

Do conflicts exist between micro and macroevolution? If so, what are they?

pollev.com/josefuyeda941

The other side of the coin...Stasis

“Stasis is data”

Microevolutionary theory can explain punctuations, but can it explain stasis?

Ephemeral divergence model

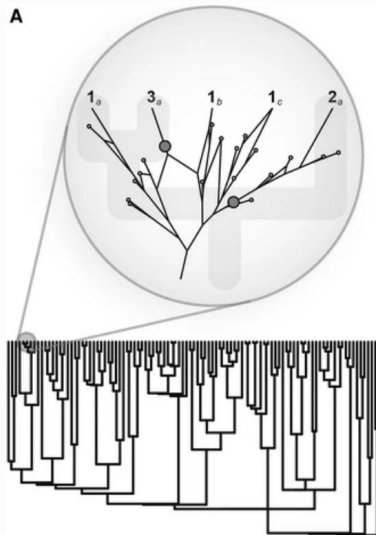
Vol. 130, No. 3

The American Naturalist

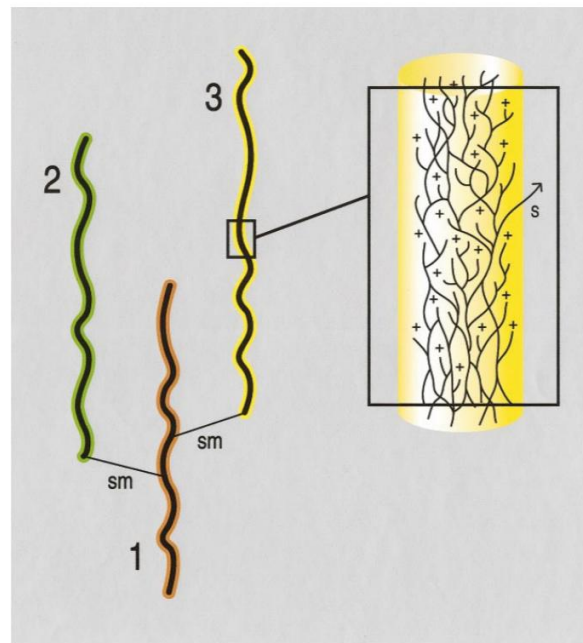
September 1987

ON THE ROLE OF SPECIES IN ANAGENESIS

Speciation is central to the hypothesis of punctuated equilibria as developed by Eldredge and Gould (1972; see also Gould and Eldredge 1977, 1986; Gould 1982) and by Stanley (1975, 1979). Without the claim that evolutionary change is



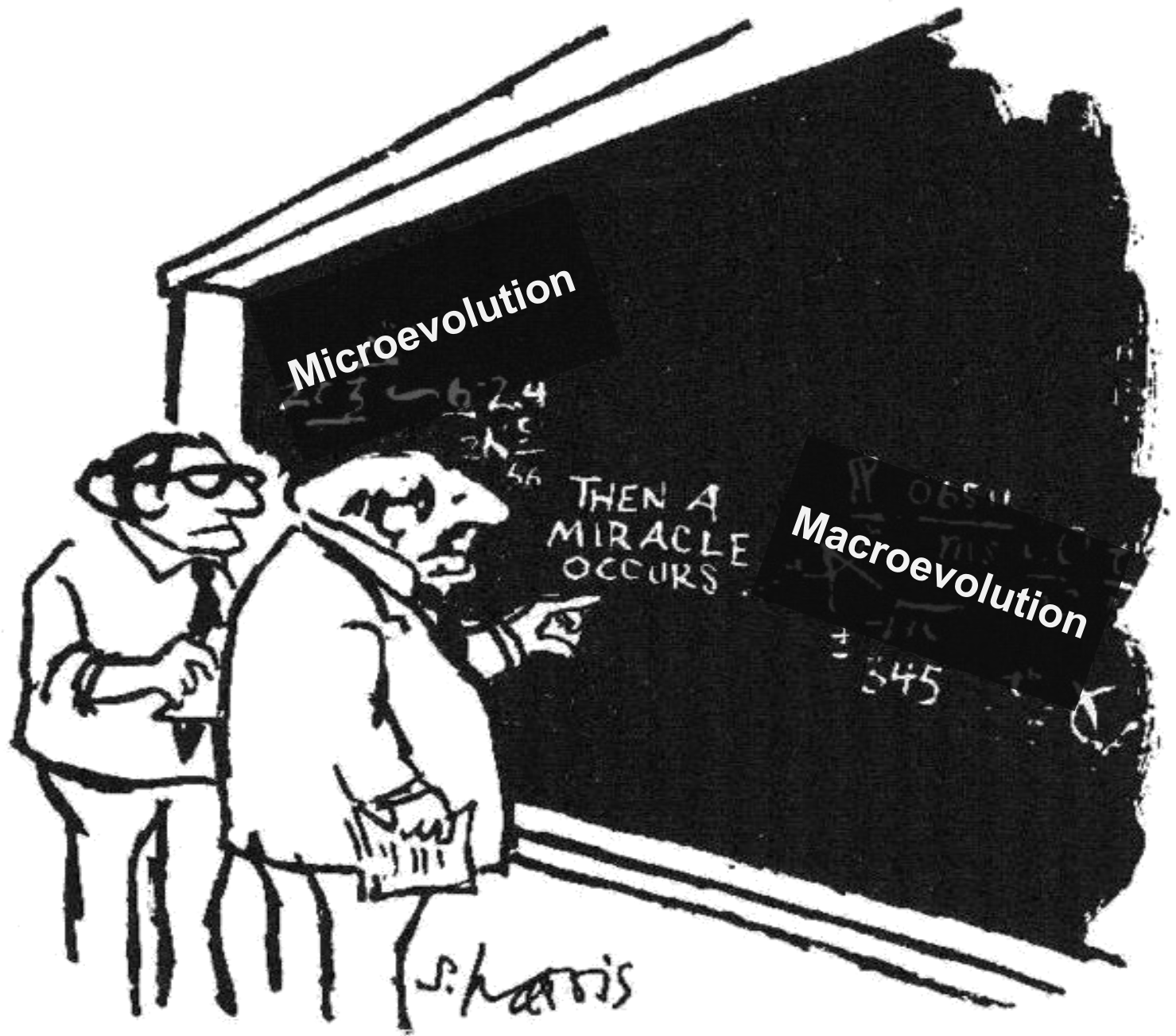
related: Ephemeral
speciation



Doug Futuyma

Rescued version of PE?

Here I point out a consequence of speciation that supports a highly qualified version of punctuated equilibrium. None of the ideas explored below is in itself original, but I am not aware that they have been explicitly developed in the present context. In brief, I propose that because the spatial locations of habitats shift in time, extinction of and interbreeding among local populations makes much of the geographic differentiation of populations ephemeral, whereas reproductive isolation confers sufficient permanence on morphological changes for them to be discerned in the fossil record. Long-term anagenetic change in some characters is then the consequence of a succession of speciation events. I have briefly referred to this argument before (Futuyma 1986*a*, pp. 404, 406; Futuyma 1986*b*, p. 377), without having developed the reasoning, evidence, and contrasts with alternative hypotheses presented here.



Microevolutionary patterns

We now know that we can study evolution in real time

Average weight
16.06 g **17.13 g**
(1976) (1978)

Response to selection

**6.7% Δ body size in
1 generation
(2 years)**

**Let's assume only 1% is
evolutionary**




(Grant and Grant, 2002)



Let's do the calculations:

If a population increased by 1% every generation starting from ~16 g:

In 200 years  43 g

In 500 years  193 g

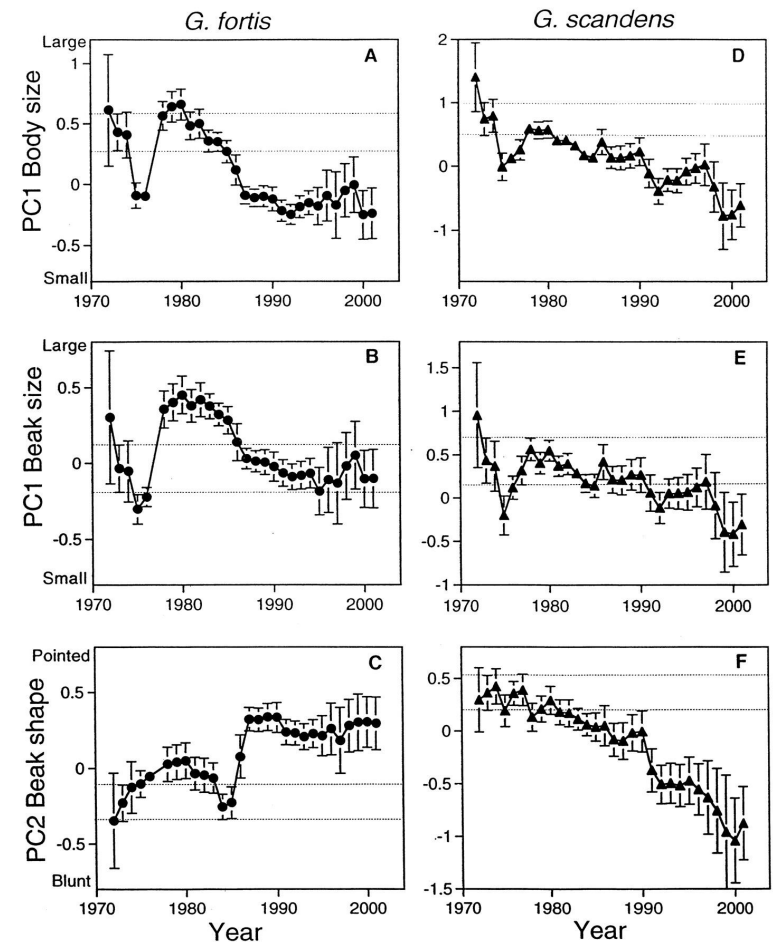
In 1,000 years  2.3 kg

In 2,000 years  335 kg

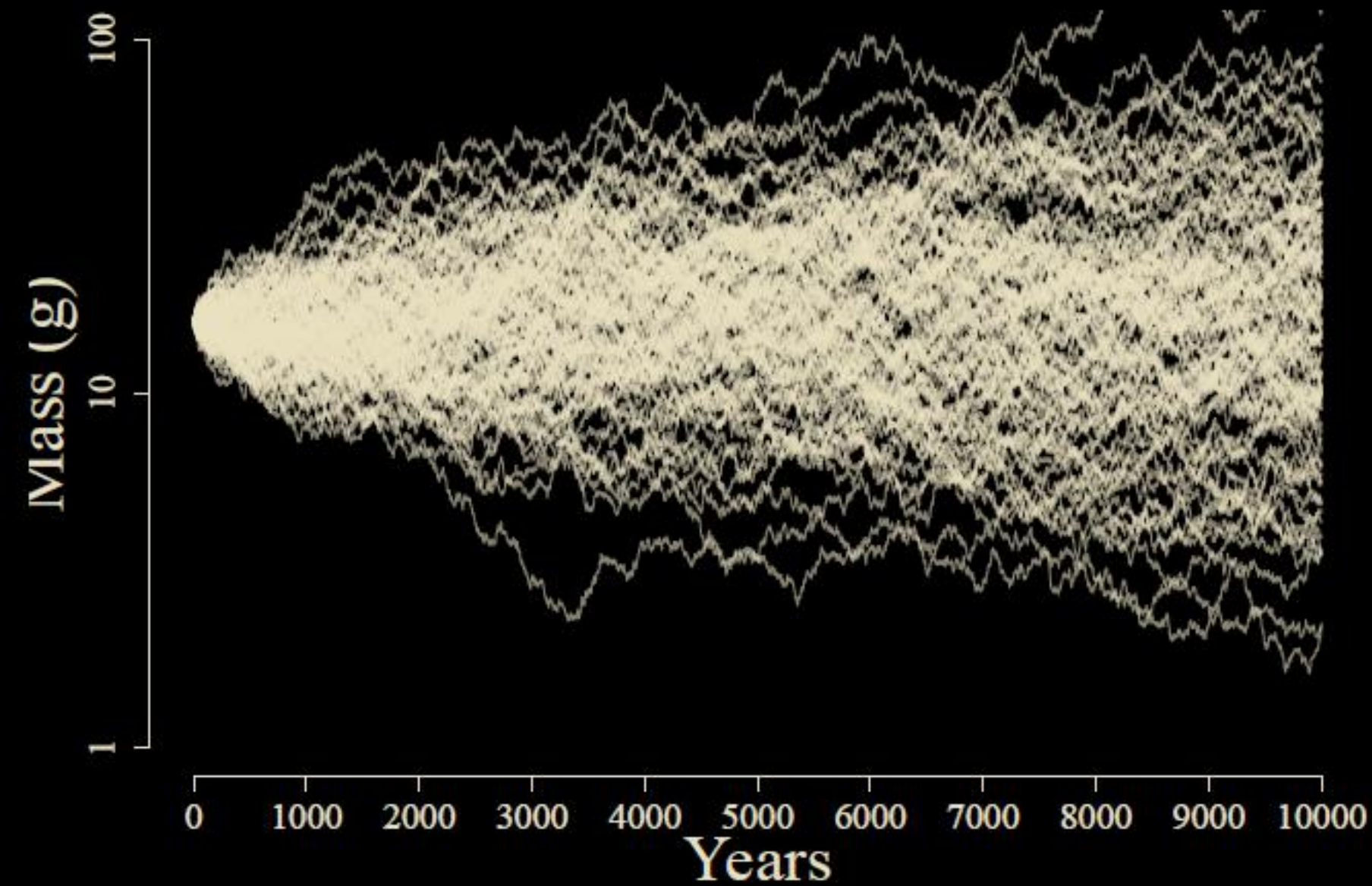
In 10,000 years  6.47×10^{19} kg

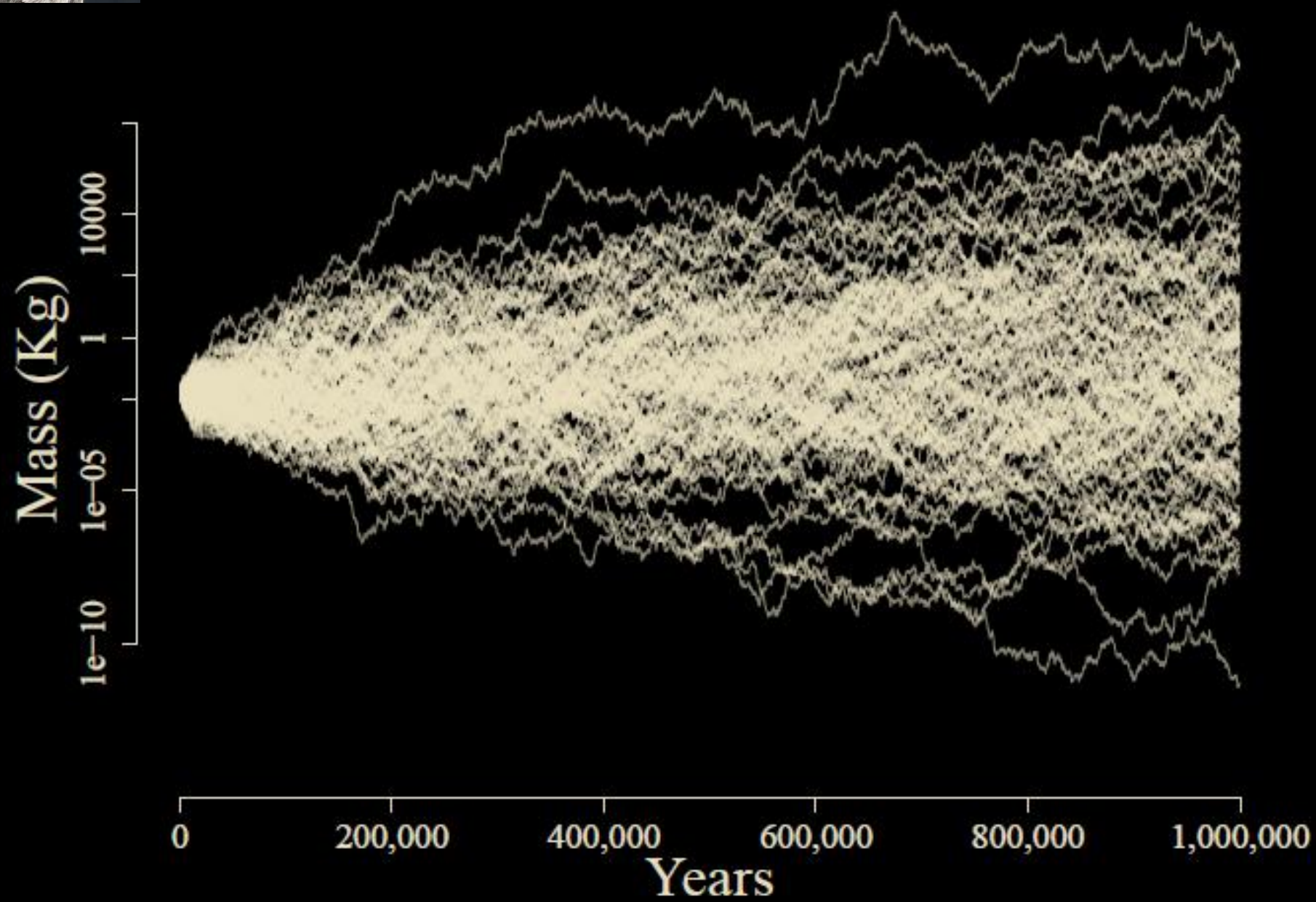
But evolution often reverses itself!

