



speciesRaster: a platform in R for integrating species ranges, morphology and phylogeny

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INTRODUCTION

Understanding what factors promote or inhibit the accumulation of species has long been a central theme in ecological and evolutionary research. Functional diversity, typically represented by a combination of traits thought to summarize the ecological characteristics of a species in its environment, has often been studied in the context of species coexistence and ecological niche theory. From the standpoint of community assembly, understanding how different aspects of functional diversity relate to each other, and to species richness, has the potential to clarify (1) the interplay between diversification and the occupation of morphological space; and, (2) how species partition ecological space and avoid competitive exclusion.

Exploring different axes of biodiversity in geographic space allows us to improve our understanding of how diversification, adaptation and environmental filtering have all contributed to the species communities observed today. In particular, quantifying spatial variation in morphology allows us to see how landscape features and climatic gradients have influenced variation in the morphospace occupied by communities, which may in turn lead to insights regarding how communities are adapted to particular conditions. Likewise, quantifying spatial variation in the phylogenetic relatedness of species can provide information regarding whether or not a community is the product of environmental filtering, or if species are the product of a recent radiation.

Although there is great potential in analyzing different axes of biodiversity in concert, it is only recently that morphological, phylogenetic and geographic data have become more broadly available for such analyses to be possible.

CASE STUDY:

THE NORTH AMERICAN DESERT HETEROMYIDAE

Multiple models predict how functional diversity should scale with species richness. North American desert rodents (especially Heteromyidae) have long been a model system for examining the relationship between ecological diversity, landscape features and community composition in western North America (e.g., Fox and Brown 1993; Dayan and Simberloff 1994; Stevens et al. 2012). A classic assembly rule predicts that functional diversity should reach its maximum when species richness equals the number of functional groups; in most of their range, two functional groups of heteromyids coexist. A quantitative analysis of phylogenetic diversity, found that, in richer communities, more similar species are packed more tightly into communities.

To demonstrate the utility of the speciesRaster framework, we integrated IUCN geographic range polygons, geometric morphometric shape (and size) data, and phylogeny (Fabre et al. 2012) for 57 species. We found that across communities of increasing richness, morphological range increases, with an asymptote at 7 species. In contrast, morphological minimum nearest neighbor distance remains relatively constant, but decreases with species richness for communities of 7 or more species.

The ratio of morphological range to minimum nearest neighbor shows that regions with greatest species richness are characterized by the maximum morphospace range and minimum nearest neighbor distance. This indicates that heteromyids achieve highest species richness by both expanding the morphospace and packing it more tightly.



