Simulated Evolutionary Reconstruction

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Peaks in species richness at mid-elevation bands have been observed in ecosystems and taxa around the globe. A number of ecological processes may contribute to this including varying autotrophic productivity, tradeoffs between competitive ability and environmental tolerance, and differences in area and isolation. Evolutionary processes have also been suggested; however, such explanations are difficult to support, as it is often unclear how speciation and extinction rates have changed over time.

Here, we use records of historical temperature and topographic changes over the past 65 Myr to construct an agent-based simulation model of Plethodontid salamander evolution in eastern North America. We then explore possible mechanisms constraining species to mid-elevation bands by using the model to predict Plethodontid evolutionary history and contemporary geographic distributions.

Our results show that models which incorporate both temperature and topographic changes are better able to predict observed patterns, suggesting that both processes may have played an important role in driving Plethodontid evolution in the region. Additionally, our model represents a proof of concept to encourage future work that takes advantage of recent advances in computing power to combine models of ecology, evolution, and earth history to better explain the abundance and distribution of species over time.

Our model tracks the evolutionary history of a single progenitor species, and all of its descendant species, from an origin 65 Mya to the present. Climatic and geologic change can be selectively enabled for this period, allowing us to tease apart their effects.

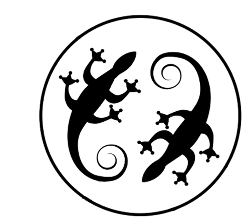
Each species is represented by one or more populations. Dynamics within populations are not explicitly simulated: Rather, we assume that individuals within a population are proximal, share the same traits, and are genetically identical. Between populations, these aspects can vary. The abundance of a species is determined by the number of populations of that species. If the genetic differences among populations within a single species become large enough, the populations diverge into separate species.

We fit this model to data species' ranges, richness, and phylogenies drawn from 95 Appalachian Plethodontid taxon groups found primarily east of the Mississippi. Finally, we compared model fits across scenarios to determine which factors were most important in driving evolution.

For each timestep

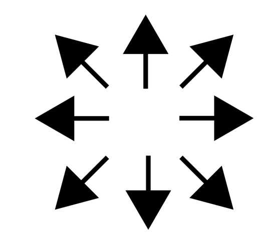
Mortality

Function of temperature and con-/heterospecific density



Mating

Genetic mutation
Crossover
New species arise



Migration

Directed, undirected, random, or external

Controls and Parameters

Primary Control Knobs
(What drives evolution?)

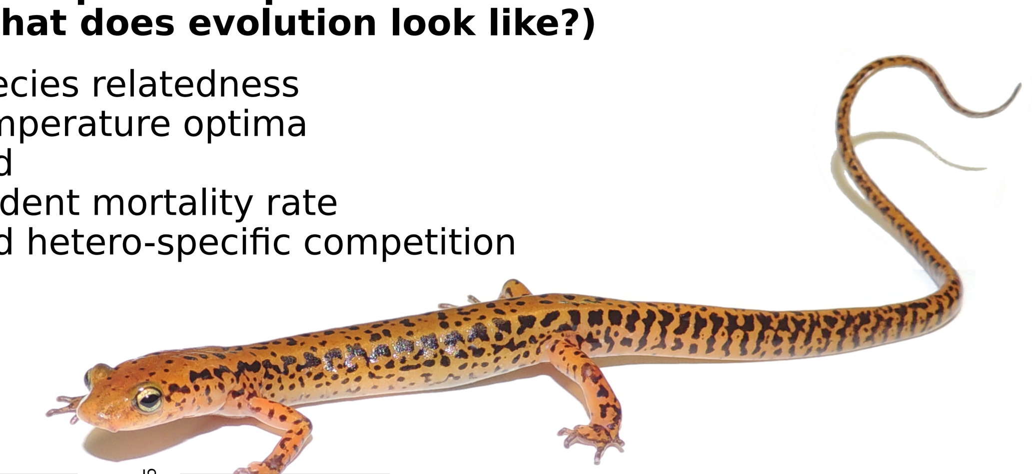
- Climate change: On/off
- Geologic change: On/off

Secondary Control Knobs
(What are the effects of our assumptions?)

