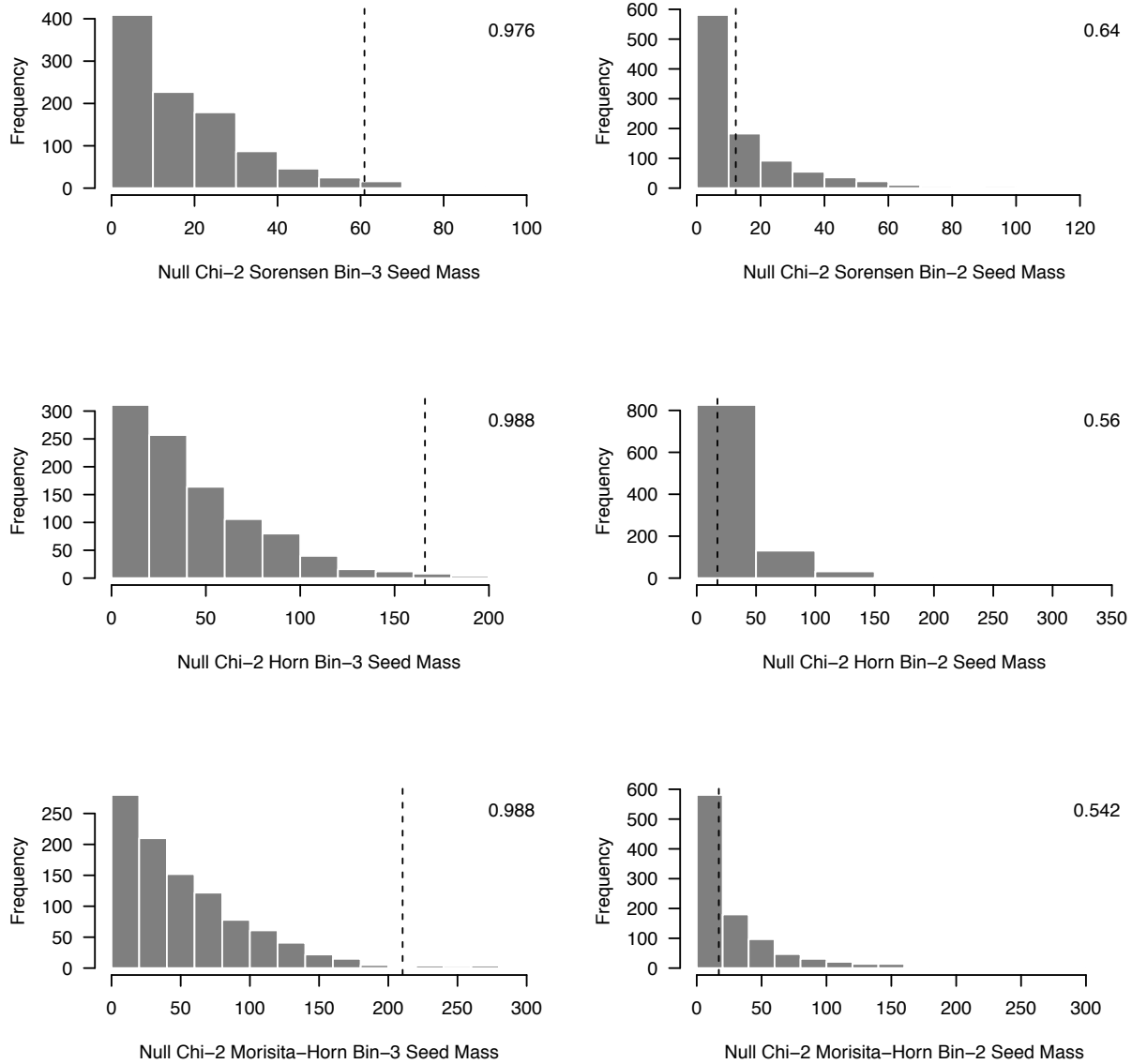


Figure S3.1. Histogram of null χ^2 values obtained from the Kruskal-Wallis test based on the null communities. The Kruskal-Wallis test compared the differences in median values of differences in trajectories (E) between trajectories that included all species (ALL) and those that excluded randomized species based on differences in seed mass (ALL _{w/o} LSM = Excl. large; ALL _{w/o} MSM = Excl. medium; ALL _{w/o} SSM = Excl. small). The vertical dashed line represents the observed χ^2 value for data that was not randomized. The numbers in the top right represent the quantile of the observed value compared to the null distribution. Observed values > 0.975 are considered significant.