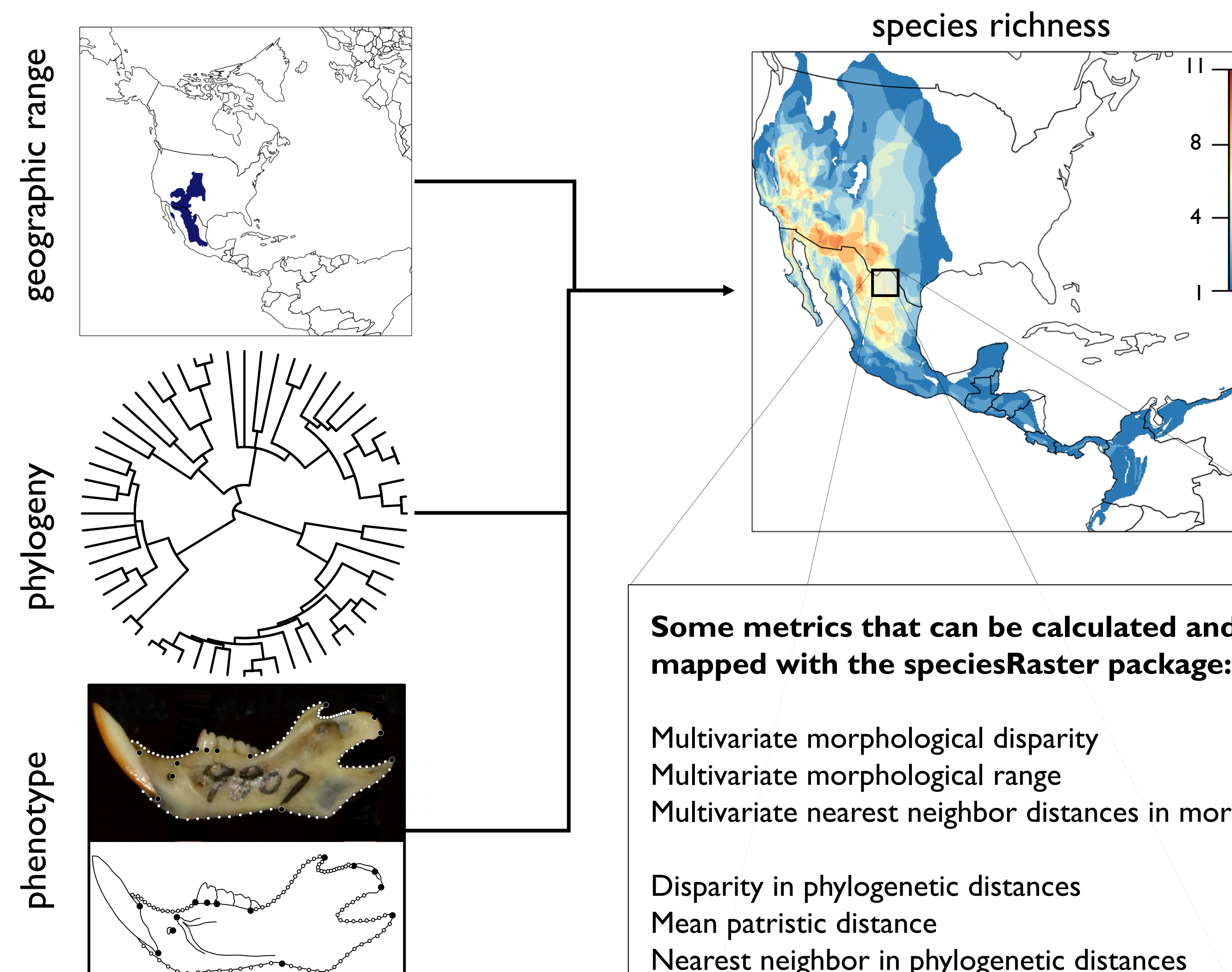
Tipton kangaroo rat (USFWS)

WHAT IS SPECIESRASTER?

We have developed a software package for the R programming environment that aims to facilitate the study of taxonomic, phylogenetic and morphological data across geographic space. In particular, we focus on the study of morphology as multivariate morphological shape, measured as high-dimensional geometric morphometric data from museum specimens.

The speciesRaster package makes it possible to create R objects of class `speciesRaster`, which are designed to hold an accounting of which species occur in each grid cell across a geographic region, as well as associated phylogenetic and morphometric shape data. The speciesRaster package can then implement a number of prepackaged taxonomic, phylogenetic and phenotypic metrics and plot these across geographic space. Users can also implement custom functions of their own, and tools are then available to apply those custom functions across all species communities.

Functions are also provided to export data to other R packages designed for the study of species community data (such as the R package picante, Kembel et al. 2010), as well as to facilitate the statistical analysis of the various data products in relation to one another, or in relation to other datasets, such as climatic or topographic data.