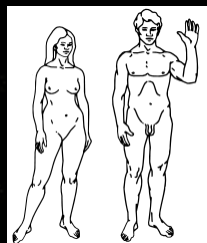
Let's instead simulate BM



(Grant and Grant, 2002)







Mass (Kg)

10000
1
1e-05
1e-10

0

200,000

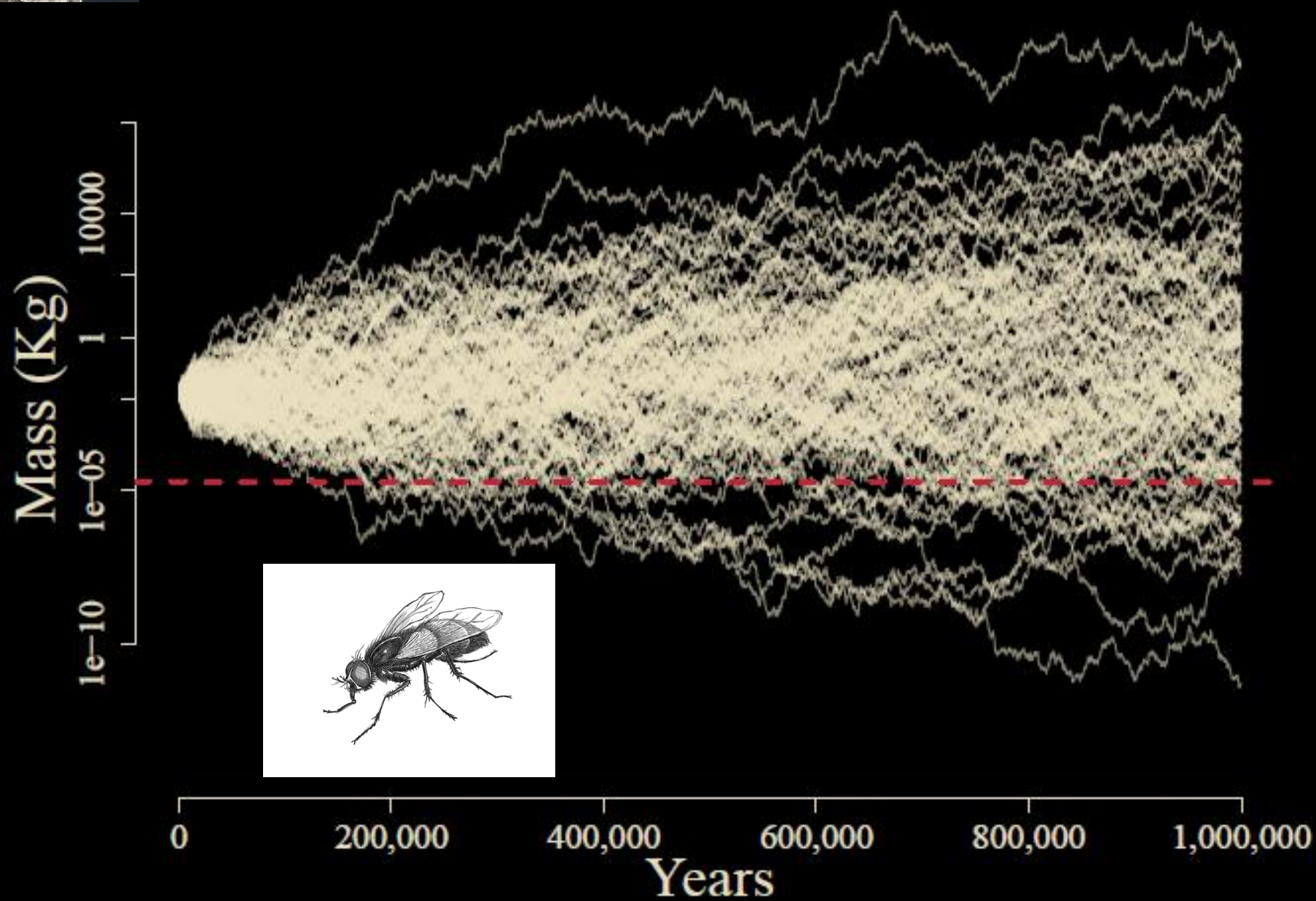
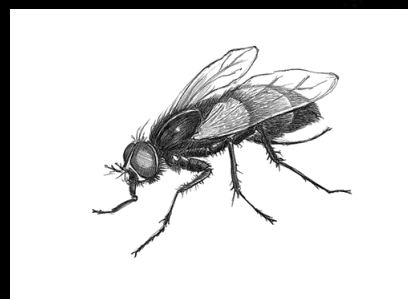
400,000

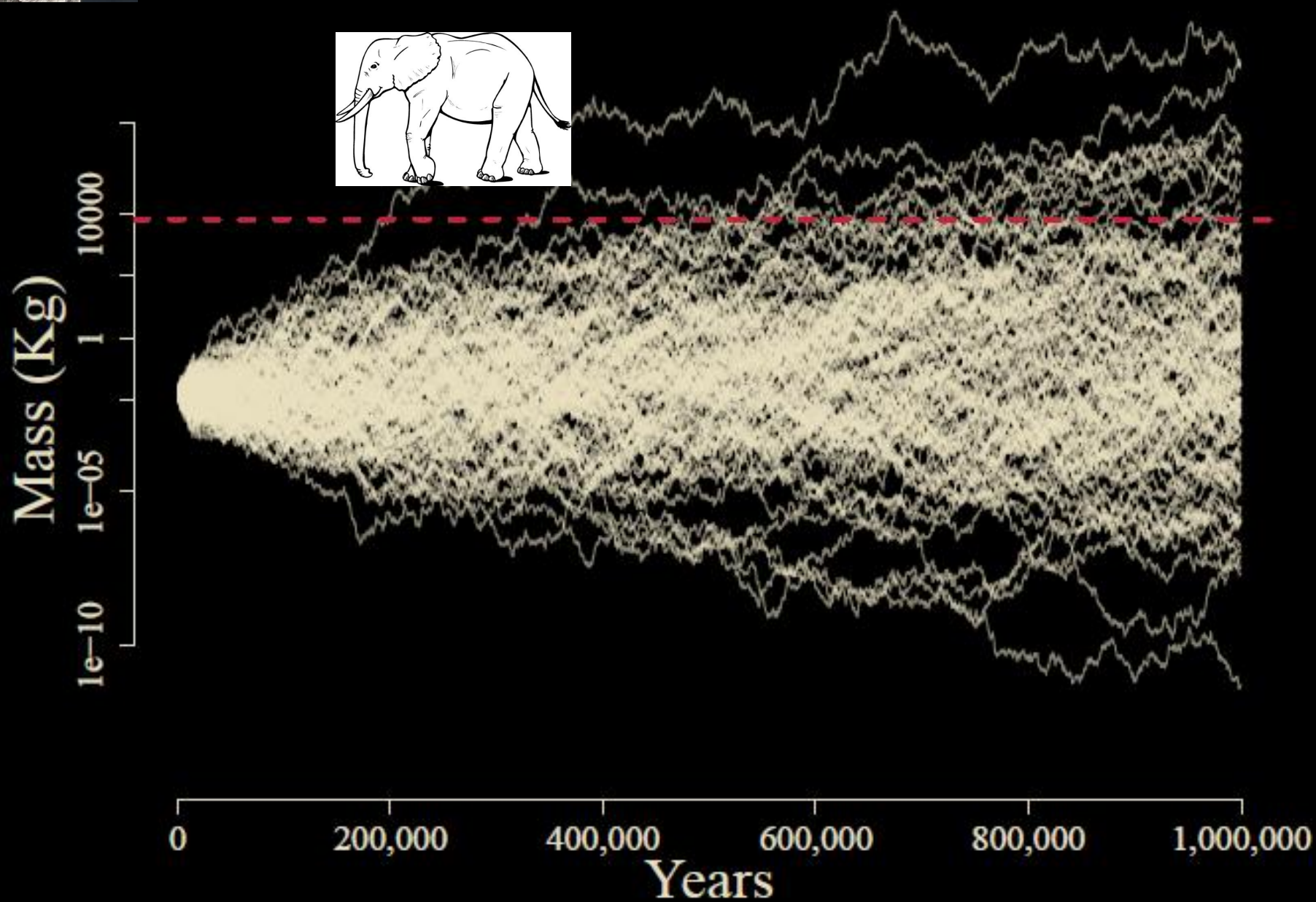
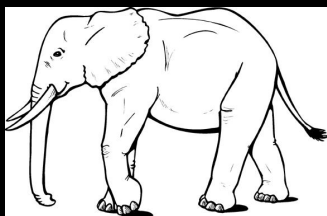
600,000

800,000

1,000,000

Years





The Breeder's Equation

$$\Delta z = V_G * \beta$$

**Response to
selection**

**Genetic
variance
for trait**

**Selection gradient
(slope of adaptive
landscape)**

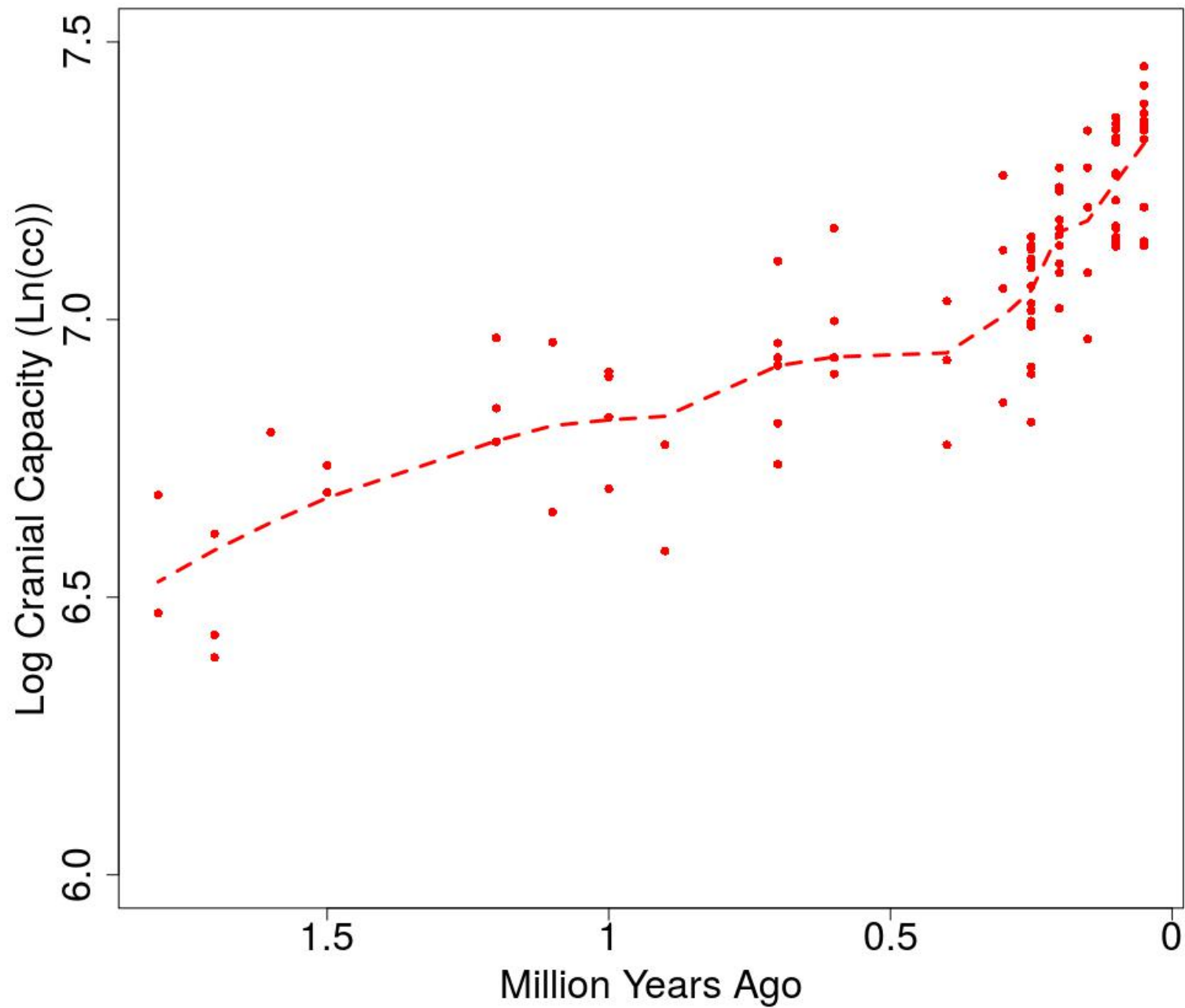
Genetic Drift (BM)

$$\Delta z = \text{sqrt}(V_G/Ne) * dW$$

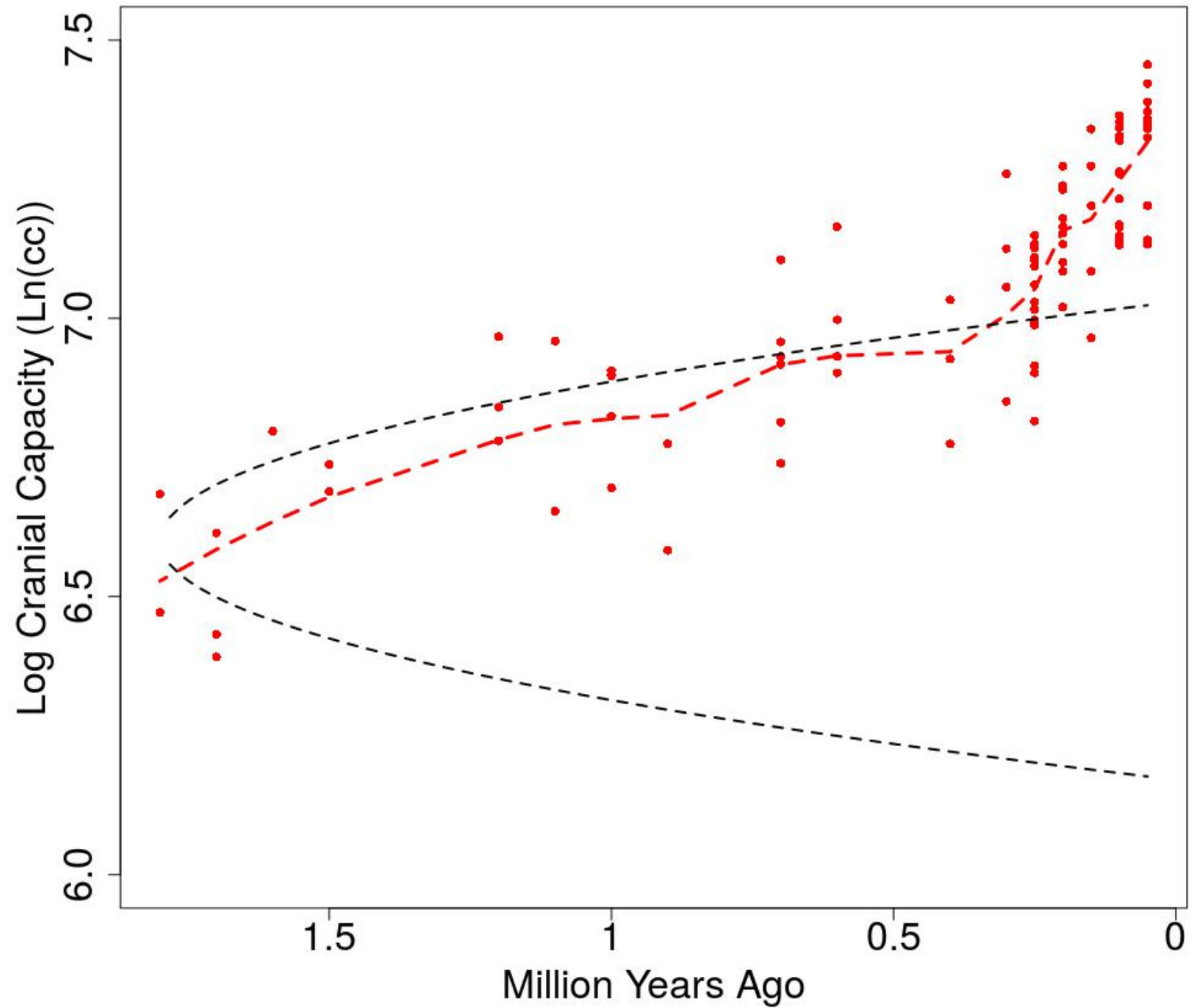
Both processes together
(OU)

$$\Delta z = V_G \beta + \text{sqrt}(V_G / N_e) dW$$

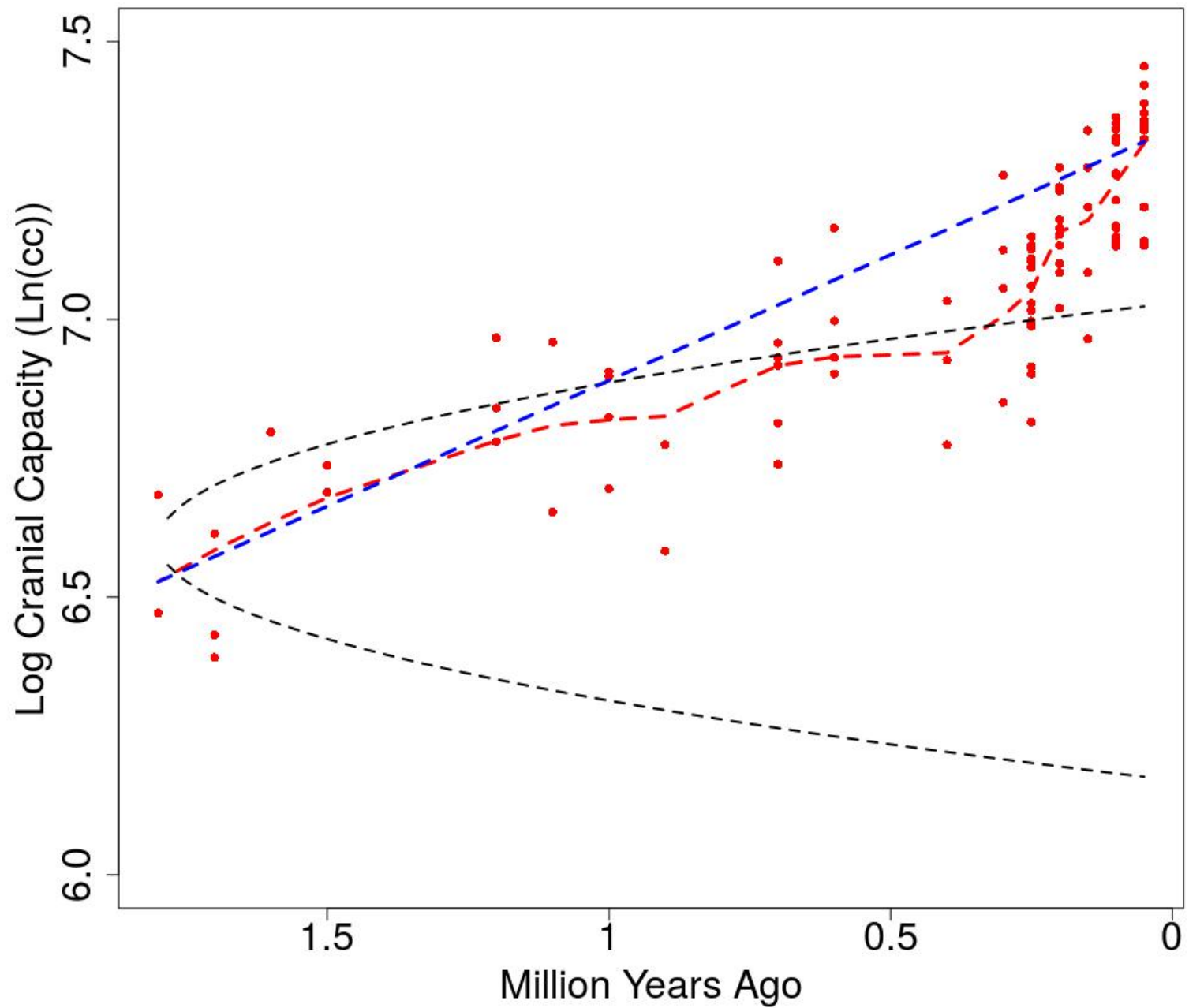
Human Cranial Capacity (past 2 million years)



