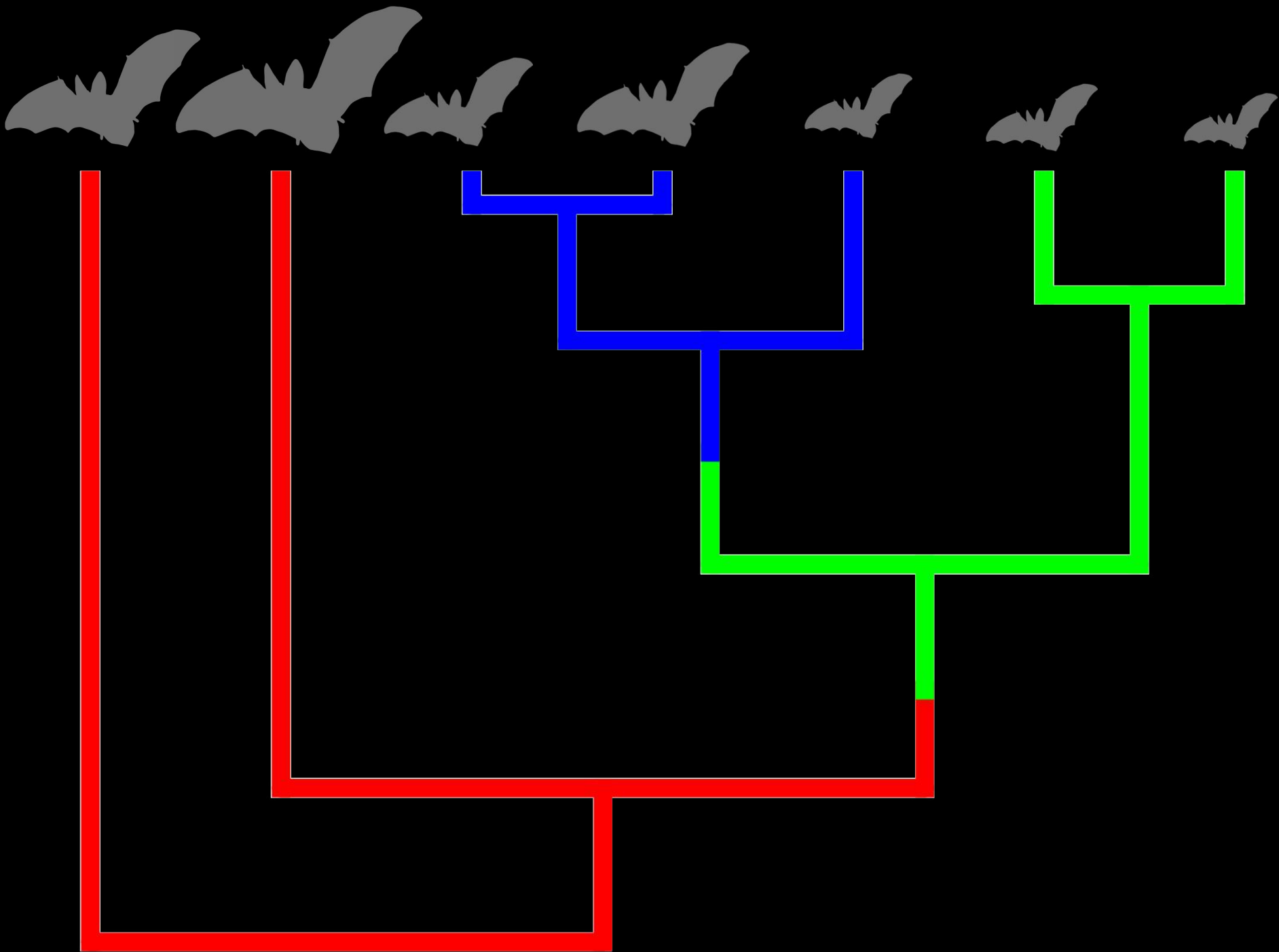


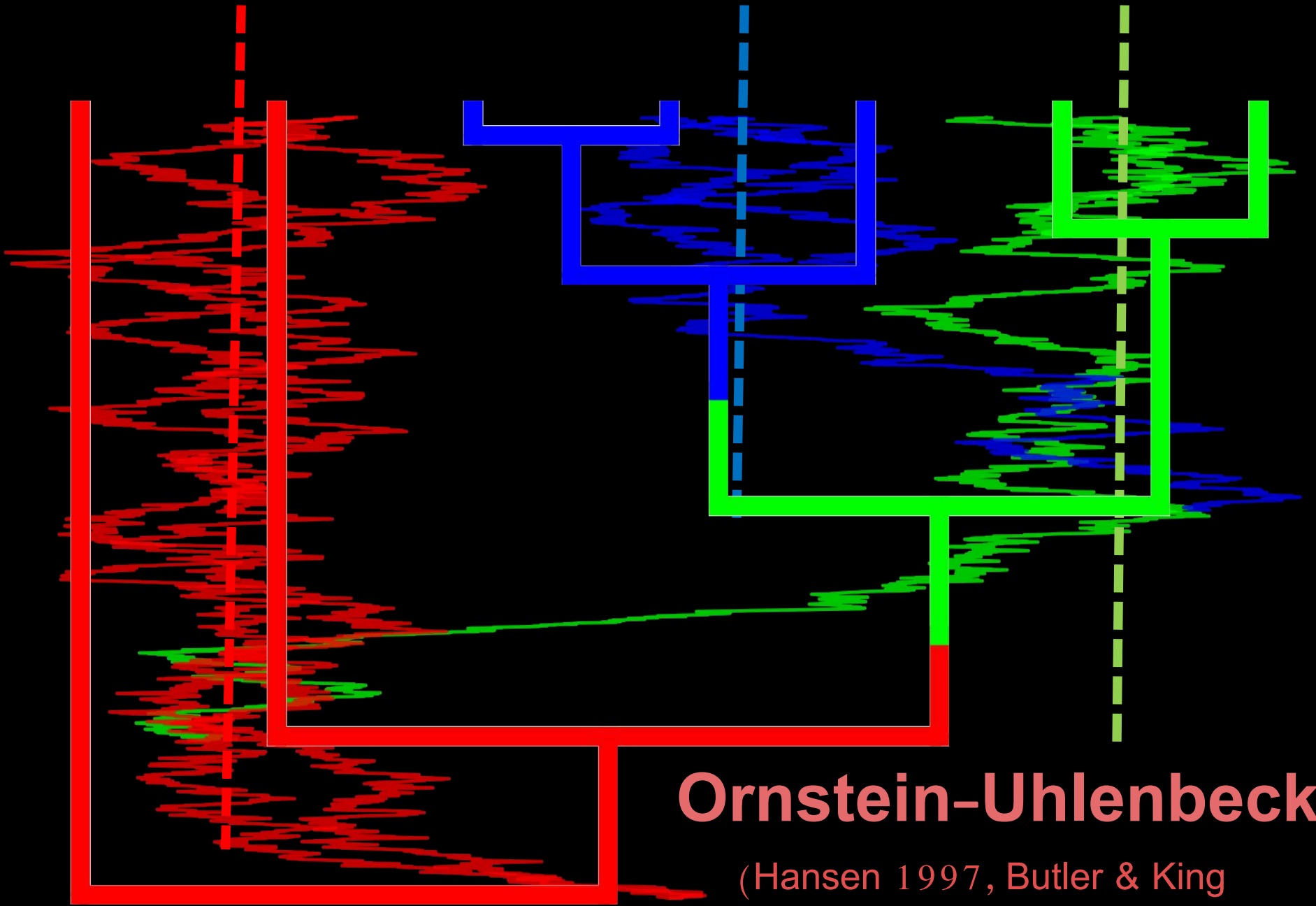
Finding evolutionary shifts



θ_1

θ_2

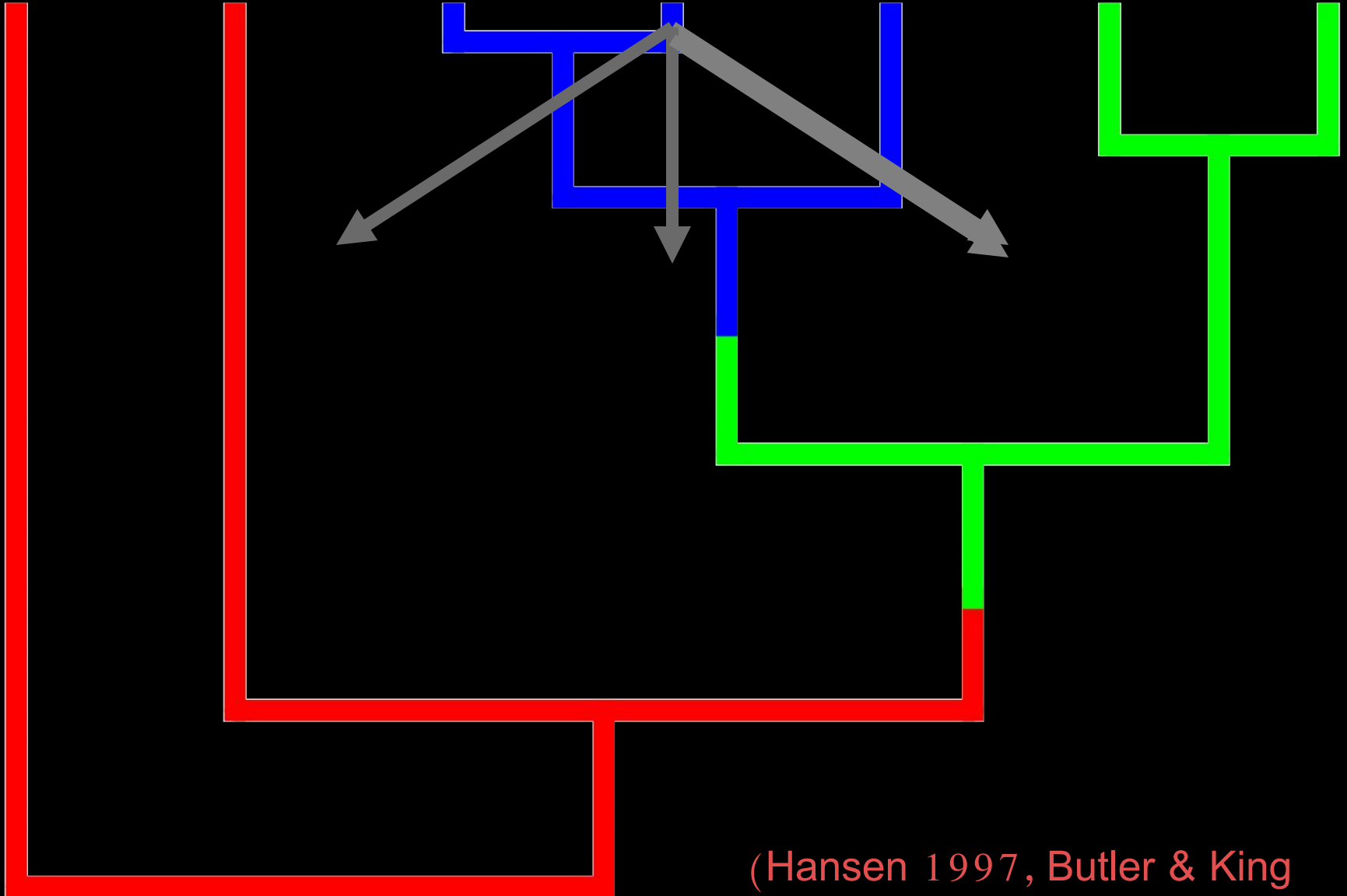
θ_3



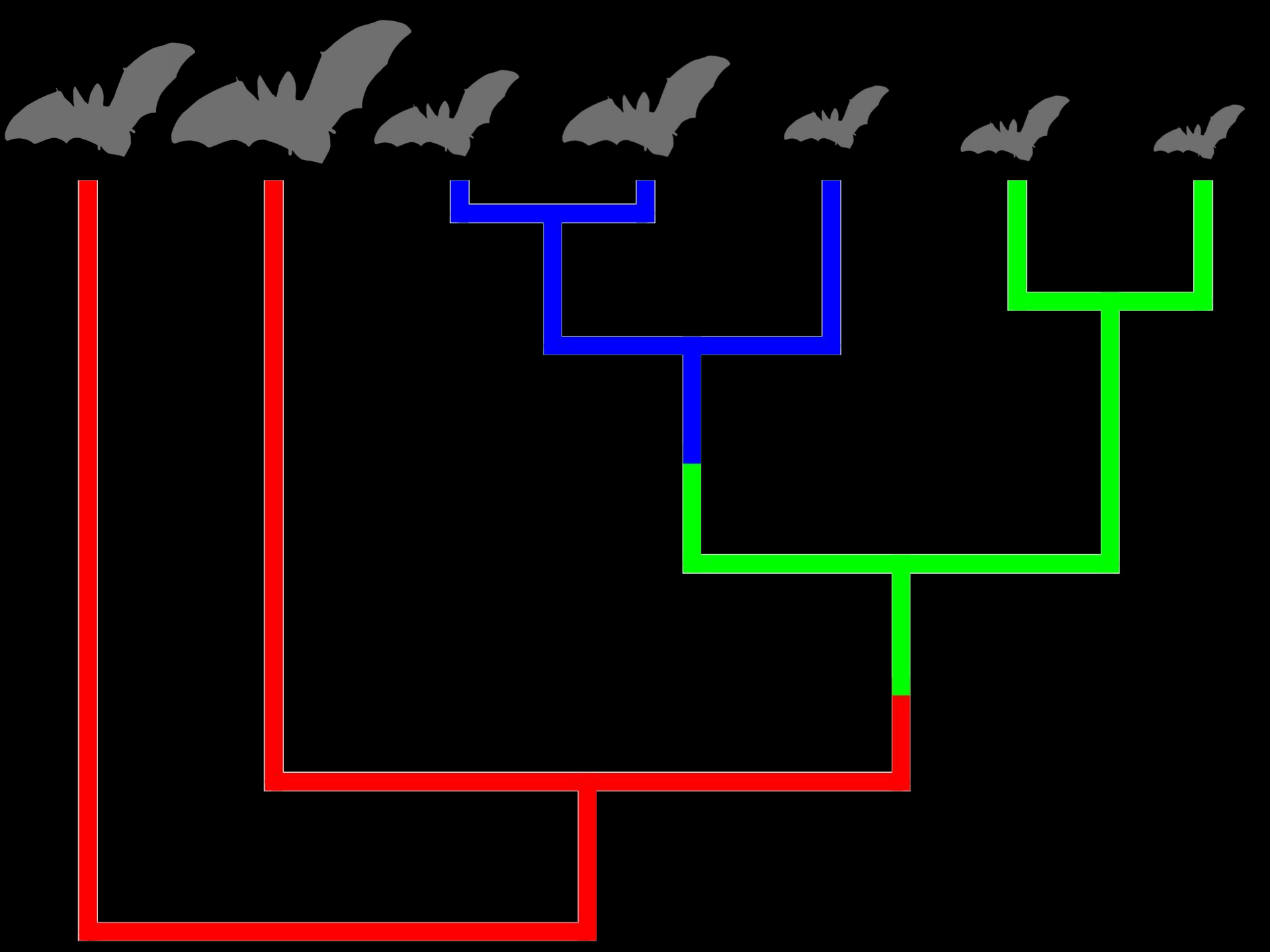
Ornstein-Uhlenbeck

