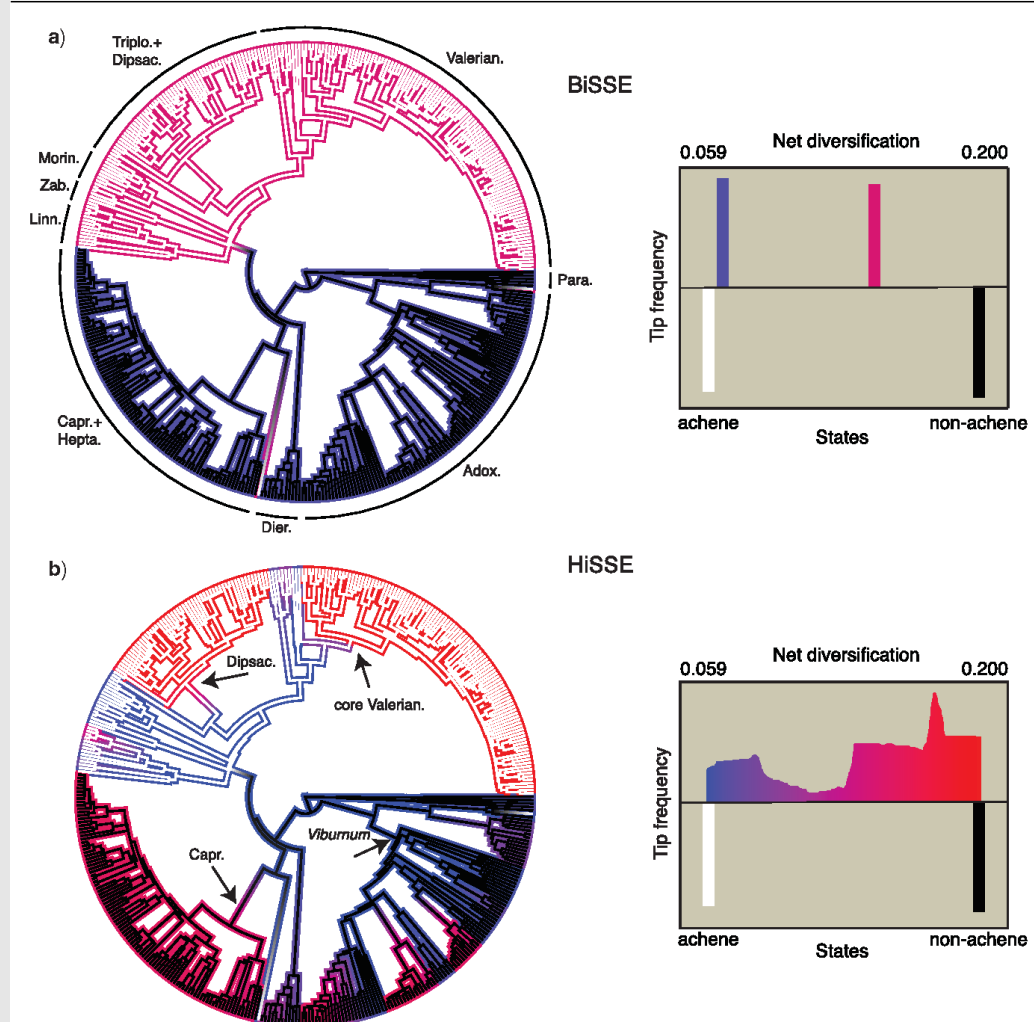


Diversification 2

598

SYSTEMATIC BIOLOGY

VOL. 65



Brian O'Meara
EEB464 Fall 2018

Learning objectives

Understand a way to examine effect of traits on diversity

Be able to extend our discussions in class into new areas

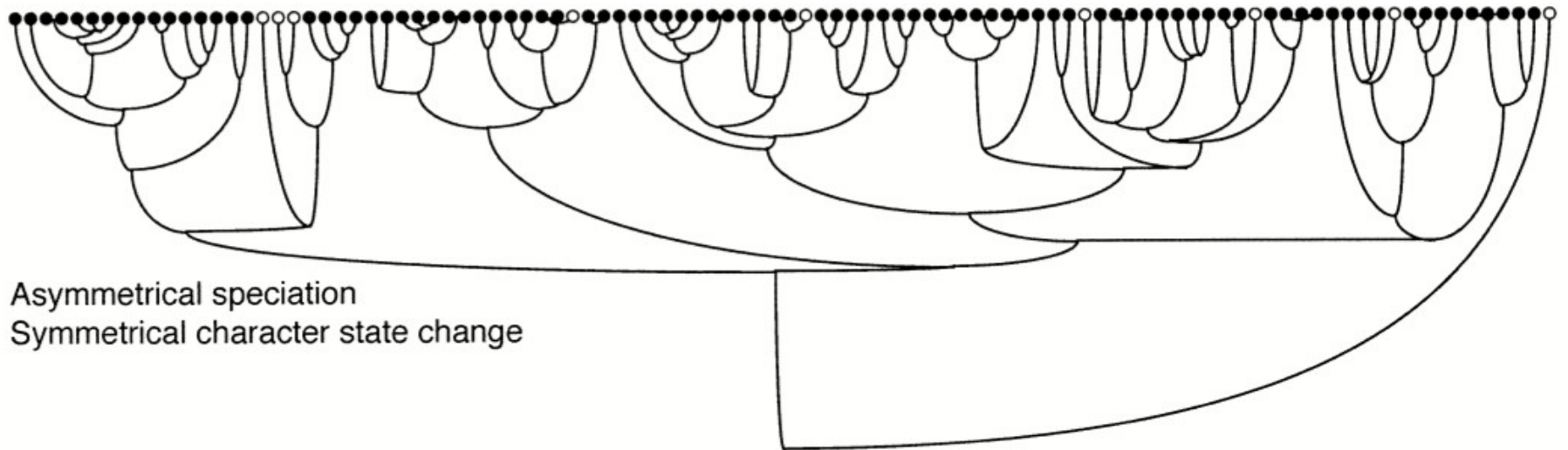


FIG. 1. An example tree and character distribution, simulated with biased speciation. Rate of speciation with state 1 (black) five times higher than rate of speciation with state 0 (white). States at internal nodes are parsimony reconstructions, not the actual ancestral states as simulated.

TABLE 1. Interpreted biases in character change (maximum likelihood estimate of ratio of gain/loss rates) for various probabilities of speciation for states 0 and 1 in each time interval of the simulation. A value of 1 indicates no