3RD CROSSING THE PALAEONTOLOGICAL-ECOLOGICAL GAP (CPEG)

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Cover Design: Kristina Girčytė
Layout: Simona Rinkevičiūtė
Logo: Monika Jasnauskaitė
Editors: Andrej Spiridonov, ORCID 0000-0002- 8773-5629
Eduardas Budrys, ORCID 0000-0001-5965-5210
Darja Dankina, ORCID 0000-0001-6226-881X
Simona Rinkevičiūtė, ORCID 0000-0001-7782-7469

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9 Saulėtekio Av., III Building, LT-10222 Vilnius
info@leidykla.vu.lt, www.leidykla.vu.lt/en/
www.knygynas.vu.lt, www.zurnalai.vu.lt

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THE "HESPDIV" R PACKAGE: CASE STUDY OF MIOCENE MAMMAL BIOGEOGRAPHY IN US

L. Daumantas[1,*], A. Spiridonov[1]

[1] Faculty of Chemistry and Geosciences, Vilnius University, Vilnius, Lithuania

* Liudas.daumantas@chgf.vu.lt

The "hespdiv" R package is a newly developed toolkit designed specifically for conducting biogeographical studies using occurrence data. This package uses an algorithm that hierarchically subdivides both the study data and study area into homogeneous units, based on predefined subdivision criteria and optimization functions. The result is a spatial hierarchy tree consisting of polygons representing distinct data clusters. When taxa occurrences are used as input data and the bioregionalization method is applied, these polygons can be interpreted as bioregions. In addition to the subdivision algorithm, the "hespdiv" package offers many visualization options and functions to assess the significance and stability of the obtained subdivisions.

To illustrate the application of the package, we conducted a case study using terrestrial Miocene mammal species occurrence dataset from the contiguous United States. This study demonstrates the capabilities of the "hespdiv" package in unravelling the biogeographical patterns of species distribution. The results deliver insights into the spatial arrangement of distinct Miocene mammal assemblages and allows to hypothesize about the underlying environmental and biotic factors driving their distribution.

Further applications of the tools provided by the "hespdiv" package, as well as the development of new tools, hold great potential in enhancing our understanding of spatial biodiversity dynamics in both past and present ecosystems.

CPEG

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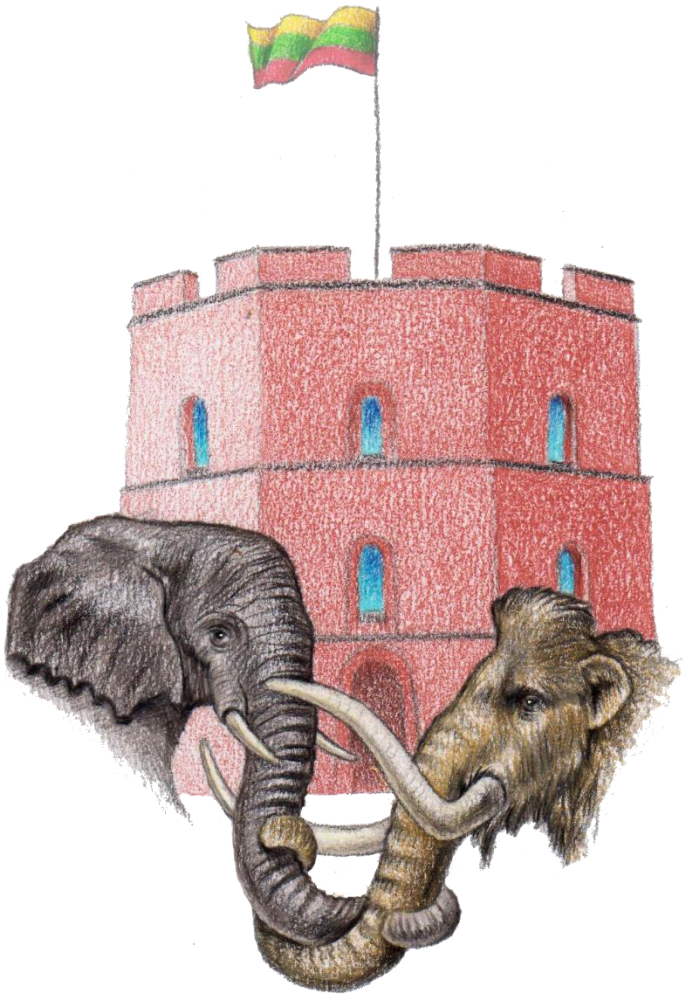

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