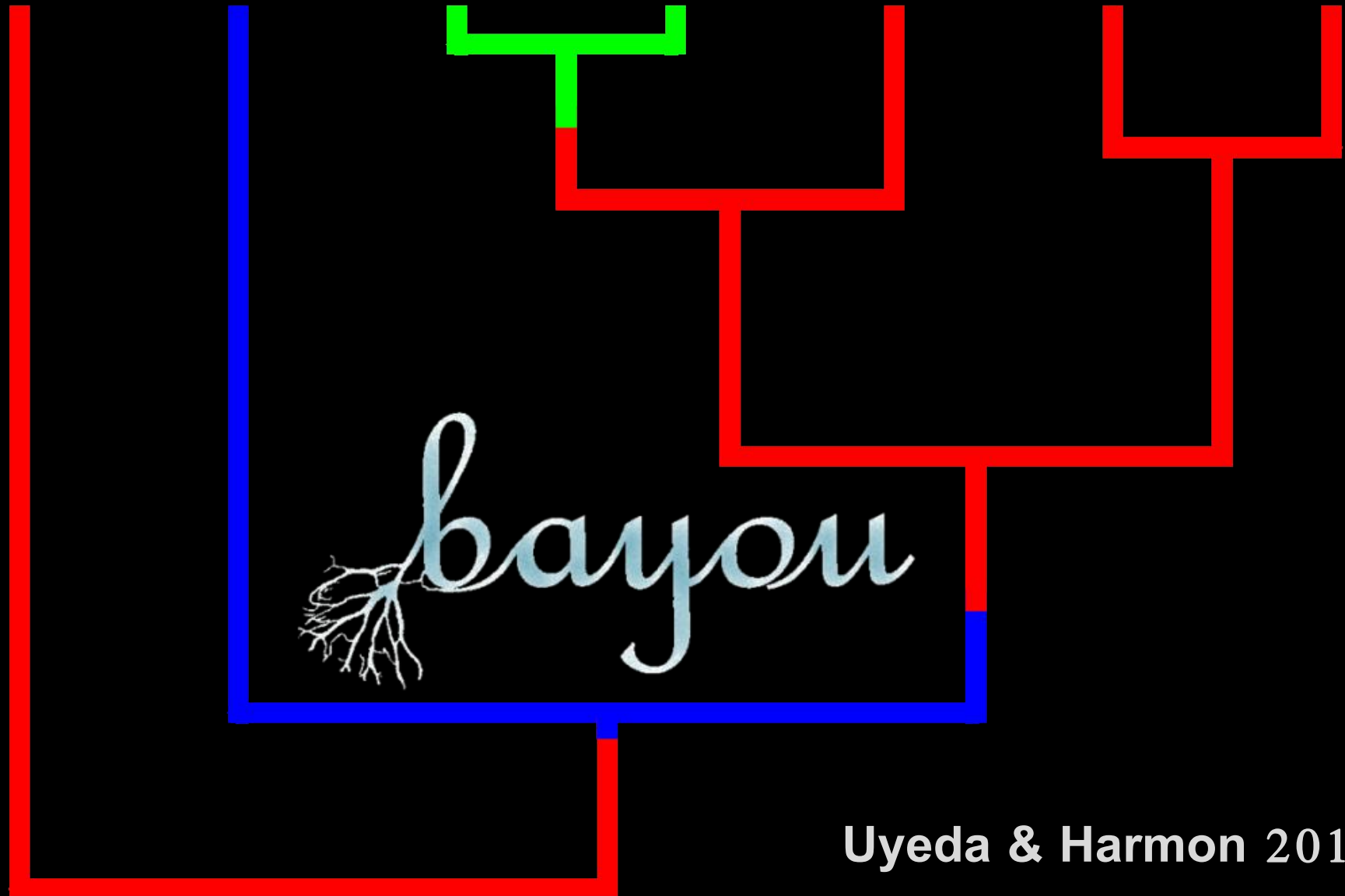
(Hansen 1997, Butler & King 2004)

Compare models (Best Model)



(Hansen 1997, Butler & King
2004)





Uyeda & Harmon 2014

Turtles and Tortoises

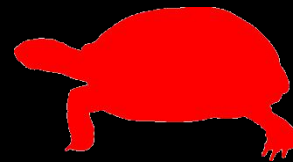
(Jaffe et al. 2011)



