

Plant functional diversity and the biogeography of biomes in North and South America

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Introduction

Understanding functional differences among biomes is critically important to modeling the global carbon cycle and the functioning of the Earth system, including responses to anthropogenic global change. Our goals in this study are (1) to document the extent of the available data that characterize the functional diversity and distinctiveness of biomes, to highlight persistent data shortfalls. (2) Given the available data, we quantify the functional distinctiveness of a biome by identifying the most common functional strategies of the most widespread species within it. (3) we explore whether biomes are in fact characterized by functionally distinct collections of species using measures of functional similarity based on multidimensional hypervolumes in functional trait space.

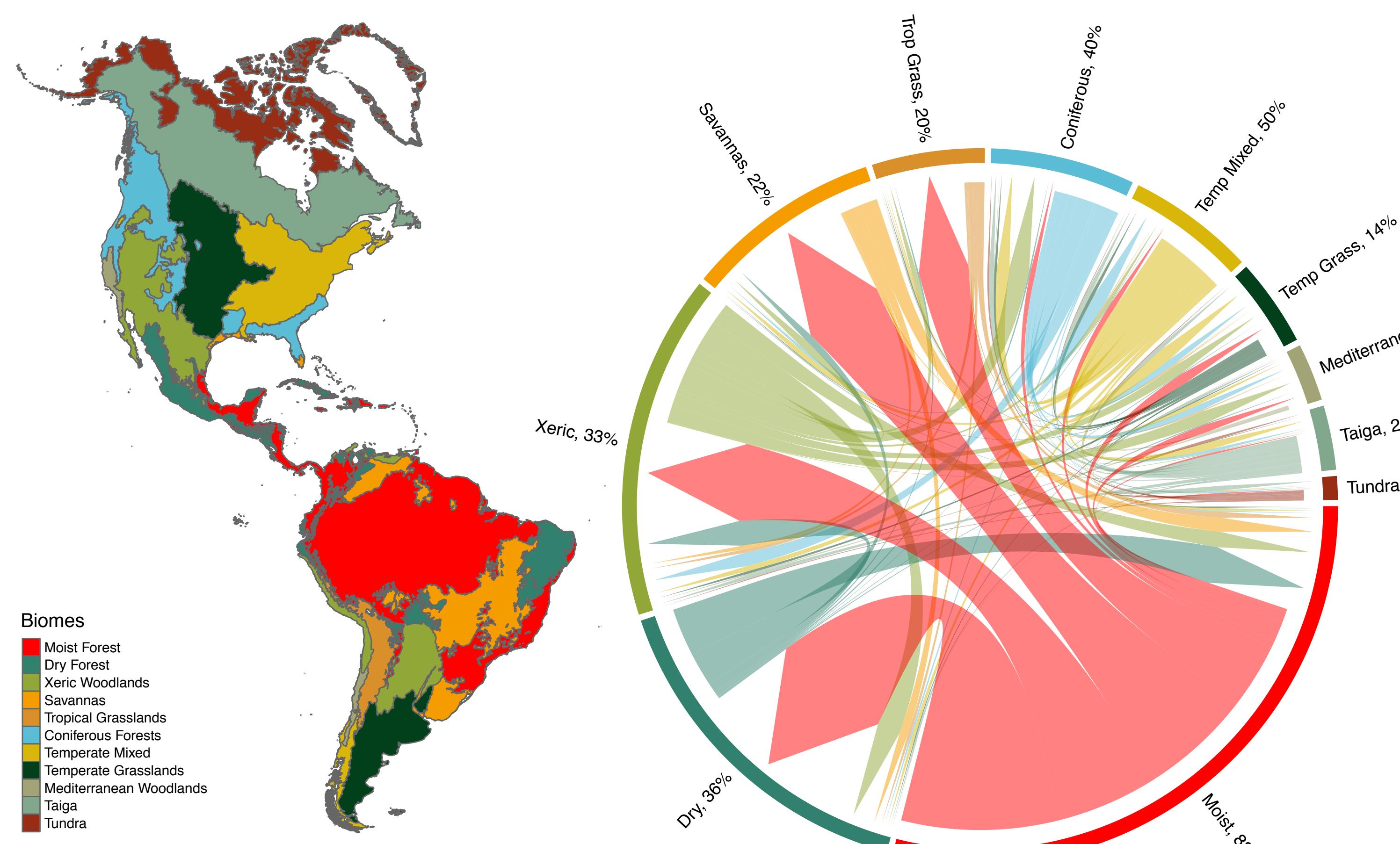


Figure 2: (A) Overlap of plant species among biomes of the New World. Percentage values express the fraction of species that have the greatest proportion of their geographic range in each biome. (B) Distribution of trait hypervolumes of 20% of randomly selected 100X100 km cells in each biome. Hypervolumes are reported in units of standard deviations to the power of the number of traits used.

