Age-rate scaling in evolution is largely artifactual

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The observation that evolutionary rates are faster over shorter or more recent time intervals has been of interest to evolutionary biologists, especially paleontologists, for decades (i.e., Gingerich 1983). This striking pattern has been shown to occur for rates of body size change, DNA substitutions, speciation rate, and genus origination rates (Rolland et al. 2023).

HMB model

O’Meara & Beaulieu (2024) showed that this pattern was largely artifactual, but we created an “**HMB**” model to separately distinguish three basic patterns in relevant data. Inspired by Kinneberg & Lysne Voje (2026), we have tried fitting this model to time series in the Phenotypic Evolution Time Series (PETS) database (Rugstad & Lysne Voje 2023). Figure 1 shows results for the largest datasets and selected datasets with interesting behavior.

H: a hyperbolic component. A hyperbola is $y = 1/x$, aka a plot of $1/x$ vs x; our thinking is that a plot of <random noise> / x vs x would approach the same (and since x is on both sides, noise in x doesn’t affect this). Basically, Δtrait / Δtime vs Δtime becomes h/t vs t.

M: in a standard $y = mx + b$ linear model, the slope. Allows for rate to increase or decrease with timespan as some people suspect happens biologically.

B: in a standard $y = mx + b$ linear model, the y-intercept. This allows there to be a nonzero rate regardless of interval.

Thus, the overall HMB model has **rate = h/t + mt + b**. We then allow restricted models: fixing h at 0, fixing b at 0, etc. and compare with AIC to find the best-fitting model. These are the lines in the first column of figure 1; the colors represent the magnitude of each of the factors at that time point. The confidence in each factor’s contribution through time are shown in the third column: thickness of the band is the potential range of contribution from each factor.

The advantage of this set of models is, once we estimate the h component, we can use the remaining parameters to fit the rate versus time correlation after removing this effect (the fourth column in Figure 1). Often the hyperbolic component explains essentially *all* the pattern, leaving the best-fitting model with fixed slopes (m) and intercepts (b) of zero, but sometimes, as in the last three datasets shown, there is information about non-hyperbolic rates.

But is the scaling real?

Recently, Kinneberg & Lysne Voje (2026) analyzed age rate scaling through both simulations and empirical results. The paper suggested that models can detect lack of age scaling in simulated data, so the empirical examples of age-rate scaling likely have a biological explanation. Fossil time series from the Phenotypic Evolution Time Series (PETS) database v1.0 were analyzed under various models and found to still show an age-rate scaling pattern. We applied our HMB model to the datasets. To ensure independence of rate estimates, we used each observation just once when calculating a contrast: if observations were made at times *a*, *b*, *c*, and *d*, we looked at *a* vs *b* and *c* vs *d*, but not *b* vs *c* as that would have used *b* and *c* twice.

Overall, there were 67 datasets (each length trait from a paper counted as a distinct dataset) with at least 20 time comparisons. Of these, 45 (67%) found a best model one that had *only* a hyperbolic component; only 8 datasets (12%) had no hyperbolic component in the best model. Total Akaike weight across all datasets for models with hyperbolic components was 86%; for linear components, 39%; for constant components, 45%. **Even when models included non-hyperbolic components, they explained little of the apparent pattern.**

For more on the methods, R package, and more:
https://brianomeara.info/posts/ageratescalingposter