- Competition: No heterospecific, equal and unequal con/heterospecifc
- Dispersal: Random local, directed local, random global
- Ancestral elevation: Sea level of mid-elevation
- Re-invasions: On/off
- Timestep: 0.1 or 0.5 Myr

Optimized parameters
(What does evolution look like?)

- Mutation rate of species relatedness
- Mutation rate of temperature optima
- Speciation threshold
- Temperature-dependent mortality rate
- Strength of con- and hetero-specific competition



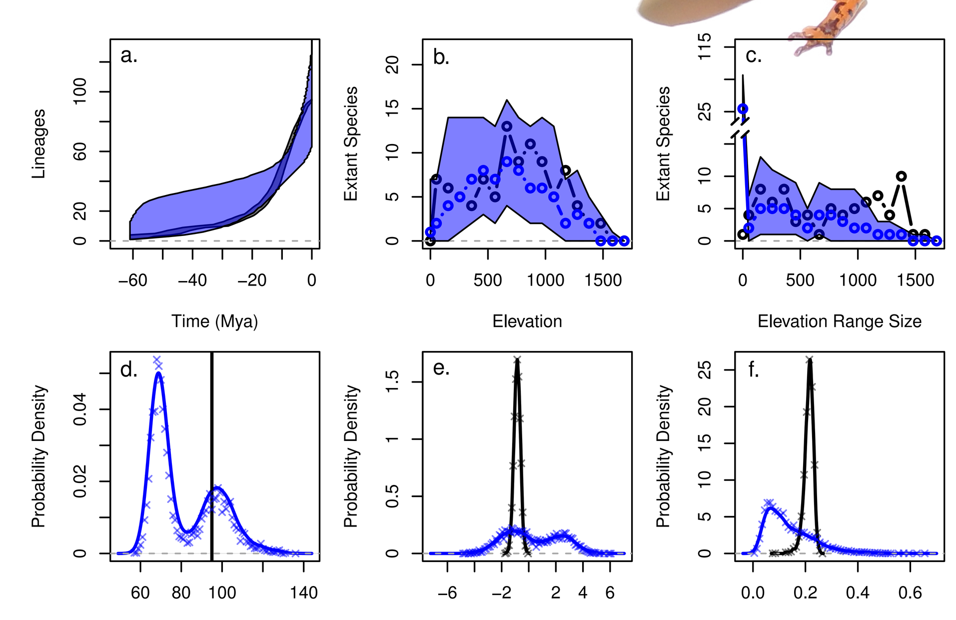


Figure 1: Comparison of observed and predicted metrics when both climatic and geologic change are included as processes (ET scenario). Black lines show observed data, while blue lines show results from simulations. Grey shaded region in (a) and blue shaded regions in (a–c) show 95% confidence intervals for observed and simulated metrics, respectively. Lines in (b–c) show values for observations, or median for simulated values. Lines in (d– f) show smoothed kernel density estimates, points show frequency calculated empirically from binned data.