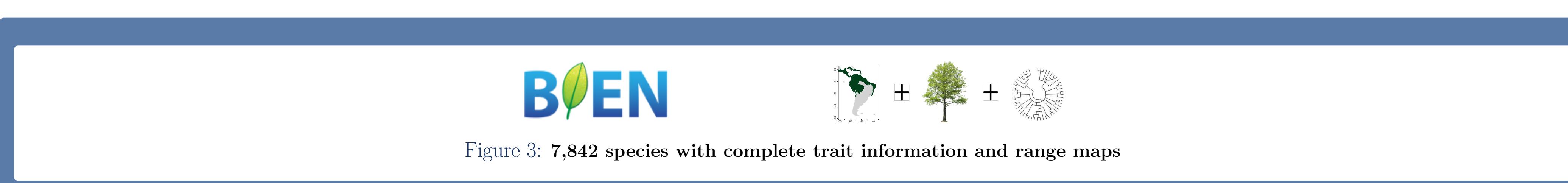


Figure 3: 7,842 species with complete trait information and range maps

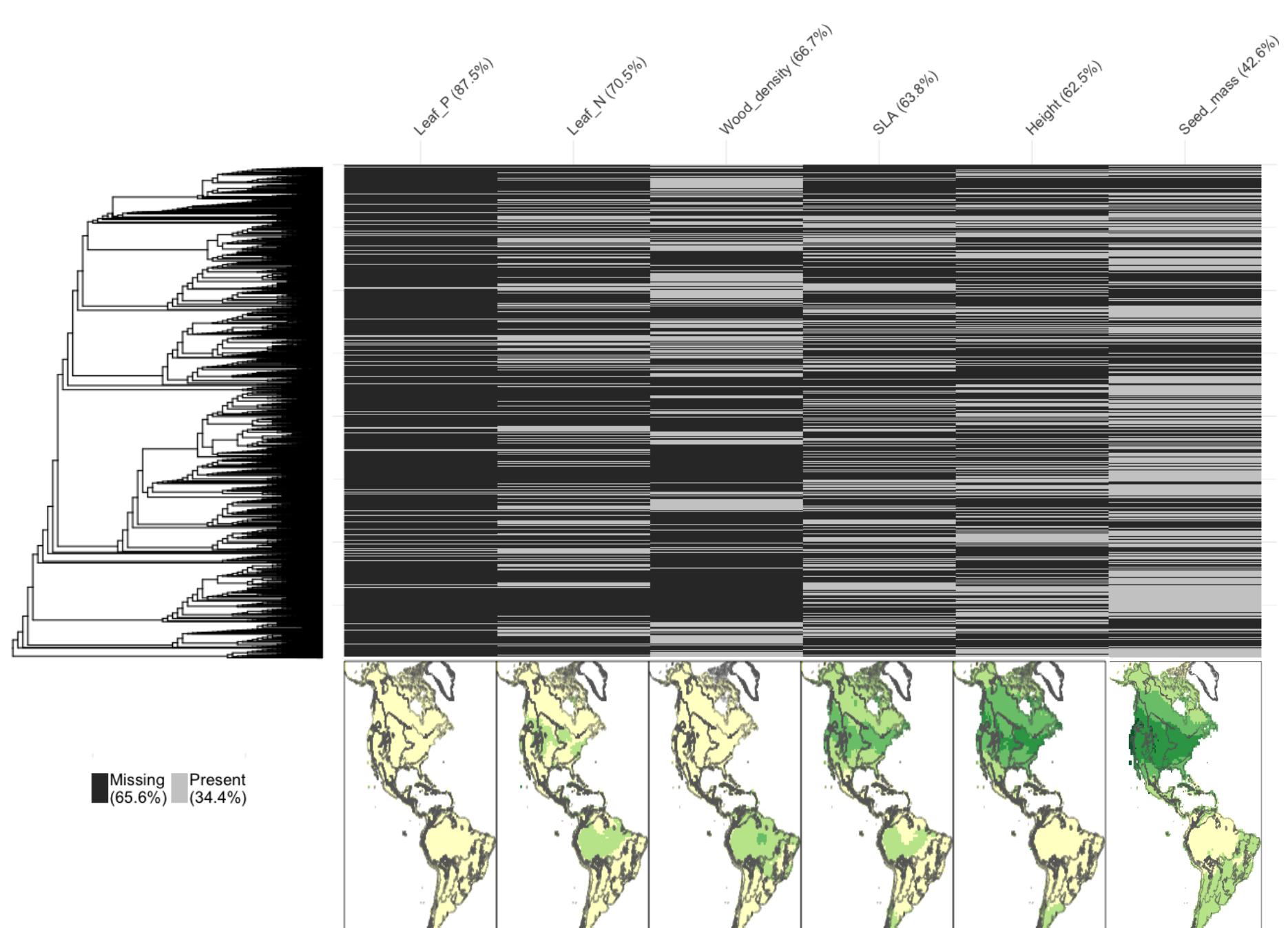


Figure 1: Proportion of species with known (gray) or missing (black) trait values to the total number of species in the BIEN 3.0 database. Phylogeny at the left corresponds to the ALLBM tree from Smith and Brown, 2018, which was used