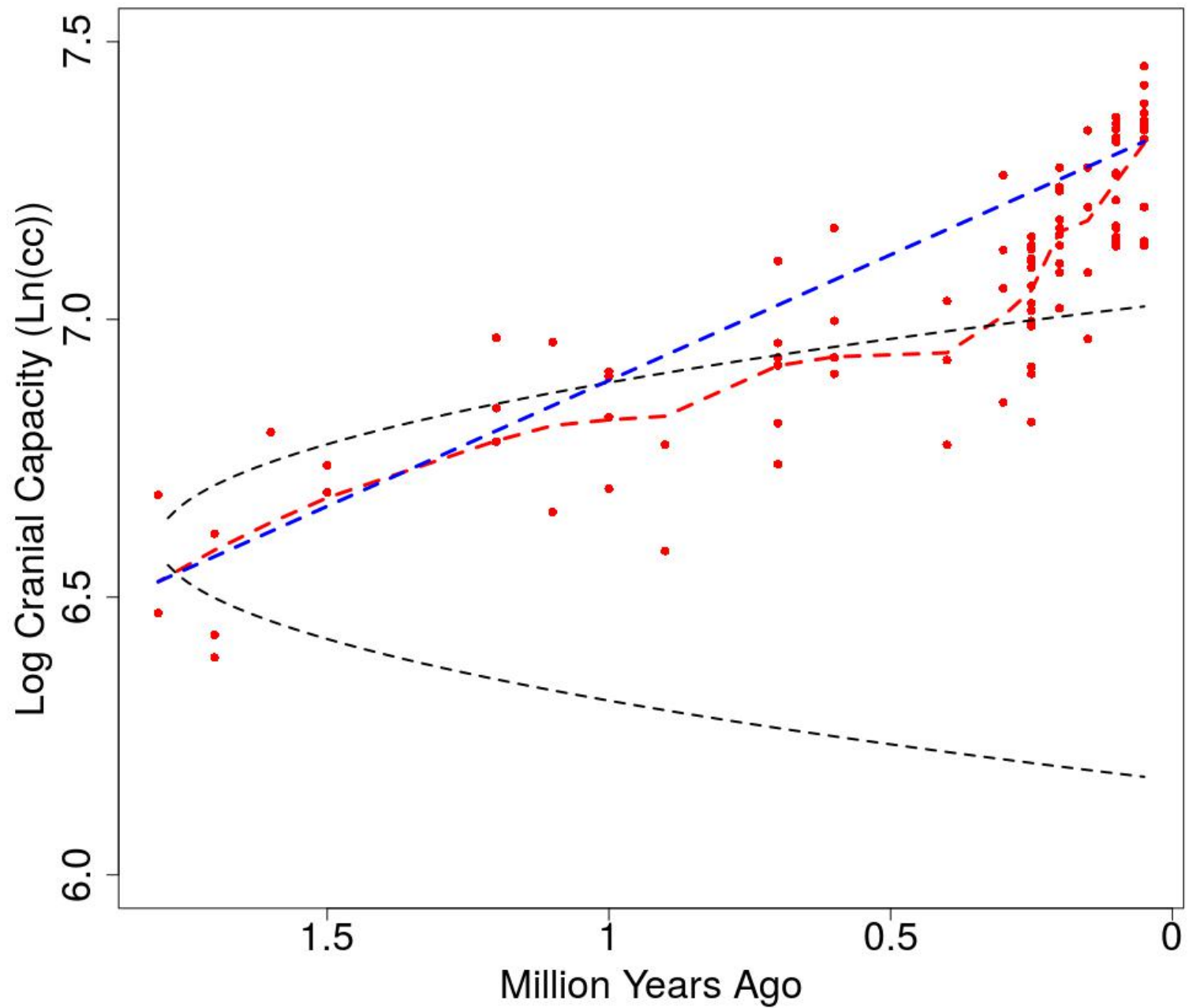
Human Cranial Capacity evolving by Genetic Drift



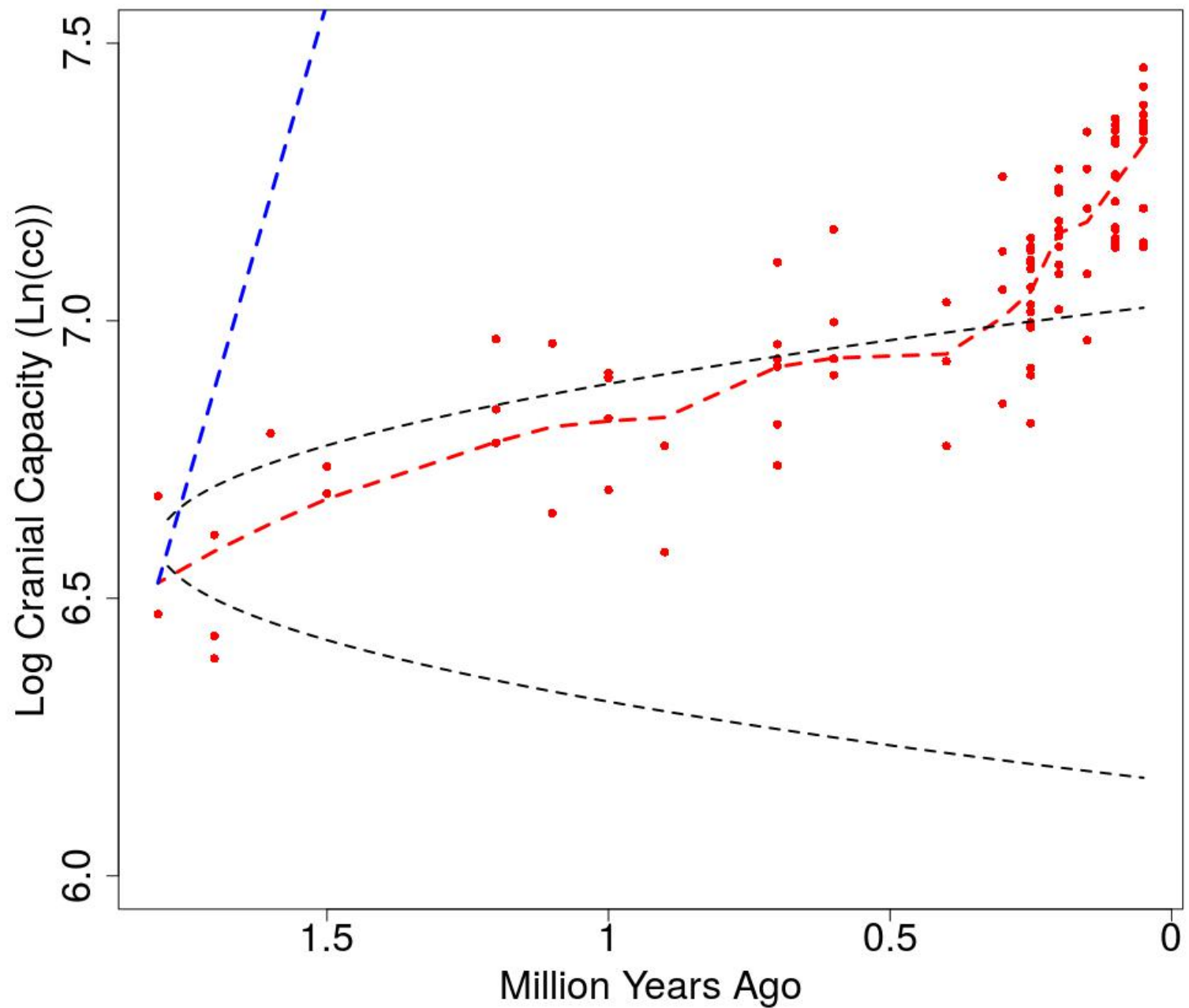
Increase cranial capacity 0.00058868 % per generation



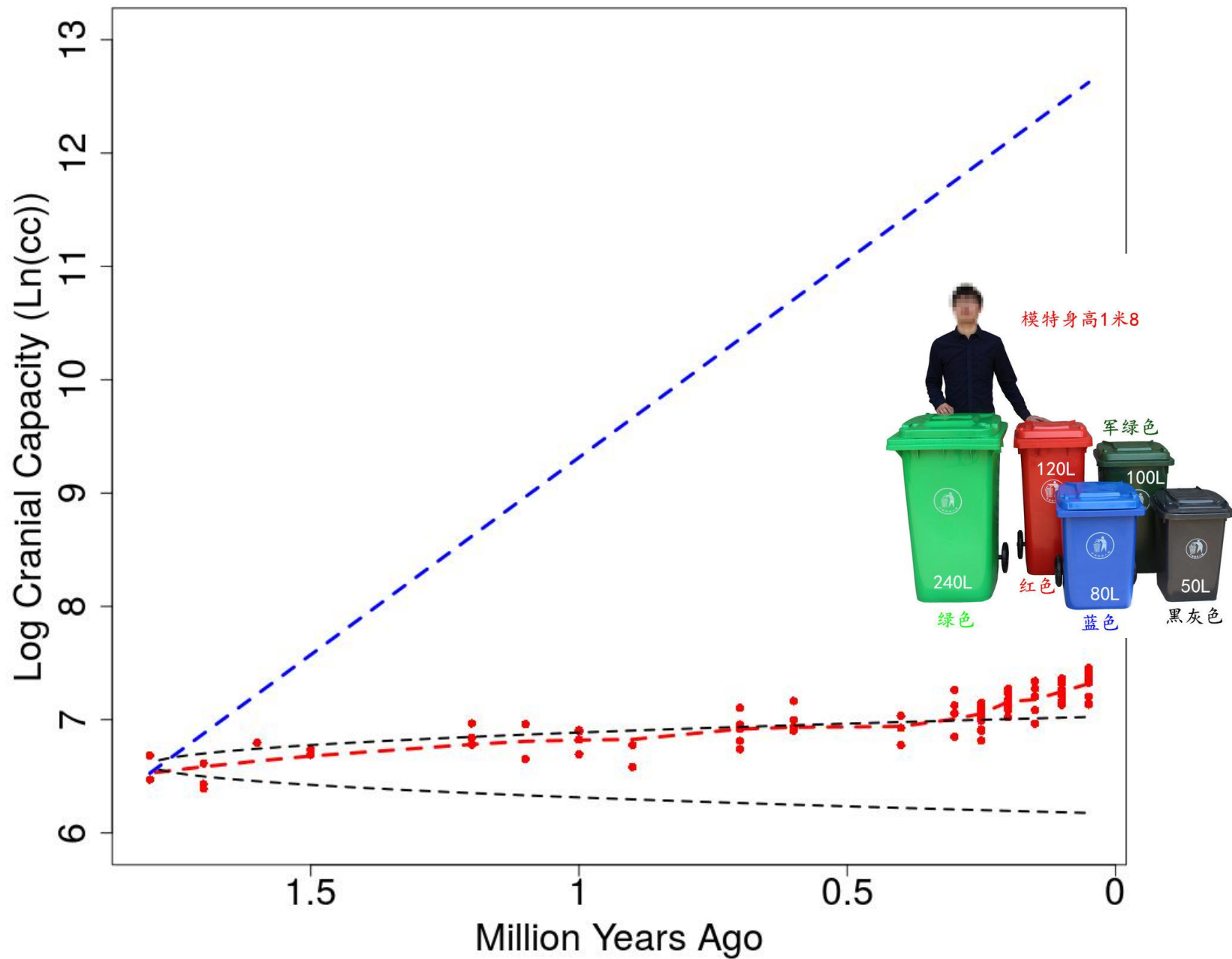
Increase cranial capacity 0.00058868 % per generation



Increase cranial capacity 0.0045284 % per generation



Increase cranial capacity 0.0045284 % per generation



The Paradox of Stasis (Hansen & Houle 2004):
Organisms seem to be able to evolve far more than they ever do

Empirical studies often find:

Strong (and often persistent) directional selection

(Hereford et al. 2004, Morrissey & Hadfield 2012)

High levels of additive genetic variance

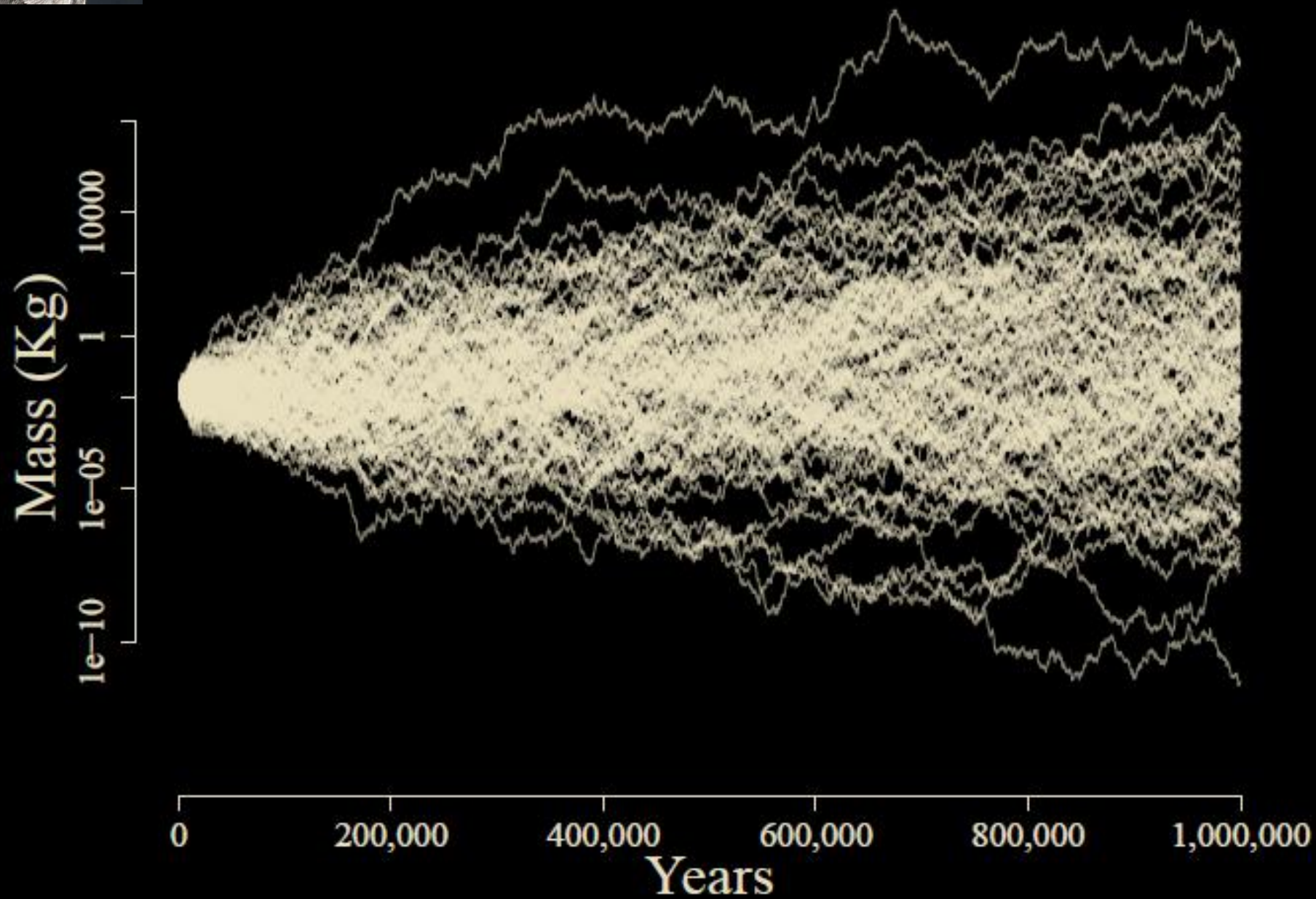
(Mousseau & Roff 1987, Houle 1992)

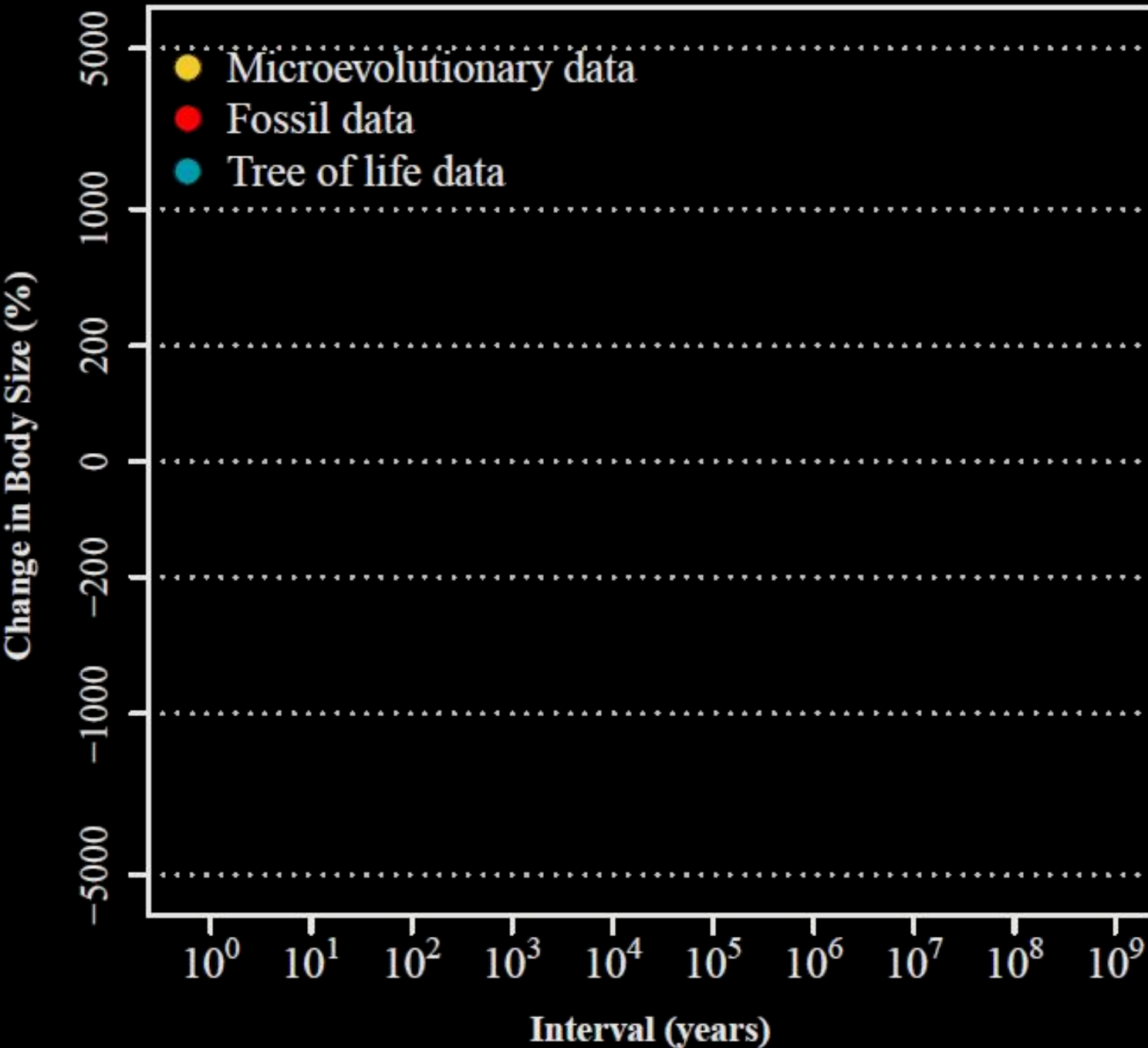
Rapid evolutionary rates

(Hendry & Kinnison 1999, Kinnison & Hendry 2002)