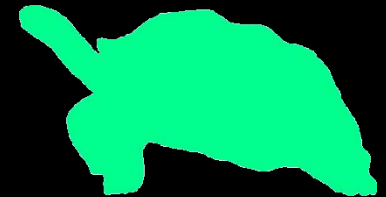
Marine



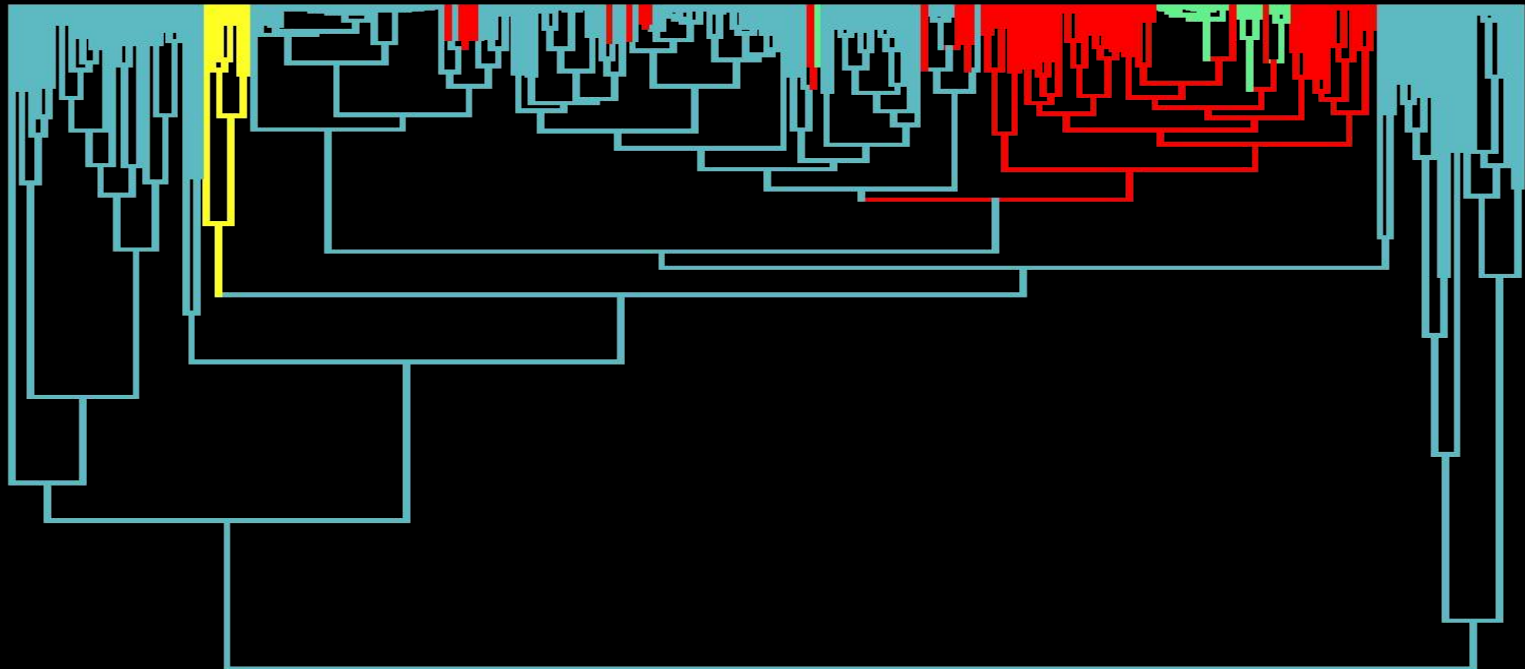
Freshwater



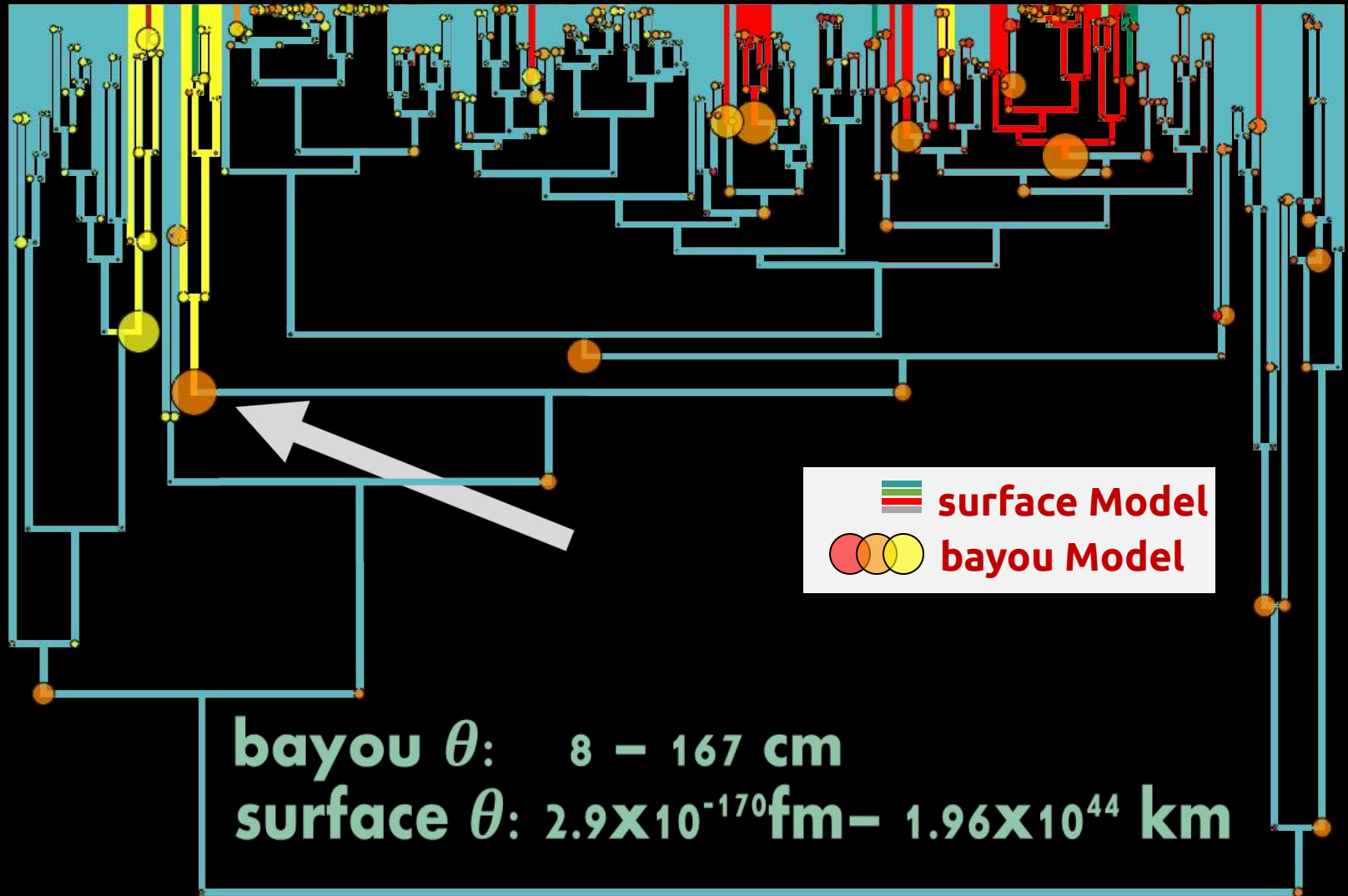
Terrestrial



Island



bayou (Uyeda and Harmon, 2014)

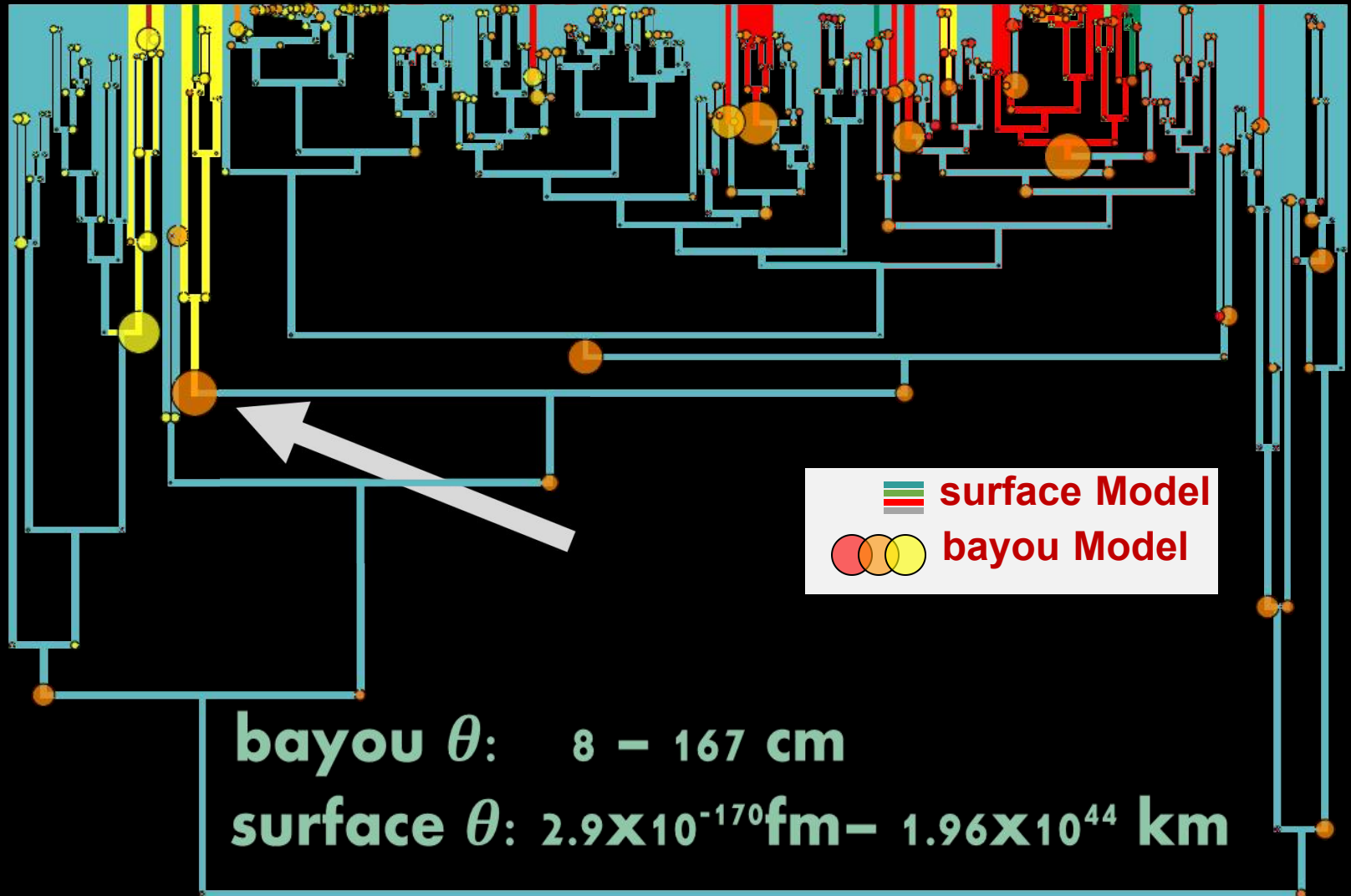


surface

(Ingram & Mahler, 2012)