to phylogenetically imputed missing trait data using the R package "Rphylopars" v 0.2.9 (Goolsby et al., 2017)

- Trait hypervolumes: R package "hypervolume" (Blonder et al., 2014, 2018)
- Functional distinctiveness: R package "funrar" (Grenié et al., 2017, Violle et al. 2017)

Acknowledgments

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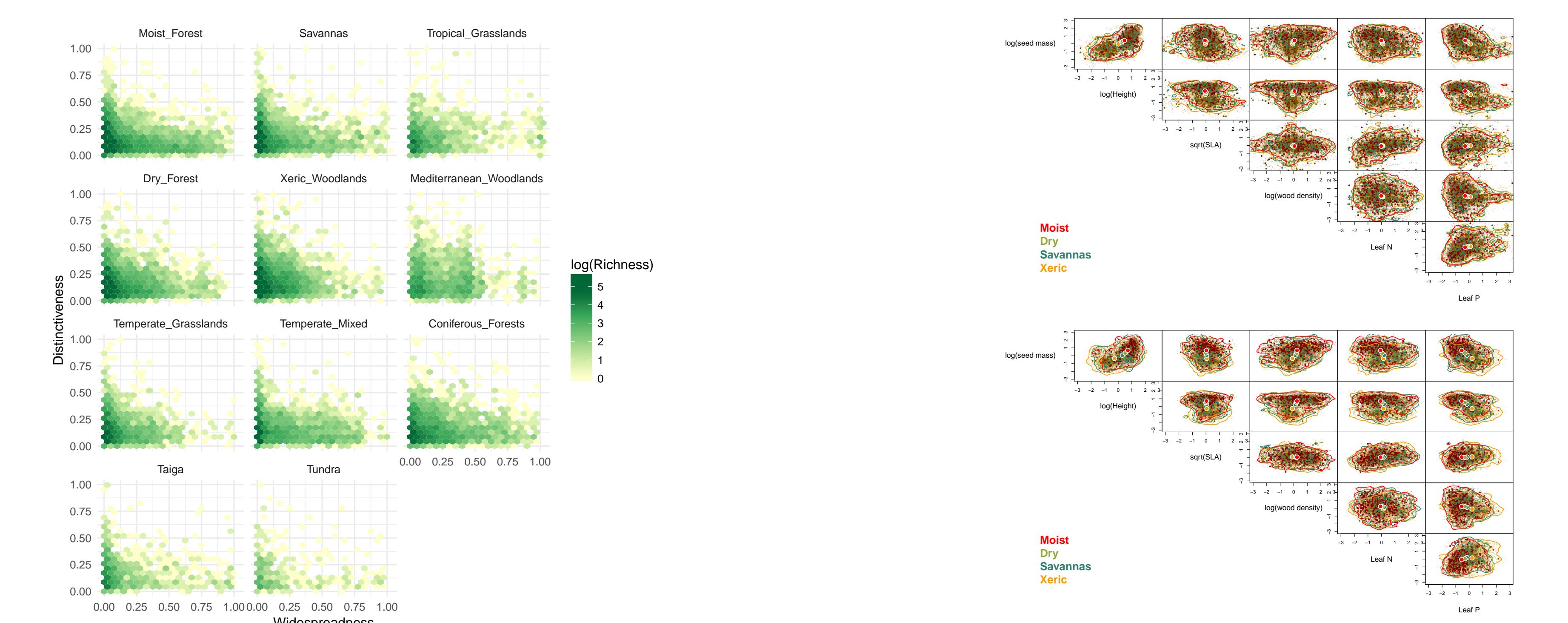