bias. Medians for 10,001 replicates. Diagonal (bold) suggests no bias is interpreted when rates of speciation are equal. Above the diagonal the (mis)interpreted biases are in favor of changes to state 1; below the diagonal to state 0.

Probability of speciation with state 0	Probability of speciation with state 1				
	0.0001	0.0002	0.0003	0.0004	0.0005
0.0001	1.00	1.44	1.79	2.16	2.41
0.0002	0.70	0.99	1.18	1.35	1.52
0.0003	0.56	0.85	1.00	1.12	1.24
0.0004	0.46	0.76	0.88	1.00	1.11
0.0005	0.42	0.66	0.82	0.89	1.00

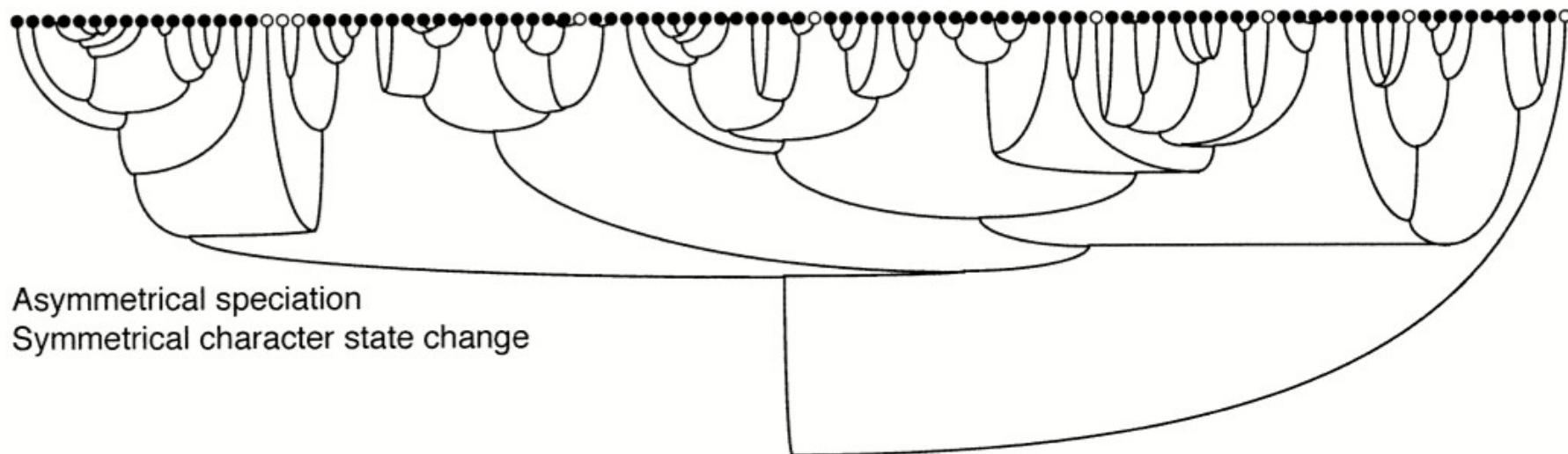


FIG. 1. An example tree and character distribution, simulated with biased speciation. Rate of speciation with state 1 (black) five times higher than rate of speciation with state 0 (white). States at internal nodes are parsimony reconstructions, not the actual ancestral states as simulated.