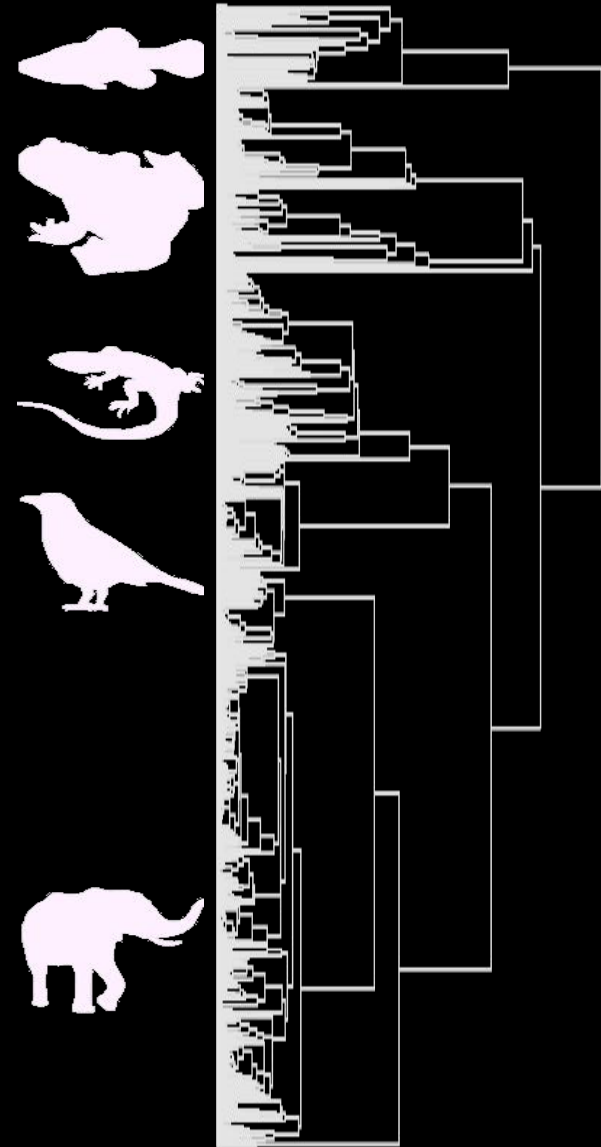
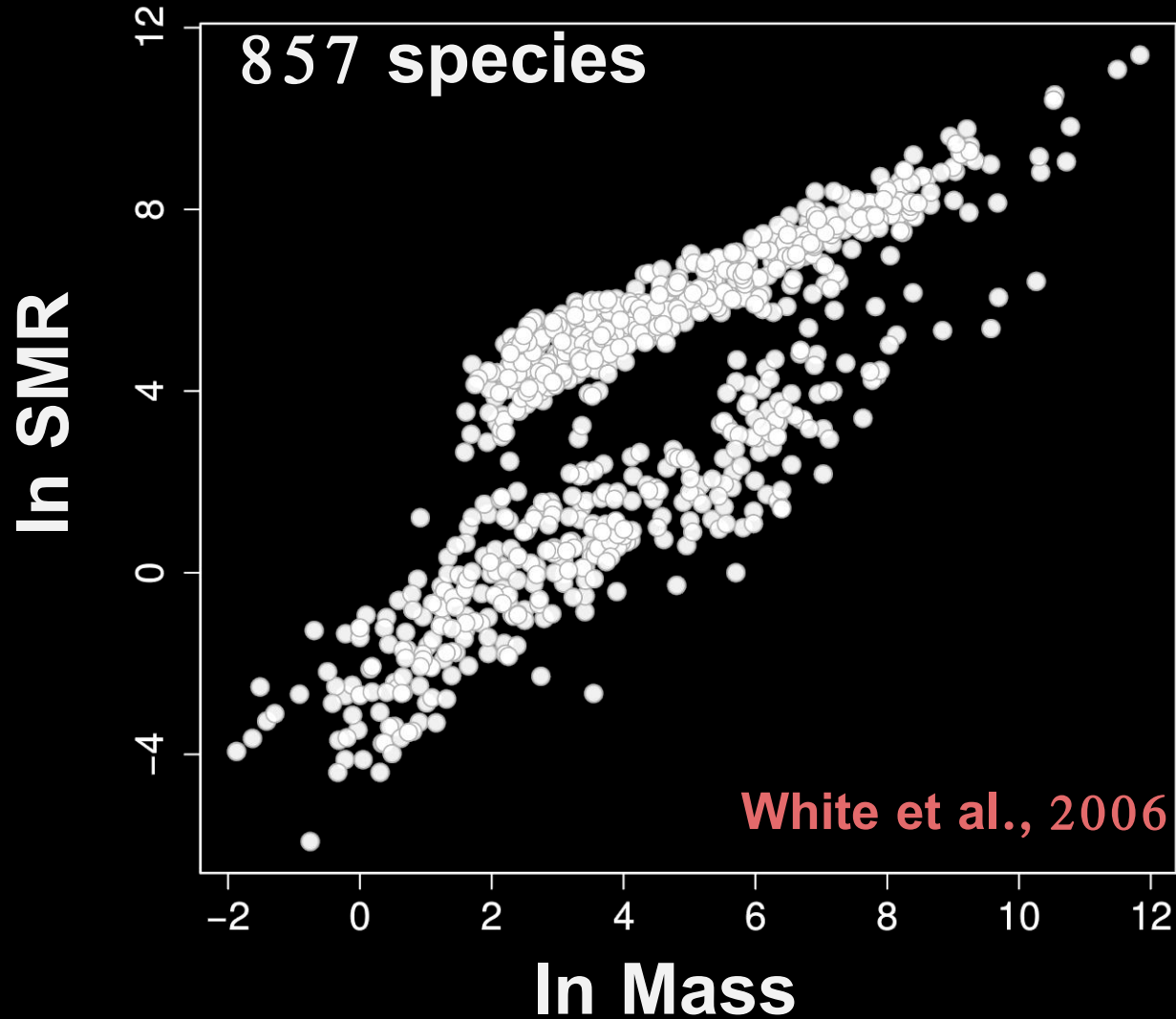


bayou (Uyeda and Harmon, 2014)

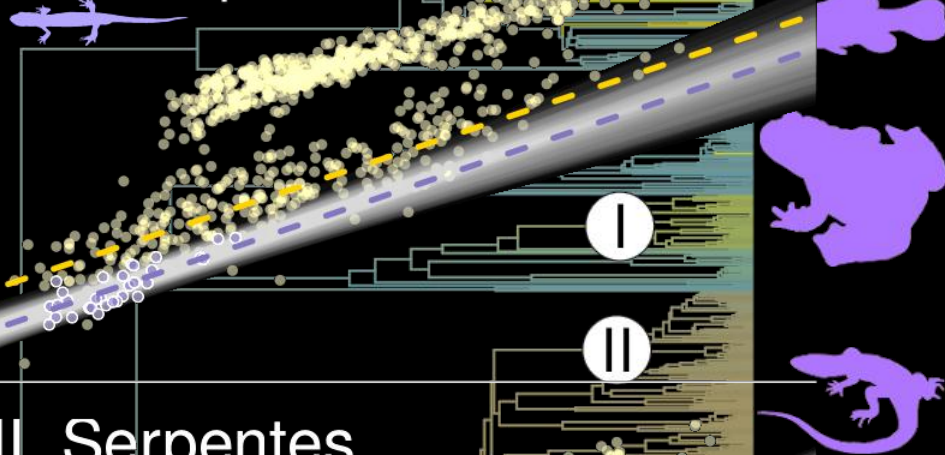


bayou phy. half-life = 3.94 million years
surface phy. half-life = 92 million years

