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# **ABSTRACT BOOK**

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## 65-HB

### **Likelihood approach to the biogeography of Atlantic Rainforest frog family Cycloramphidae**

Diego Silva, Universidade Federal do ABC; Bruna Bolochio, Universidade Estadual Paulista - UNESP; Ricardo Sawaya, Universidade Federal do ABC; Matheus Nogueira, Universidade Federal do ABC; Vanessa Verdade, Universidade Federal do ABC

The neotropical anuran family Cycloramphidae, with 36 valid species in the genus *Thoropa*, *Cycloramphus* and *Zachaeus*, occurs over the Atlantic Forest. Most of the species have restricted distributions, bonded by mountains. Despite that making sense for stream-dwelling species, there is a litter-dwelling clade that could have larger distributions. Also, there are species with disjunct distributions, suggesting that there were widespread ancestors. This brings to debate the historical questions behind the distributional patterns currently observed. Herein, we analysed this historical role in a previous phylogeny of 20 Cycloramphidae species based on 91 morphological characters from the group. We implemented six Maximum Likelihood models in the R package BioGeoBEARS to estimate the ancestor's distributional patterns and the biogeographic processes involved. We defined seven areas for the regionalisation of the Atlantic Forest according with the Biotic Elements from a previous study for anurans of this domain. The best fitted model (BAYAREALIKE+j) suggests that the region between the southern Serra da Mantiqueira and Serra dos Órgãos was the Cycloramphidae ancestors' range of distribution, as for the most part of the internal nodes. It also seems to be the region with the higher diversification on the family, especially between 30–20 mya. The most common biogeographic processes along the phylogeny were founder-event and dispersal. Our results are still preliminary, but this model is a good fit to explain the disjunct distribution in some species, and the inclusion of more *Thoropa* species could clarify this effect.

## 66-HB

### **SSDM: An R package to predict distribution of species richness and composition based on stacked species distribution models**

Sylvain Schmitt, UMR BIOGECO - Université de Bordeaux; Robin Pouteau, Zhejiang Key Laboratory of Plant Evolutionary Ecology and Conservation, Taizhou University; Dimitri Justeau, UMR AMAP - Cirad; Florian de Boissien, UMR TETIS - IRSTEA; Philippe Birnbaum, UMR AMAP - Cirad; Lukas Baumbach, University of Freiburg

There is growing interest among conservationists in biodiversity mapping based on stacked species distribution models (SSDMs), a method that combines multiple individual species distribution models to produce a community-level model. However, no user-friendly interface specifically designed to provide the basic tools needed to fit such models was available until now. The “ssdm” package is a computer platform implemented in R providing a range of methodological approaches and parameterisation at each step in building the SSDM: e.g. pseudo-absence selection, variable contribution and model accuracy assessment, inter-model consensus forecasting, species assembly design, and calculation of weighted endemism. The object-oriented design of the package is such that: users can modify existing methods, extend the framework by implementing new methods, and share them to be reproduced by others. The package includes a graphical user interface to extend the use of SSDMs to a wide range of conservation scientists and practitioners.