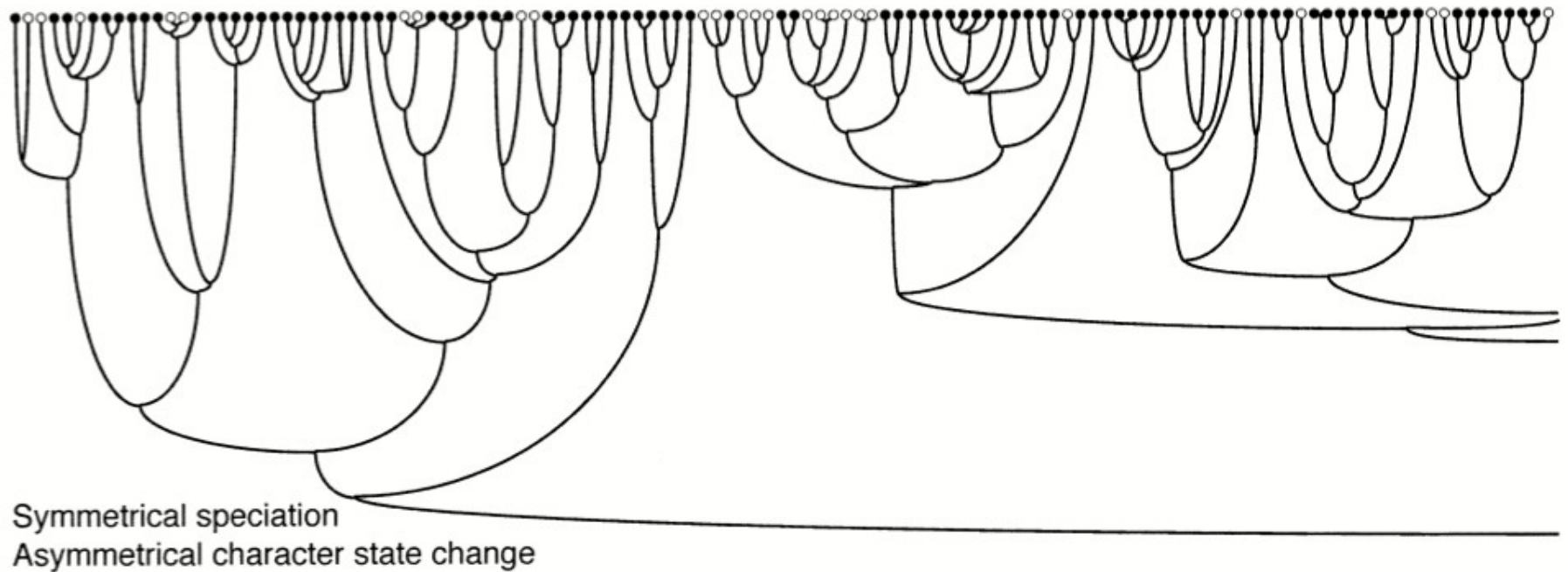
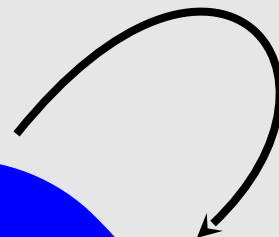
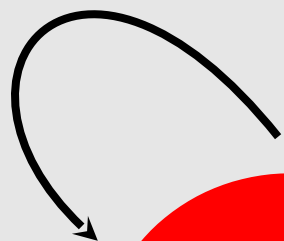


FIG. 2. An example tree with character distribution from the simulations of biased character change. Rate of 0 to 1 change is four times greater than rate of 1 to 0 change. States at internal nodes are parsimony reconstructions.