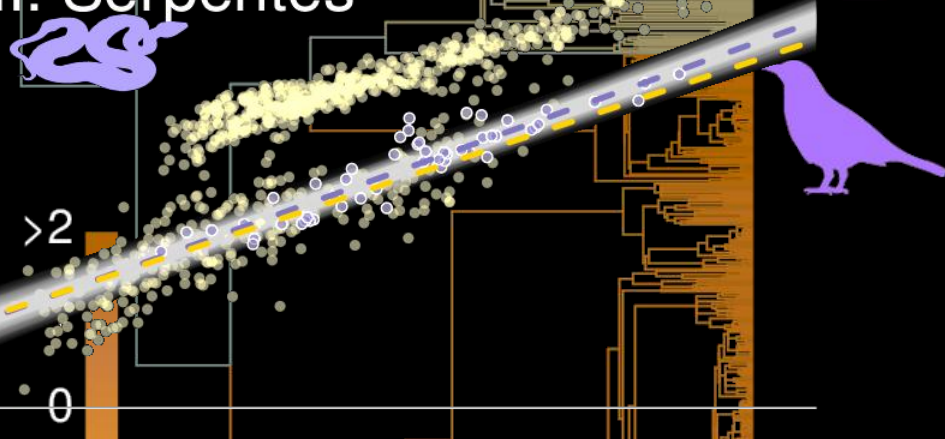
Metabolic Rate Allometry



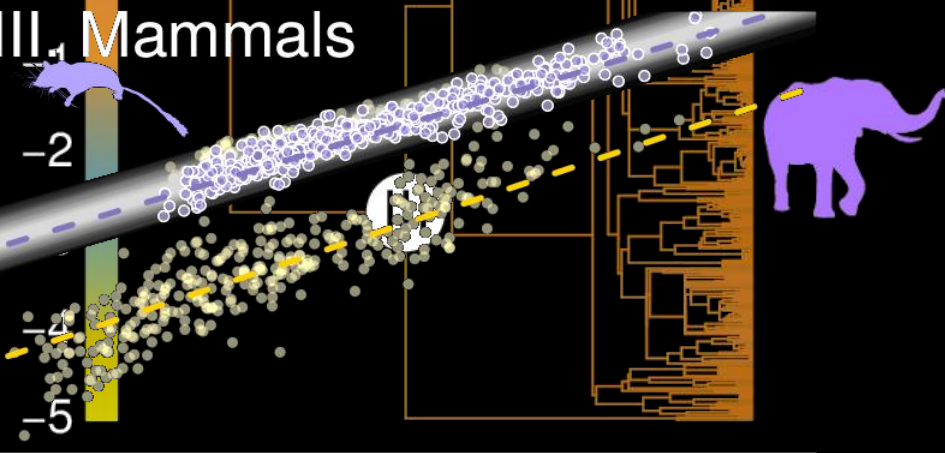
I. Pteropontidae



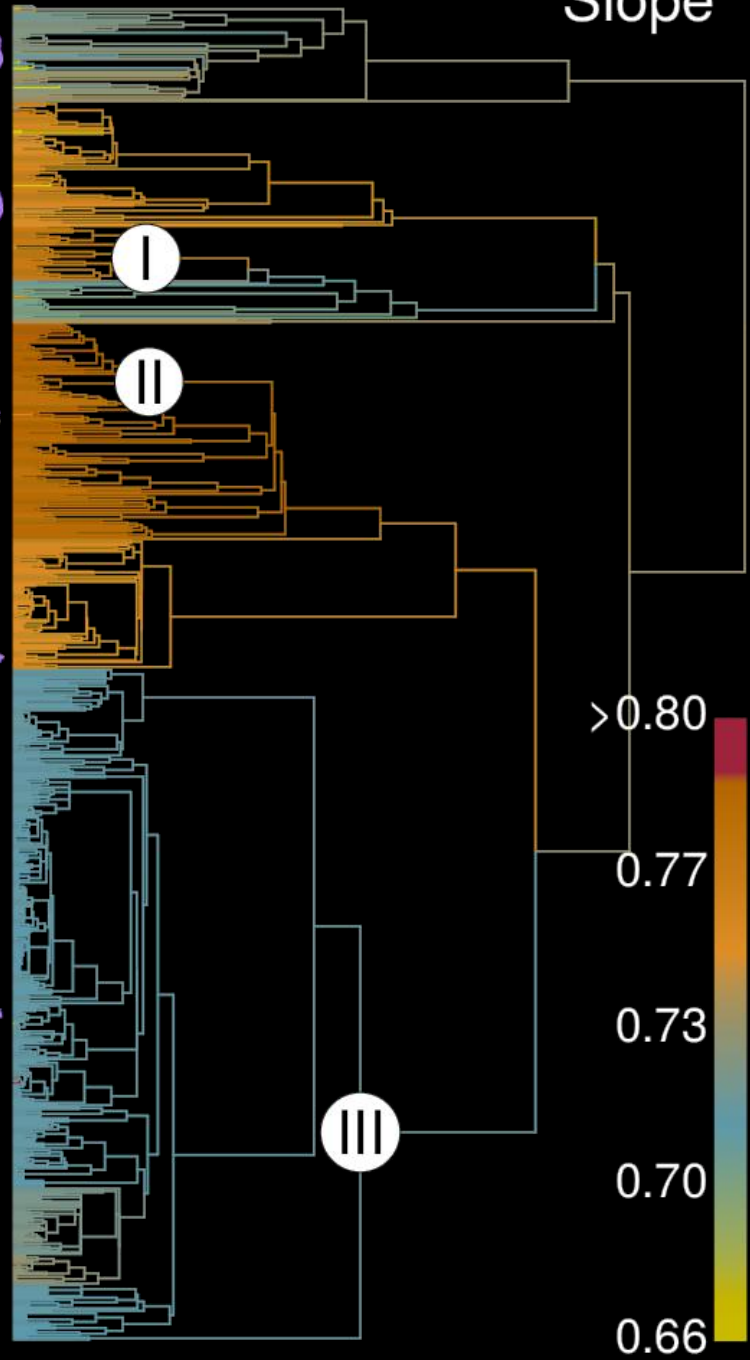
II. Serpentes

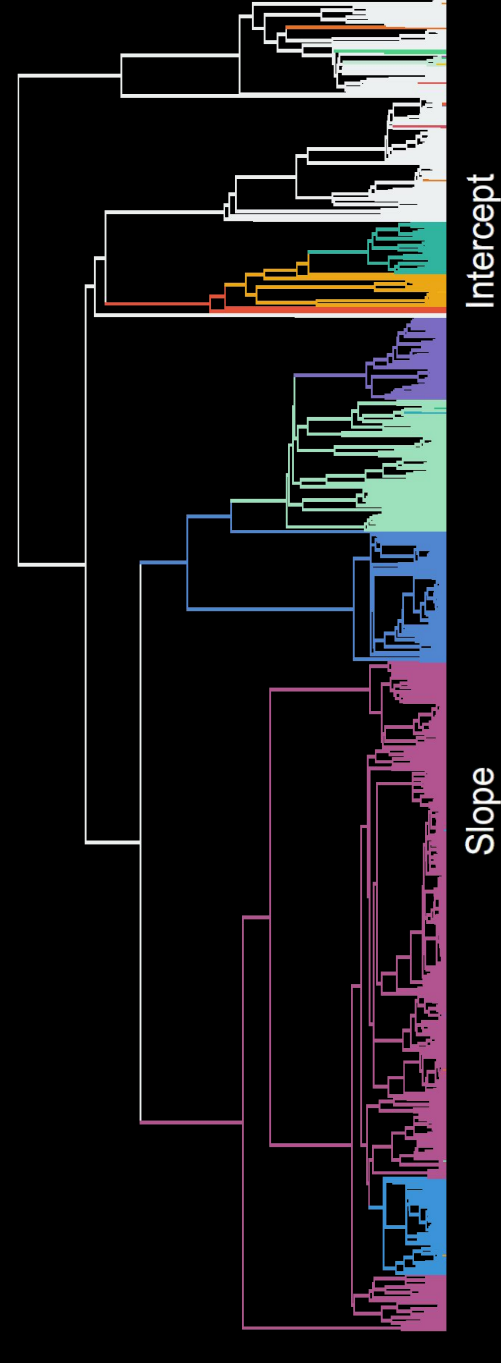


III. Mammals

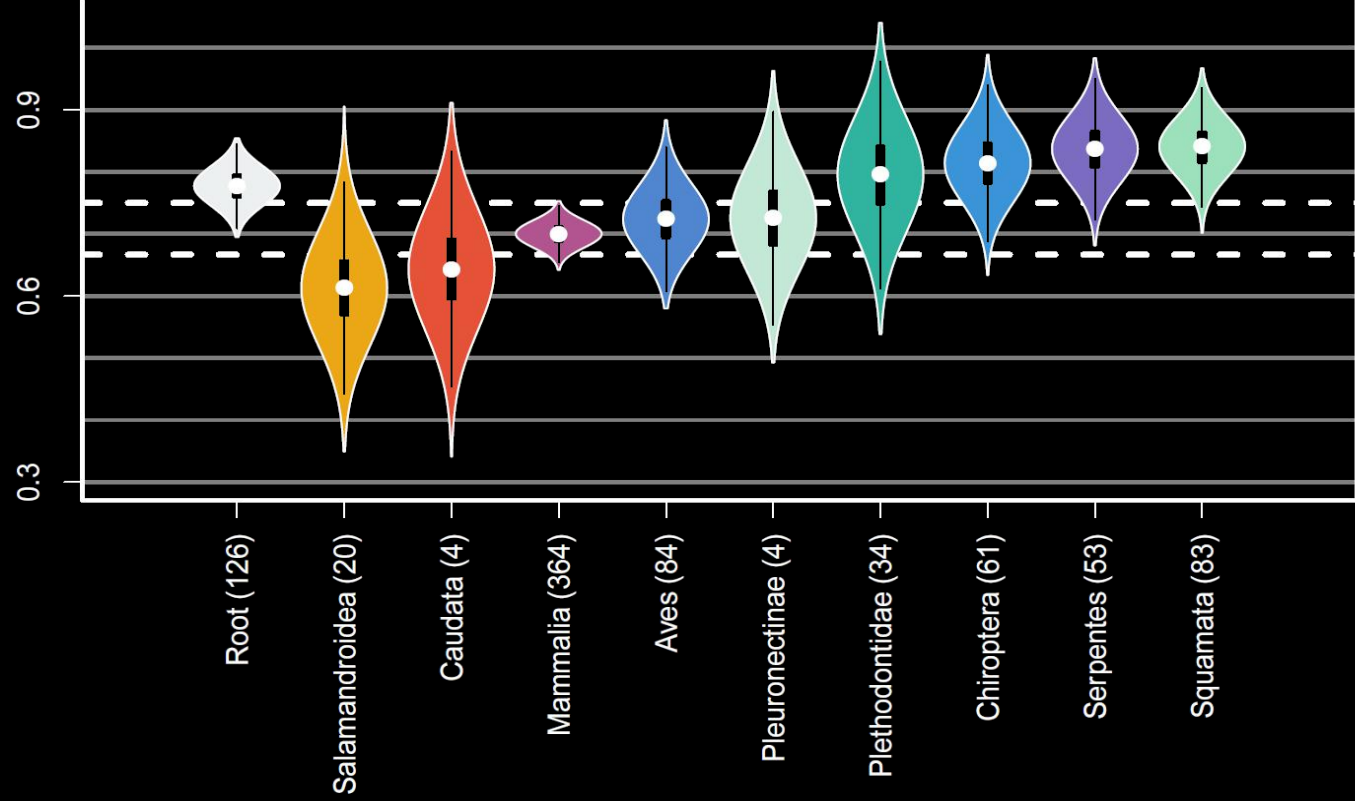


Slope

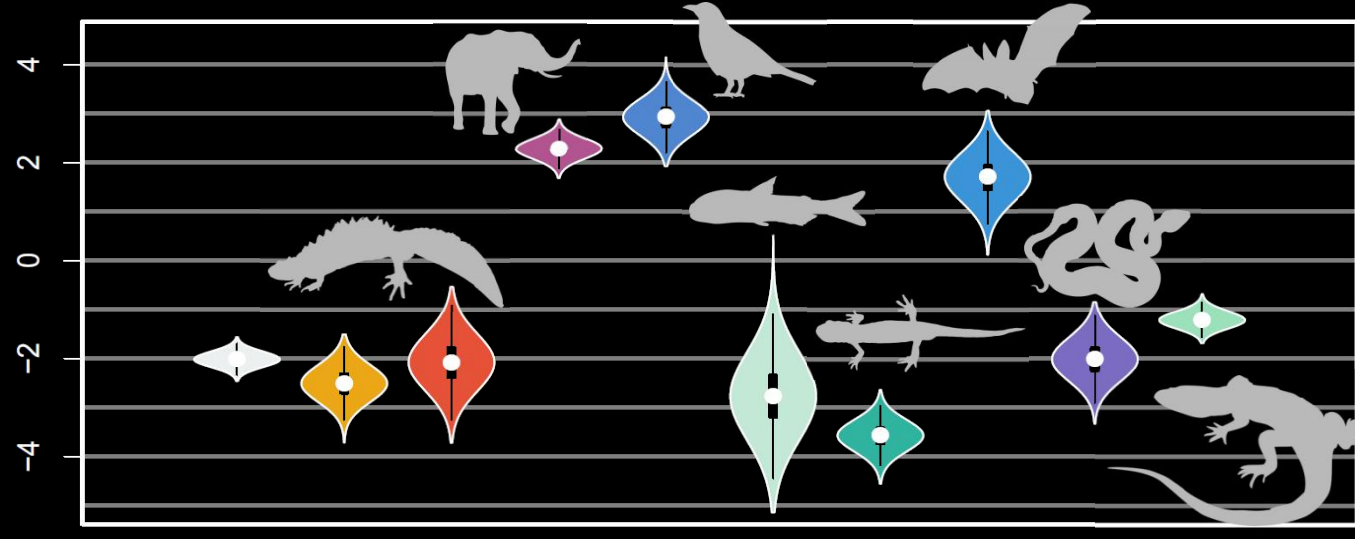




Slope



Intercept

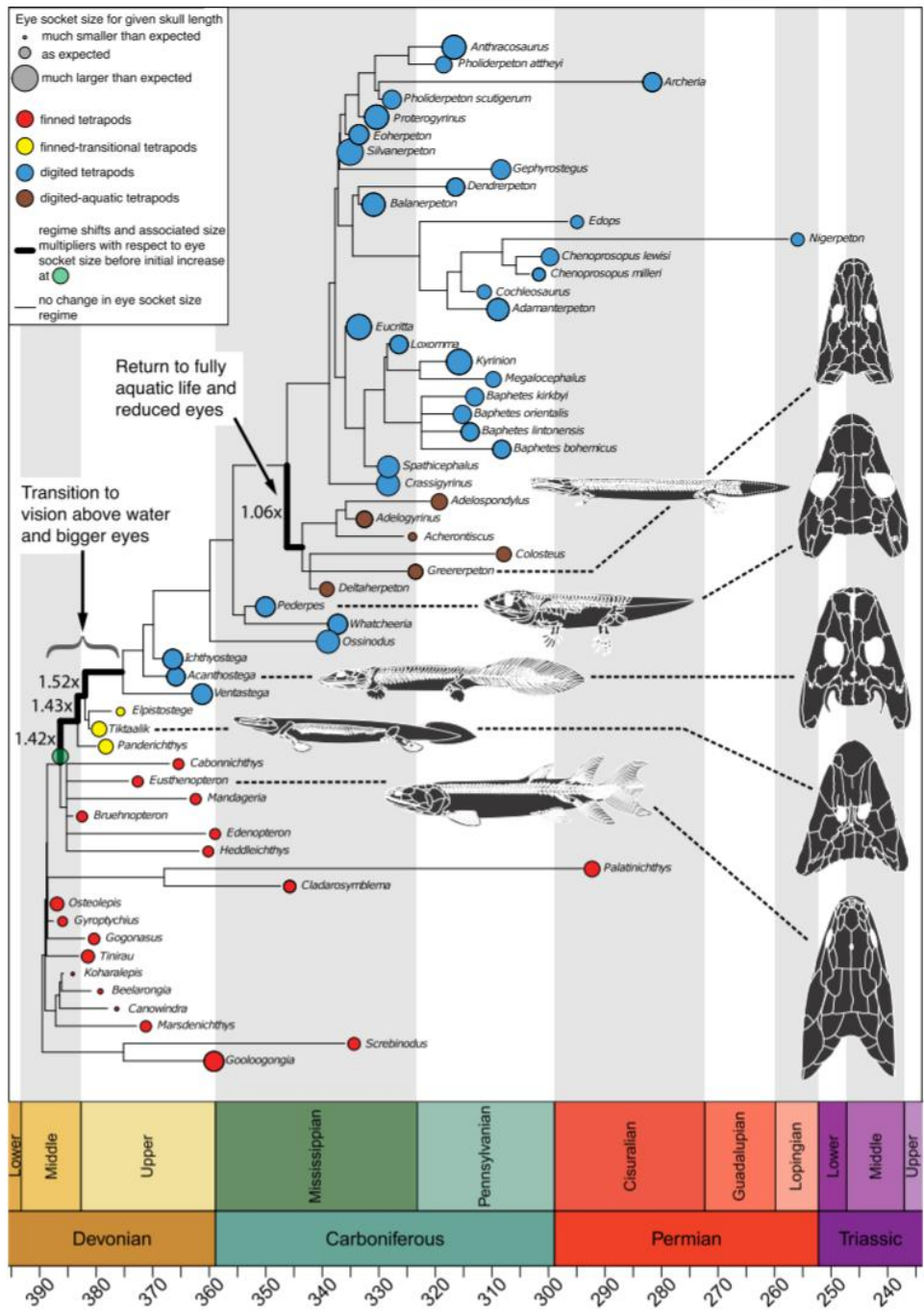
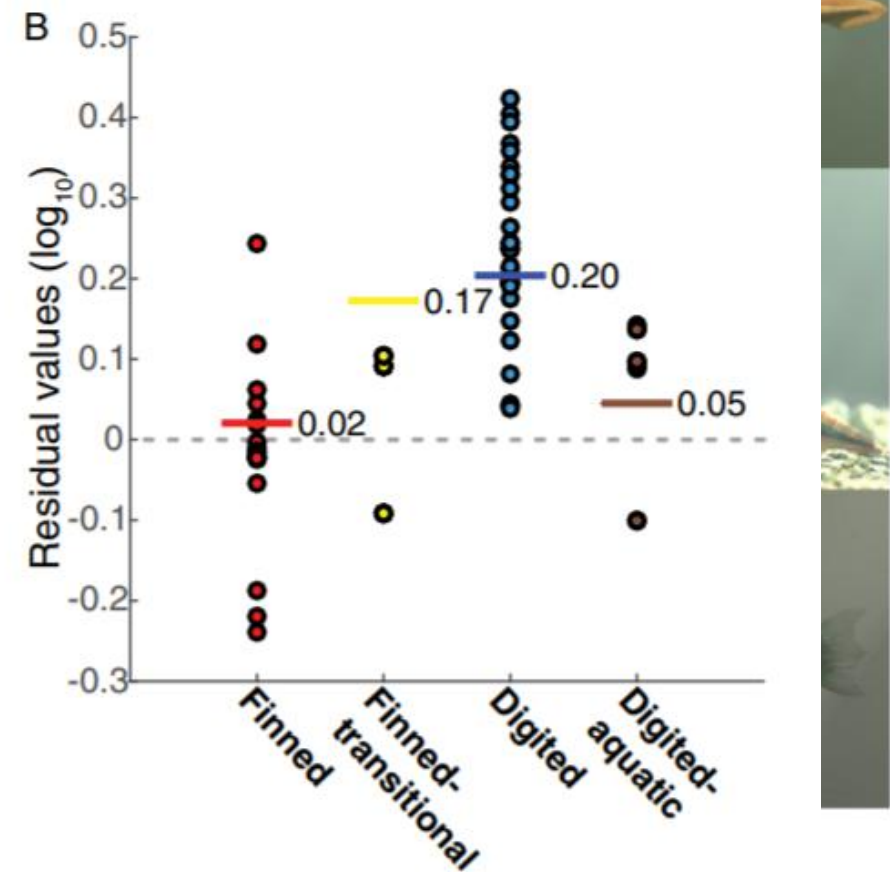


Shifts in Fossil Data: Unique Opportunities

Mclver et al. 2017,
PNAS



halflife =
5.79 my



Hunt, Bell & Travis 2007

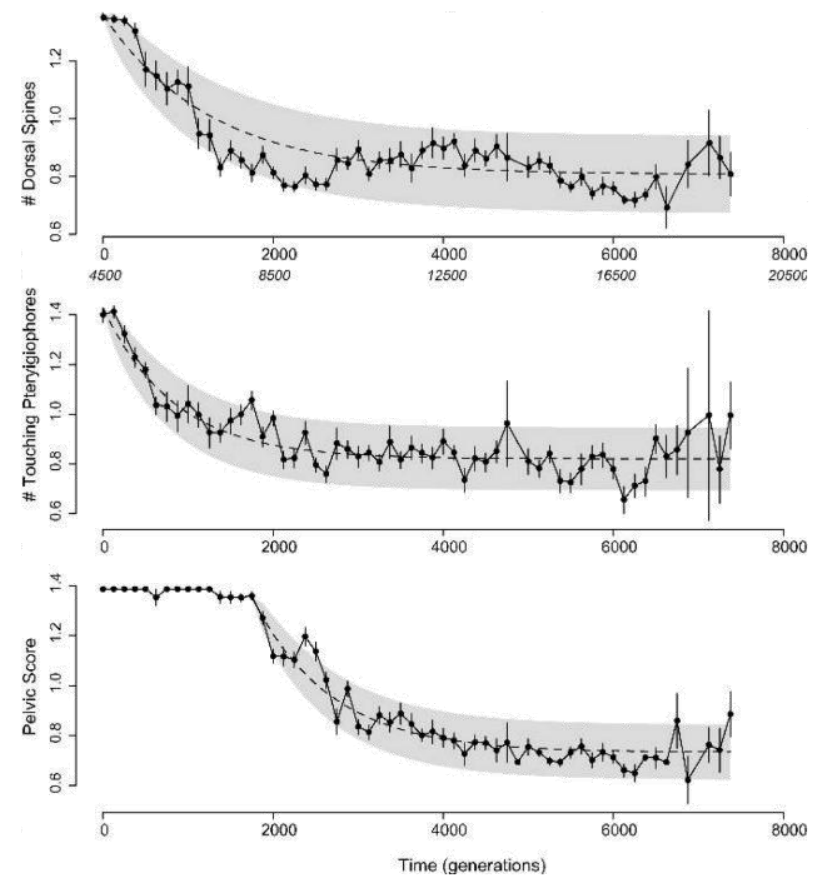
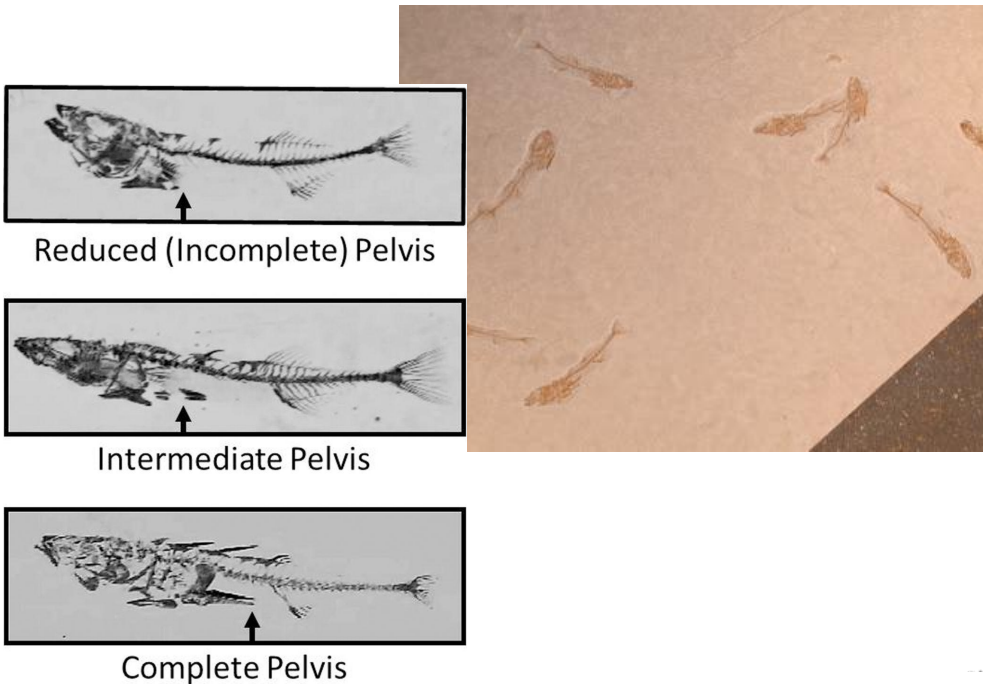


Table 3. Estimates and ranges for population genetic and selective parameters, derived from the maximum-likelihood parameter estimates for the adaptive model. Displacement is the phenotypic distance between the starting morphology and the optimal morphology, in standard deviation units (computed from the phenotypic variance pooled across samples, σ^2_p). Calculations of the effective population size (N_e) and strength of stabilizing selection (ω^2) require knowledge of trait heritabilities, which were assumed to range between 0.1 and 0.7. The ranges reported for N_e and ω^2 reflect calculation using these two different end-member heritability values. Finally, $t_{1/2}$ is the expected time it takes the population to traverse half the distance to the phenotypic optimum, in generations. For details on the calculation of these quantities, see the Appendix.

Trait	Displacement	σ^2_p	N_e	ω^2	$t_{1/2}$
No. of dorsal spines	-2.80	0.041	575–4023	5.0–35.2	853
Pterygiophores	-2.13	0.081	851–5957	6.7–47.3	580
Pelvic score	-2.57	0.059	889–6222	5.3–37.5	635

Strength of OU models: It looks like evolution! Parameters (could potentially) have biological meaning!

Weaknesses: Statistical “bad dog”. Without constraints, can behave wildly.

**But what if the optimum doesn't
have discrete shifts?**

What if it moves continuously?