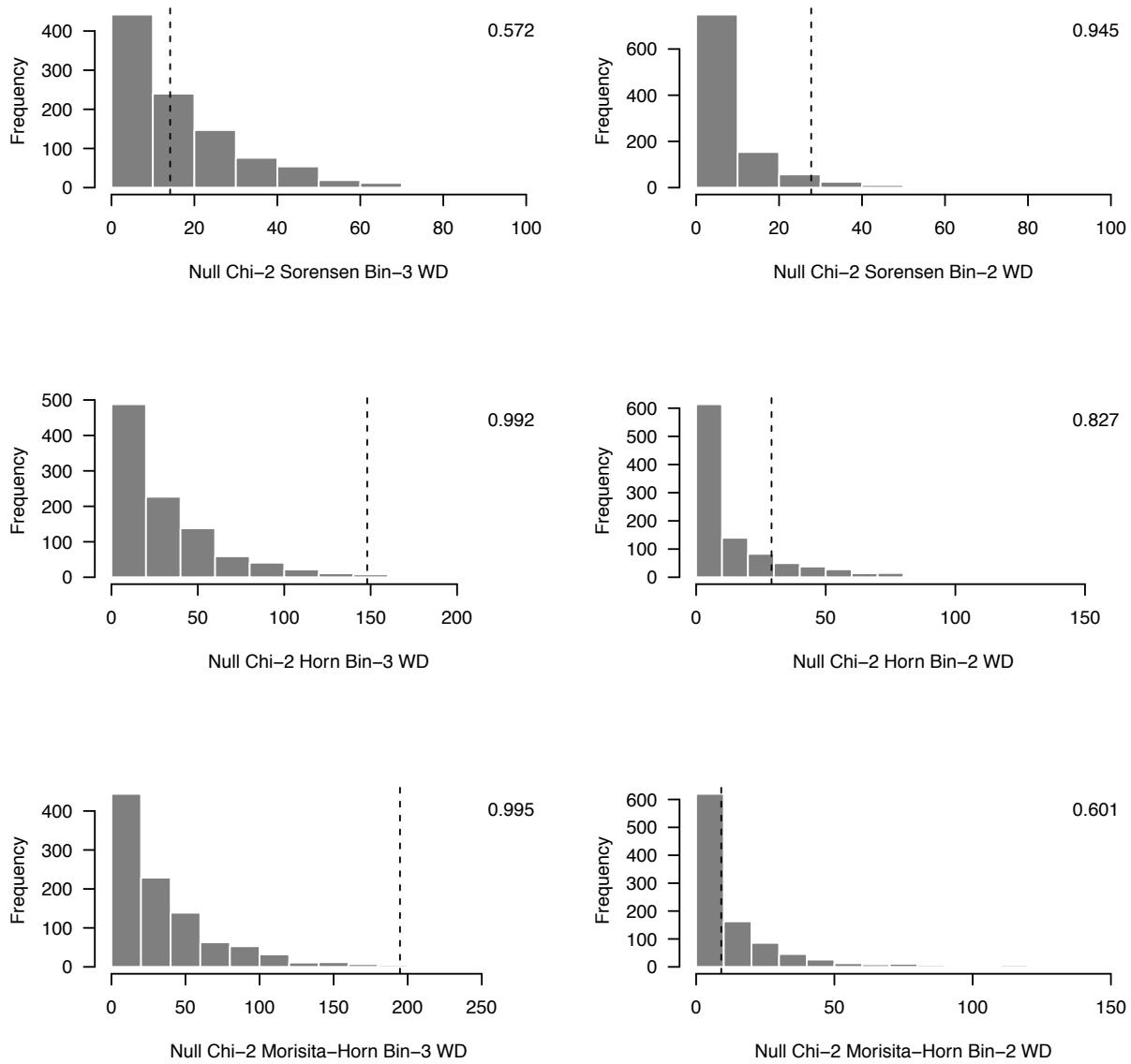


Figure S3.2. Histogram of null χ^2 values obtained from the Kruskal-Wallis test based on the null communities. The Kruskal-Wallis test compared the differences in median values of differences in trajectories (E) between trajectories that included all species (ALL) and those that excluded randomized species based on differences in wood density (ALL w/o HWD = Excl. high; ALL w/o MWD = Excl. medium; ALL w/o LWD = Excl. low). The vertical dashed line represents the observed χ^2 value for data that was not randomized. The numbers in the top right represent the quantile of the observed value compared to the null distribution. Observed values > 0.975 are considered significant.