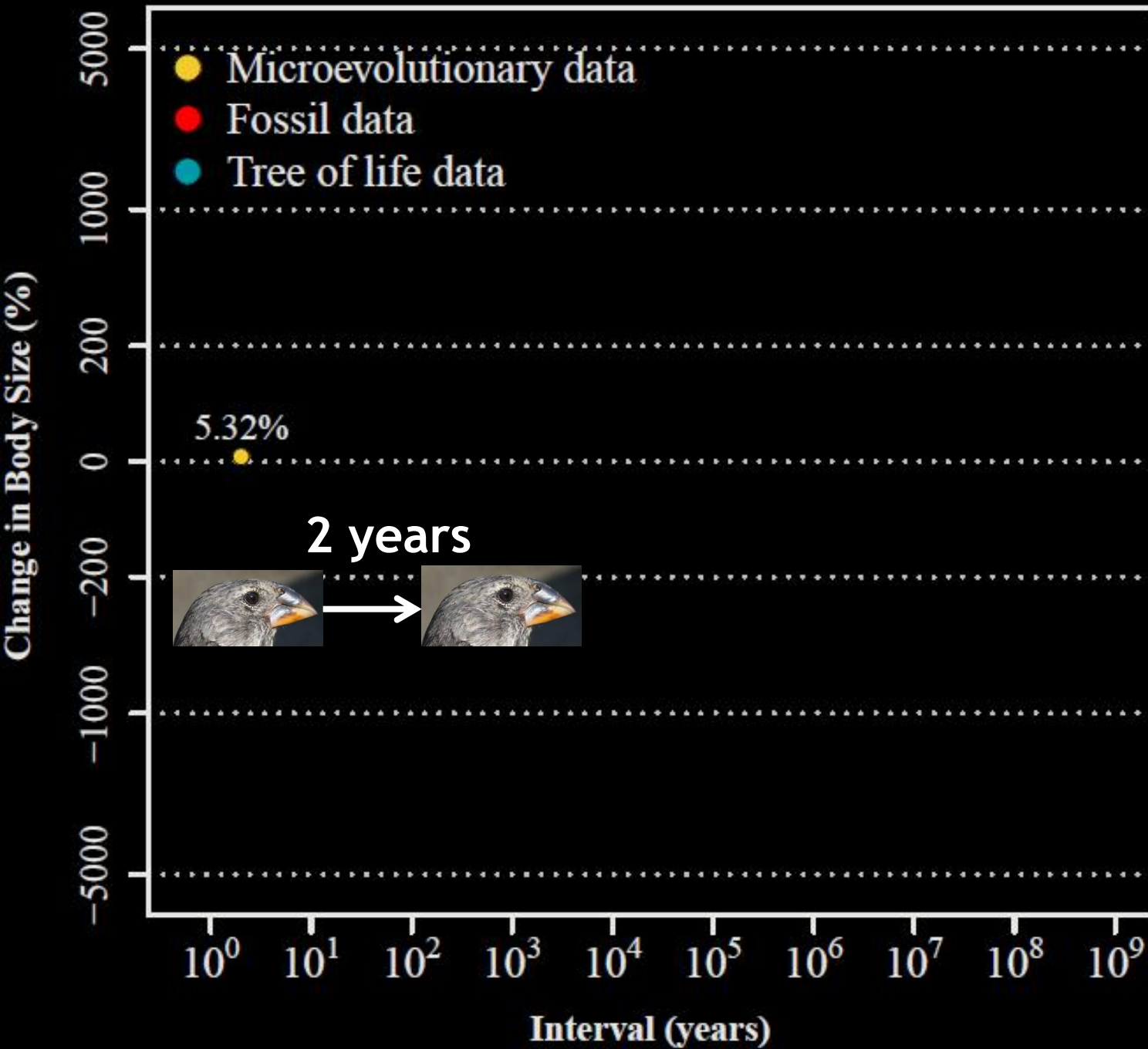
...yet stasis in the fossil record

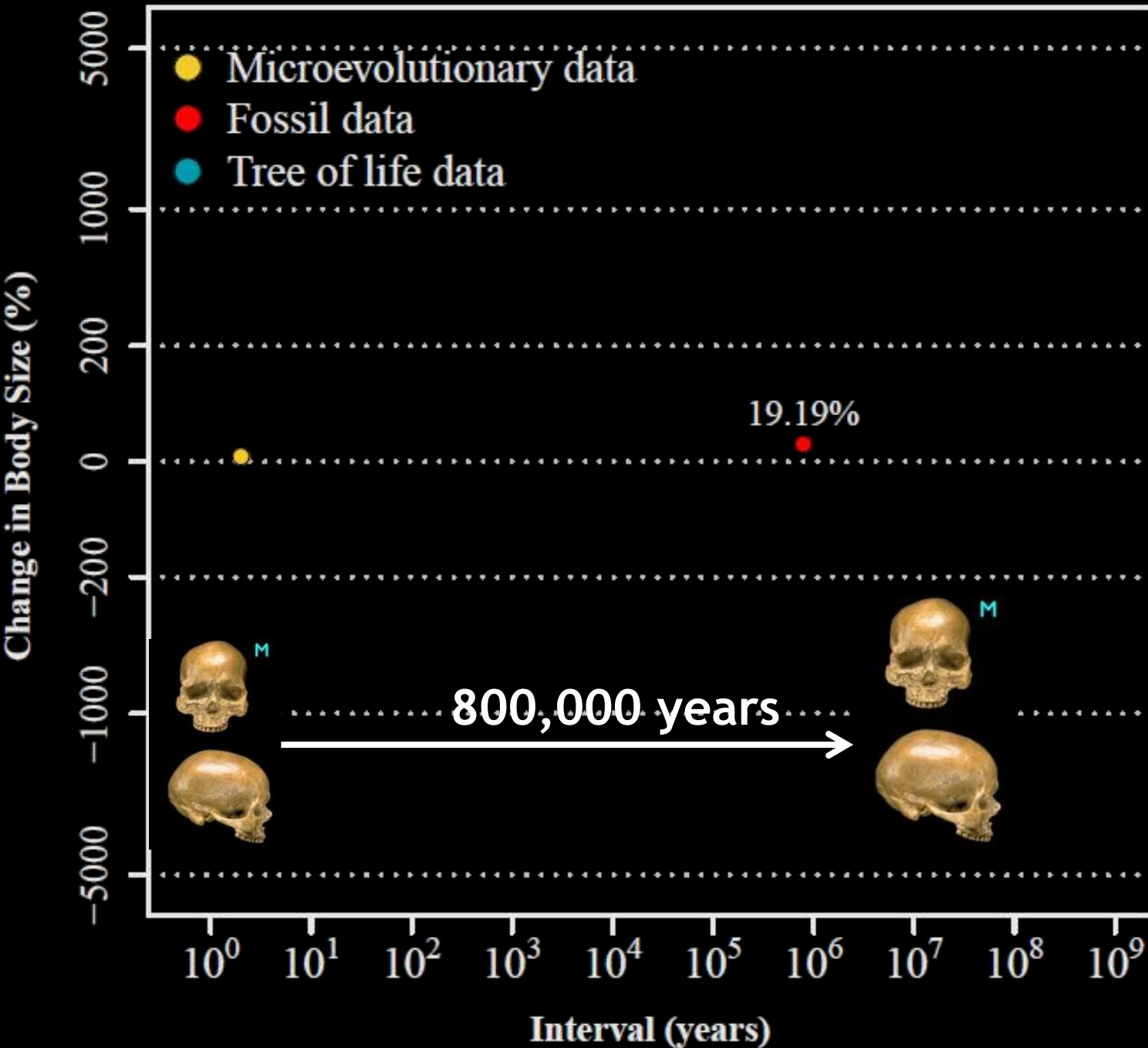
(Gingerich 1983, 2002)



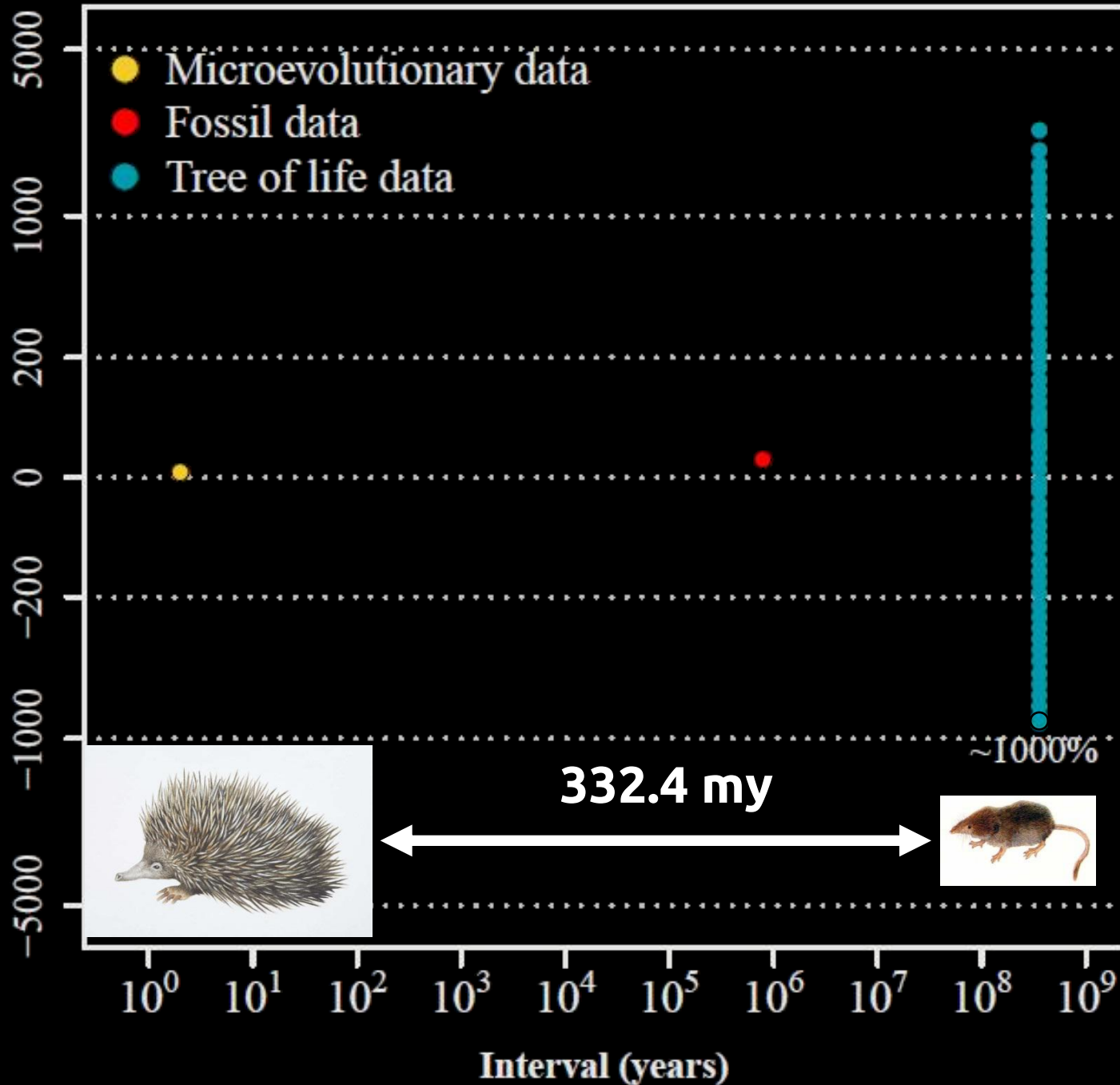


Uyeda et al.,
PNAS, 2011

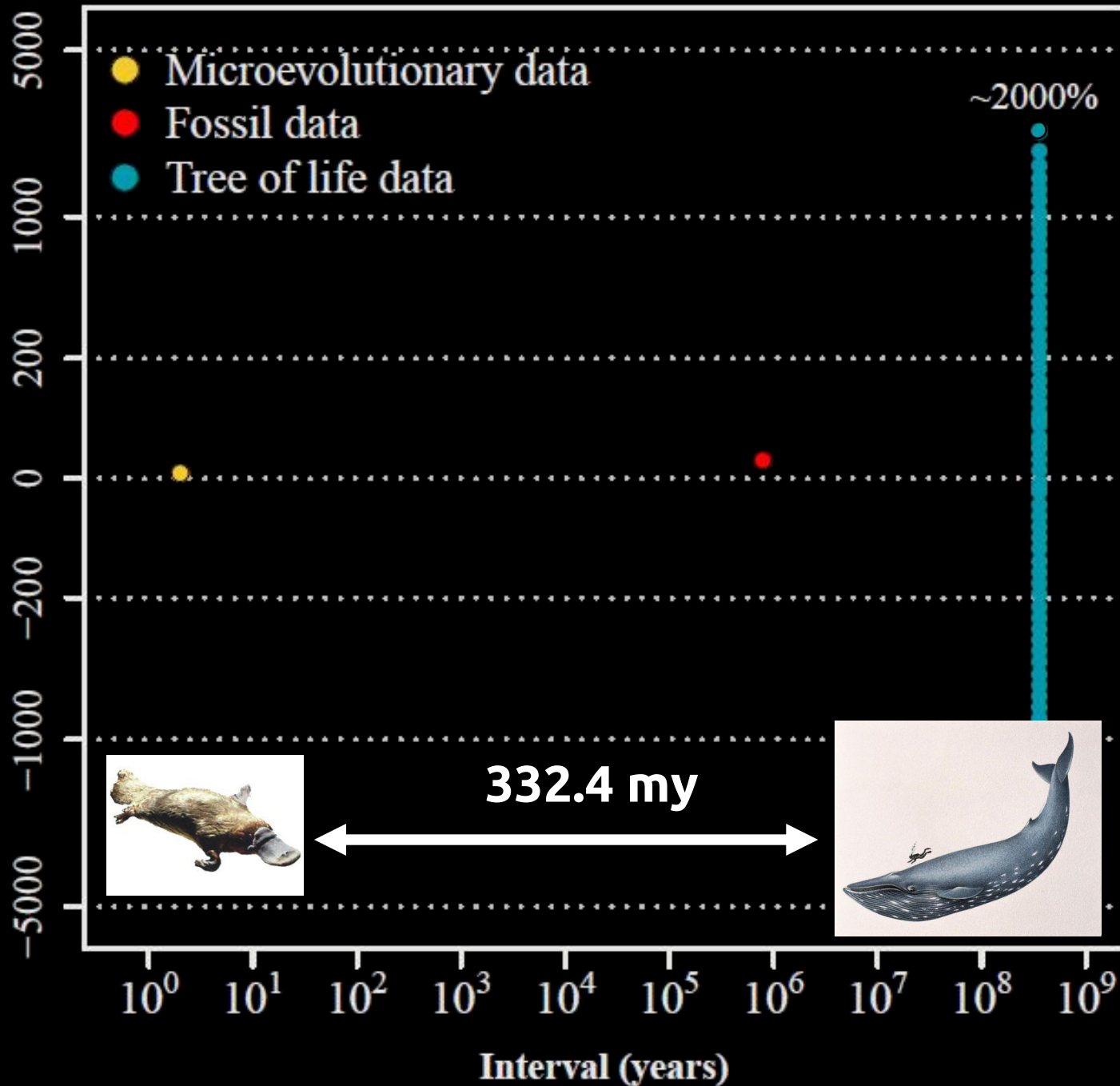




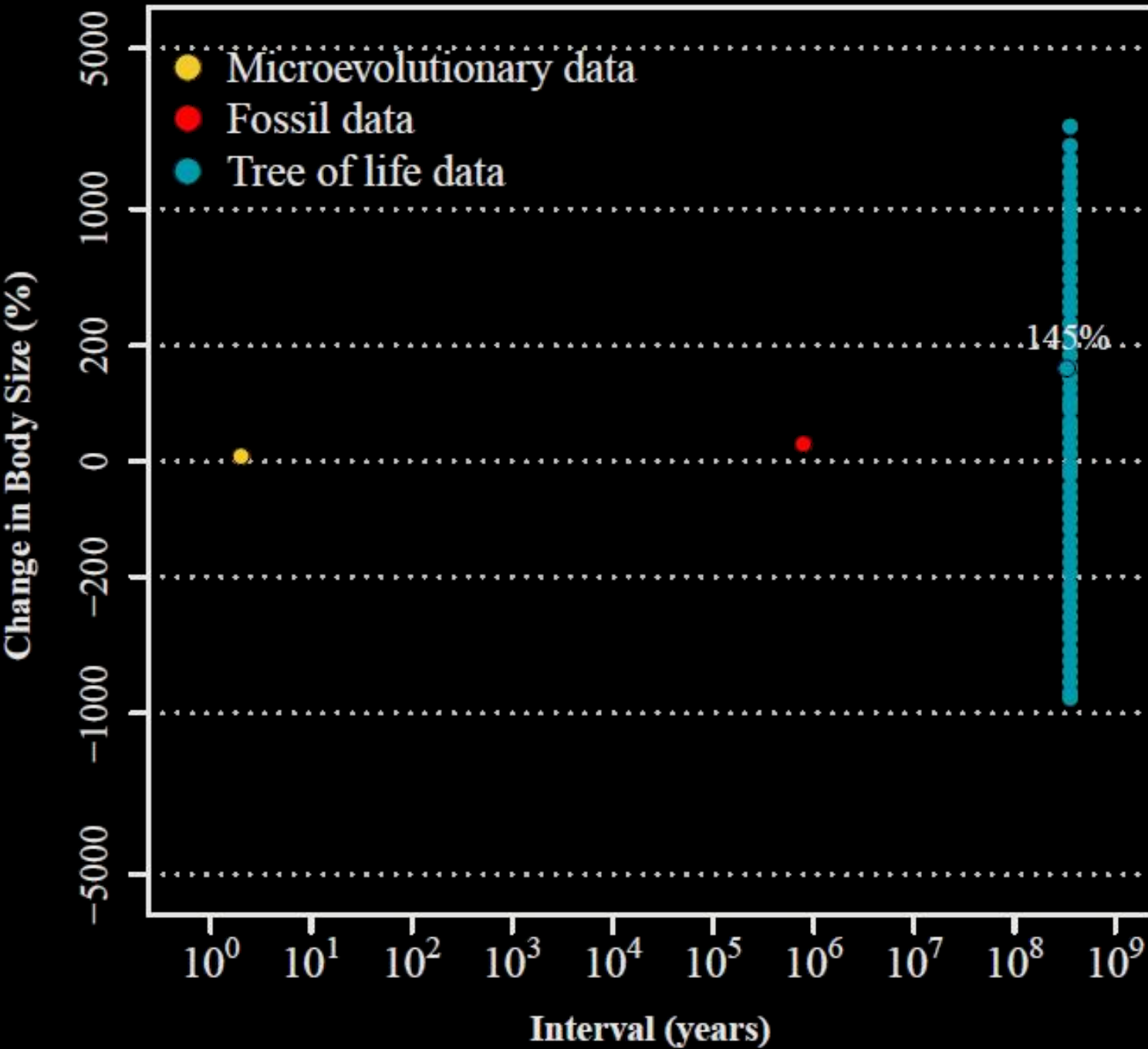
Change in Body Size (%)