SLOUCH (Hansen, Pienaar & Orzack 2008)

ORIGINAL ARTICLE

doi:10.1111/j.1558-5646.2008.00412.x

A COMPARATIVE METHOD FOR STUDYING ADAPTATION TO A RANDOMLY EVOLVING ENVIRONMENT

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²*Department of Biological Sciences, Florida State University, Tallahassee, Florida 32306*

³*E-mail: thomas.hansen@bio.uio.no*

⁵*Fresh Pond Research Institute, Cambridge, Massachusetts 02140*

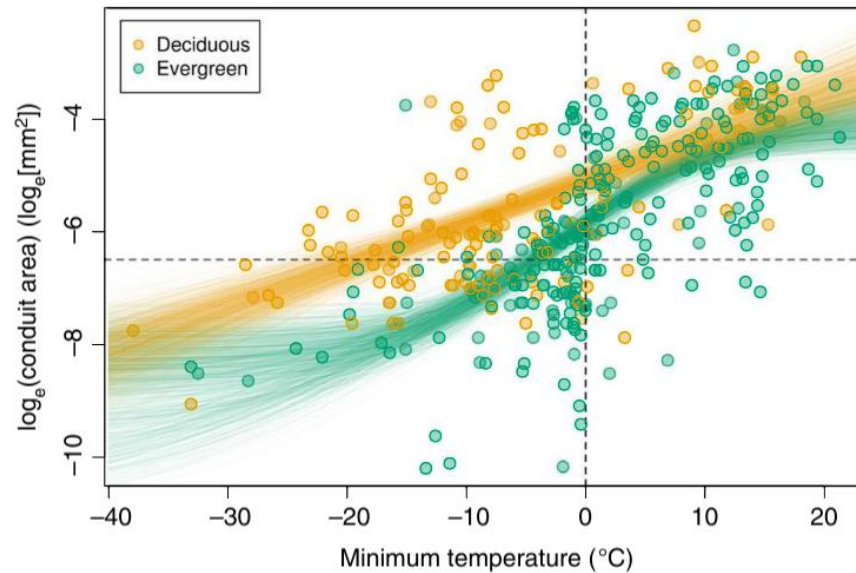
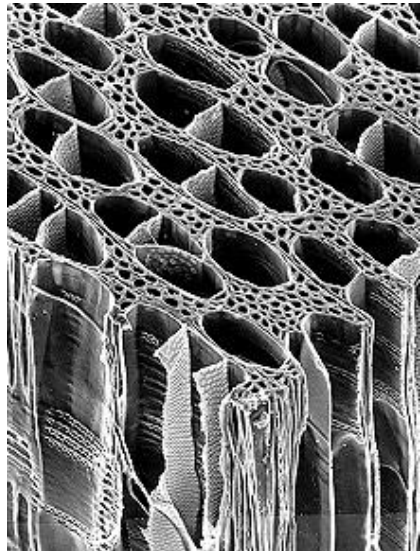
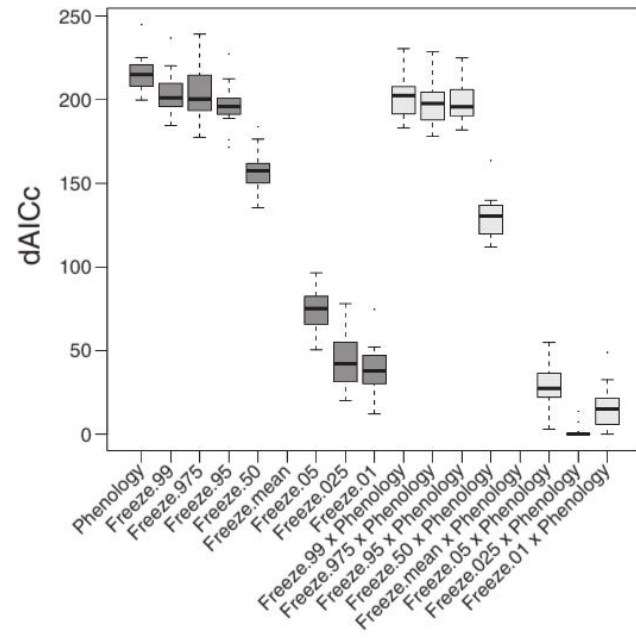
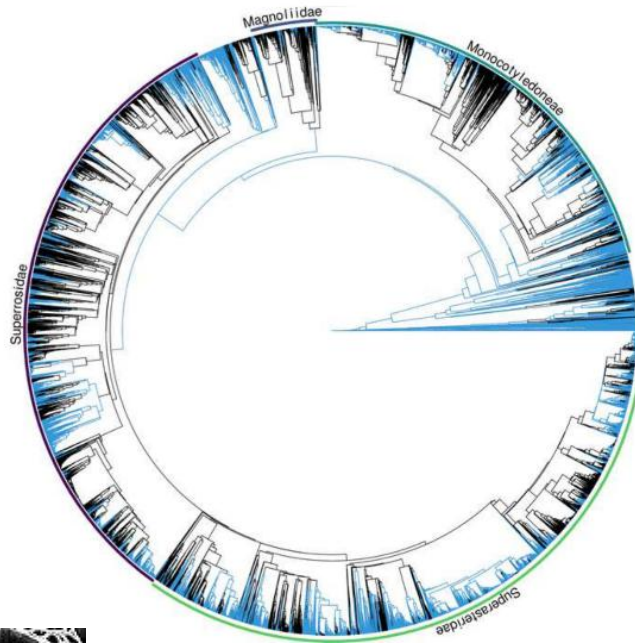


Fig. 6 Bayesian posteriors of estimates of best-fitting functional relationships between macroevolutionary adaptive optima for natural log of conduit area and minimum temperature at the 2.5th percentile of geographic distribution. Functions are fit separately for deciduous (gold) and evergreen (green) species. Best-fitting models for deciduous species are linear, whereas evergreen species follow a sigmoid relationship with the center around freezing (vertical dashed line). The horizontal black dashed line is at 0.0015 mm² (i.e. the 0.044 mm diameter threshold above which freezing induced embolisms are believed to become frequent at modest tensions; Davis *et al.*, 1999).

Method	Shift mapping	α & σ	Multivariate?	Optimum change	Inference approach	Predictors?	Convergent regimes?
OUCH (Butler & King 2004)	User hypotheses	Global	Yes	Discrete	Maximum Likelihood	Discrete regimes	Yes
Ouwie (Bealieu et al. 2012)	User hypotheses/ simmap	Regime-specific	No	Discrete	Maximum Likelihood	Discrete regimes	Yes
mvMORPH (Clavel 2015)	User hypotheses/ simmap	Global	Yes	Discrete	Maximum Likelihood	Discrete regimes	Yes
SLOUCH (Hansen et al. 2008)	None	Global	No	Brownian Motion	Maximum Likelihood	Continuously-evolving predictors	N/A
mvSLOUCH (Bartoszek et al. 2012)	None	Global	Yes	Brownian Motion/OU	Maximum Likelihood	Continuously co-evolving	N/A
SURFACE (Ingram & Mahler 2013)	Data driven (Stepwise AIC)	Global	Pseudo	Discrete	Maximum Likelihood	No	Yes
l1ou (Khabbazian et al. 2016)	Data driven (Lasso)	Global	No	Discrete	Maximum Likelihood	No	Yes
PhylogeneticEM (Bastide et al. 2018)	Data driven (Expectation maximization)	Global	Yes	Discrete	Maximum Likelihood	No	Yes
Bayou (Uyeda & Harmon 2014)	Data driven (RJMCMC)	Global	No	Discrete +	Bayesian	Regression framework	Not with RJMCMC

Overwhelmed? Take-home:

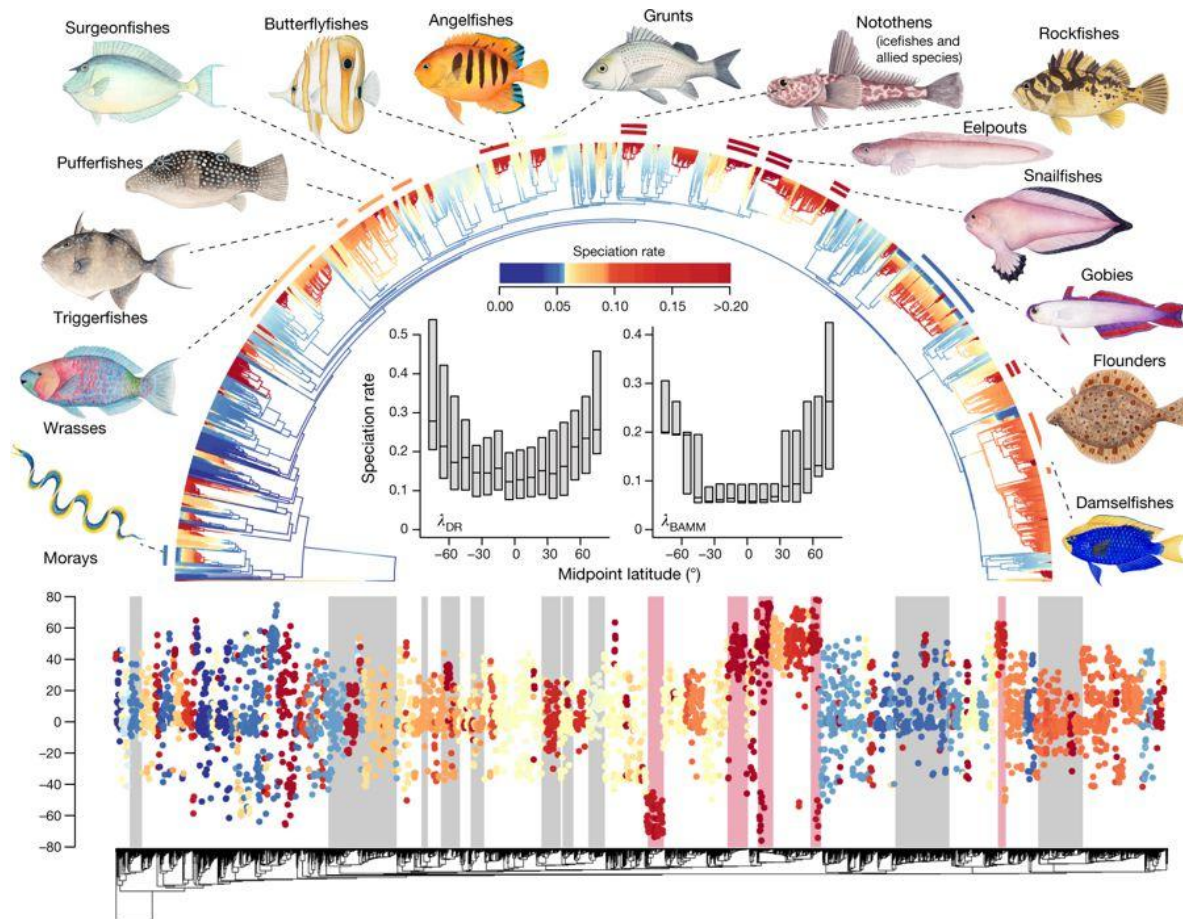
Lots of variations on a basic model (OU)

Models where everything vary ->
Probably too complicated to fit to real data!

How you can simplify the model with what you KNOW.