Figure 4: Patterns of functional distinctiveness among biomes. Distinctiveness represents how species are functionally distant from another within a biome (i.e., the mean pairwise phenotypic distance from a species that are functionally redundant and widespread in each biome). The larger the value, the more distant a species is to the centroid of the 2D projection using the combination of all six trait axes implemented in this study. The main traits are log(Richness), log(Height), log(Seed_Mass), log(Wood_Density), log(SLA), and log(Dry_Wood_Density). Widespreadness measures how geographically common a species is. A value of 0 indicates that a species is present in a single biome cell.

Figure 5: Trait hypervolumes for tropical biomes using (A) the whole pool of species and (B) using species that are functionally redundant and widespread in each biome. Hypervolumes are shown in a 2D projection using the combination of all six trait axes implemented in this study. The main traits are log(Richness), log(Height), log(Seed_Mass), log(Wood_Density), log(SLA), and log(Dry_Wood_Density). The hypervolumes are shown as 2D projections of the 6D trait space.

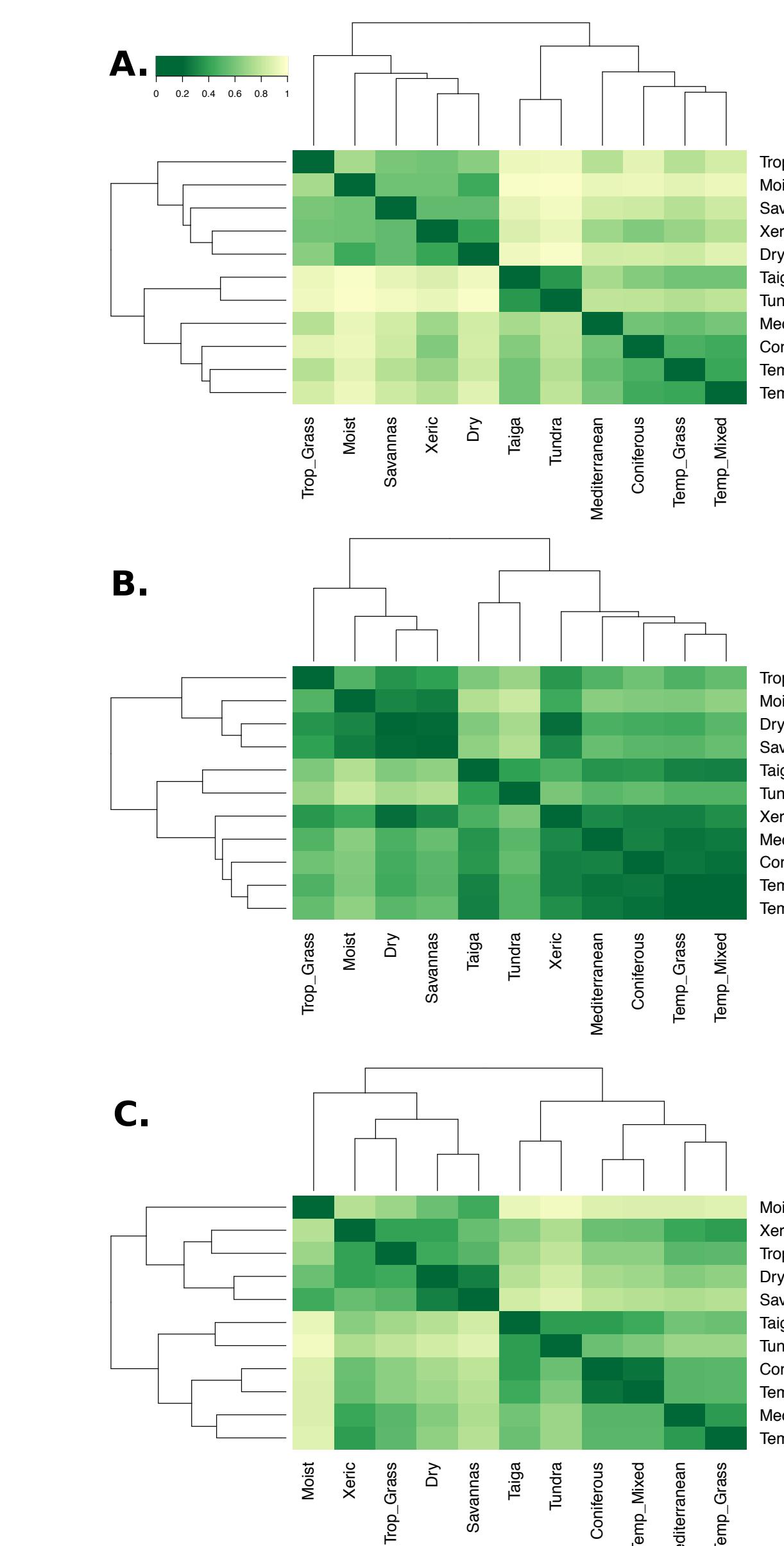


Figure 6: (A) Pairwise dissimilarity in species composition among biomes. (B) Pairwise dissimilarity in trait hypervolumes (1-Sørensen similarity) among biomes using the total number of species. (C) Pairwise dissimilarity in trait hypervolumes (1-Sørensen similarity) among biomes using only those species that are considered as functionally redundant and widespread. The lighter the cell the greater the dissimilarity.

