**Supplementary Information**

For the manuscript: Oliver et al. (2025). “Limited dispersal and differing evolutionary trajectories across geographically proximate continental and insular regions in an Australasian lizard radiation (*Gehyra*).”

**Supplemental Methods**

*Biogeographical analyses*

*Gehyra* biogeography was discretized into 6 areas in order to capture the major coarse-scale features of the clade’s geographic distribution, while limiting computation time over a series of inferential models. The six areas were abbreviated as follows.

O = Australia

N = New Guinea

W = Wallacea

E = East Melanesia

P = Pacific

A = Asia

The dated phylogeny of 96 *Gehyra* taxa (described species, or genetically isolated populations thought to be likely species/lineages) was displayed in ladderized format in FigTree and saved to Newick. We constructed a geographic ranges text file coding each taxon as present or absent in each of the 6 areas. The maximum number of areas occupied was 4 (by *G. insulana*, found in N, W, E, P). Nevertheless, while constructing the list of possible geographic states in the states list (i.e., the list of possible ranges), we set max\_range\_size to 6, to allow maximum flexibility. The null range (0 areas occupied) was also allowed in the state space (Massana et al. 2015). This resulted in 2^6=64 possible ranges in the state space.

*BioGeoBEARS analysis*

An initial analysis was conducted in the R package BioGeoBEARS (Matzke 2013) version 1.1.4 (Matzke 2025). Six common base models were compared: DEC (Ree & Smith 2008); DIVALIKE, a likelihood implementation of the events allowed in the parsimony DIVA program (Ronquist 1997); and BAYAREALIKE, a likelihood implementation of the BayArea model (Landis et al. 2013), plus “+J” variants of these models, which add the possibility of jump dispersal/founder-event speciation at cladogenesis (Matzke 2014; for a defense of the +J model variant against criticisms, see Matzke 2022). DEC, DIVALIKE, and BAYAREALIKE make different assumptions about how cladogenesis (speciation) can change geographic ranges at nodes (see Figure 1 of Matzke 2013), and +J models use a free parameter, *j*, to measure the relative weight of jump dispersal events at cladogenesis versus the other cladogenetic range inheritance events allowed under the base model.

Parameters were inferred for each model using Maximum Likelihood (ML) inference. Model fit was statistically compared using AICc and AICc weights (Franklin et al. 2001; Burnham & Anderson 2002; Anderson 2008).

*Testing the effect of including lineage extinction in biogeographical models using PhyBEARS.jl*

A legitimate criticism of the biogeographical models implemented in BioGeoBEARS and previous software packages is that they take the phylogenetic tree as complete, i.e. the only cladogenesis events that can change geographic ranges are the speciation events in the observed tree. This amounts to a Yule process assumption, i.e. a “pure birth” process with 0 extinctions (Matzke 2022), which is extremely unlikely to represent reality (Marshall 2017). While a simulation study suggested that ignoring extinction may not dramatically bias the inference of ancestral geographic ranges, at least with random extinction (Matzke 2014), newer technology enabling SSE models (state-dependent speciation/extinction models; Maddison et al. 1997 [and other references]) to be run on large biogeographical state spaces allows the possibility of lineage extinction being added to biogeographical modes. The Julia package PhyBEARS.jl (Matzke and Bland, 2024a, 2024b) implements BioGeoBEARS models in a full cladogenesis SSE (ClaSSE; Goldberg & Igic 2011) framework. PhyBEARS.jl uses the Julia library DifferentialEquations.jl (Rackauckas & Nie 2017) to calculate SSE likelihoods using Ordinary Differential Equation (ODE) solvers designed for large state spaces (typically CVODE\_BDF). The runtimes for ML inference using this Julia implementation of the ODE SSE calculations are typically similar or slightly faster than the simpler non-ODE BioGeoBEARS calculations in R using matrix exponentiation, and much faster that R’s ODE solving libraries (Bland 2024).