Some metrics that can be calculated and mapped with the speciesRaster package:

Multivariate morphological disparity
Multivariate morphological range
Multivariate nearest neighbor distances in morpho-space

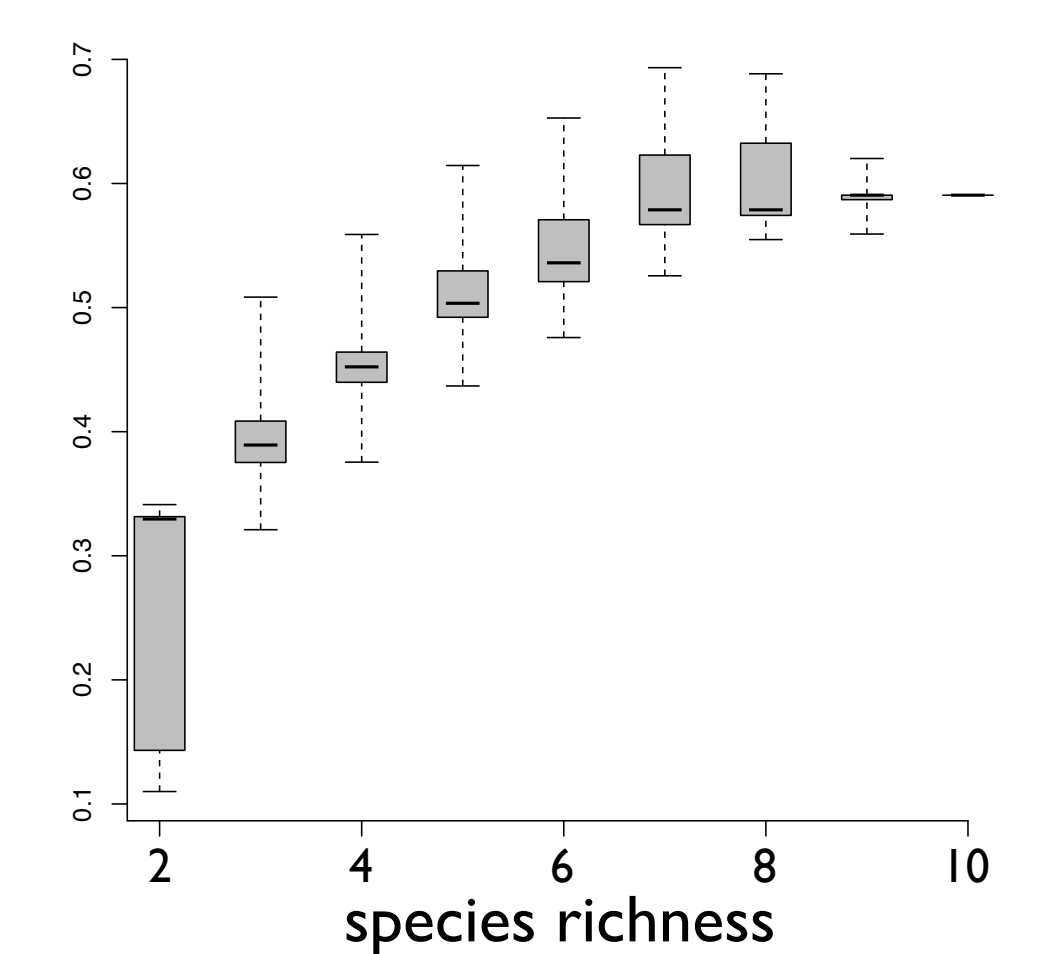
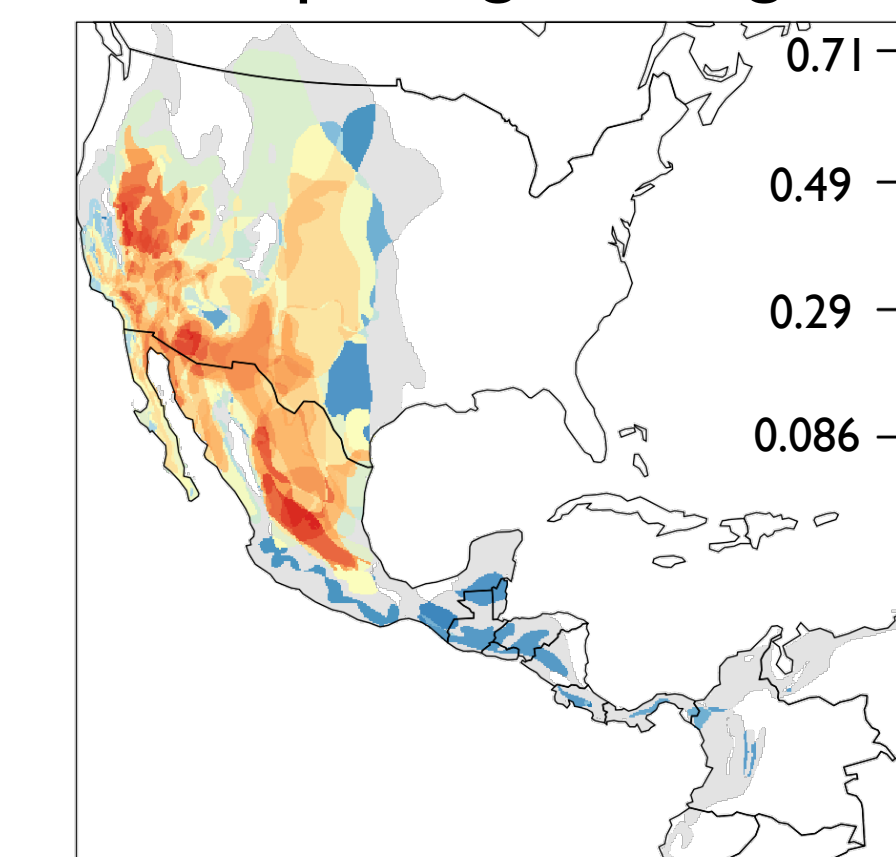
Disparity in phylogenetic distances
Mean patristic distance
Nearest neighbor in phylogenetic distances