speciation₀

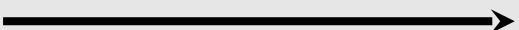
speciation₁



q_{10}



q_{01}



extinction₀



extinction₁



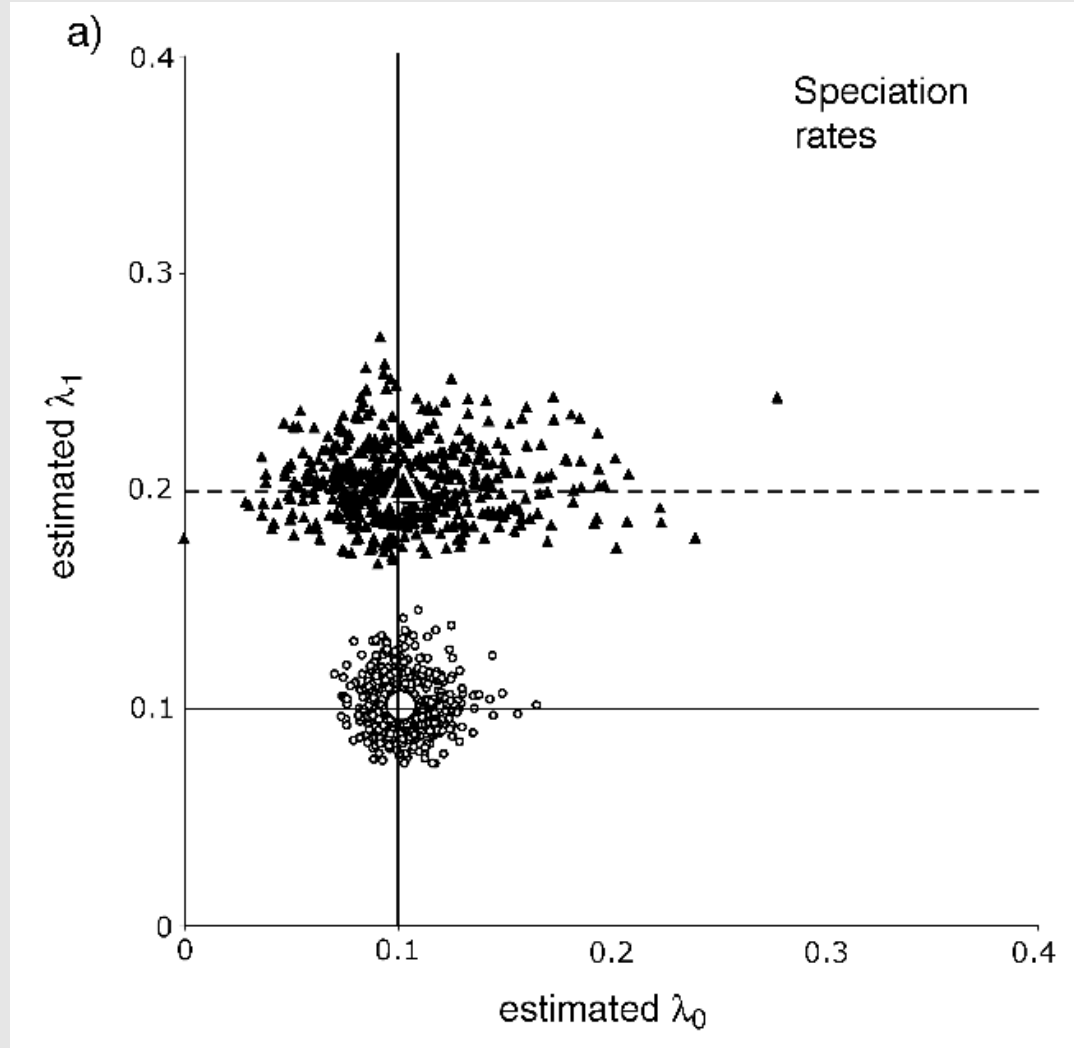


FIGURE 4. Estimated parameter values from simulated trees and characters. Lines indicate true parameter values of the simulations (solid, equal rates for the two states; dashed, unequal). Small symbols represent estimates; large symbols represent mean values of estimates. Open circles represent parameter estimates from symmetrical simulations; i.e., equal parameter values for states 0 and 1 (speciation rates 0.1, extinction rates 0.03, character change 0.01). Closed triangles represent estimates from simulations with asymmetries in the respectively estimated parameters. Asymmetries shown are (a) speciation rate asymmetry ($\lambda_1 = 0.1$ versus 0.2), (b) extinction rate asymmetry ($\mu_0 = 0.03$ versus 0.06), and (c) character state change rate asymmetry ($q_{10} = 0.01$ versus 0.005). In the maximum likelihood analysis, all six parameters were free to vary, but each scatterplot focuses only on the parameters of interest in each case.