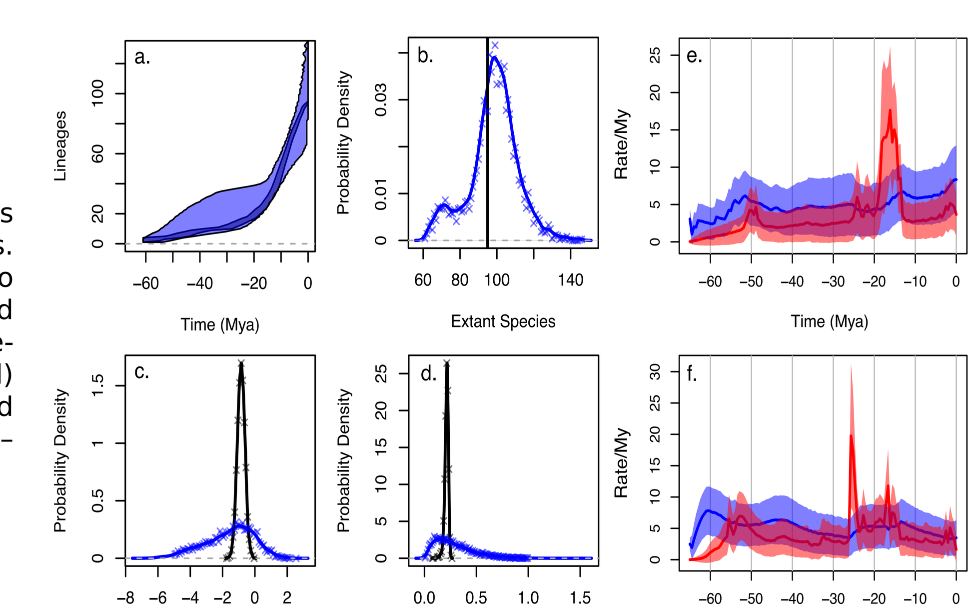


Figure 2: Examples of metric comparisons and time trends for other fitted scenarios. Panels (a), (b), and (e) are for the scenario with directed dispersal. Panels (c), (d), and (f) are for the scenario with multiple re-invasions. Symbols and intervals for (a–d) are as described in Fig. 1 (a), (d), (e), and (f), respectively. Colors and intervals in (e–f) are as described in Fig. 2 (b).

Barnes and Clark (2016). 65 Million Years of Change in Temperature and Topography Explain Evolutionary History in Eastern North American Plethodontid Salamanders. American Naturalist: 190(1). doi: 10.1086/691796.
code: https://github.com/r-barnes/BarnesClark2017-Salamanders

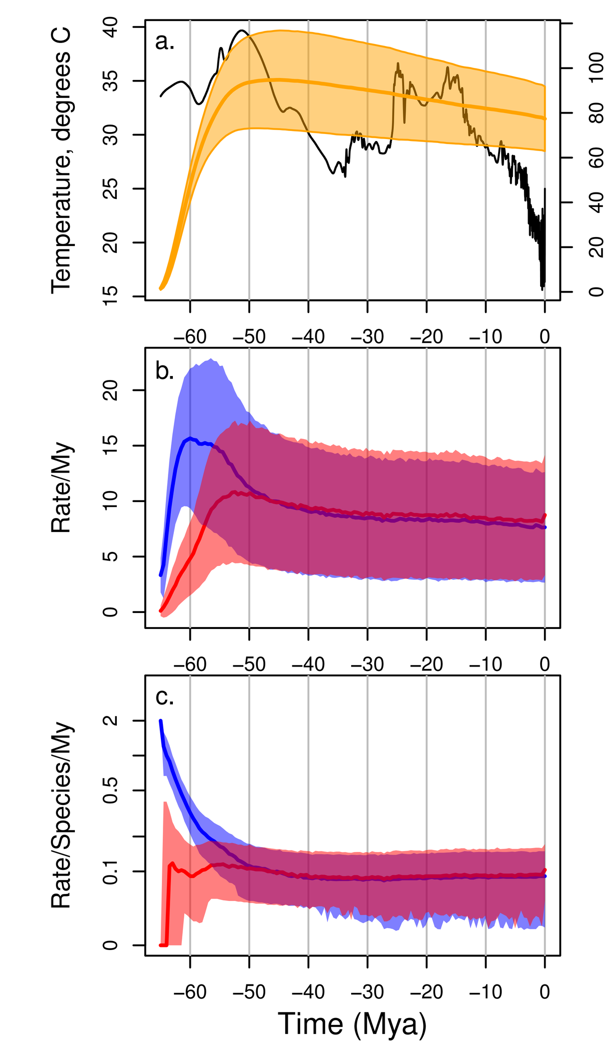


Figure 3: Time trends predicted from the fitted scenario with climatic and geologic change (ET scenario). Lines show mean ± one standard deviation. (a) Black line shows temperature trend over time, and orange shows species richness. (b–c) Blue and red shows rates for speciation and extinction, respectively. Darker regions show overlap between confidence intervals.