Weighted endemism (Crisp et al. 2001)
Phylogenetic weighted endemism (Rosauer et al. 2009)

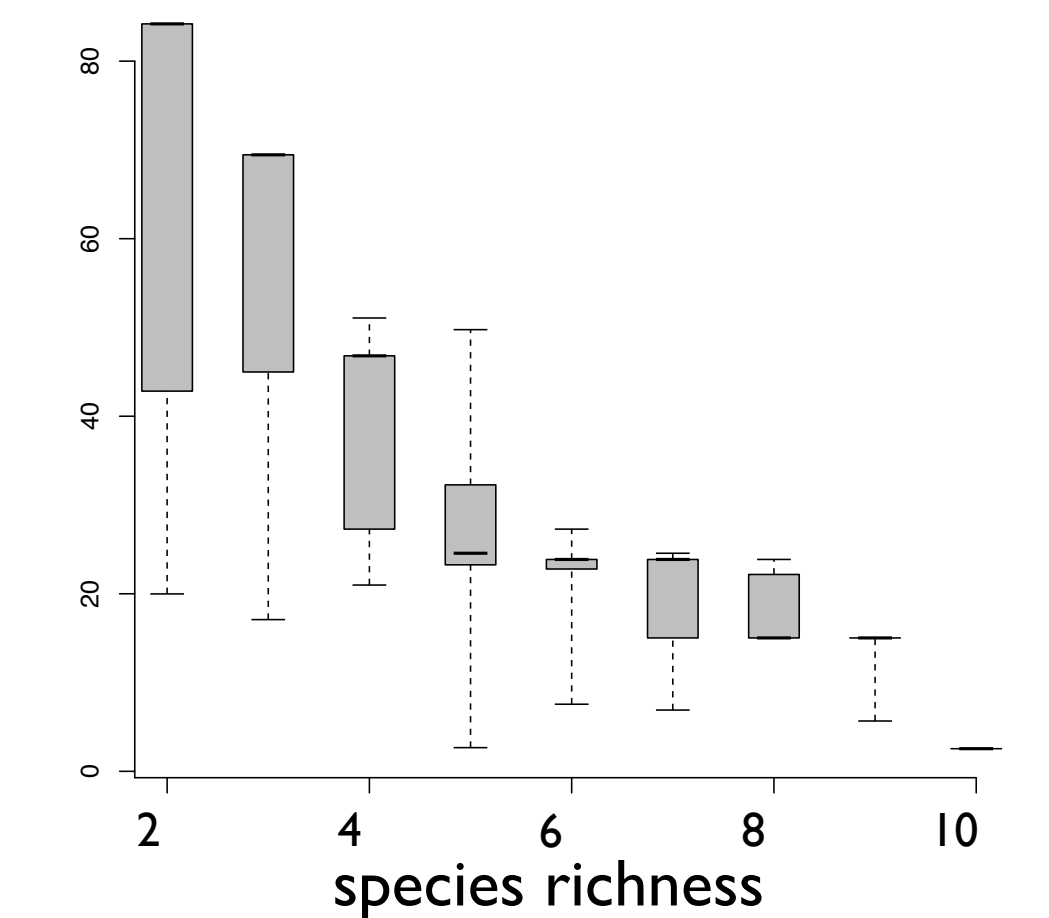
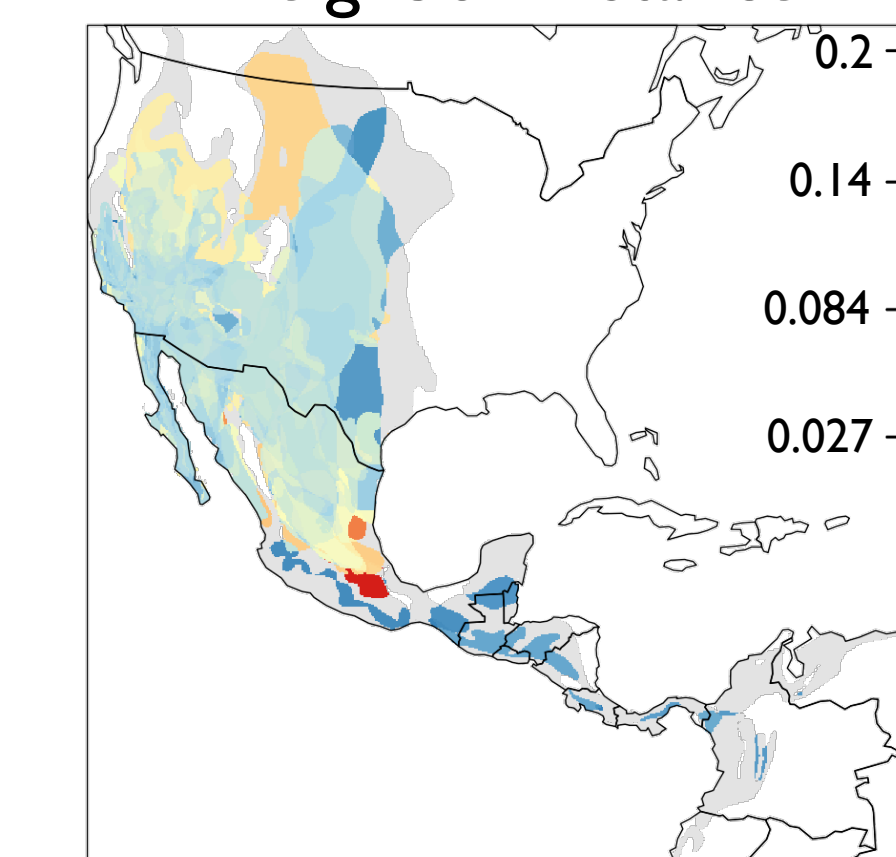
Moving window beta diversity metrics:
Spatial turnover in taxonomic diversity
Spatial turnover in phylogenetic diversity
Spatial turnover in morphological shape
Spatial turnover in morphological disparity