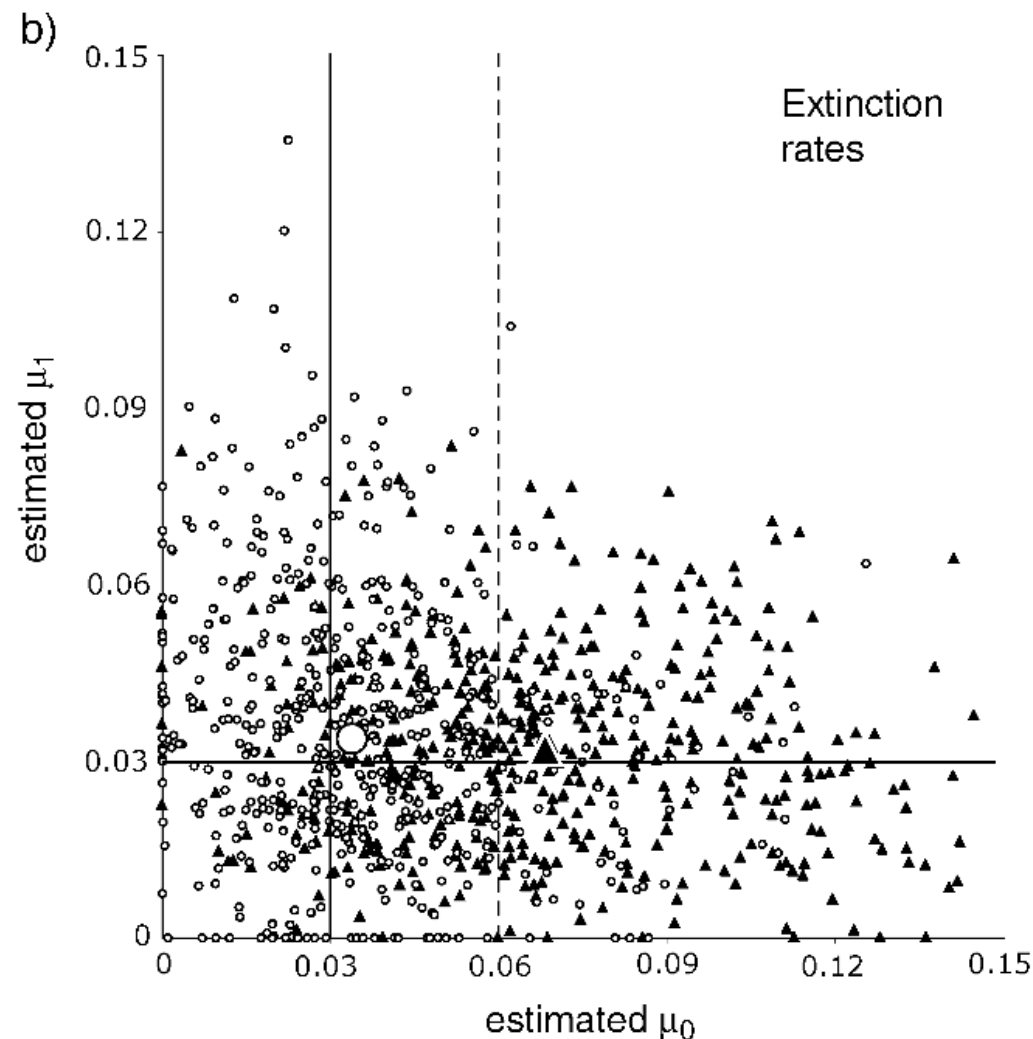


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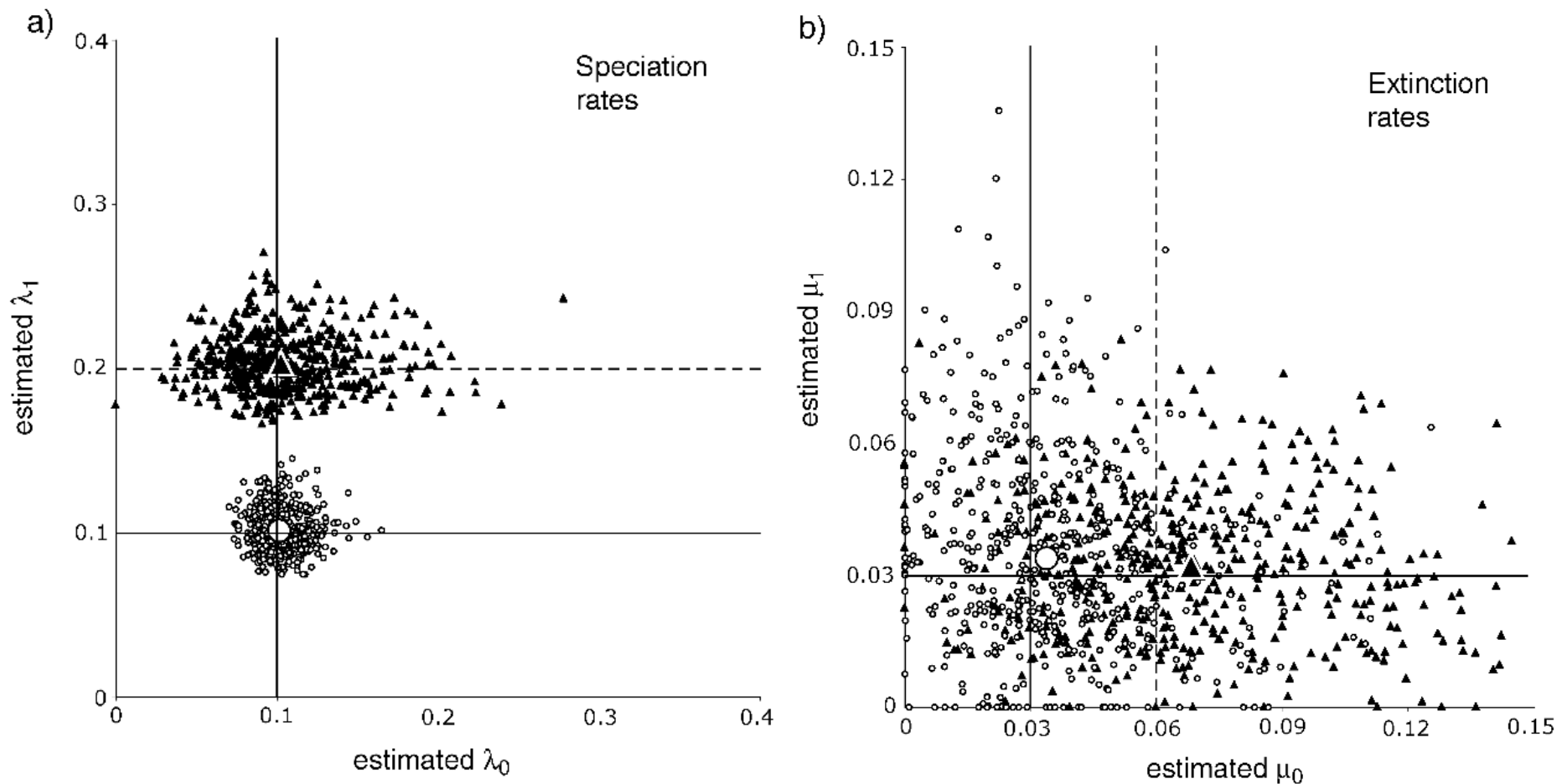


