Running head: Simulation-based examination of priors in biogeographic dating

Title: Towards a methodological background for using Biological data to inform Geological models: Interaction of Biological and Paleoeographic priors in Biogeographic Dating

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# Abstract

Biological and geographic data have long reciprocally informed one another. In this study, we simulate 10 simple molecular phylogenies with known histories and date them with historic biogeographic priors of varying information levels and accuracy in order to test the influence of biogeographic knowledge and molecular data on phylogenetic dating. In our simulations, models prohibiting gene flow with unknown biogeographic histories performed just as well as models prohibiting gene flow with correctly informed biogeographic priors. The result that accurate molecular data performs similarly under correct and unknown geographic knowledge shows promise for the utilization of the geogenomic method, which has been used to date geographic events with biological data. However, the introduction of gene flow or the incorporation of incorrect historic biogeographic data shifted the accuracy of our phylogenetic dating. These findings show that systematists must remain cautious when conducting biogeographic dating.

Keywords: biogeography, geogenomics, dating, molecular, simulation

# Introduction

The recognition of the interplay of biological evolution and geological change laid the foundation for the field of historical biogeography (cite Wallace’s 1852 foundational work here). Centering on the study of how the geographic distribution of organisms has changed over evolutionary time and how those changes are shaped by Earth’s geological history, historical biogeography forces the interpretation of biological data in reference to a specified geological background. This analytical approach has led to the description of generalizable patterns in for example island biogeography (), and to the description of broad patterns of organismal distribution through time ().

That organismal evolution proceeds in parallel to changes in abiotic conditions (e.g., landscape or climate shifts), has prompted the use of patterns of co-variation in geographic distributions and genomic data, as proxies to infer shared abiotic processes (e.g., formation of a barrier to gene flow) that may have driven those patterns (). From the formulation (and later rejection) of the forest refugia hypothesis to explain a mechanism for the high biodiversity observed in regions like the Amazon and Central African rainforests (), to the characterization of the timing and mode of uplift of mountain ranges (), and the timing of river connectivity through time (Bedoya et al., 2021), biological data has been used to propose and inform geological models. This approach was unified in a theoretical framework named geogenomics (Baker et al., 2014), which involves the reciprocal integration of geological, climatic, ecological, paleontological, and genomic data to test landscape or climate evolution hypotheses from biological data (Dolby et al., 2022).

Using biological and geological data independently, or interpreting them in reference of each other (e.g., establishing a geological analyses as ground truth against which biological data are interpreted) may introduce biases inherent to each biology and geology. First, geological models carry great uncertainty and consensus in the interpretation of some data (e.g., provenance analyses) is challenging. Second, the response of organisms to a common paleogeographical event is idiosyncratic, with gene flow, migration, and other evolutionary processes getting in the way so evolutionary patterns of organisms don’t all mirror a common underlying process. (talk about what makes for good model systems in geogenomics without mentioning the term geogenomics i.e., strong affinity to the habitat to be reconstructed, very limited gene flow, small population sizes? Read Bedoya et al., 2024) Therefore, not all organisms carry the signal from the evolution of a given landscape feature.

An example of the biases mentioned above for the use of biological and geological data to date the timing of geomorphic events is the closure of the Isthmus of Panama and the Great American Biotic Interchange. The traditional model for the evolution of the Panama Isthmus suggests that its formation took place ~4.2–3.5 Ma (late Pliocene; (Keigwin, 1978, 1982; Coates *et al.*, 1992; Jackson & O’Dea, 2013) or earlier at 2.8 Ma (O’Dea *et al.*, 2016). Geochronological data and provenance analyses have challenged this model, pushing back the timing of closure of the Central American Seaway to 13–15 Ma (middle Miocene; Montes *et al.*, 2012a,b, 2015). This more recently published model is based on the interpretation of detrital zircon provenance data (Montes *et al.*, 2015), and has been called into question (O’Dea *et al.*, 2016). However, the evidence used to this end has in turn been challenged (Jaramillo *et al.*, 2017; Molnar, 2017; Jaramillo, 2018). Inferred divergence times of several taxa distributed across the Americas —including freshwater fishes, ground sloths, shrimp, and several plant taxa— are older than 3 Ma, supporting the notion of pre-Pliocene contact (Erkens *et al.*, 2007; Hurt *et al.*, 2009; Weir *et al.*, 2009; Cody *et al.*, 2010; Pinto-Sánchez *et al.*, 2012; Bacon *et al.*, 2013; Leigh *et al.*, 2014; Barker *et al.*, 2015). Multiple pulses of migration across the Isthmus prior to 3.5 Ma were inferred by Bacon et al., 2015, in opposition to the traditional model of formation of the Isthmus. While earlier pulses of organismal migration between the Americas may be evidence for an earlier onset of a land bridge connecting the Americas, earlier divergence times have sometimes been interpreted as episodes of stochastic long-distance dispersal by defendants of the traditional model of closure of the Isthmus of Panama (). This underscores the importance of considering species-specific traits when interpreting bio/phylogeographic patterns used for inferring geological models.