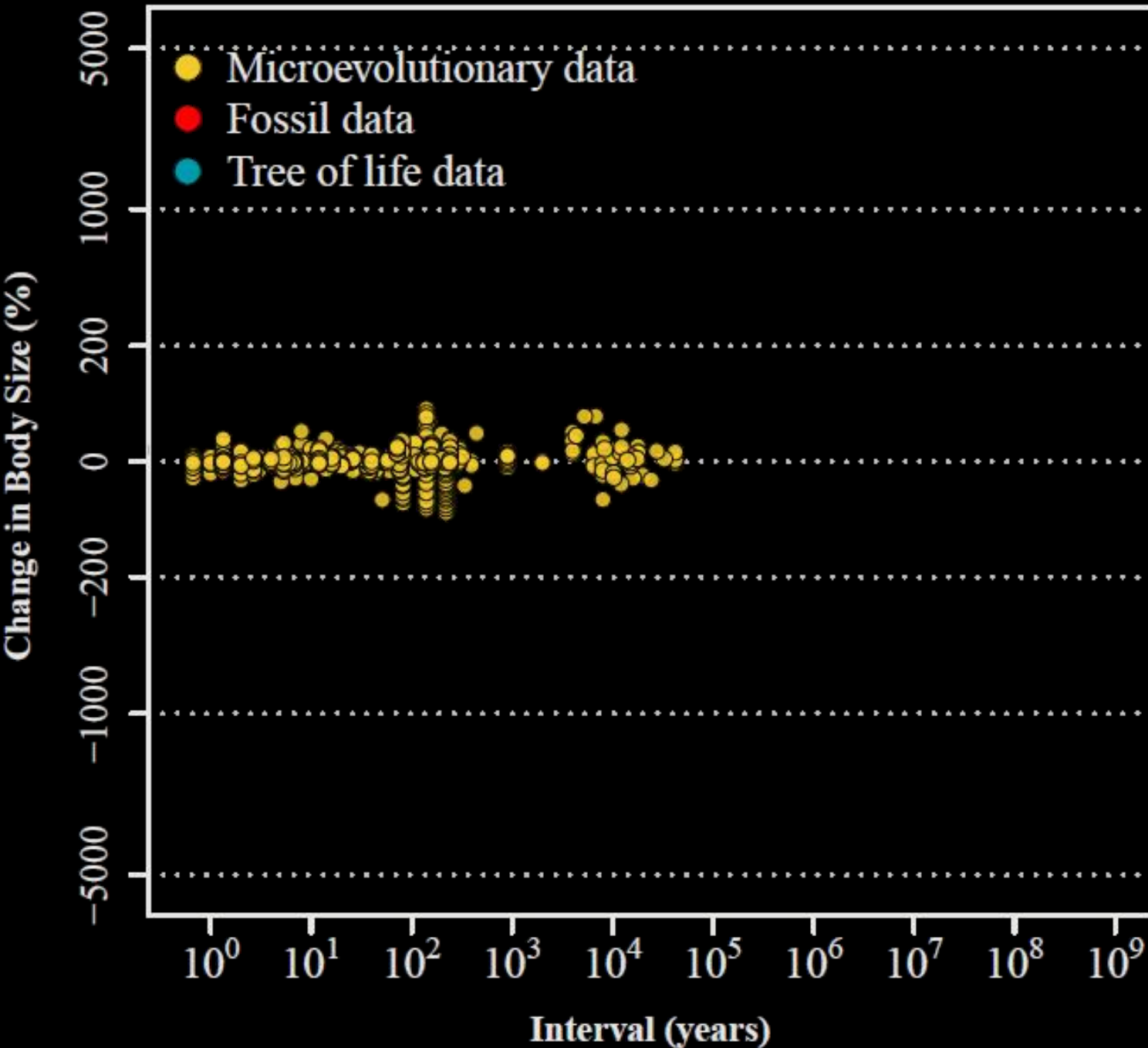


Change in Body Size (%)

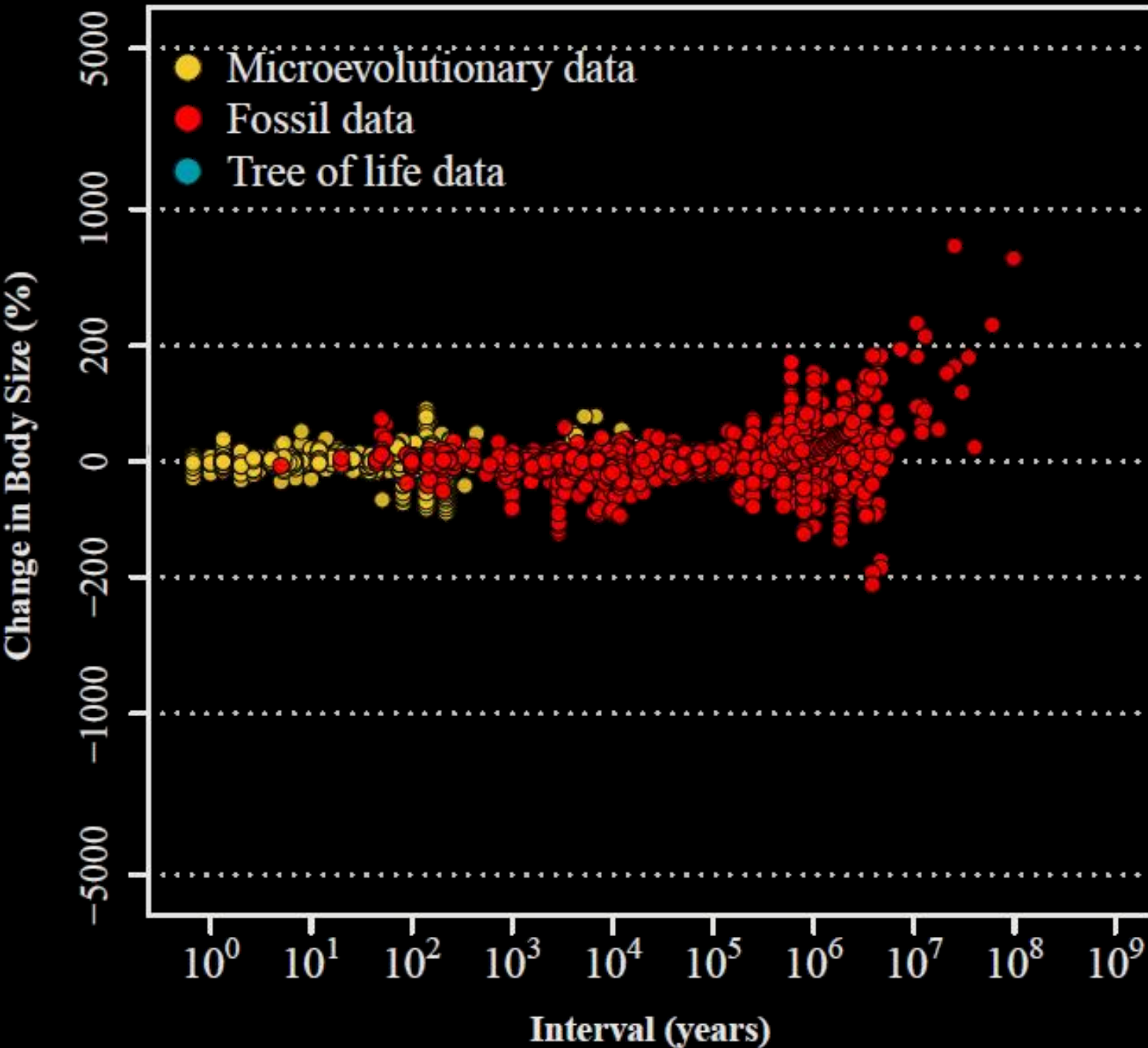


Uyeda et al.,
PNAS, 2011



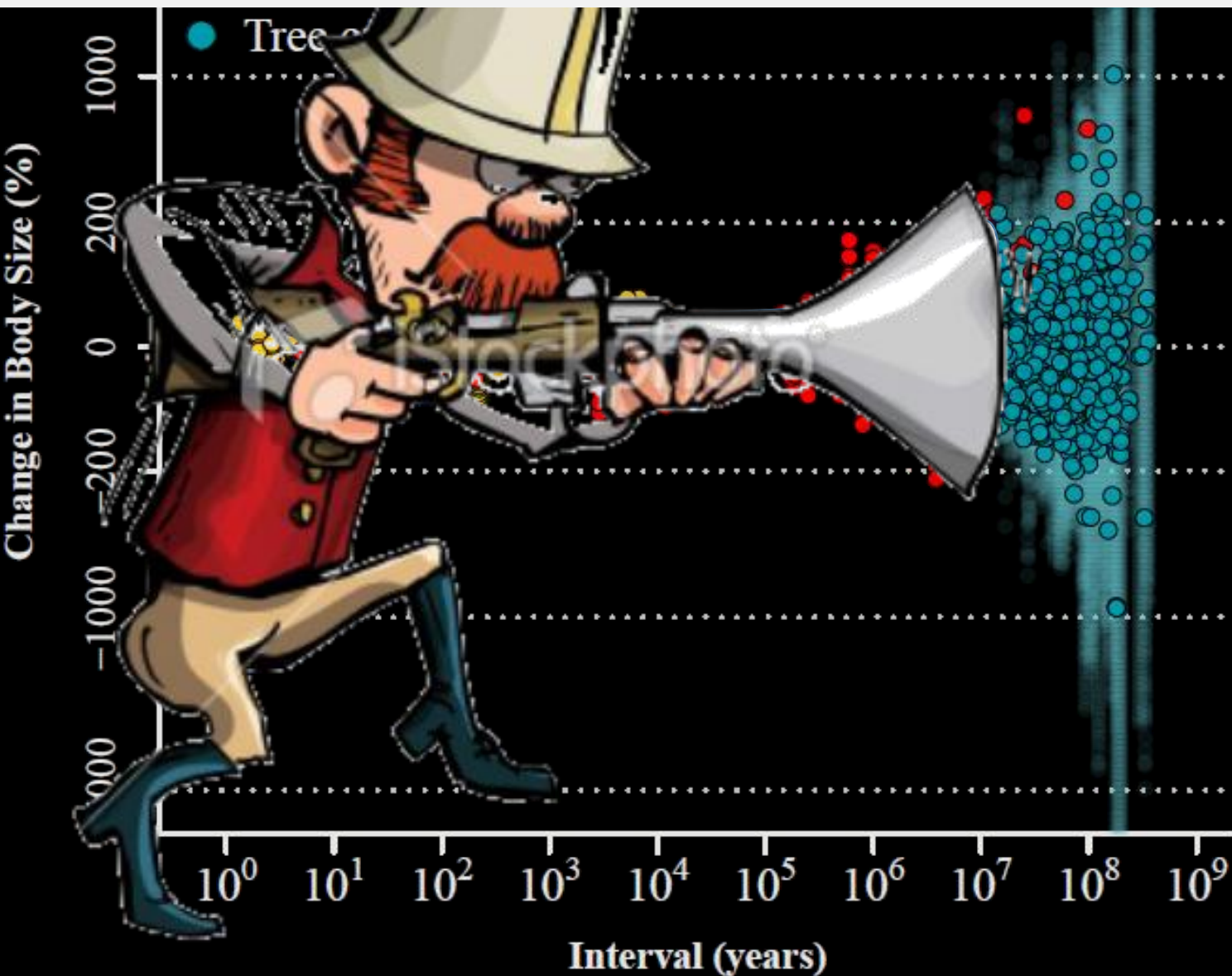


Uyeda et al.,
PNAS, 2011



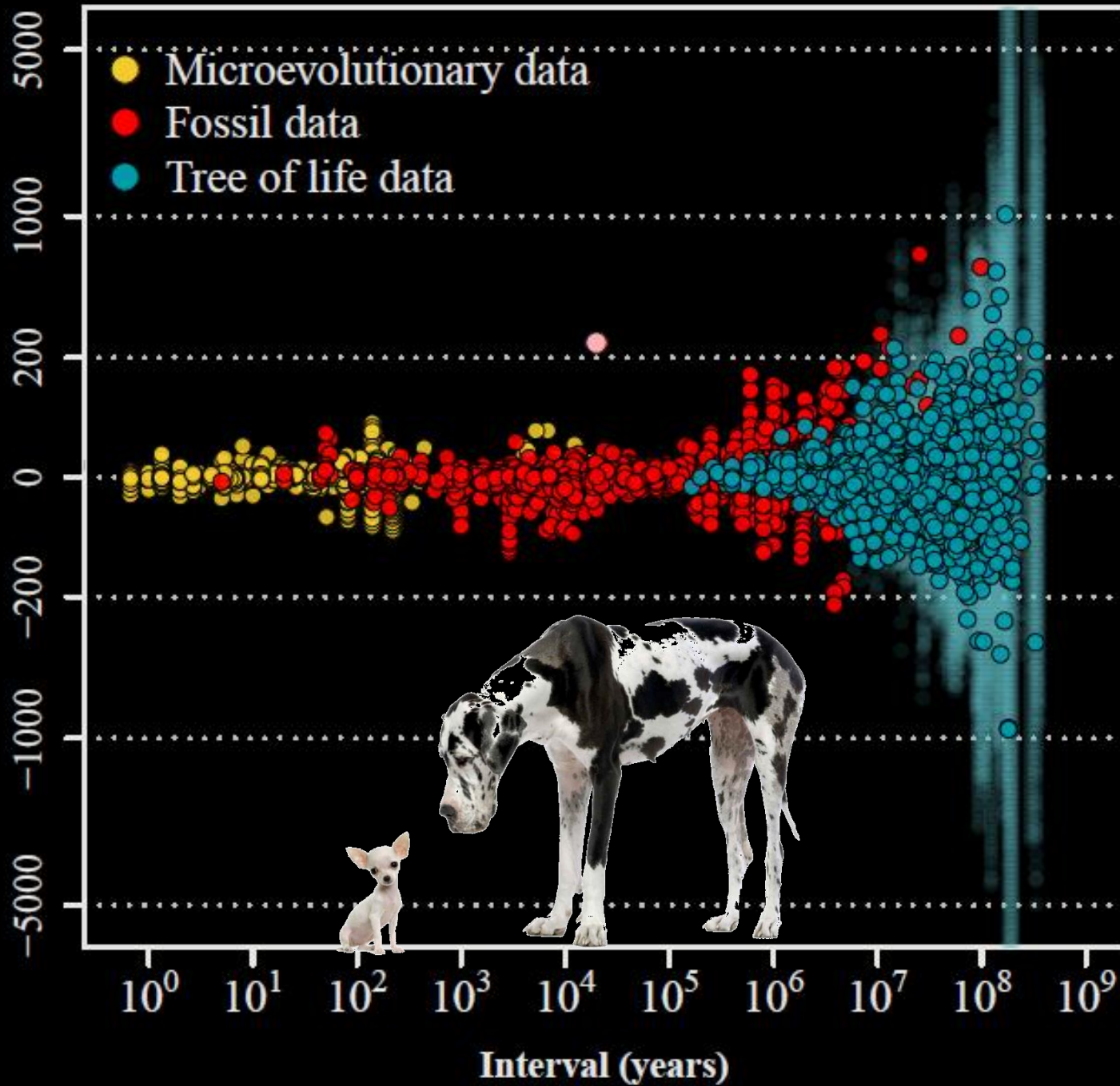
Uyeda et al.,
PNAS, 2011

"The Evolutionary Blunderbuss"



Uyeda et al.,
PNAS, 2011

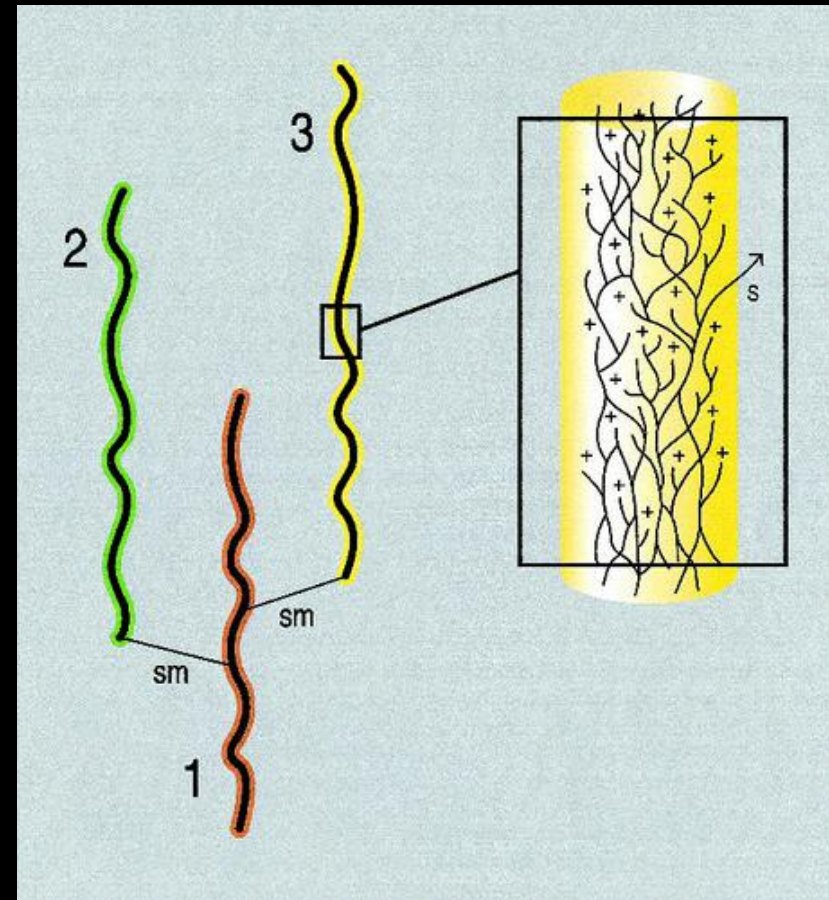
Change in Body Size (%)



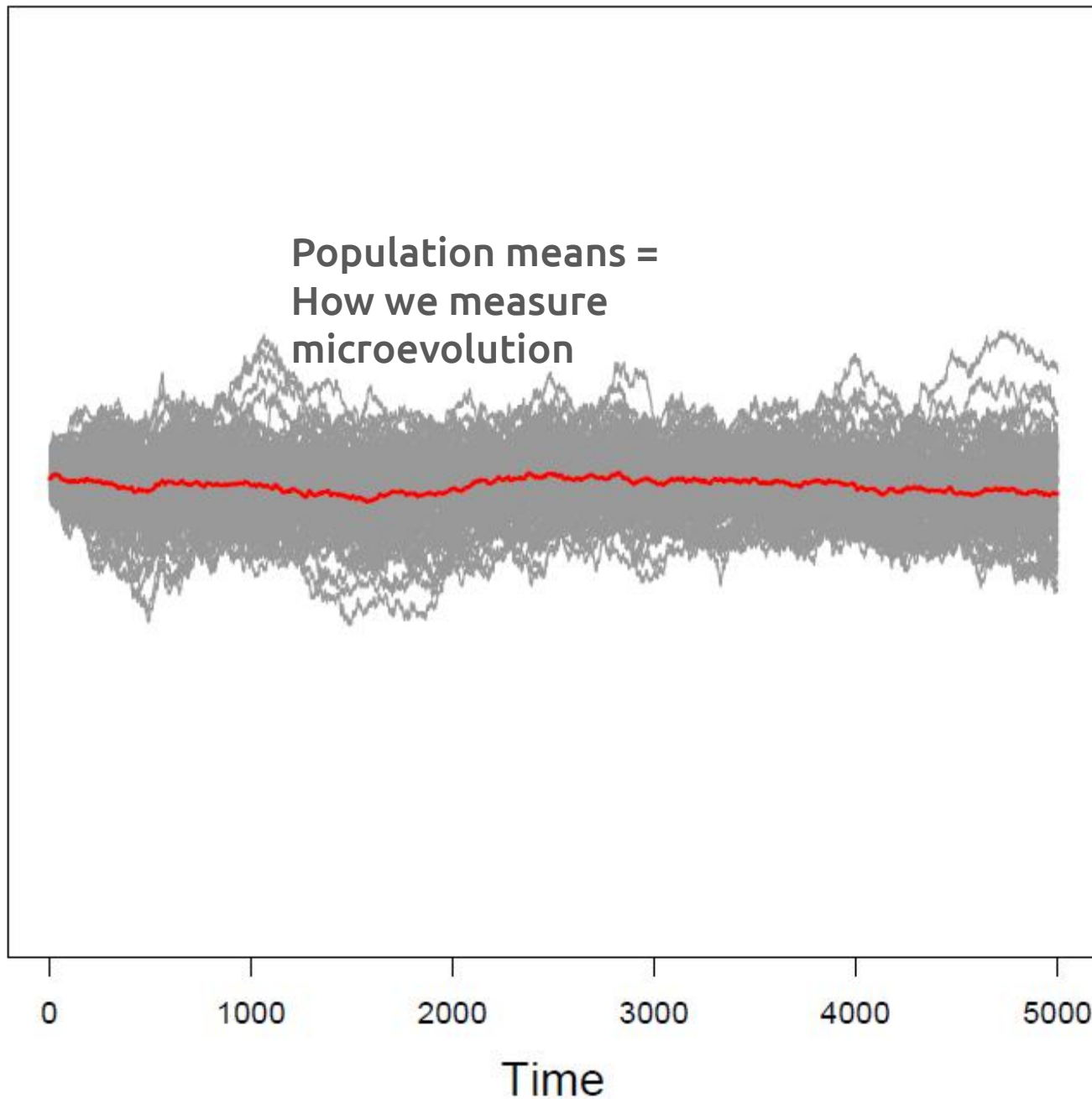
Uyeda et al.,
PNAS, 2011

Eldredge, et al. 2005. *The dynamics of evolutionary stasis*. *Paleobiology*.