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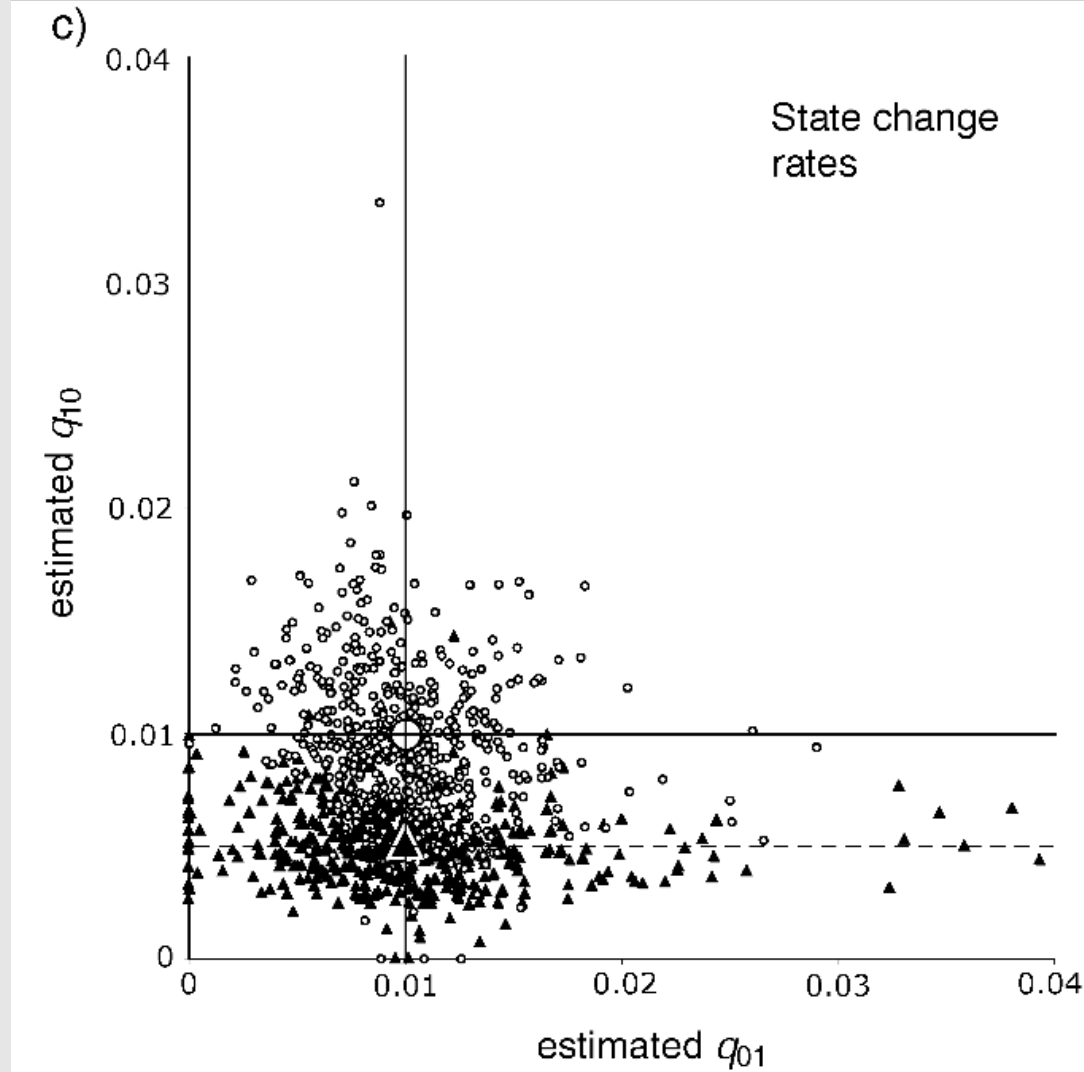
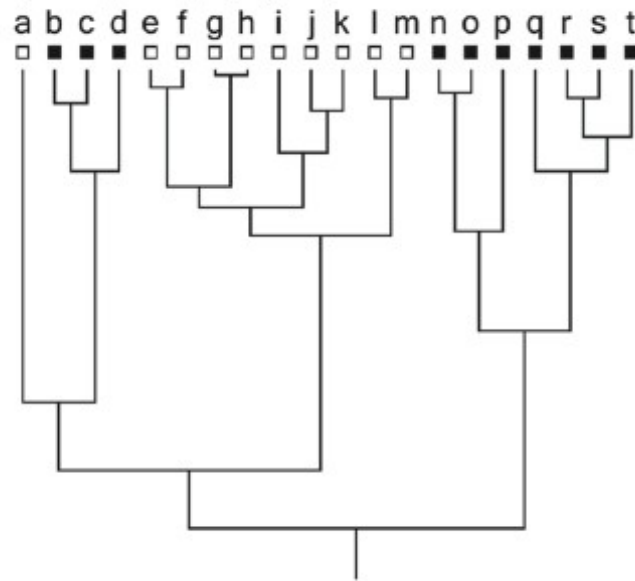
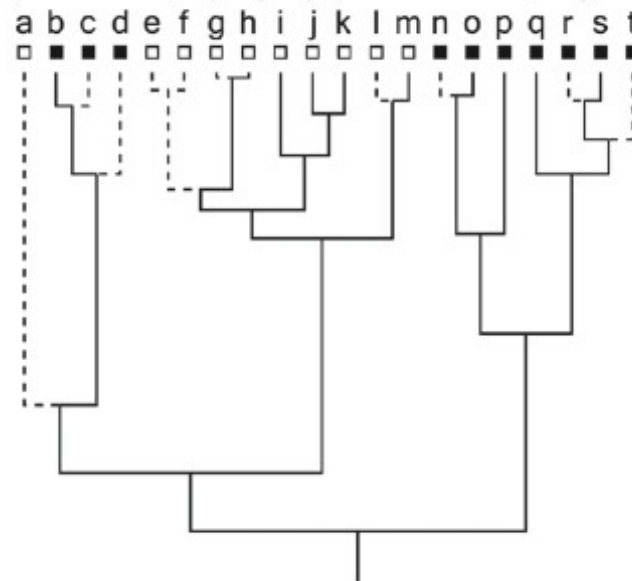