Basic validation of PhyBEARS calculations and estimates against BioGeoBEARS and simulated data was conducted by Bland (2024), as well as 511 unit tests implemented in the PhyBEARS.jl tests directory (Matzke and Bland, 2024a). However, although PhyBEARS.jl makes it feasible to extinction in the likelihood calculations for large problems, accurate inference of extinction rates from molecular phylogenies is still a very difficult problem (Marshall 2017; Louca & Pennell 2021; Legried & Terhorst 2023). However, it is still useful to conduct sensitivity tests to see biogeographical inference is substantially changed by including lineage extinction.

For the *Gehyra* dataset, we implemented the standard DEC and DEC+J models in PhyBEARS, first with a Yule process (lineage extinction set to 0). Then we created a series of model variants with the lineage extinction set to be a free parameter, or with the extinction rate constrained to equal the speciation rate (this reflects the typical rough balance in the fossil record; Marshall 2017).

An alternative model tested was to set the extinction rate is set to match *e*, the rate of range loss, with the model set up so that (1) the null range was not an allowed state in the state space, (2) the extinction rate for a lineage occupying multiple areas was 0.0, and (3) extinction occurred only when an *e* range contraction event occurred in a single-area range.

*Biogeographical Results*

The statistical model comparison of BioGeoBEARS models are found in Table BioGeoBEARS1. The estimated ancestral ranges are available in *Gehyra\_BioGeoBEARS\_results\_M0\_unconstrained\_v1.pdf*. A comparison of PhyBEARS models is shown in Table PhyBEARS1. DEC+J dominates in both model sets, but in PhyBEARS models, likelihood and AICc differences were small between the DEC+J model variants, with all of them being in the credible set except for model 10, where the single-area extinction rate was set to equal the birth rate.

The AICc-best model was PhyBEARS Model 12, a DEC+J+birth-death model where both *e* and *deathRate* are constrained to equal *d*, the range-expansion rate. However, this model (AICc weight 46.8%) was only slightly better than standard DEC+J (AICc weight 42.8%) implemented in PhyBEARS (termed DEC+J+Yule, indicating that standard DEC+J ignores the possibility of lineage extinction). Inference of the geographic history under Model 12 (Figure *pdf\_graphics/best\_model\_phyBEARS\_Gehyra2\_DEC+J+B+d=e=D\_M0\_unconstrained\_v1.pdf*) was similar to that under standard DEC+J. This probably occurred due to the low inferred *d*=*e*=*deathRate* parameter (0.0015, compared to an inferred speciation rate of 0.17 events per million years). The lowness of these parameters in DEC+J models suggests that that the observed geographic ranges can mostly be explained by cladogenetic jump events, and that postulating range loss and lineage extinction is not particularly necessary to explain the data under consideration (note that this is different than saying these low rates are biologically plausible).

To get a sense of how much a realistically high extinction rate could change biogeographic inference, the PhyBEARS ancestral range estimates (*Gehyra\_PhyBEARS\_results\_M0\_unconstrained\_v1.pdf*) for Models 4 and 10 (in both, *deathRate* was constrained to equal *birthRate*) can be compared to the results above. Forcing a high extinction rate into the model results in higher uncertainty at many nodes, especially deep nodes, but overall, most nodes have the same plurality-favoured range estimates.

[Overall summary: differences are pretty minor ]

**References**

Anderson, David R. (2008). *Model Based Inference in the Life Sciences: A Primer on Evidence*. New York, Springer. doi: [10.1007/978-0-387-74075-1](http://dx.doi.org/10.1007/978-0-387-74075-1)

Bland, Wallis Miyuki (2024). *Improving realism in biogeographic simulation and inference with state-dependent speciation and extinction models using GPlates palaeogeography and the Julia programming language*. Ph.D. thesis, School of Biological Sciences, University of Auckland. Published by: ResearchSpace@Auckland. pp. 1-203. <https://hdl.handle.net/2292/70305>

Burnham, Kenneth P.; Anderson, David R. (1998, first edition; 2002, second edition). *Model Selection and Multimodel Inference: A Practical Information-Theoretic Approach*. New York, Springer. doi: [10.1007/b97636](http://dx.doi.org/10.1007/b97636)

Franklin, Alan B.; Shenk, Tanya M.; Anderson, David R.; Burnham, Kenneth P. (2001). "Statistical Model Selection: An Alternative to Null Hypothesis Testing." *Modeling in Natural Resource Management: Development, Interpretation, and Application*. Edited by T. M. Shenk and A. B. Franklin. Washington, Island Press: 75-90.