While geogenomics established a theoretical background for discussing the characteristics that study systems, as well as geographic and geological scales must meet for the reciprocal interpretation of data to infer past geological events, the integration of biological, paleontological, and geological data in a unified methodological framework is still lacking. Such unified framework would allow to test how geological priors and biological data interact. This would help test the effect of bad (deviates from reality), broad (lots of uncertainty), and good (accurately describes the timing of a geomorphic event) geological models and the use of good and bad geogenomics model systems. We here address this gap using biogeographic dating, a data-dependent and process based method that uses biogeographic information alongside time-calibrated paleogeographical priors for divergence dating (Landis, 2017; 2018). In biogeographic dating the observed biogeographic states of extant taxa induce a posterior distribution of dated speciation times. Specifically, observed distributional data are used to model dispersal rates between areas. The estimation of such dispersal rates results from the interaction of tip data with a specified paleogeographic prior (i.e., for the emergence or disappearance of a barrier), where the latter influences the expected probability that a particular dispersal event between areas takes place (Fig. 1a).

We aimed to test the reciprocal influence of biological and geological data and priors, leveraging biogeographic dating as a method where both are specified and analyzed simultaneously. We aimed to 1) and 2) xxx. We generated a hypothetical scenario where a temporal and spatial correspondence of biological and geological processes was enforced, such that divergence times are a proxy for the timing of a landscape change event (Fig. 1b). We also considered the opposite scenario, where the evolution of organisms was not strictly shaped by an underlying geological event. Under these scenarios, we simulated nucleotide data used as input for divergence times estimation. In using this simulated dataset with known evolutionary and biogeographic histories, we test the potential for well-calibrated phylogenies to estimate paleogeographic events and the impact of incorrect assumptions in geographic history.

**Fig 1**

# Materials & Methods

## *Evolutionary and Geological scenarios*

In our model scenario, a river-dwelling angiosperm lineage occurs in a river basin that has experienced two historic biogeographic barriers. This model group of aquatic riparian species is suitable for analyses, because individuals do not migrate, and species are restricted to highly specific and diagnosable ranges. We assume a barrier, such as mountain uplift, creates a branching in a river ecosystem at three and one million years before present. The ensuing three distinct river branches allow for speciation, with a phylogeny whose branches mirror the river ecosystem (Fig. 1b).

## *Demographic and Sequence Simulation*

A model phylogeny containing three taxa was generated with msprime (Baumdicker et al., 2022). The model phylogeny has taxon C splitting from taxa A and B three million years ago and taxon A splitting from taxon B one million years ago. Each taxon has a generation time of one year. Model sequences of 10,000 base pairs were generated for each taxa using the HKY model, which was used to limit the number of assumptions about our simulated dataset. We selected a mutation rate of 1e-8 and a recombination rate of 4.8e-8, realistic for angiosperms (Koch et al., 2000; Salomé et al., 2011). Divergence times were calculated for each node. All invariant sites were filled in with randomly selected bases. In one demographic model, gene flow between taxa was never allowed. In a second demographic model, gene flow occurred between ingroup taxon A and outgroup taxon C from 0.8–0.6 Ma. Demographic models were visualized in python using the package DemesDraw (Gower et al., 2022).