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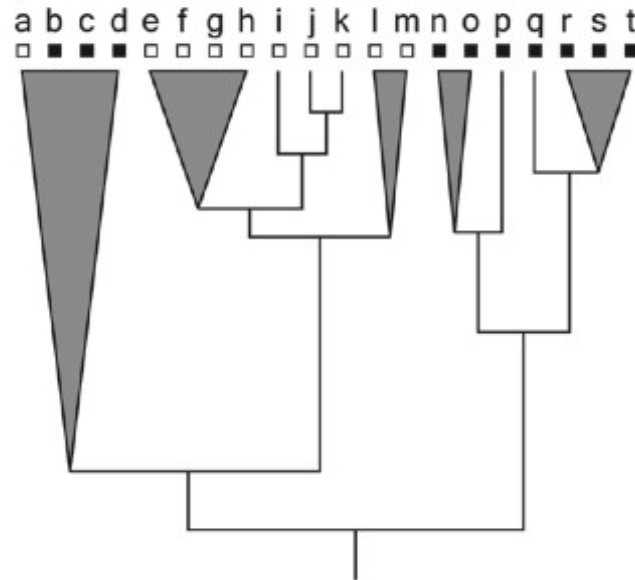
a) Complete phylogeny



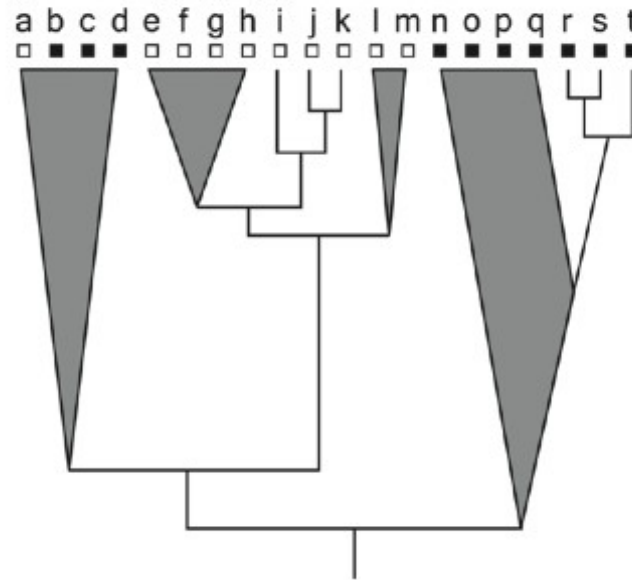
b) Skeleton phylogeny (random sampling)