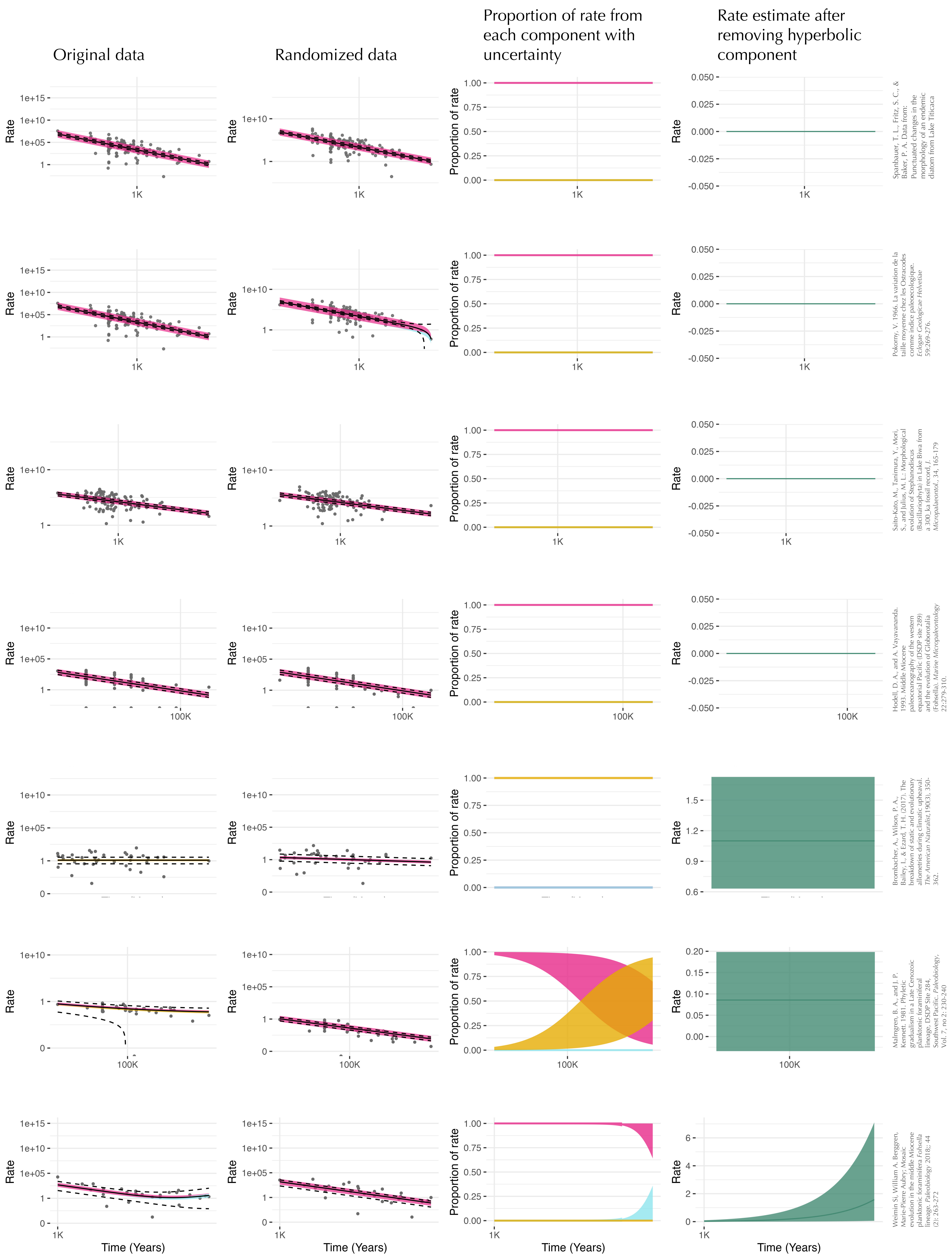

Figure 1: Sample results from running Phenotypic Evolution Time Series through HMB in the hyperr8s package. The four largest datasets are shown first (as they have the best chance of having enough power to pick up interesting dynamics) as well as other datasets illustrating interesting behavior. The first column shows the rates versus time (each point represents a comparison) with the fitted rate model (solid line) and uncertainty in the model (dashed lines). The second column shows the pattern if we back transform the comparison to amount of change and time, randomize the two, and re-fit the model (see the **So random** section of the poster for more on the procedure). The third column shows the proportion of rate from the hyperbolic (pink), constant (goldenrod), and linear (blue) components and the uncertainty in this proportion (thickness of the line). The fourth column shows the estimate of the rate versus time pattern once the hyperbolic component is removed.

Figure 2: Plot of original and randomized data from Uyeda et al. (2011) from O’Meara & Beaulieu (2024). The animal icons represent three particular data comparisons that are then randomized, as are all the other points. Similar patterns come from randomized points as from the original points, though with enough time and morphological change, there does appear to be a different pattern between the original and random datasets.

So random

Models, shmodels. Let’s just randomize stuff. Rate = Δtrait / Δtime, so since we know rate and Δtime for a given point, we can multiply them to backcompute Δtrait. We can then take all the Δtrait for a given dataset, all the Δtime for a given dataset, and shuffle them so that the Δtrait and Δtime are reordered, then recompute rate = Δtrait / Δtime for each randomized pair, then plot it against the Δtime for that couple. This is shown in Figure 2 in the Replicate 1 and Replicate 2 images (using data from Uyeda et al. (2011) and in the second column of Figure 1 (using data from PETS). The remarkable empirical pattern of age-rate scaling is often nearly indistinguishable from thew pattern for randomized data. There are some datasets where this is not the case, however, showing that not all is lost: for example, in Figure 1, the fifth row has as a best-fitting model one with no hyperbolic component, only an intercept.

Conclusion

We suspect the underlying biological reality is no general trend in rate versus time interval: there is a nonzero rate of change, but it will vary through time and across taxa. It is possible to sometimes tease this pattern out from the data, as in the last rows of Fig 1. However, the hyperbolic pattern so common in many datasets does not reflect the biology but rather noisiness and artifacts from plotting a ratio versus its denominator, something long known to be problematic (Pearson 1893). Biologists seeking to understand age-rate scaling would be best served by fitting a model (like HMB or something better) or by moving on to questions with a higher signal-to-noise ratio. There are nonzero rates of evolution, and they might change in interesting ways, but we have to account for the major factor of uncertainty as an explanation before getting to the cool inferences.

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