Comparing conservation metrics in a case study of lemurs

Deciding to which areas or species conservation actions should be allocated is, unfortunately, a very difficult process. On the one hand, time, money and resources are limited. On the other hand, it is unclear which points of focus (e.g. biodiversity hotspots, endangered or rare species, or charismatic species that are loved by the general public) most require conservation actions. Additionally, it is unclear where conservation would have the biggest chance of success, i.e. of saving species from going extinct. Various metrics have been developed to facilitate conservationist's decisions. Traditional metric focussed on rareness, geographic spread and genetic uniqueness.

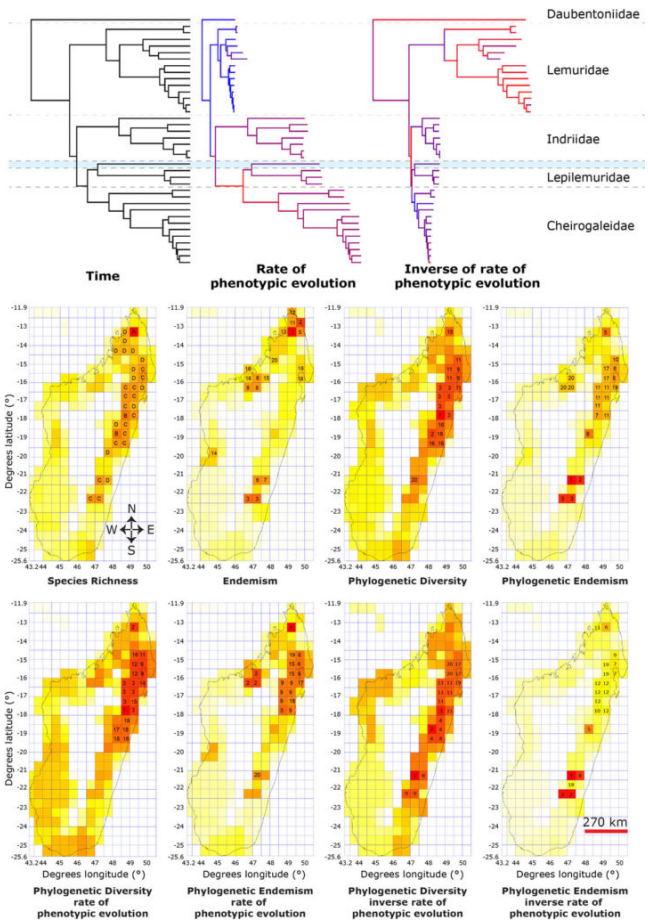

Fig. 1. We adjusted the branch lengths of the lemur phylogeny (left) according to the rate of body mass evolution (middle) and its inverse (right). The dashed lines show where the different lemur families are located on the tree (the species highlighted by blue shading is Phaner furcifer, a species from the Cheirogaleidae family). The maps underneath show where high levels of conservation value, indicated by red grid cells, are found in Madagascar.

One traditional metric, species richness, is used to determine where the most species are located. Endemism focusses on geographically rare species, prioritizing species which only occur in a limited number of geographical regions. Another form of rarity, genetic rarity, takes the shared history among species into account, by using phylogenies (tree structures that describe how species are related to each other).

The best-known phylogenetic conservation metric is phylogenetic diversity, which focusses on the most genetically unique species, by summing the branch lengths connecting all species occurring in a particular geographical region. Phylogenetic endemism combines endemism and genetic uniqueness to identify the rarest species, both spatially and genetically, by dividing phylogenetic branches among the number of geographical regions where the species descended from that branch occur.

While researchers are enthusiastic about phylogenetic conservation metrics, they have not often been incorporated in actual conservation planning. One of the most important reasons for this is that evolution is not a homogeneous process through time, which means that differences between species are not linearly increasing through time. This means that species that underwent a speciation event recently may differ more from its closely related species than a species that split off much earlier.

It is possible to account for evolutionary patterns by adjusting the differences between species to the rate of evolution of a given morphological characteristic (e.g. body size). Here, we show how rates of phenotypic evolution can be included to identify areas containing species that underwent high or low levels of phenotypic evolution. High rates of trait evolution may relate to opposite processes; generalisation or specialization. Traits can be flexible in generalists, for example, body size in animals can vary according to environmental factors, such as food resources, while specialists have a specific size, adapted to their ecological niche.

We predict that specialist species are more at risk by environmental changes, and thus require conservation attention. While high rates may indicate specialism, low rates may too, when little variation allows little evolution. Because the phylogenetic metrics focus on branch lengths, they may not succeed in the identification of specialized species with low rates of evolution. Therefore, we also determined the conservation values of phylogenetic diversity and phylogenetic endemism by using the inverse of the rate of evolution.

We applied these different conservation metrics to 38 lemur species, which occur on the island of Madagascar. In our paper we discuss and compare these conservation metrics in relation to our results (Fig. 1). We also suggest which metric could be used in order to meet specific conservation goals.

Renske Marleen Gudde
School of Biological Sciences, Philip Lyle Building,

University of Reading, Reading, United Kingdom

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