## *Biogeographic dating with differing Biological data and Geological Priors*

Biogeographic dating analyses for the model data was performed in RevBayes (Höhna et al., 2016) according to the Dispersal-Extinction-Cladogenesis (DEC) model (Landis, 2017; also see Landis et al., 2018). We modified the code for biogeographic dating in RevBayes (cite github here. In this model, molecular sequence data, a phylogeny, present ranges, distances between areas, geological epoch times, and dispersal probabilities across the latter, are defined as inputs to jointly estimate phylogenetic relationships, divergence times, and biogeography. Two MCMC chains were run with 10 million generations for each of the ten model scenarios. For all of the model scenarios, we manually set the root age of the tree to a uniform distribution between three and four million years ago and set the extirpation rate to zero. Results were visualized using Tracer v1.7.2 (Rembaut et al., 2018) and convergence assessment for each pair of the two model runs was examined with the R package Convenience (Fabreti & Höhna, 2022) to confirm adequate run times. The two generated log and tree files for each model were then combined with the cat command after applying a 0.25 burn-in on each file, resulting in a concatenated file with 15 million generations. The final generated trees were visualized in FigTree v1.4.4.

# Results

**Figure 3**

When using correctly informed geological priors (Figs. S2, S3, S7, S8), the age distribution for node two began at the true date of one million years ago (Table S1), regardless of the introduction of gene flow after the split of taxa A and B at node two. However, the age distribution node two became much younger when gene flow was incorporated into our demographic model. The absolute age of node two was predicted to be about 0.7 million years younger in models permitting gene flow. For correctly informed models, the choice between uniform and normal paleogeographic models had little influence on absolute node age regardless of gene flow, but the normal model did have a slightly older age distribution for node two when gene flow was prohibited.

In the geology unknown models (Figs. S4, S9), when both prohibiting and permitting gene flow, the models found an absolute age for both nodes similar (around 0.1 million years) to the correctly informed models. Like the correctly informed model, the introduction of a short period of gene flow in the demographic history of geology unknown models had a large influence on the predicted absolute age of node two. The absolute age of node two was found to be around 0.5 million years younger when gene flow was included when compared to the unknown model prohibiting gene flow. Additionally, the age distributions for node two were similar to the correctly informed models when gene flow was permitted. However, in the unknown model prohibiting gene flow, the age distribution for node two was dated more broadly than the correctly informed models that prohibited gene flow.

When incorrect geological priors were used in the model (Figs. S5, S6, S10, S11), results for absolute node age and the age distribution for node two shifted in models prohibiting gene flow. The absolute age for node two was about 0.5 years older in both incorrect models prohibiting gene flow, and the age distribution for node two was dated as older as well. Interestingly, in the models that permitted gene flow, the incorrect, correctly informed, and unknown models all produced similar (around 0.1 million years) results. Predictably, the estimated absolute age for node one remained roughly unchanged, as it was not manipulated in the epoch time estimation nor the demographic model. There were no notable differences in the age estimations between using the uniform or normal distributions in the incorrect models.

# Discussion

## *Geologically unknown prior data dates phylogenies comparably to accurate geological priors*

Our results found that models with a flat, unknown geological prior performed nearly as well at estimating divergence times as models with a uniform or normal geological prior centered around correct times. Correct, well-informed simulated data successfully being able to predict the timing of the emergence of biogeographic barriers without prior historic geographic information suggests exciting opportunities to test new biogeographic hypotheses. These results confirm the critical idea in geogenomics that biology and geography may reciprocally inform each other.

While the strong performance of the molecular data is exciting, it should be noted that in our simulations, our molecular data was “perfect”: a model scenario in which genetic sequences had no missing data. Additionally, we assume our taxon sampling was complete; there were no unknown extant taxa nor extinct taxa in our group that lacked molecular data. Yet, has been thought that missing data at the molecular (Roure et al., 2013) and taxonomic levels (Zwickl & Hillis, 2002) may negatively influence the accuracy of phylogenies, which could in turn create issues downstream in dating methods. Additionally, our model dataset lacked common informatic errors like inaccurate molecular alignment (Ogden & Rosenberg, 2006) or erroneous taxonomic identification (de Almeida et al., 2023) both of which may lead to inaccurate phylogenies and biogeographic dating. In realistic datasets, imperfect molecular data may interfere with the ability of molecular data to accurately test geographic hypotheses.

Furthering genomic data acquisition and empirical analyses in model systems such as montane or riparian species has been proposed (Bedoya, 2024) as the next steps in furthering the empirical testing of reciprocal geographic-biological dating methods. Model systems such as these that lack known demographic histories of gene flow, have strongly-supported biogeographic histories, and already have accepted dated phylogenies through adequate fossil calibrations (such as Landis et al., 2021) will be necessary to explore the possibilities of dating geographic events through biological data.

