

## A Note on Phylogenetic Patterns of Biodiversity

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### Abstract

The threats to biodiversity in the world today are numerous and expanding quickly. Approaches that combine bioinformatics, extensive phylogeny reconstruction, utilization of digital specimen data, and complex post-tree analysis (such as niche modelling, niche diversification, and other ecological analyses) are necessary to address these biodiversity concerns. Incomparable opportunities for mobilizing and integrating vast amounts of biological data are now available thanks to recent advancements in phylogenetics, emerging cyber infrastructure, and new data sources. This has led to the identification of complex patterns and the development of novel research hypotheses. These findings are significant because the global biodiversity data that are now being gathered and examined are intrinsically complicated. We refer to the systematics, ecology, and evolution-related research that is being made possible by the ongoing integration and development of the biodiversity tools outlined here as “biodiversity science.” To speed up research in these fields, new training that combines data science expertise with domain knowledge in biodiversity is also required. The future of global biodiversity depends on integrative biodiversity science. We cannot simply respond to the ongoing threats to biodiversity; instead, we must anticipate them. Using an integrative, multifaceted, big data approach, researchers can now project biodiversity and provide vital information for the general public, land managers, policy makers, urban planners, and agriculture, as well as for scientists.

**Keywords:** Cyber Infrastructure; Phylogenetics; Biodiversity; Ecology

### Introduction

A significant factor in the reduction of biodiversity, particularly in biodiversity hotspots where many rare and vulnerable species thrive, is climate change. The Mediterranean Basin, which makes up more than 60% of the Mediterranean climate’s global range and has about 22500 plant species, including 11700 endemics, is one of the world’s top hotspots for plant biodiversity. Because of this unusual concentration of plant diversity, conservation biologists are under pressure to develop ways to reduce the anticipated loss of biodiversity in the area. Planning for conservation measures might be more effective if we are aware of the link between biological characteristics of species and susceptibility to extinction. There is a conspicuous lack of consistency throughout research, and the association between the vast majority of qualities investigated and extinction risk remains mostly mysterious, despite the fact that few traits have been identified as potential biological drivers of extinction risk in both plants and animals. Importantly, this lack of empirical consistency makes it difficult to pinpoint the species that may require conservation efforts the most. The evolutionarily conserved nature of several features associated with the danger of plant extinction, such as phenology and biotic pollination, raises the possibility that phylogenetically, extinctions caused by climate change may not be random events [1].

On the other hand, if we assume that the biological causes of extinction susceptibility are evolutionarily conserved, the association between extinction risk and species phenotypes appears to vary geographically, suggesting that the clades that are threatened by climatic stressors may be region-specific. For instance, representatives of the *Asteraceae* family might be threatened in the tropics but not in drylands if pseudanthia, a floral characteristic that is highly preserved, were linked to a high risk of extinction in humid environments. Therefore, even if the underlying biological drivers are unknown, identifying the clades that accumulate a disproportionate number of threatened species in particular regions may help to guide proactive conservation actions to mitigate potential increases in extinction risk among currently unthreatened (or near threatened) species in these clades. Additionally, taking extinction into

account from a phylogenetic perspective enables assessing its effects on the tree of life as the loss of evolutionary history, a viewpoint that is becoming more and more valued within conservation objectives. Phylogenetic data and community data are increasingly being analyzed simultaneously by community ecologists and conservation biologists. To comprehend the mechanisms governing community assembly, for instance, the phylogenetic structure of local communities is contrasted with that of larger species pools. Similar to this, Phylogenetic Diversity (PD) maps are used to identify conservation regions that best preserve evolutionary history [2, 3].

Despite the rising popularity of PD, patterns of species diversity have traditionally been the focus of spatial biodiversity study. The species-area relationship, which depicts the rise in species richness with geographic area, has been described in hundreds of papers. The species-area relationship, hailed as one of the few general principles in ecology, has been vital to the development of ecological theory and for calculating the danger of extinction in the face of environmental change. Similar to this, analytical characterizations of the distance-decay relationship, a curve that shows how the similarity in species composition between two communities decreases as a function of distance, have been used to predict the complementarity of sites within reserve networks and infer the relative importance of dispersal limitation and environmental filtering in explaining patterns of diversity. Research on the spatial scaling of PD is still in its infancy, in contrast to the decades of study on the spatial scaling of species diversity. Recent research has shown that phylogenetic similarity decreases with geographic or environmental

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distance and that PD increases with area. There haven't been any attempts to generalize these diversity patterns' shape or mathematical form, though. Given that patterns explicitly incorporating information on evolutionary history will probably be more effective than patterns that do not (such as the species-area and distance-decay relationships) for testing and estimating parameters of biodiversity theory, there is a significant gap in our knowledge of these patterns. Additionally, in order to determine conservation priorities for preserving evolutionary history in a spatial context, phylogeny-based spatial patterns are required [4-6].

The geographical scaling of species diversity, the phylogenetic tree describing these species' evolutionary history, and their position in the phylogeny are the three key factors that determine the spatial scaling of PD. Various evolutionary and ecological processes, including as speciation and extinction, dispersion restriction, environmental filtration, and intra- and inter-specific interactions, in turn, drive these three elements. The third factor, often known as community phylogenetic structure or the position of co-occurring species in a phylogeny, has recently received a lot of attention. The degree to which species assemblages depart from randomly occurring assemblages is measured by phylogenetic structure, which has been applied as a method to infer the mechanisms governing community formation [7].

## Discussion

For conservation biologists, minimizing projected plant diversity loss in biodiversity hotspots is a critical concern. Phylogenetic methods may be helpful in assessing present and potential threats in these areas rich in endemic species. Here, we demonstrate that the phylogeny of the unique angiosperm flora of the Iberian Peninsula largely clusters extinction risk and that there is generally little specificity in the link between IUCN categories and phylogenetic clades. Due to the poor phylogenetic signal found in our comparison analysis, there is no correlation between clades and threat categories, which suggests that species that are closely related often have different threat statuses. Overall, our findings show that the extinction-risk gradient in the endemic flora of the western Mediterranean is concentrated in a small number of phylogenetic clades, and monitoring programmers should pay special attention to these extinction-prone lineages [8].

## Conclusion

The threats to biodiversity in the world today are numerous and expanding quickly. Approaches that combine bioinformatics, extensive phylogeny reconstruction, utilization of digital specimen

data, and complex post-tree analysis (such as niche modeling, niche diversification, and other ecological analyses) are necessary to address these biodiversity concerns. However, the creation of tools for the study of biodiversity is still in its infancy and often does not scale as required. Furthermore, there is a lot of trait data that is "locked" in the metadata and pictures of natural history collections and is only partially retrievable. This data is relevant to evolutionary and ecological study as well as conservation. To speed up research in these fields, new training is required that combines data science expertise with expertise in the biodiversity domain. We can't just respond to the ongoing threats to biodiversity; instead, we must make biodiversity projections using an integrative, multifaceted, big data approach to provide essential information not only for scientists but also for the general public, land managers, policy makers, urban planners, and agriculture [9, 10].

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## Conflict of Interest

None

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