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 Paleogeographic 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 geological priors of varying information levels and accuracy in order to test the influence of geological knowledge and molecular data on phylogenetic dating. In our simulations, models prohibiting gene flow with unknown geological histories performed just as well as models prohibiting gene flow with correctly informed geological 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 geological 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 (Wallace, 1854). 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 inherently forces the interpretation of biological data in reference to a specified geological background. This analytical approach has led to the description of generalizable patterns, such as in island biogeography (Whittaker et al., 2017), 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 the timing of formation of shared abiotic processes that may have driven those patterns (e.g., formation of a mountain as a barrier to gene flow; Landis et al., 2021). 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 (Haffer, 1969), to the characterization of the timing and mode of uplift of mountain ranges (Sanín et al., 2022), 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; Rahbeck et al., 2019; Badgley et al., 2017).

Using biological and geological data independently, or interpreting them in reference of each other (e.g., establishing geological analyses as ground truth against which biological data are interpreted) may introduce biases inherent to each biology and geology. Geological models inherently carry uncertainty for example in the interpretation of zircon data in provenance analyses (Weltje & von Eynatten, 2004). On the other hand, standard approaches for the analysis of biological data and subsequent interpretation of geological hypothesis may introduce biases (e.g., divergence dating analyses (). Further, as the responses of organisms to a shared paleogeographical event are idiosyncratic, careful attention should be placed to the model system used to infer geological models from biological data. Organisms best serve as appropriate model systems for inferring geological history with biological data when they mirror geological history. However, even if the evolutionary trajectories of a given set of organisms are shaped by a landscape event, the predictability of landscape hypotheses from evolutionary patterns may be affected by common and stochastic processes (e.g., gene flow).

An example of the overall biases for the use of biological and geological data to date the timing of geomorphic events is the closure of the Isthmus of Panama, which facilitated 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, 2012b, 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 (O’Dea et al., 2016). This underscores the importance of considering species-specific traits when interpreting bio/phylogeographic patterns used for inferring geological models.

Biogeographic hypotheses renewed by the emerging geogenomics field have established a theoretical background for discussing the characteristics that study systems must meet for the reciprocal interpretation of data to infer past geological events, as well the geographic and geological scales that study systems may effectively inform one another. Yet, the integration of biological, paleontological, and geological data in a unified methodological framework is still lacking. A unified framework such as this would allow tests of how geological priors and biological data interact. This would test the effect of bad (deviates from reality), broad (lots of uncertainty), and good (accurately describes the timing of a geomorphic event) geological models, providing clarity on the impact using different geogenomics model systems of varying quality. 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; Landis et al., 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. To do this, we examined varying levels of accuracy in geological priors, and created two demographic models to examine the influence of gene flow. In order to control other influences, 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. In this alternative case, a pair of taxa experienced a period of gene flow despite inhabiting distinct rivers. Under these two 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. We assume a barrier, such as mountain uplift, creates a branching in a river ecosystem at three and one Ma. The ensuing three distinct river branches X, Y, and Z allow for the speciation of taxa A, B, and C, respectively, producing a phylogeny whose branches mirror the river ecosystem (Fig. 1b). This model group of aquatic riparian species is suitable for analyses because we can assume individuals do not migrate and that species are restricted to highly specific and diagnosable ranges.

## *Demographic and Sequence Simulation*

A model demographic scenario consisting of three taxa was created with msprime (Baumdicker et al., 2022) to generate molecular sequence data of 10,000 base pairs per taxa under the coalescent model. The demographic model enforced taxon C splitting from taxa A and B three Ma and taxon A splitting from taxon B one Ma. This means that our demographic model exactly mirrored the known geological history of the river system. In the model, each taxon has a generation time of one year, similar to other river-dwelling angiosperms (Philbrick & Retana, 1998). We used the HKY model to limit the number of assumptions about our simulated dataset, and selected a mutation rate of 1e-8 substitutions per site per generation (equal to per year in our model) and a recombination rate of 4.8e-8 per base pair, both rates realistic for angiosperms (Koch et al., 2000; Tiley & Burleigh, 2015). All invariant sites were filled in with randomly selected bases. In one demographic model, gene flow between taxa was never allowed, simulating a scenario where geological events completely isolated taxonomic groups. We the simulated gene flow in a second demographic model otherwise consistent with the previously described scenario. In this scenario where geological events created a gradual, weak, or incomplete isolation between taxon A and taxon B for the time period from 1 to 0.5 Ma, we simulated a gene flow using the migration function in msprime (rate = 0.2). Demographic models (Fig. 2) were visualized in python using the package DemesDraw (Gower et al., 2022). When prohibiting gene flow, our demographic model produced a phylogeny of the structure (C:3, (A:1, B:1):2), mirroring the known geological event times. Contrastingly, the demographic model permitting gene flow produced a phylogeny of the structure (C:3, (A:0.5, B:0.5):2.5), inconsistent with the geological history known in our model. These phylogenies were used in the ensuing analyses. We enforced a root age for the tree as a uniform distribution from 3 to 4 Ma for all models.

**Fig 2**

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

We ran five geological knowledge-level scenarios by creating different priors (Fig. 3); uniform-informed, normal-informed, normal-uninformed, normal-incorrect, and unknown. We then simulated the same five geological knowledge-level scenarios with the second demographic model that allowed for a period of gene flow.

**Fig 3**

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 created new scripts adapted from Landis, 2017 for biogeographic dating in RevBayes available at https://github.com/Bedoya-Research-Group/BioGeoDating\_Geogenomics.git. 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 Ma 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 after applying a 0.25 burn-in on each file, resulting in a concatenated file with 15 million generations. The final generated trees and posterior distributions were visualized in R using RevGadgets (Tribble et al., 2021).

# Results

**Fig 4**

When using correctly informed geological priors (Figs. S1, S2, S6, S7), the age distribution for node two began at the true date of one Ma (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. S3, S8), 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. S4, S5, S9, S10), 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 geological 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 geological 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 geological 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 geological 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) and in areas with ephemeral geological barriers (Araya-Donoso et al., 2022).

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

# 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 1a:** Biogeographic model for simulated organisms modelled in our phylogeny. Dotted lines represent known geological dates of uplift marking epoch transitions at three and one Ma.

**Figure 1b:** The methodological approach of geogenomics that allows reciprocal influence of biological and geological data to test hypotheses.

**Figure 2:** Demographic models used to generate sequence data and inform phylogenies, for a system prohibiting gene flow (left) and permitting gene flow (right).

**Figure 3:** Prior distributions for five geological 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.

**Figure 4:** Posterior distributions produced from ten different models with varying demographic models, knowledge levels and correctness, and geological prior distributions.

# 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 |

**Figures S1-S10:** Maximum clade credibility trees constructed for the ten biogeographic models tested in this study.