

Editorial

Modeling the Ecology and Evolution of Biodiversity: Introduction to the Special Issue

Dwueng-Chwan Jhwueng 

Department of Statistics, Feng-Chia University, Taichung 40724, Taiwan; dcjhwueng@fcu.edu.tw;
Tel.: +886-975-662-326

Applying relevant statistical models to empirical data analysis has been considered a very important procedure for scientists to answer research questions in the fields of biodiversity, phylogeography, evolutionary biology, paleoecology, phylogenetics, and geography. This is due to the limitation of resources or geographical barriers where the data collected might not reveal sufficient straightforward information by fundamental statistical analysis. This motivation calls for developing robust methods for analysis and hence makes a significant contribution to our understanding of biodiversity.

This Special Issue aims to propose to the scientific community a collection of articles on the application of statistical phylogenetics, phylogeography, and geography analysis for these fields. Special attention will be paid to the use of various types of mathematical models or statistical methods, associated with applications for the empirical analysis of the biological variety and variability of life.

The first paper [1] documents the spatial shifts in species richness in response to climate and environmental change. The authors used the data collected in the Czech Republic and then adapted the EUROMOVE model to quantify the impact of climate change on plant species diversity within the European region. They found that the species' habitat expanded between 1990 and 2018. Due to the rising temperatures, species generally shifted towards highlands, which greatly altered plant habitats, which results in greater biodiversity loss at different scales. The authors also concluded that the impact of climate and environmental change on individual species distribution is very diverse, but varies with the local topography.

The second paper [2] developed a novel phylogenetic method for tree selection by testing substitution numbers in a clade. The method was based on testing the nucleotide substitution number between sequences to select trees. The authors applied their method to analyze Ebolavirus datasets where the phylogenetic relationship for five species was studied and analyzed under the proposed novel method. The authors urged that while there is no guarantee that their method will always select the true tree, a reasonable tree will be reported. This provides a useful reference to the literature when considering choosing an appropriate tree among tree sets space.

The third paper [3] evaluated the climate change impacts on the global distribution of the calliphorid fly *Chrysomya albiceps* using geographical information system (GIS). The authors proposed to use the maximum entropy for modeling species niches and distributions and then used their model to predict the current and future potential global geographic distribution. Their modeling tools helped scientists to understand the mapping distributions of insect pests in many areas in each continent, especially on the Mediterranean coasts of Europe and Africa, Florida in the USA, and the coasts of Australia.

The fourth paper [4] studied the phylogeographic structuring of the Kuroshio-Type Prawn *Macrobrachium japonicum* (Decapoda: Palaemonidae) in Taiwan and Ryukyu Islands. The authors hypothetically defined five demographic scenarios to determine the possible demographic history of *M. japonicum* and implemented approximate Bayesian computation (ABC) methods to investigate the possible historical demographic scenarios of *M. japonicum*. The authors reported that the topology of the haplotype minimum-spanning



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network revealed a star-like structure, which suggested a recent range expansion. The results offered both practical and theoretical value for the further study of conservation genetics, management, and sustainable resource utilization.

In the final paper [5], the authors investigated the effect of polytomy on parameter estimation and goodness of fit of the phylogenetic linear regression models. By fitting various popular models to the datasets generated under different types and levels of polytomy in the given phylogenetic tree, the authors found that the lambda model and the Ornstein–Uhlenbeck process model have stable and reliable estimates when encountering the polytomy issue for trait evolution.

Overall, the papers in this Special Issue collectively addressed many interesting questions relating to the application of methods in diversity. Readers can find answers to understand how spatial shifts in species richness are in response to climate and environmental change; how to select phylogenetic trees by testing the substitution number in clades; how to use geographic information systems for evaluating the climate change impacts on the global distribution of the calliphorid fly; the phylogeographic structuring and demographic history of *M. japonicum* in Taiwan and the Ryukyu Islands; and how the polytomy effect affects the models and parameter estimates when applying phylogenetic comparative analysis. These answers are not just relevant and limited to those statistical methods that can be addressed, but provide a broader impact to better understand our biodiversity.

Conflicts of Interest: The author declares no conflict of interest.

References

1. Tangwa, E.; Pechanec, V.; Brus, J.; Vyvlečka, P. Spatial Shifts in Species Richness in Response to Climate and Environmental Change: An Adaption of the EUROMOVE Model in the Czech Republic. *Diversity* **2022**, *14*, 235. [[CrossRef](#)]
2. Chen, W.; Wang, H. Phylogenetic Tree Selection by Testing Substitution Number in Clade. *Diversity* **2022**, *14*, 543. [[CrossRef](#)]
3. Hosni, E.M.; Al-Khalaf, A.A.; Naguib, R.M.; Afify, A.E.; Abdalgawad, A.A.; Faltas, E.M.; Hassan, M.A.; Mahmoud, M.A.; Naeem, O.M.; Hassan, Y.M.; et al. Evaluation of Climate Change Impacts on the Global Distribution of the Calliphorid Fly *Chrysomya albiceps* Using GIS. *Diversity* **2022**, *14*, 578. [[CrossRef](#)]
4. Han, C.C.; Lai, C.H.; Huang, C.C.; Wang, I.C.; Lin, H.D.; Wang, W.K. Phylogeographic Structuring of the Kuroshio-Type Prawn *Macrobrachium japonicum* (Decapoda: Palaemonidae) in Taiwan and Ryukyu Islands. *Diversity* **2022**, *14*, 617. [[CrossRef](#)]
5. Jhwueng, D.C.; Liu, F.C. Effect of Polytomy on the Parameter Estimation and Goodness of Fit of Phylogenetic Linear Regression Models for Trait Evolution. *Diversity* **2022**, *14*, 942. [[CrossRef](#)]

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