Bartoszek et al. 2017. *Using the Ornstein-Uhlenbeck process to model the evolution of interacting populations*, *J. of Theoretical Biology*

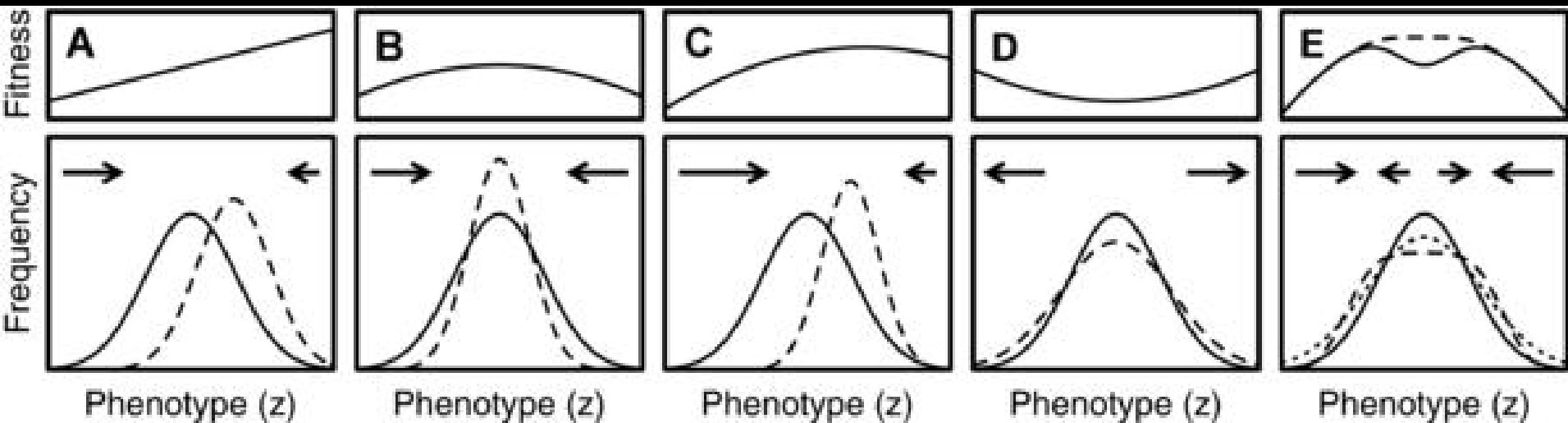


Population means =
How we measure
microevolution

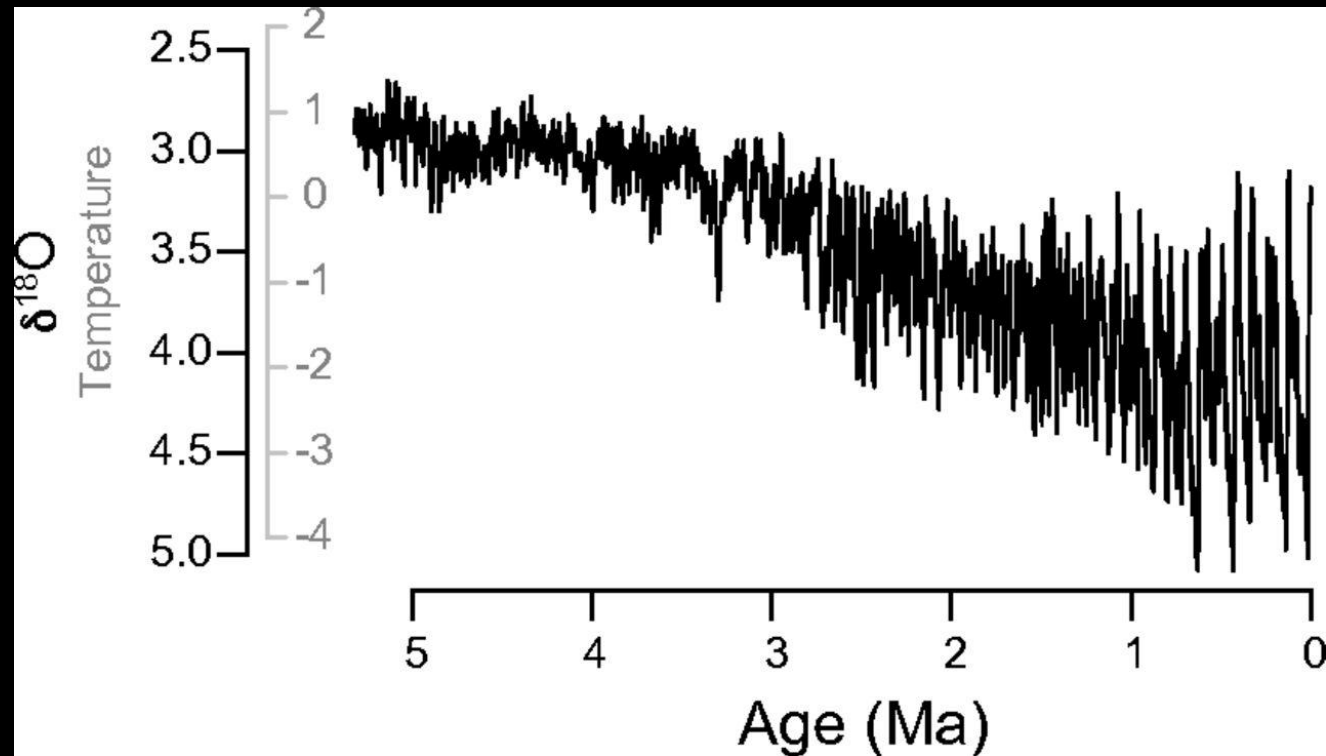


Species means =
How we measure
macroevolution

Haller & Hendry. 2014. *Solving the paradox of stasis: Squashed stabilizing selection and the limits of detection, Evolution*



Hunt et al. 2015. *Simple vs complex models of trait evolution and stasis as a response to environmental change, PNAS*



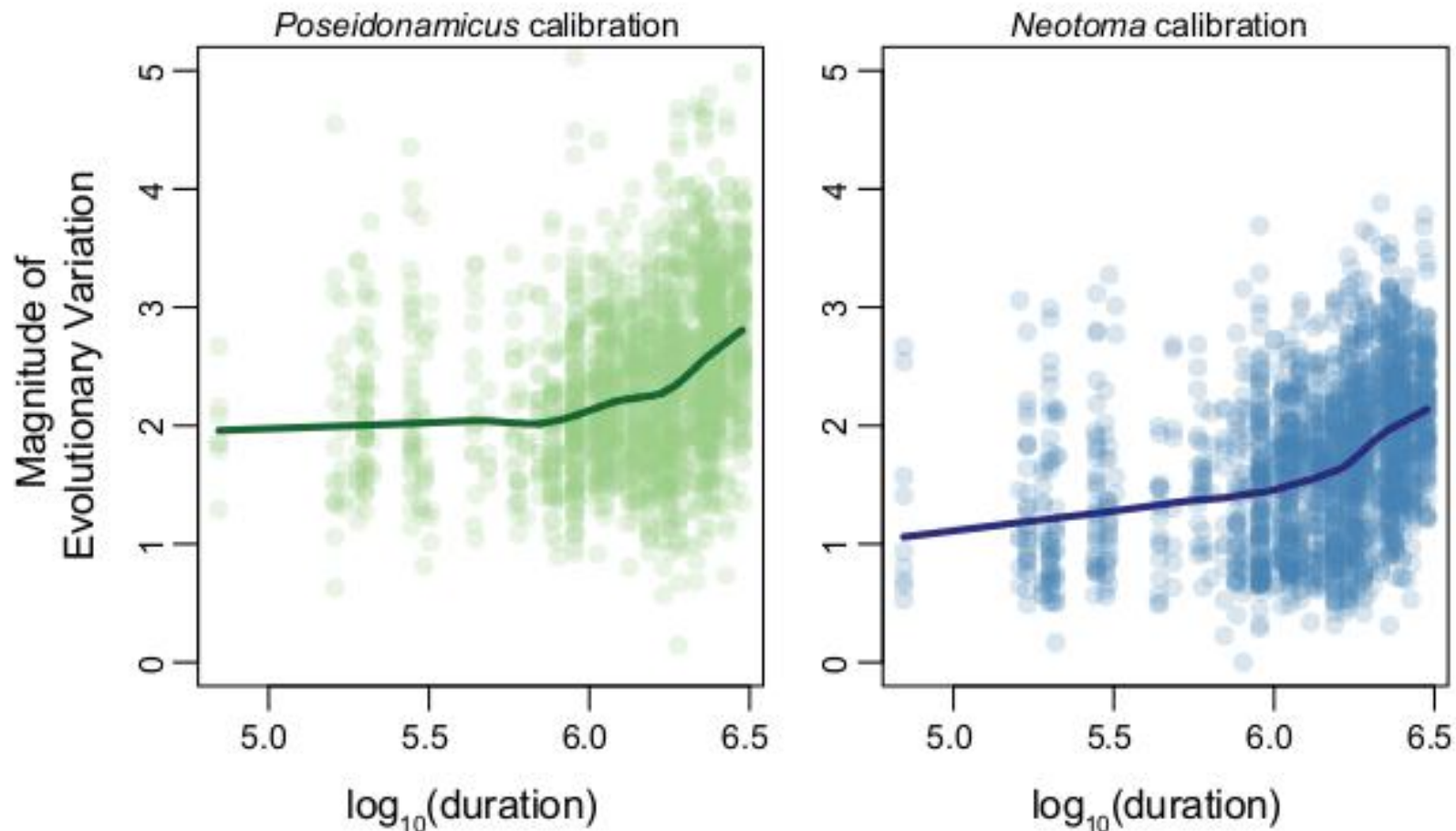
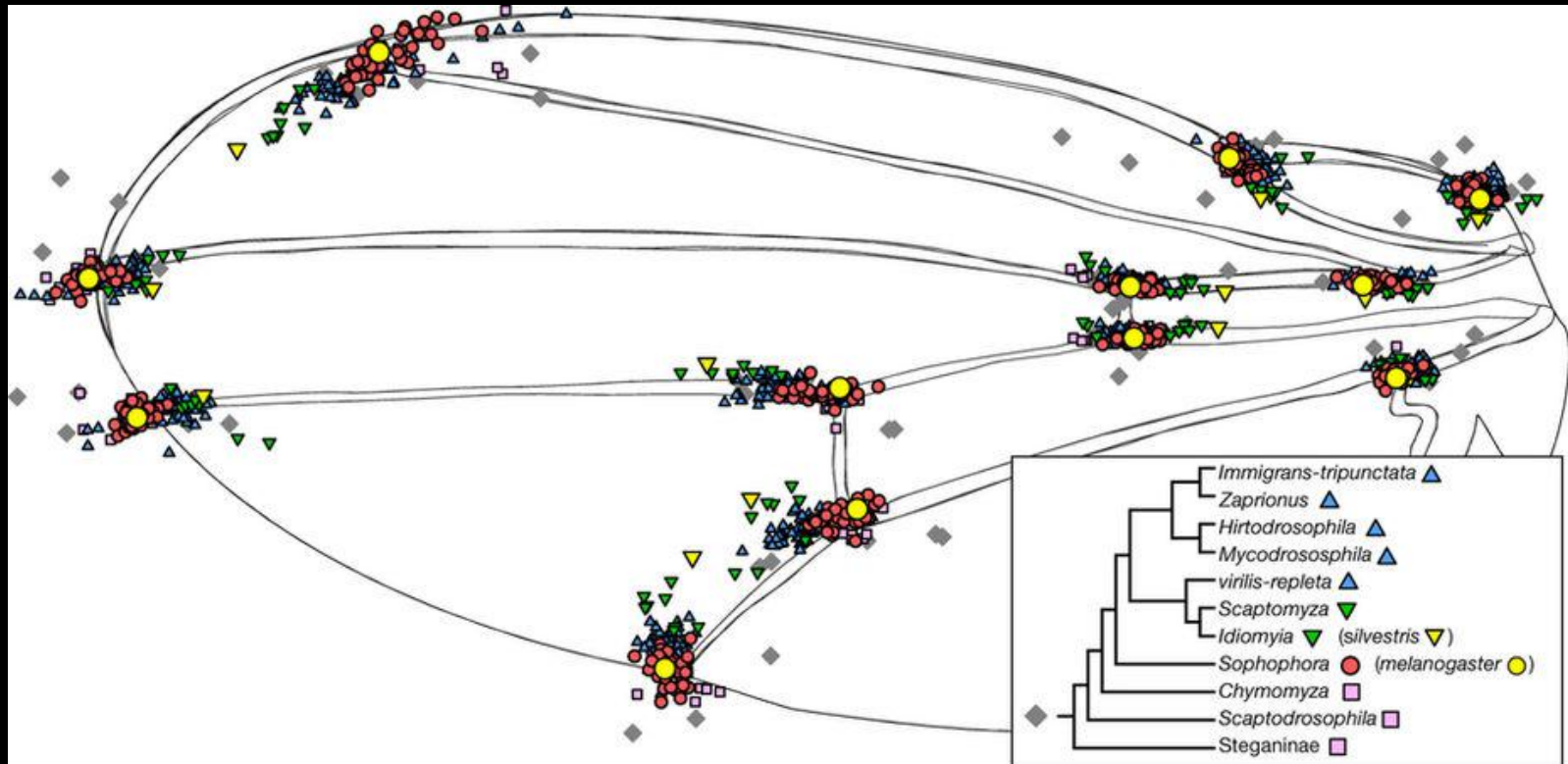


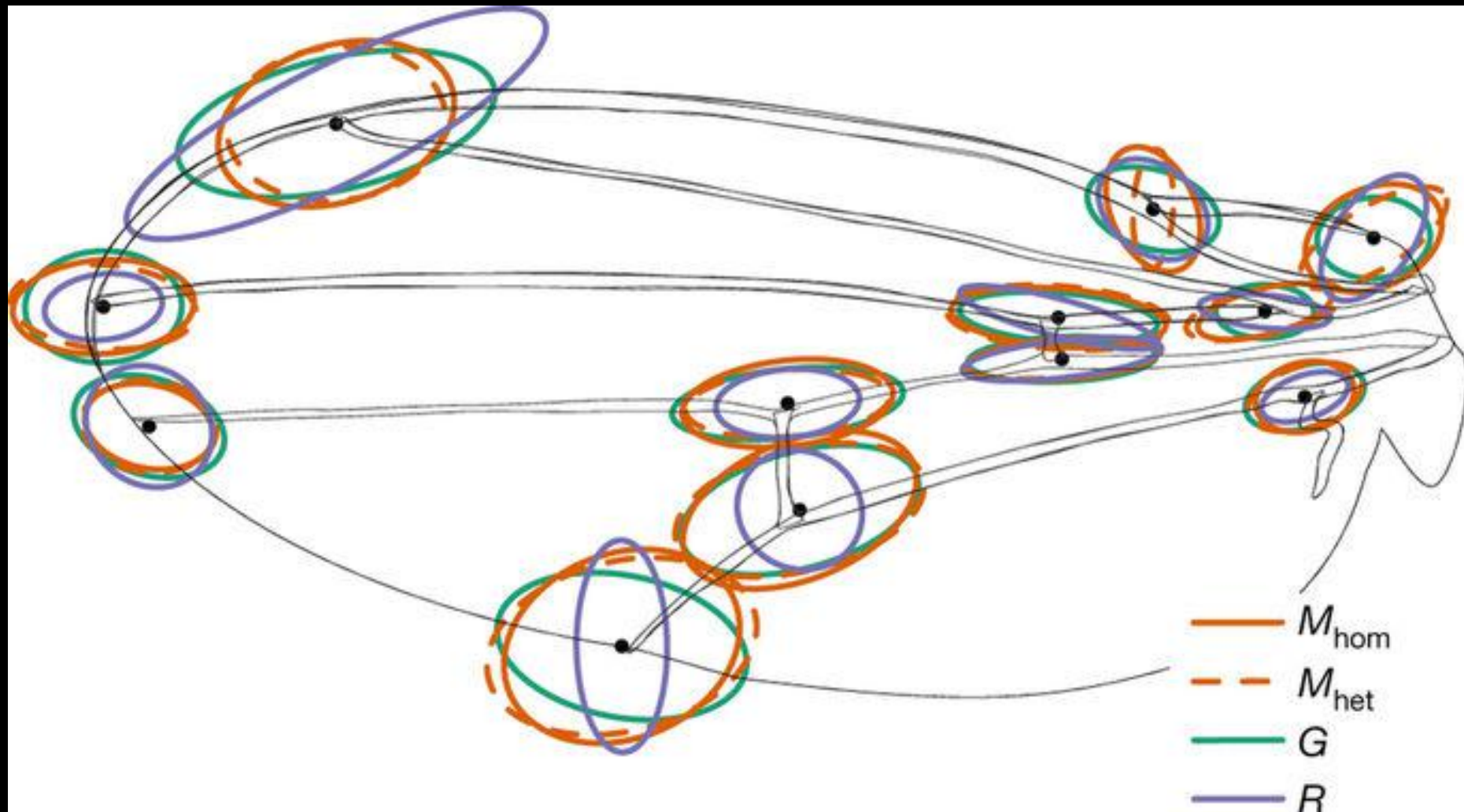
Figure S6. Results of simulations from the temperature-tracking model, calibrated by *Poseidonamicus major* (left) and *Neotoma cinerea* (right). Vertical axis is magnitude of evolutionary variation measured as the standard deviation of samples in a sequence, with the contribution from measurement error removed (see Methods). Horizontal axis is sequence duration, in years and on a log₁₀ scale (a value of 6 is 1 Myr). Points are semi-transparent and lines represent locally weighted (lowess) regressions with a smoother span = 0.5.