CASE STUDY RESULTS

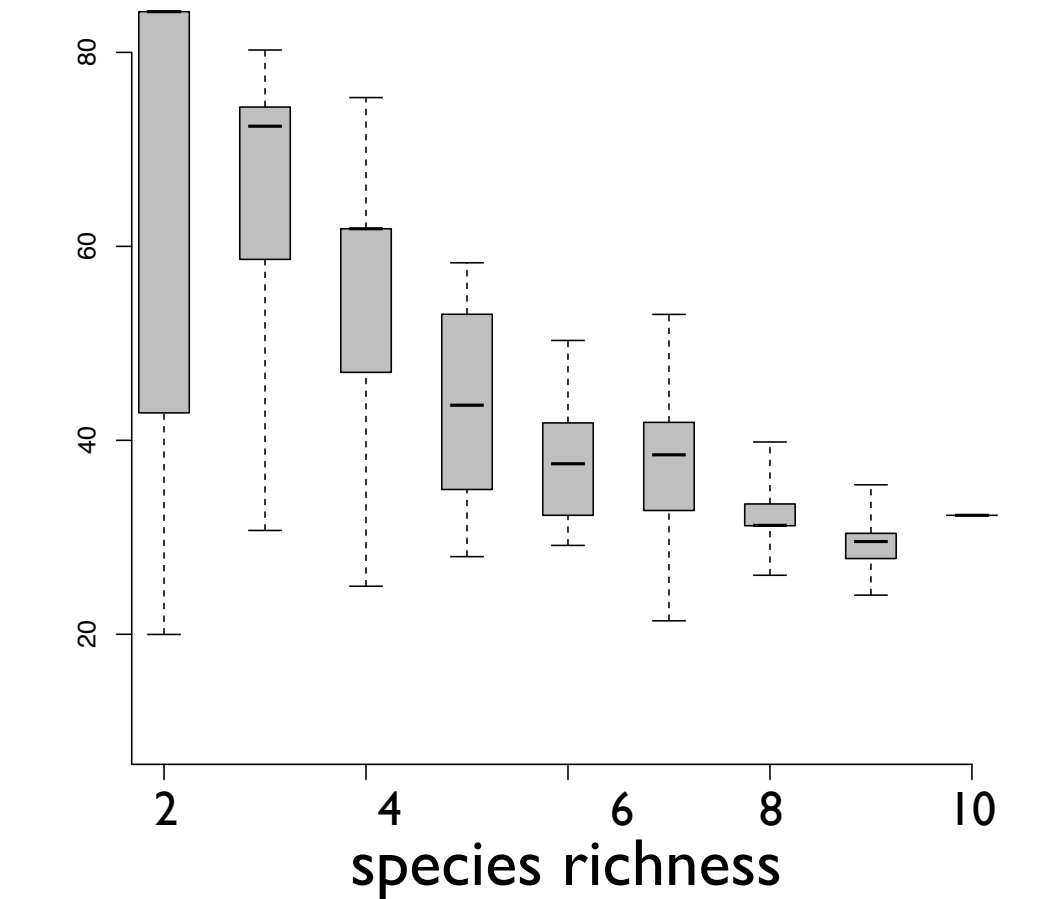
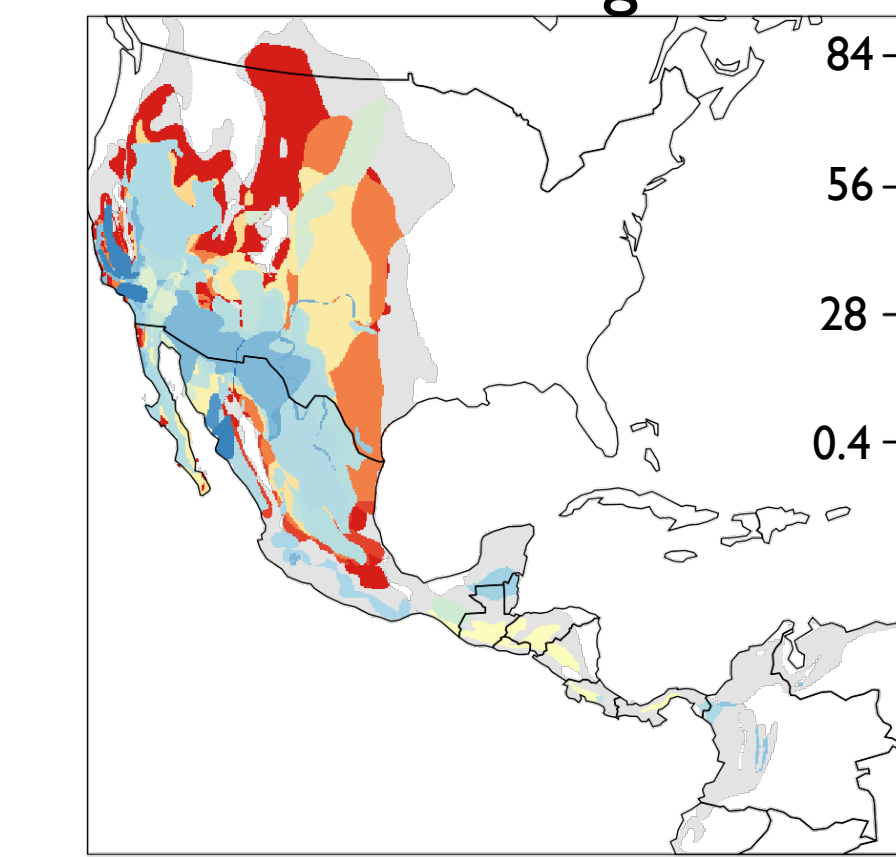
morphological range