Landis, Michael J., Matzke, Nicholas J.; Moore, Brian R.; Huelsenbeck, John P. (2013). "Bayesian Analysis of Biogeography when the Number of Areas is Large." *Systematic Biology*, 62(6), 789-804. <http://dx.doi.org/10.1093/sysbio/syt040>

Legried, Brandon; Terhorst, Jonathan (2023). Identifiability and inference of phylogenetic birth-death models. *Journal of Theoretical Biology*, 568:111520. doi: 10.1016/j.jtbi.2023.111520

Louca, S.; Pennell M. W. (2021). Why extinction estimates from extant phylogenies are so often zero. *Current Biology*, 31(14):3168-3173.e4. doi: 10.1016/j.cub.2021.04.066

Goldberg, E. E., & Igic, B. (2012). Tempo and mode in plant breeding system evolution.

*Evolution*, 66(12), 3701-3709. doi:10.1111/j.1558-5646.2012.01730.x

Maddison, W. P., Midford, P. E., & Otto, S. P. (2007). Estimating a binary character's effect on speciation and extinction. *Systematic Biology*, 56(5), 701-710. doi:10.1080/10635150701607033

Marshall, Charles R. (2017). Five palaeobiological laws needed to understand the evolution of the living biota. *Nature Ecology & Evolution*. 1(6):165. doi: 10.1038/s41559-017-0165.

Massana, Kathryn A.; Beaulieu, Jeremy M.; Matzke, Nicholas J.; O'Meara, Brian C. (2015). Non-null Effects of the Null Range in Biogeographic Models: Exploring Parameter Estimation in the DEC Model. *bioRxiv*, 026914. <http://dx.doi.org/10.1101/026914>

Matzke, Nicholas J. (2013). "Probabilistic historical biogeography: new models for founder-event speciation, imperfect detection, and fossils allow improved accuracy and model-testing." *Frontiers of Biogeography*, 5(4), 242-248. <https://doi.org/10.21425/F5FBG19694>

Matzke, Nicholas J. (2014). "Model Selection in Historical Biogeography Reveals that Founder-event Speciation is a Crucial Process in Island Clades." *Systematic Biology*, 63(6), 951–970. <http://dx.doi.org/10.1093/sysbio/syu056>

Matzke, Nicholas J. (2022). Statistical comparison of DEC and DEC+J is identical to comparison of two ClaSSE submodels, and is therefore valid. *Journal of Biogeography*, 49(10), 1805-1824. doi: [10.1111/jbi.14346](http://dx.doi.org/10.1111/jbi.14346)

Matzke, N. J., & Bland, W. (2024a). PhyBEARS.jl: Phylogenetic biogeography SSE models for large state spaces (Version 1.0). <https://github.com/nmatzke/PhyloBits.jl>

Matzke, N. J., & Bland, W. (2024b). PhyloBits.jl: Phylogenetic tree tables and other

phylogenetic utilities (Version 1.0). <https://github.com/nmatzke/PhyloBits.jl>

Matzke, Nicholas J. (2025) BioGeoBEARS: BioGeography with Bayesian (and likelihood) evolutionary analysis in R Scripts. Version 1.1.4. <https://github.com/nmatzke/BioGeoBEARS/>

Rackauckas, C., & Nie, Q. (2017). DifferentialEquations.jl – A Performant and Feature-Rich Ecosystem for Solving Differential Equations in Julia. *Journal of Open Research Software*, 5(1). doi:10.5334/jors.151

Ree, R. H., & Smith, S. A. (2008). Maximum likelihood inference of geographic range evolution by dispersal, local extinction, and cladogenesis. *Systematic Biology*, 57(1), 4-14. doi:10.1080/10635150701883881

Ronquist, F. (1997). Dispersal-vicariance analysis: A new approach to the quantification of historical biogeography. *Systematic Biology*, 46(1), 195-203. doi:10.2307/2413643