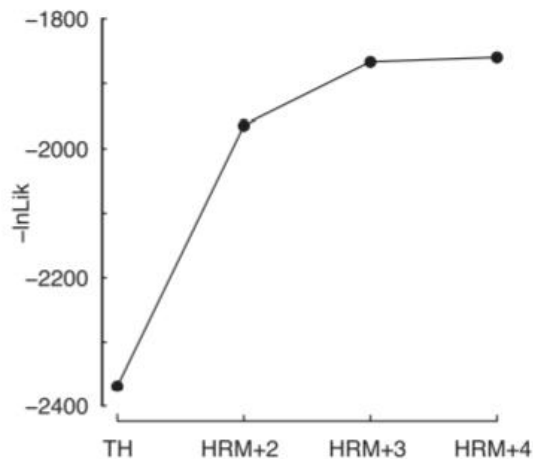
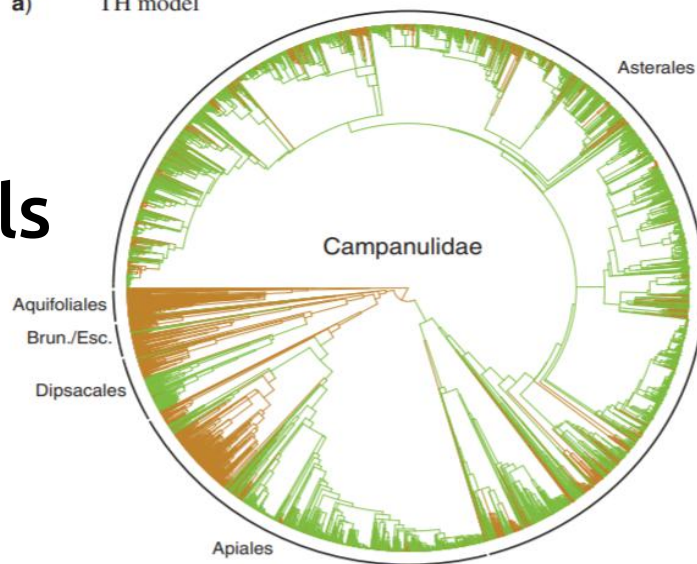
Choose software that tests YOUR hypothesis and lets you incorporate YOUR knowledge

Similar models for Diversification: BAMM (Rabosky 2014)



Shifts in Discrete Character Data: Hidden State Models

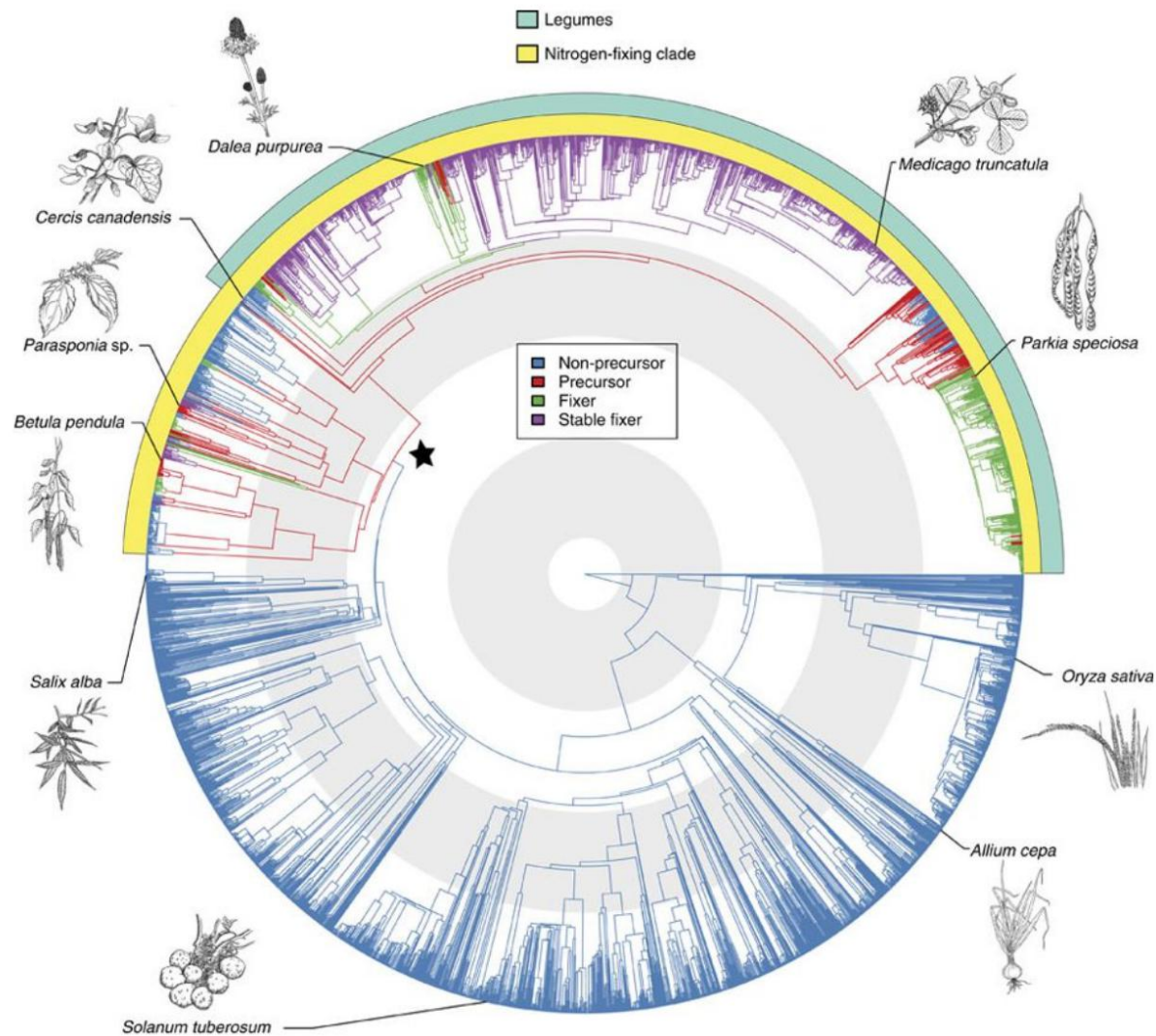
a) TH model



Identifying Hidden Rate Changes in the Evolution of a Binary Morphological Character:
The Evolution of Plant Habit in Campanulid Angiosperms

JEREMY M. BEAULIEU^{1,*}, BRIAN C. O'MEARA², AND MICHAEL J. DONOGHUE¹

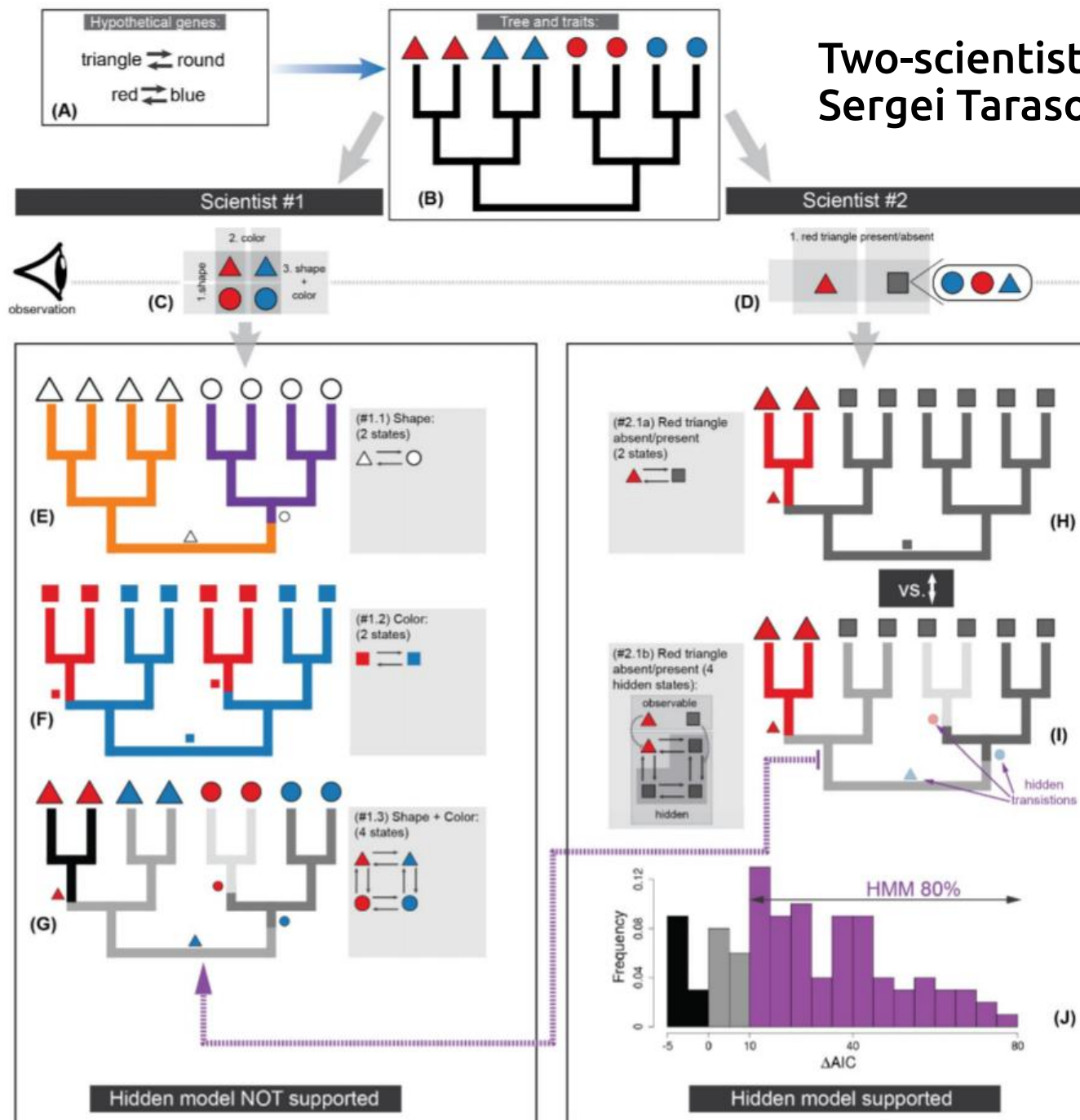
`install.packages("corHMM")`



A single evolutionary innovation drives the deep evolution of symbiotic N₂-fixation in angiosperms

Gijsbert D.A. Werner¹, William K. Cornwell^{1,†}, Janet I. Sprent², Jens Kattge^{3,4} & E. Toby Kiers¹

Two-scientist Paradox Sergei Tarasov



Like phylogenetic models, lots of PCMs devoted to *heterogeneity in the tempo & mode of evolution*

Continuous traits:

BM (bayestraits, Auteur, BAMM, OUwie)

OU (bayou, l1ou, PhylogeneticEM)

Discrete traits

Hidden State Models (corHMM)

Diversification Models (BAMM, HiSSE, FiSSE)

The PCM “Sweet Spot”