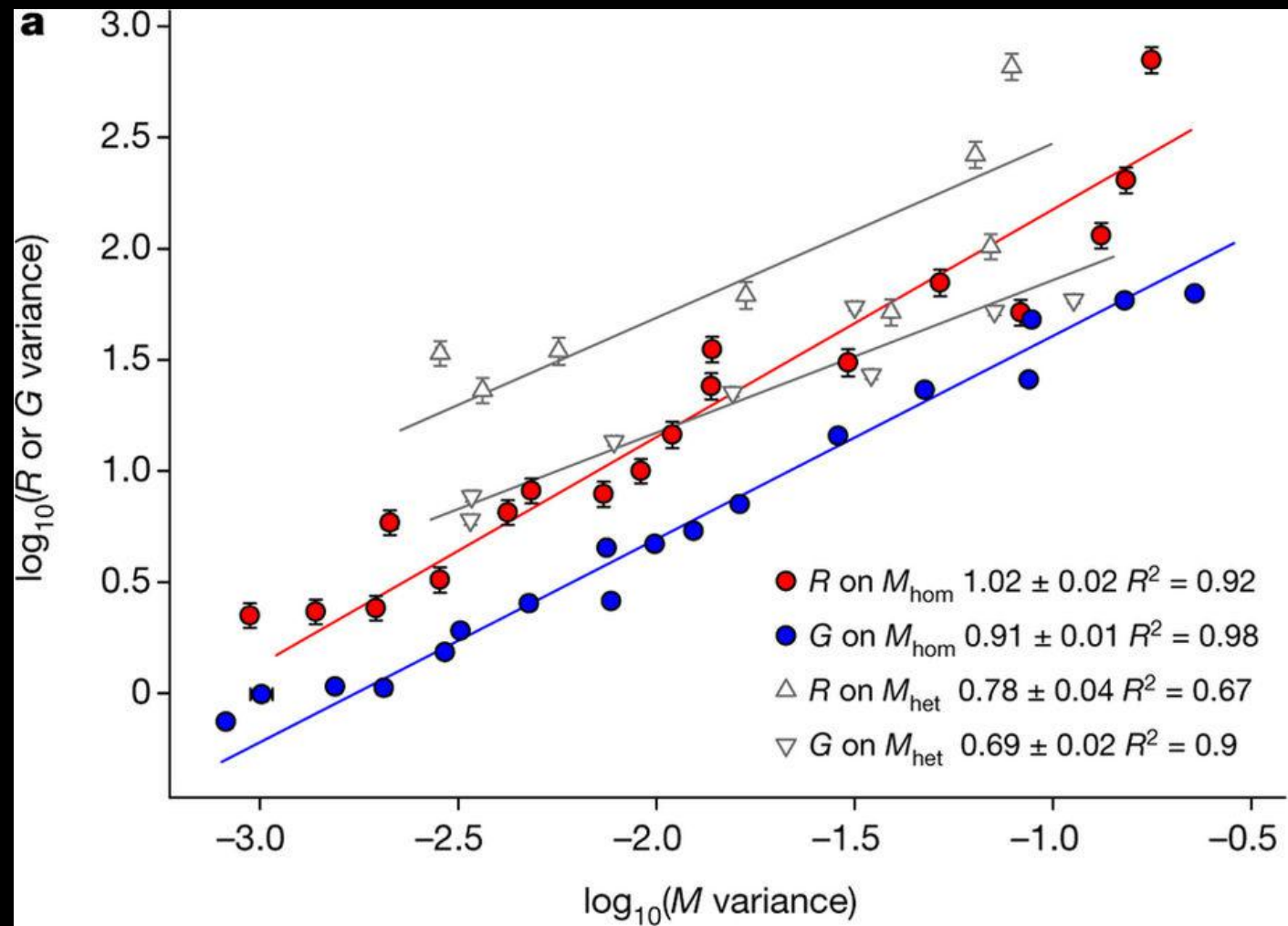
Multivariate genetic constraints

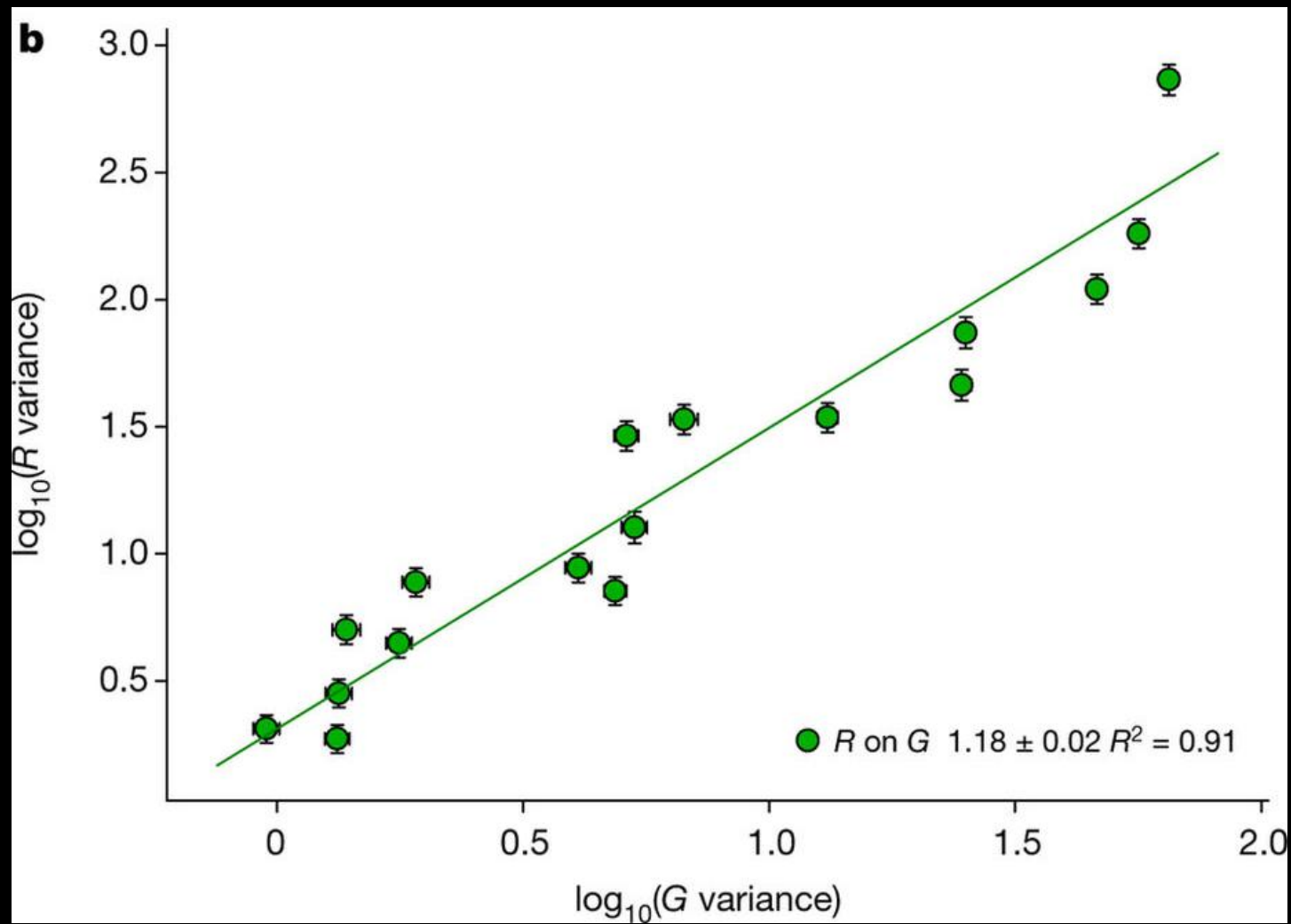
Mutation predicts 40 million years of fly wing evolution

Houle et al. 2017, Nature









**...but it's hard to imagine that
they don't all contribute**

2001 5 yr prediction

- Genomic data for phylogeny, and using phylogeny to understand genome evolution
- Modelling and representing reticulate evolution.
- Supertree methods
- Bayesian methods
- Large data sets (computational problems, testing hypotheses)



Mike Steel

2006 5 yr prediction

- The ‘tree of life’: better ways to represent it, and insights into the early history of life by improved rooting and ancestral data reconstruction.
- Closer integration of population-genetic factors in phylogenetics, including further insights into gene-tree/species tree, and horizontal gene transfer.
- Better methods for relating phylogenies to geological processes and species radiations
- Novel types and uses of genomic data for resolving difficult phylogenetic questions
- Applications of phylogenetics in evolutionary ecology and biodiversity conservation.



Mike Steel

2011 5 yr prediction

- Development of network-based methods to display 'evolution as it happened' including reticulation (LGT, endosymbiosis, hybrid species etc) up to the limits of what can be discerned from extant data.
- Phylogenetic approaches for handling patchy taxon coverage and analyzing large numbers of short reads from next generation sequencing.
- Phylogenetic approaches to early life using non-stationary models and protein structural constraints
- Statistical approaches for analyzing non-aligned sequence data.
- More realistic models of speciation and extinction that better describe the shape of 'real' phylogenies.



Mike Steel

2016 5 yr prediction

- Improved methods for using phylogenies to study processes on trees (including the evolution of morphological and continuous characters).
- Development of techniques for updating/refining/enlarging existing phylogenies as new data are added.
- Development of phylogenetic methods based on models that allow site-specific rates and processes that change across a tree.
- Statistical methods for generating random phylogenetic networks and inferring networks based on the trees they display.
- Improved techniques for posterior estimation of large trees, and further development of invariant-based phylogeny reconstruction methods.



Mike Steel

What I don't like about these:

Most of Steel's predictions don't address the questions, but are purely methods

What will be the big advances in terms of the questions we can answer, and with what tools?

Brainstorm: What big questions in macroevolution have we not addressed in this class?

What will happen in macroevolution in the next 5-20 years?

What questions do the models we have talked about seem ill-equipped to answer?

Our Tools:

Discrete traits: Continuous-Time Markov Chains

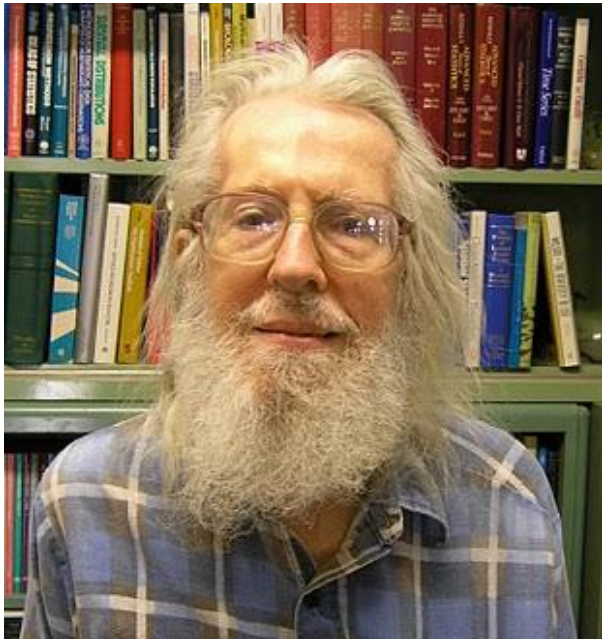
Continuous traits: Gaussian diffusion models
(BM/OU etc)

Diversification: Birth-Death Models

Comparative method: Regression models

Biotic Interactions

Red Queen - The Law of Constant Extinction



Leigh Van Valen

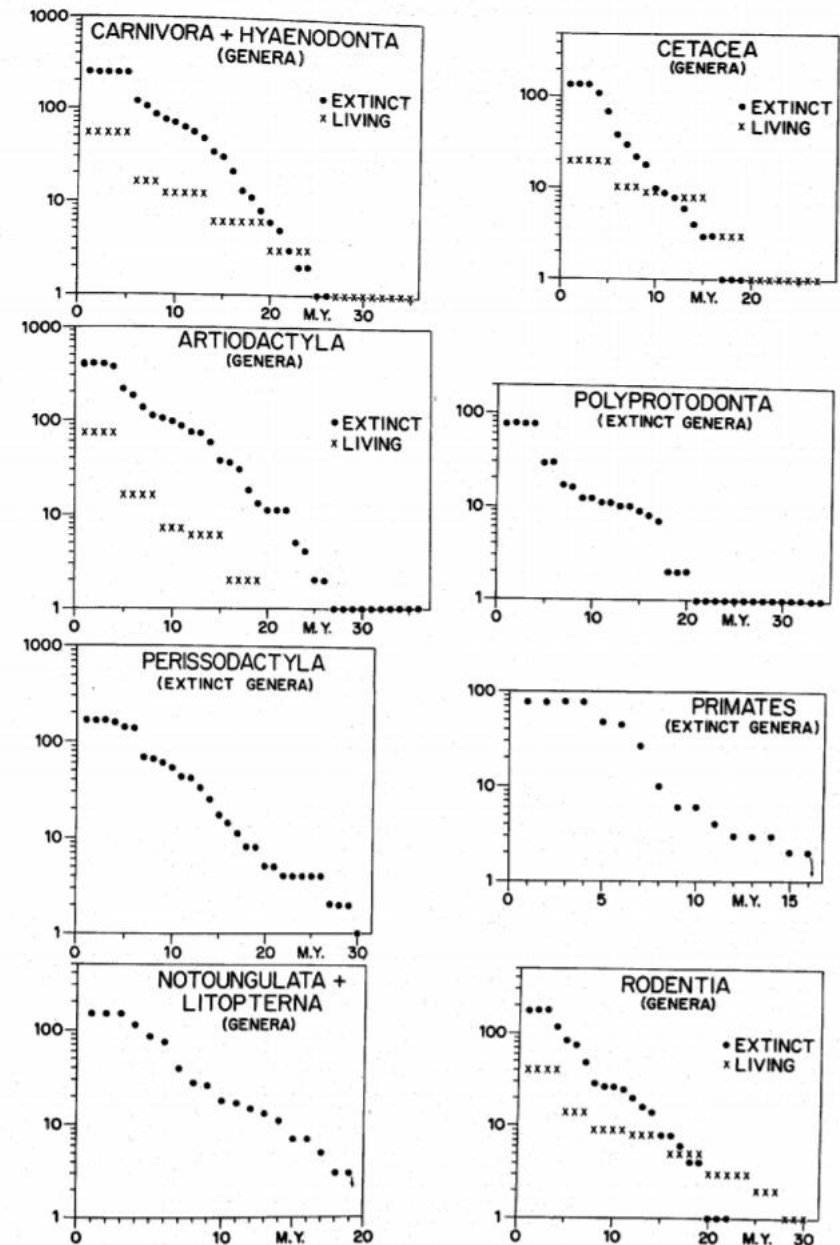


Fig. 5. Taxonomic survivorship curves for mammals. For Primates, Madagascar genera are omitted because the island lacks pre-Pleistocene fossils. Polyprotodonta includes Caenolestidae.

The Rise and Fall of Species

Remember: Why million year timescales?

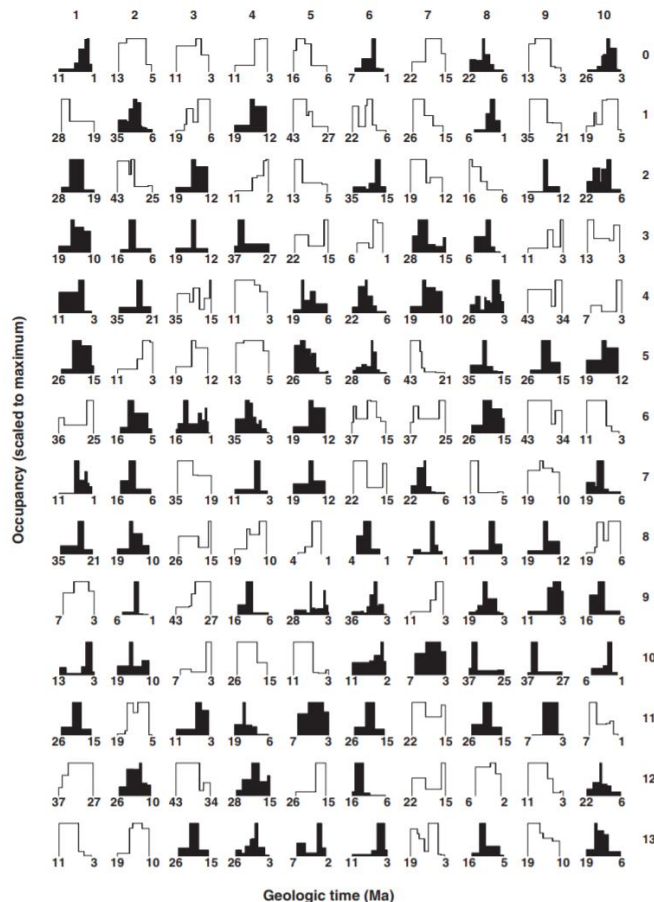
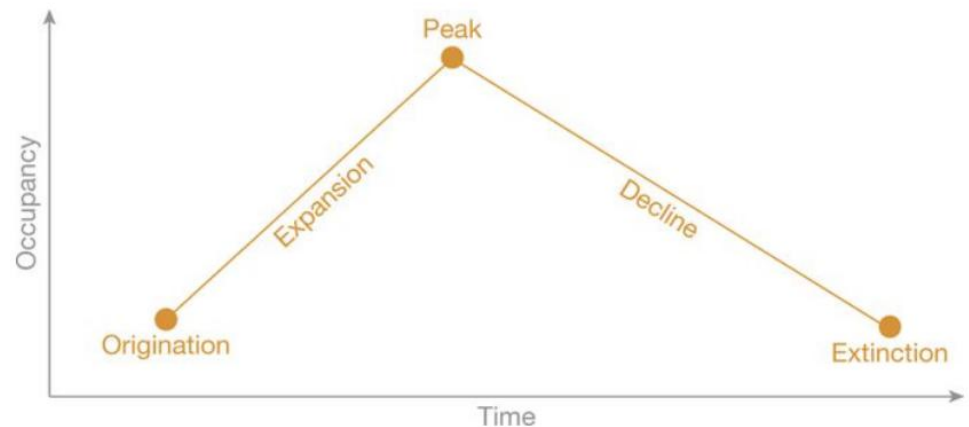


Figure 1: The hat-like pattern of a taxon's history in the fossil record.



A taxon's history can be conceptualized as containing five distinct phases: origination, expansion, peak, decline and extinction. The observed trajectories are typically monotonic in expansion and decline, with a clearly expressed peak.

