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BAYESIAN NETWORK ANALYSIS REVEALS THE ASSEMBLY DRIVERS AND EMERGENT STABILITY OF PLEISTOCENE LARGE MAMMAL COMMUNITIES

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The nature of community assembly is one of the oldest questions in ecology. The structure of fossil communities is driven by a number of environmental, biogeographic, ecological and taphonomic processes acting at different spatial scales and timescales. A Bayesian network is a directed acyclic graph that specifies a joint probability distribution between the entities of interest (nodes) in a modular way, as a product of local conditional distributions at each node. The graph structure determines the qualitative dependences between the variables, whereas the local conditional distributions allow quantitative inference of relationships. Using Bayesian network inference methods we determine the degrees of association between 12 large mammal families and their local environment, global temperature, locality age and large-scale geographical extent throughout the Pleistocene. With an exception of Hominidae, we do not find significant associations between external variables (latitude, age, mean surface temperature) and the families analysed here, demonstrating that the majority of families showed remarkable resilience to extreme climatic variability of the Pleistocene. The associations between the mammal families themselves seem to be structured by the degree of generalism in carnivores and omnivores, and by similar environmental preferences in herbivores. To our knowledge, this is the first Bayesian network inference study of motile land animal palaeocommunities. We also discuss possible further applications of this method.

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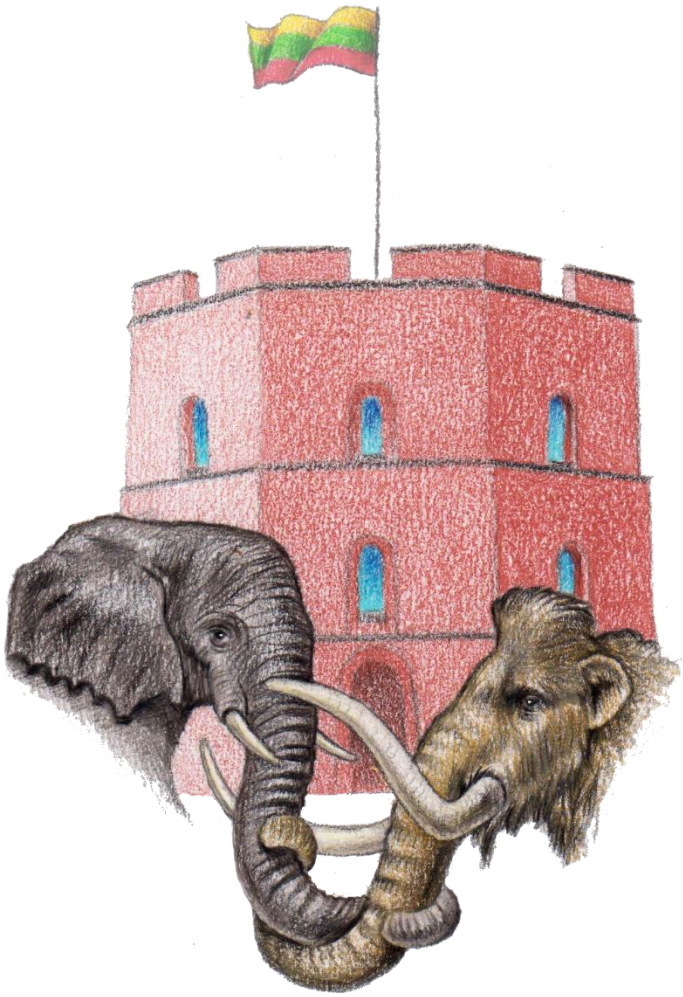

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