## *Incorrect geographic historical data alters dating accuracy*

With the introduction of incorrect prior information, however, models performed significantly worse in predicting geological history. This supports previous studies that have indicated incorrect assumptions within the DEC (Magalhaes et al., 2021) and fossilized birth-death (Barido-Sottani et al., 2020) models have large impacts on inference in biogeographic estimations. Considering debate continues over the timing of influential biogeographic events (White et al., 2013; Zheng, 2015), the selection of accurately resolved paleogeographic priors is critical. Further work should also explore the impact of these historic geographic assumptions in other biogeographic models like DEC+J (Matzke, 2014), which have been debated regarding ability to accurately parameterize the rates of speciation (Ree & Sanmartin, 2018), as the accuracy of model assumptions likely plays a large role in the accuracy of phylogenetic dating results.

Researchers should be conservative and cautious when creating strict priors in biogeographic dating methods, especially considering the fact that with our accurate simulated molecular data, a flat geological prior performed nearly as well as correctly-informed priors.

## *Demographic models that allow gene flow alter dating accuracy*

When demographic models allowed for gene flow, the predicted cladogenesis times were found to be significantly younger, regardless of the historic geographic prior used. The fact that all models allowing gene flow, regardless of the biogeographic information present, produced similar results suggests that the existence of gene flow in molecular data creates a significant barrier to the accurate implementation in using biogeographic data to date phylogenies. Current work continues to reveal histories of introgression (Stull et al., 2023), including from extinct lineages (Tricou et al., 2022), which did not exist in our model system. Researchers should take caution in using biogeographic priors to date phylogenies with known or suspected gene flow.

While gene flow may interfere with inferring the correct biogeographic history, further research may develop methods that allow systematists to properly date phylogenies of systems that include rampant gene flow. In fact, if properly diagnosed, the detection of gene flow itself may be a tool to understand the history of past biogeographic connections, as gene flow is more likely to occur between species that have geographic overlap (Liu et al., 2024).

# Acknowledgements

Code used to run our model simulations was adapted from existing code produced in Landis, 2017 and Landis et al., 2018.

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# Data Availability Statement

All code for the generation data and analyses included here is available at the following GitHub repository https://github.com/Bedoya-Research-Group/River\_phylogeography

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# Figures

**Figure 1:** Biogeographic model for simulated organisms modelled in our phylogeny. Dotted lines represent known biogeographic dates of uplift marking epoch transitions at three and one million years ago.

**Figure 2:** The methodological approach of geogenomics that allows reciprocal influence of biological and geological data to test hypotheses.

**Figure 3:** Maximum clade credibility trees produced from ten different models with varying geographic historical knowledge, prior distributions, and demographic models.

# Supplemental Information

**Table S1**: The absolute ages predicted for node 1 (taxa C and stem group AB), node 2 (taxa A and B), and the distribution of age ranges for the demographically manipulated node 2 (taxa A and B)

|  |  |  |  |
| --- | --- | --- | --- |
| **Model** | **Node 1 Absolute Age** | **Node 2 Absolute Age** | **Node 2 Age Distribution** |
| Informed uniform, no gene flow | 3.6051 | 2.1222 | 3.3801, 0.9284 |
| Informed normal, no gene flow | 3.6012 | 2.1295 | 3.2818, 1.0217 |
| Unknown, no gene flow | 3.5304 | 2.0042 | 3.5133, 0.5983 |
| Incorrect uniform, no gene flow | 3.633 | 2.6246 | 3.5475, 1.7175 |
| Incorrect normal, no gene flow | 3.6297 | 2.6844 | 3.5546, 1.9654 |
| Informed uniform, gene flow | 3.5067 | 1.3893 | 2.9633, 0.2038 |
| Informed normal, gene flow | 3.5074 | 1.403 | 2.9705, 0.2054 |
| Unknown, gene flow | 3.5198 | 1.4953 | 3.0648, 0.2794 |
| Incorrect uniform, gene flow | 3.5086 | 1.4076 | 2.9846, 0.2103 |
| Incorrect normal, gene flow | 3.5084 | 1.4034 | 2.9679, 0.2042 |

**Figure S1:** Prior distributions for five biogeographic knowledge-level scenarios. Red dotted line represents the true time for the node where taxon C splits from taxa A and B, and green dotted line represents the true time for the node where taxon A splits from taxon B.**Figures S2-S11:** Maximum clade credibility trees constructed for the ten biogeographic models tested in this study.

**Figures S2-S11:** Maximum clade credibility trees produced by each of the 10 models.