Species interactions on trees

Trait evolution models

Estimating the Effect of Competition on Trait Evolution Using Maximum Likelihood Inference

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Institut de Biologie de l'Ecole Normale Supérieure (IBENS), CNRS, Inserm, Ecole Normale Supérieure, PSL Research University, F-75005 Paris, France

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Received 31 July 2015; reviews returned 24 February 2016; accepted 1 March 2016

Associate Editor: Luke Harmon

ECOLOGY LETTERS

Ecology Letters, (2015) **18**: 17–27

doi: 10.1111/ele.12384

LETTER

Predicting rates of interspecific interaction from phylogenetic trees

Abstract

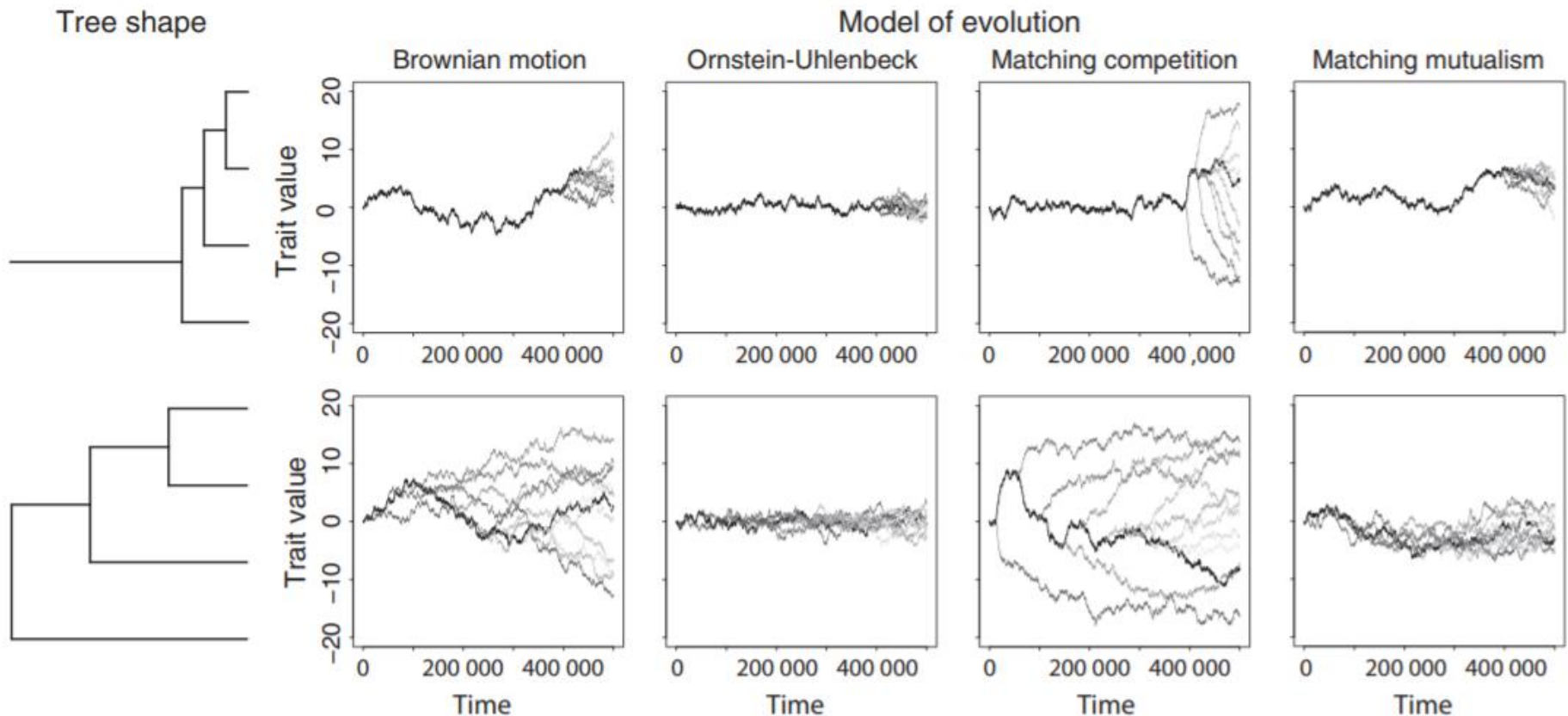
Integrating phylogenetic information can potentially improve our ability to explain species' traits, patterns of community assembly, the network structure of communities, and ecosystem function. In this study, we use mathematical models to explore the ecological and evolutionary factors that

Scott L. Nuismer* and Luke J. Harmon

Department of Biological Sciences

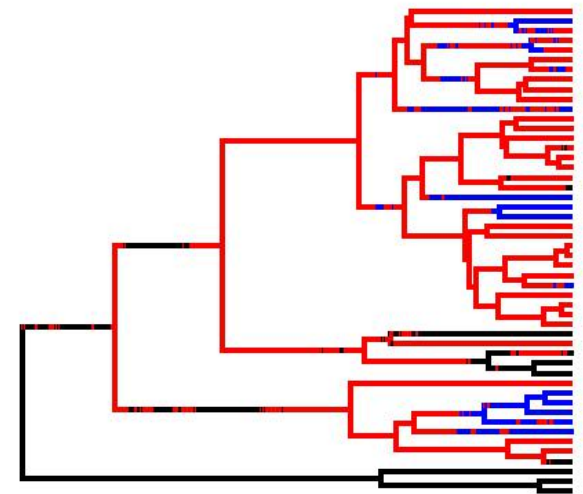
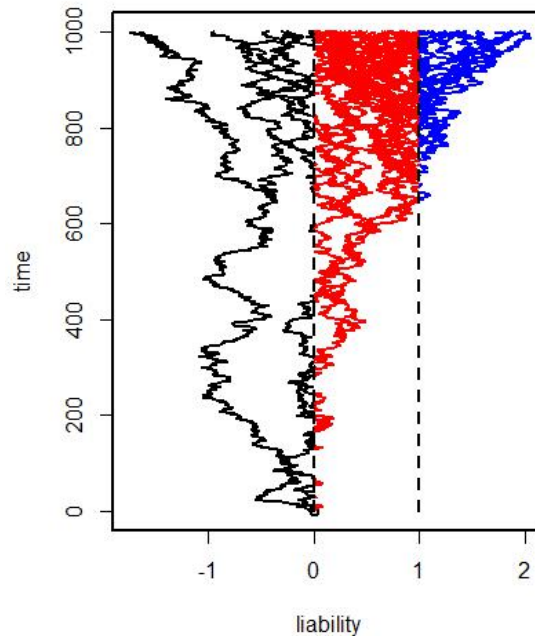
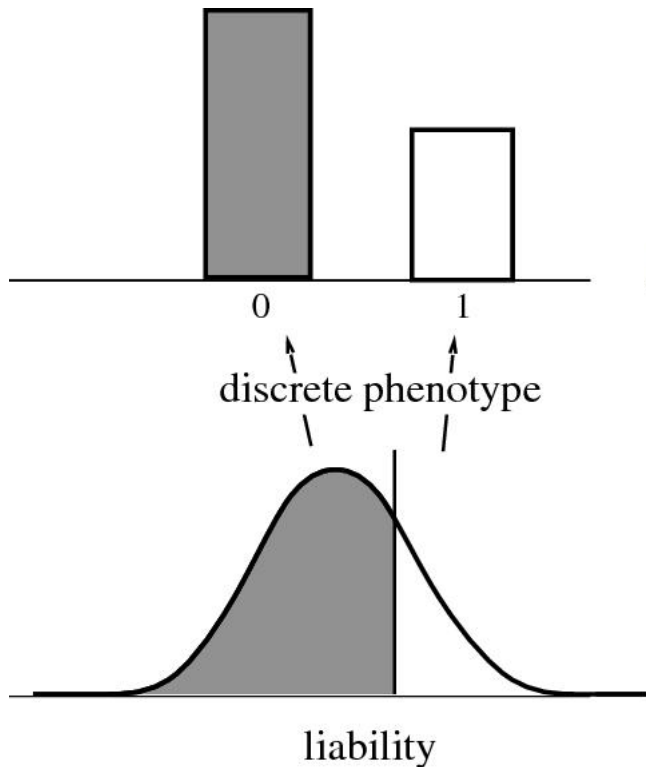
Species interactions on trees

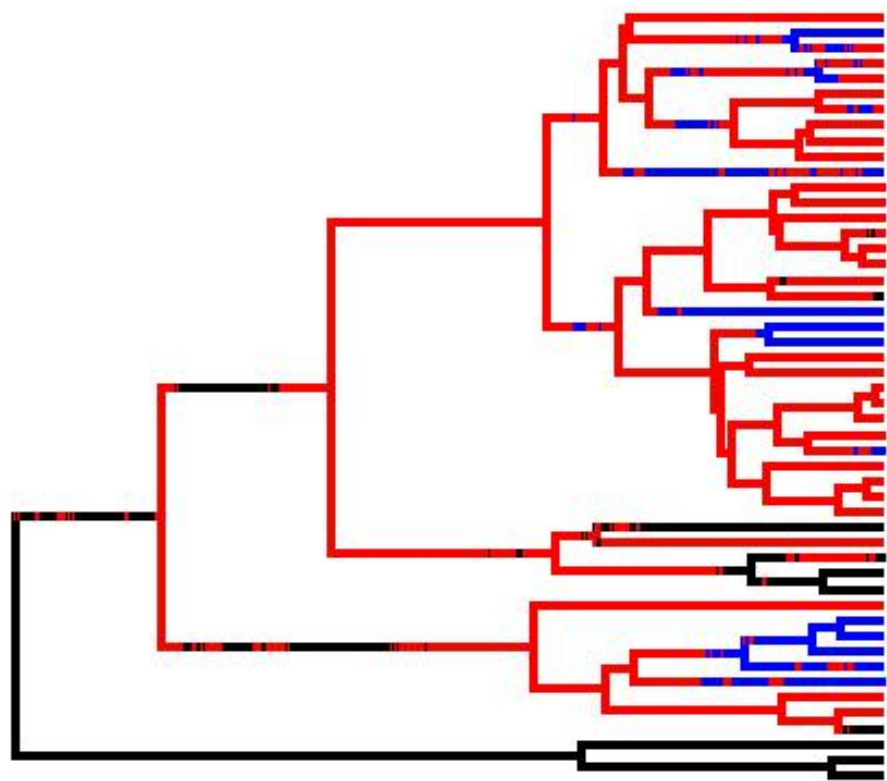
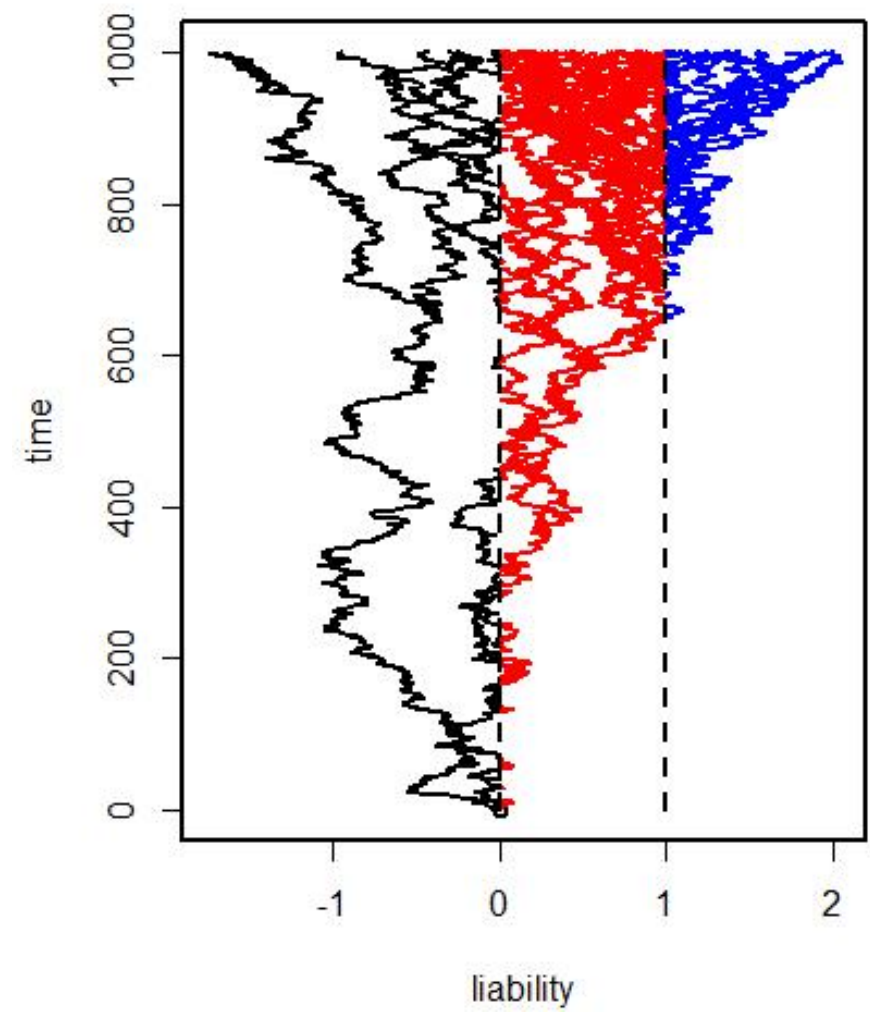
Trait evolution models



Evo-Devo: The Genotype-Phenotype Map

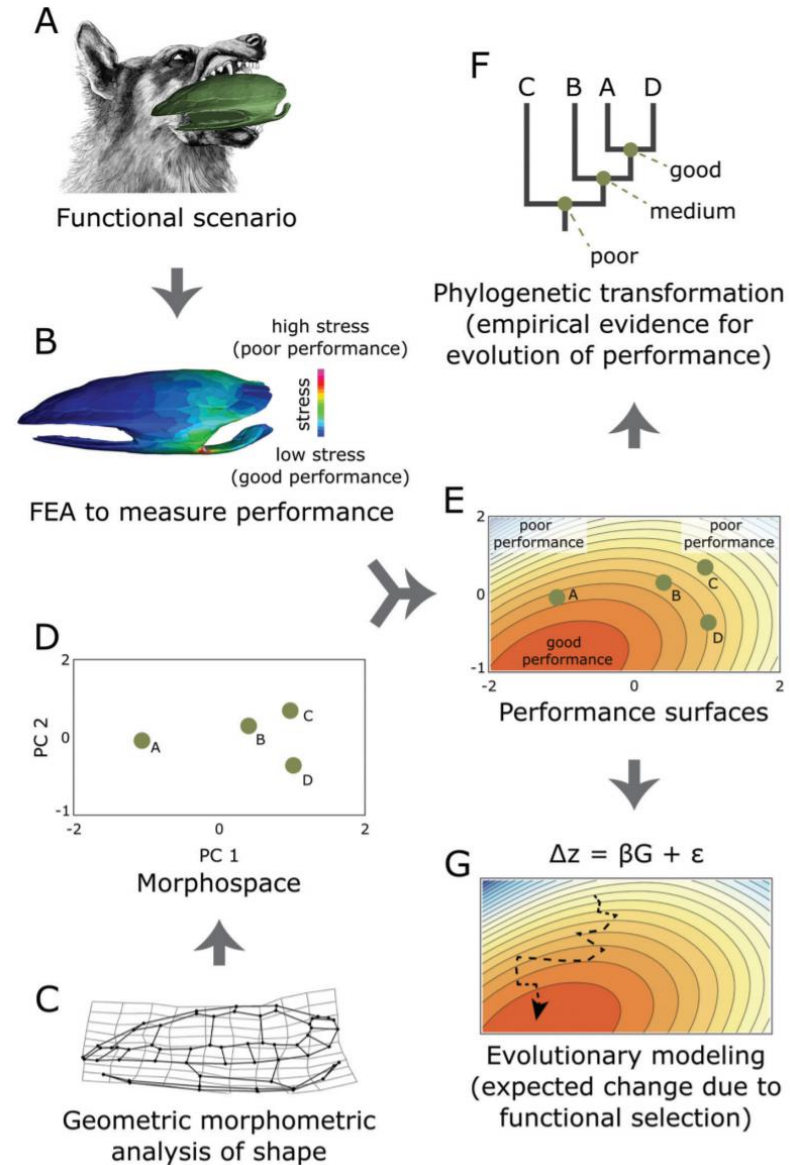
Simple example: Threshold traits





Biomechanics:

Performance as a bridge between phenotypes & macroevolutionary adaptive landscapes

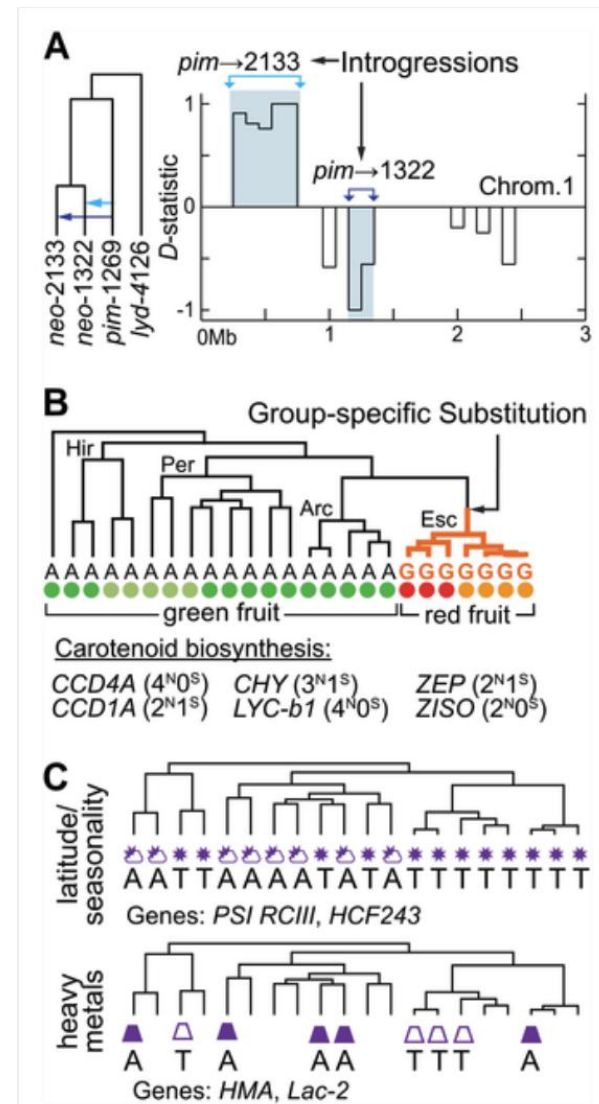


Combining geometric morphometrics and finite element analysis with evolutionary modeling: towards a synthesis

Genomics

e.g. phyloGWAS

Genomics broke most of our “good” models...need to figure out how to intelligently see signal through noise



Phylogenomics Reveals Three Sources of Adaptive Variation during a Rapid Radiation

James B. Pease, David C. Haak, Matthew W. Hahn, Leonie C. Moyle

Published: February 12, 2016 • <https://doi.org/10.1371/journal.pbio.1002379>

My 5 yr predictions/hopes:

- Introduction and expansion of statistical causal inference to macroevolution
- Integration of dynamic evolutionary process models into comparative models (demographic processes, sexual selection, coevolution, competition, symbioses, pathogen-host)
- Increasing usage of phylogenetic prediction and cross-validation as methods for evaluating models, methods for integrating streaming data building on previous analyses rather than starting from scratch
- Elucidation of scaling processes (e.g. gene interactions/networks to phenotypes; populations to species; microevolution to macroevolution)
- More customized joint analyses that integrate over uncertainty across many different types of data
- Tests and integration of biomechanics, physiological models, and other types of functional models into macroevolutionary adaptive landscapes
- Taking the consequences of population variation within lineages seriously for trait evolution (e.g. hemiplasy, polymorphism, etc.)
- Improved methods for dealing with multivariate and multitrait datasets.
- Increased application of comparative models to analyzing genomic basis of adaptation, e.g phyloGWAS.