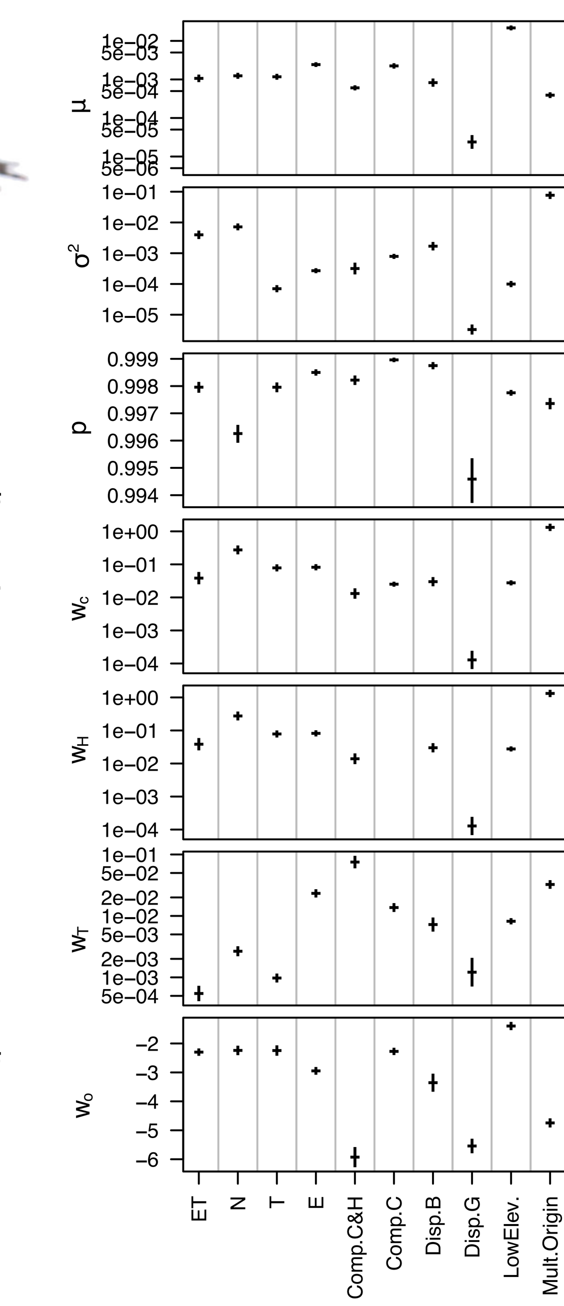


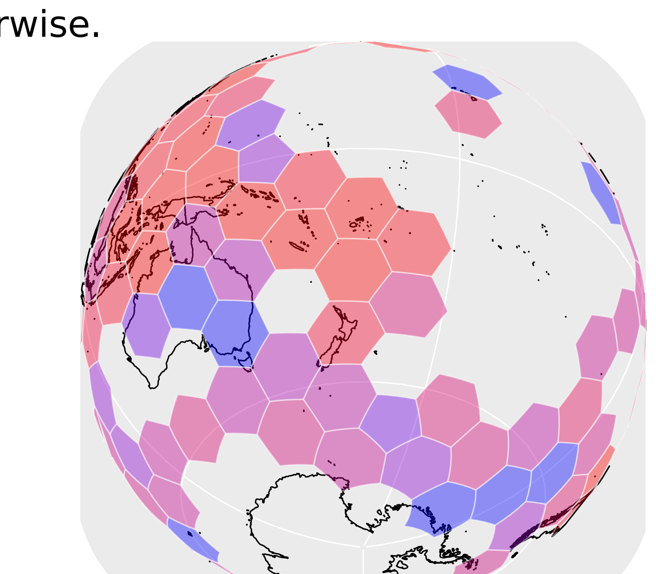
Figure 4: Estimates for the optimized parameters in the model. μ and σ^2 control mutation rates of species relatedness and temperature optima, respectively; p controls relatedness threshold for breeding and speciation; w0 and wT control mortality rates as a function of temperature; wC and wH control the strength of conspecific and heterospecific competition, respectively. Points and intervals show mean and standard deviation averaged across simulated annealing iterations, weighted by parameter set likelihood. Because the sampling window contracts over time in simulated annealing, this estimate of the standard deviation is biased towards smaller values, and should only be interpreted as a general indication of the shape of the likelihood surface, not as a tool for significance testing.

And another thing: webglobe

Your data's spatial and it spans large areas. You're nervous about viewing it using flat projections like Mercator because of the bad intutions they will give you: in your head you know Greenland isn't that big, but your heart tells you otherwise.

webglobe can help! It allows you to interactively visualize your data in R using either a 3D globe, a flat map, or the mysterious "Columbus view".

Available on CRAN and at https://github.com/r-barnes/webglobe



webglobe is the perfect accompaniment to dggridR: a package for doing spatial statistics with equally-sized bins. Do stats right. Get dggridR from CRAN or https://github.com/r-barnes/dggridR