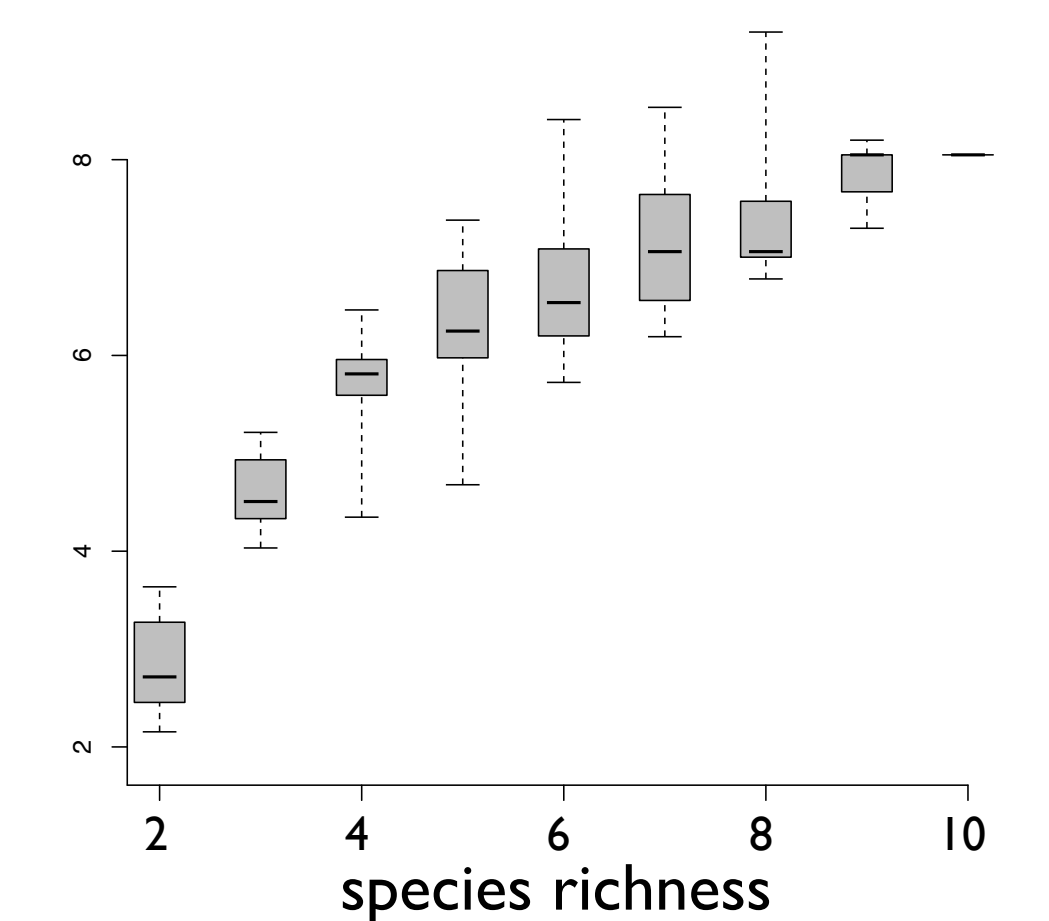
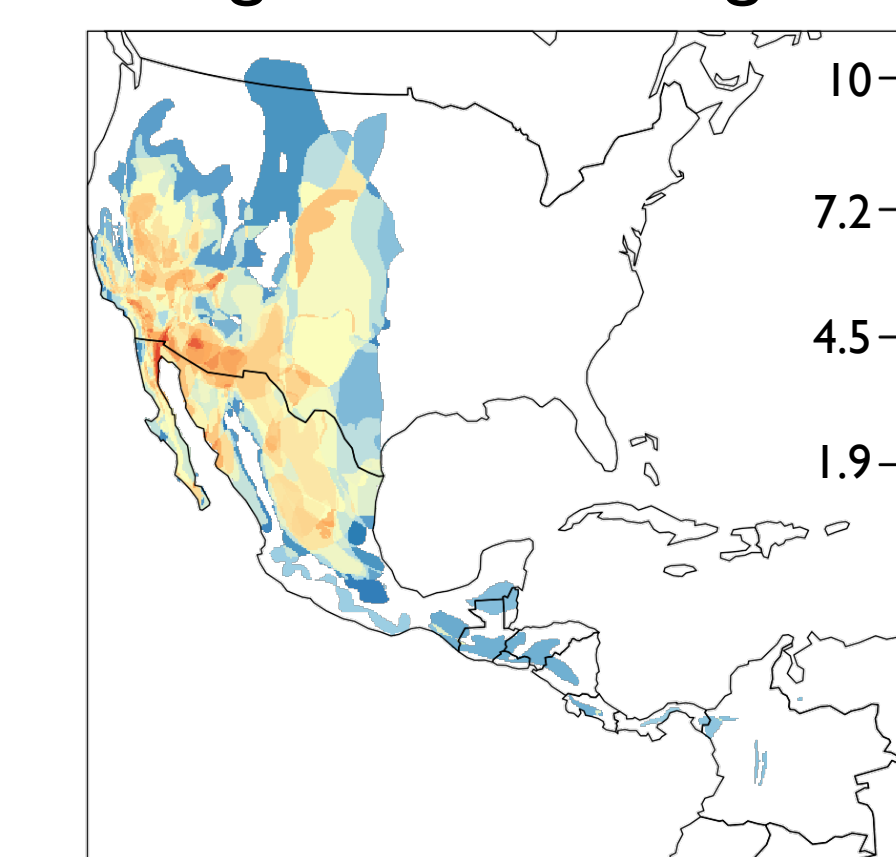
morphological nearest neighbor distance



patristic nearest neighbor



range / nearest neighbor



Coming soon!

<https://github.com/ptitle/speciesRaster>

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