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Computational tools to quantify biodiversity

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Effective protection of our planet's biodiversity is central to maintaining fundamental ecological processes and thus crucial to human well-being and survival. However, biodiversity is declining globally at an alarming and unprecedented rate, mainly due to habitat destruction, over-exploitation and effects of ongoing human-induced climate change. To counteract this trend, many governments and institutions make considerable efforts to characterise existing biodiversity and understand the patterns and drivers of its distribution. For this purpose, a large amount of data is being collected in various dedicated monitoring projects, such as direct observations, counts of animal tracks, vocalisations, tissue to sequence DNA or images collected using camera traps. However, drawing reliable conclusions about the state of biodiversity from such data is often challenging, for two reasons. First, efforts to conduct biodiversity research are spatially biased towards wealthy and accessible regions, leaving a large amount of the world's regions critically understudied. Second, even in regions where data are available, the inherent complexity of biodiversity, ranging from genes to organisms to entire ecosystems, along different spatial and temporal scales, often render statistically meaningful inference challenging. A common issue in ecological data analysis are noisy or unevenly sampled data, which may violate underlying assumptions of existing methods. To achieve maximum benefits for biodiversity given limited conservation budgets, we therefore one the one hand need to make efforts to study biodiversity in so far undocumented regions and, on the other hand, we equally need dedicated statistical methods that can draw robust and valid conclusions from resulting ecological monitoring data.

The goal of my PhD thesis was to develop such statistical methods suited to analyse noisy and unevenly sampled ecological data and to show their applicability using a variety of available data sets. For this, I focused on data sampled within the Aire de Conservation de Chinko, a remote and understudied protected area in the east of the Central African Republic. In Chapter 1 I introduce TOMCAT, a method that characterizes species distributions in space and time, allowing to study habitat requirements and daily activity patterns of a species as well as spatio-temporal niche partitioning between multiple species. By not summarising the available data in a simple detection/nondetection matrix, TOMCAT can also estimate and predict relative species densities within its habitat range. In Chapter 2 I present BIRP, a method that directly tests for population trends and changes in populations trends using time series data of animal observation counts. BIRP has greater statistical power to estimate such trends compared to current approaches, as we focus on the change itself, allowing us to combine data from different survey methods while avoiding the need to explicitly estimate detection probabilities. I expect this method to be particularly useful to conservation managers who are looking for feedback concerning a newly implemented conservation intervention. In Chapter 3, I used BIRP and other methods to study the spatial distribution and temporal trends of livestock damages caused by wolves in Europe. We show that damages are not uniformly distributed across Europe and that a small set of environmental variables explain more than 50% of the observed differences between regions. Moreover, we argue that temporal trends, in conjunction with their spatial distribution, are an important tool for the effective monitoring of the wolf-human conflict in Europe. Both methods presented in this thesis are well-documented and publicly available, and will help ecologists and conservation managers to characterize the spatio-temporal distribution of biodiversity and thus to conduct relevant and effective conservation work.

Jury:
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