Conclusions

- Despite progress in the compilation and synthesis of primary biodiversity data, significant knowledge shortfalls persist that may limit our ability to quantify the functional biodiversity of biomes on continental to global scales.
- Biomes can be more distinguished functionally, when only the widespread and functionally redundant species are considered, and patterns of dissimilarity between biomes appear to reflect a correspondence between climate and plant functional niche space.
- While the study of the functional diversity of biomes is still in its formative stages, further development of the field will yield insights linking evolution, biogeography, community assembly, and ecosystem function.

References

- Blonder, B., Lamanna, C., Violle, C., and Enquist, B. J. *Glob. Ecol. Biogeogr.* **23**, 595-609 (2014).
- Blonder, B., Morrow, C. B., Maitner, B., Harris, D. J., Lamanna, C., Violle, C., et al. *Methods Ecol. Evol.* **9**, 305-319 (2018).
- Enquist, B. J., Condit, R., Peet, R. K., Schildhauer, M., and Thiers, B. M. *PeerJ Preprints No. e2615v1* (2016).
- Grenié, Matthias, et al. *Diversity and Distributions* **23**, 1365-1371 (2017).
- Goldsmith, G. R., Morueta-Holme, N., Sandel, B., Fitz, E. D., Fitz, S. D., Boyle, B., et al. *Methods Ecol. Evol.* **7**, 960-965 (2016).
- Goolsby, E. W., Bruggeman, J., and Ané, C. *Methods Ecol. Evol.* **8**, 22-27 (2017).
- Smith, S. A., and Brown, J. W. *Am. J. Bot.* **105**, 302-314 (2018).
- Violle, C., Thuiller, W., Mouquet, N., Munoz, F., Kraft, N. J. B., Cadotte, M. W., et al. *Trends Ecol. Evol.* **32**, 356A-367 (2017).