

Open-access data is uncovering past responses of biodiversity to global environmental change

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Research emerging at the frontiers between paleoecology, paleoclimatology and paleogenomics is offering exciting new prospects for unveiling the ecological and evolutionary mechanisms that have shaped past and current-day patterns of biodiversity (Nogués-Bravo et al. 2018). This frontline in paleo research is being driven by developments in high-throughput sequencing; dating and computational technologies; and open access to curated georeferenced and dated fossils, collections of genetic sequences and paleoclimate simulations. These publicly available e-resources are the result of decades of fieldwork and their combination provides innovative opportunities to use ecological and evolutionary models to connect past observed responses of biodiversity to environmental processes, particularly during the late Quaternary (from 120,000 years ago) (Barnosky et al. 2017). This integration of open-access data into biodiversity models is allowing fundamental theories in ecology and evolution to be tested and better connected to the on-ground design and implementation of effective measures to protect biodiversity (Fordham et al. 2016; Fig 1).

Until recently biodiversity modelers and other non-climate scientists have had difficulty accessing simulations of late-Quaternary climate change at the spatial and temporal scales needed to understand population-, species- and community-level responses to climatic change. Now, spatially explicit paleoclimate simulations are readily downloadable at the short-temporal scales (decades to centuries) needed to detect biotic responses to paleoclimatic change (Fordham et al. 2017).

These spatially explicit paleoclimate simulations are being used to better understand past biodiversity dynamics, and inform future conservation policies. Open-access databases, such as Neotoma (neotomadb.org) or the European Pollen Database (euro-pollendatabase.net) provide geographic localities of fossils that can be intersected with paleoclimatic simulations, then passed to statistical models to analyze changes in species climate niche properties through time, and provide spatial representations of past distributions of species, their climatic refugia and potential migration pathways (Gavin et al. 2014). These results can be used to formulate ecological hypotheses concerning changes in past population sizes and population structures, which are then testable with independent genetic sequence data from ancient DNA and modern populations – much of which is freely available via GenBank. This integrated analytical approach is providing fascinating insights into the historical biogeography of species,

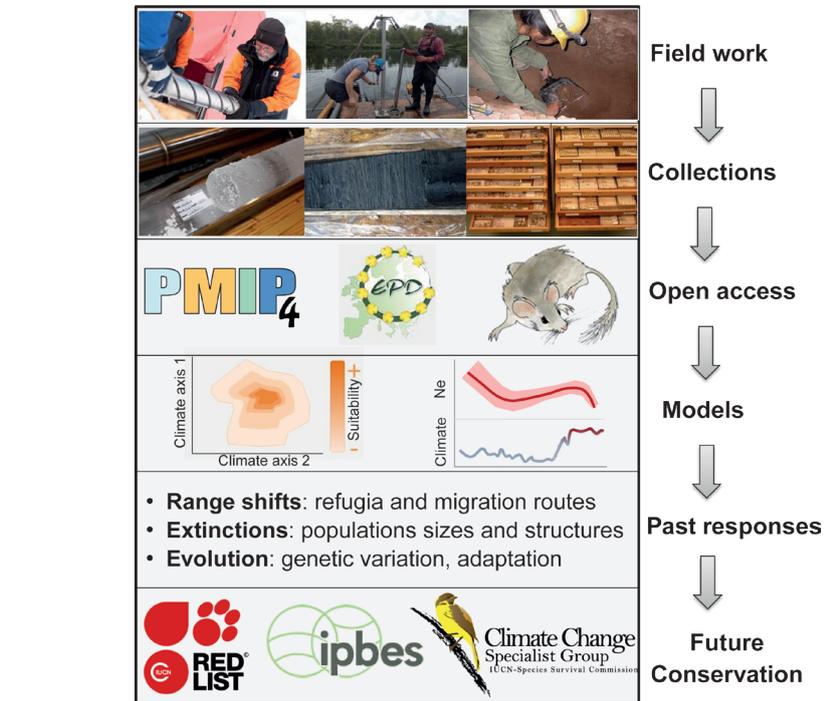


Figure 1: Information flow for using open-access data (i.e. PMIP4, European Pollen Database [EPD] and Neotoma) to uncover past ecological and evolutionary responses to environmental change, so as to improve the conservation of future biodiversity.

facilitating a better understanding of why species' population sizes and distributions change over time, and why some species survived pronounced climatic shifts during the late Quaternary and not others (Nogués-Bravo et al. 2018). Moreover, recent developments in paleogenomics are providing unparalleled opportunities to estimate not only the demographic histories of species and populations through time, but also to understand the evolutionary mechanisms that govern responses to past global environmental change (Shapiro and Hofreiter 2014).

Since genetic-sequence or genomic-level information stored in digital open-source databases often lack geographic coordinates, deep-diving algorithms and artificial intelligence are being used to georeference hundreds of thousands of genetic sequences from the peer-reviewed literature, providing new opportunities to determine the role of paleoclimatic change in structuring genetic diversity (Miraldo et al. 2016). Another major barrier is the scarcity of continuous paleoclimate simulations for the late Quaternary, which are only publicly available from the Last Glacial Maximum (LGM) to the present day (Fordham et al. 2017). Since many important biotic responses to paleoclimatic changes occurred prior to the LGM, high temporal resolution paleoclimate simulations from the last interglacial to the present day, from multiple atmosphere-ocean global circulation models, are urgently needed.

Open access to paleo resources, and their integration into macroecological models, has already played an important role in improving our understanding of how ecological and evolutionary processes regulate the severity of threats from global environmental change, providing a "real-world" foundation for better anticipating what the future may bring. The continued expansion of paleoecological information in online databases, including emerging resources, such as georeferenced ancient and modern DNA, are opening new frontiers in our understanding of past responses of biodiversity to global change.

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