c) Terminally unresolved phylogeny

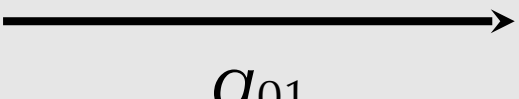
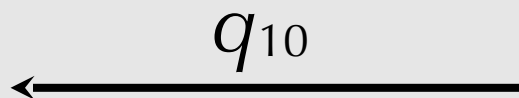
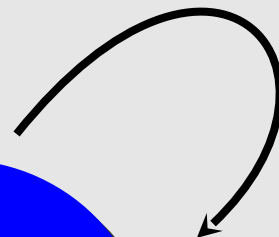
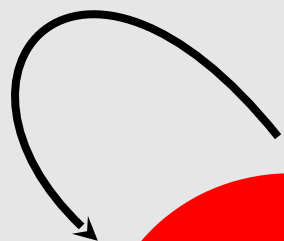


d) Other phylogeny, not handled



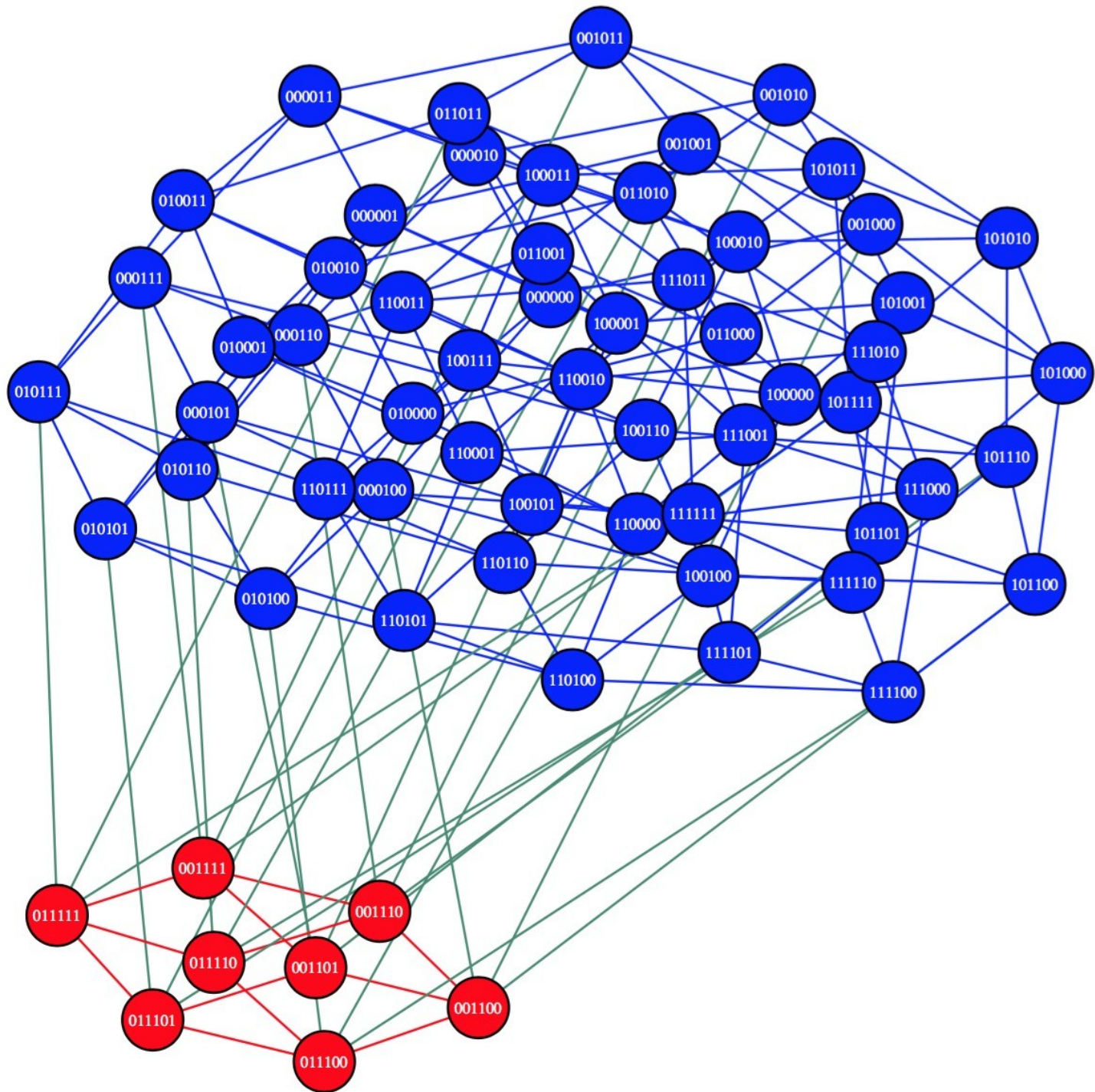
speciation₀

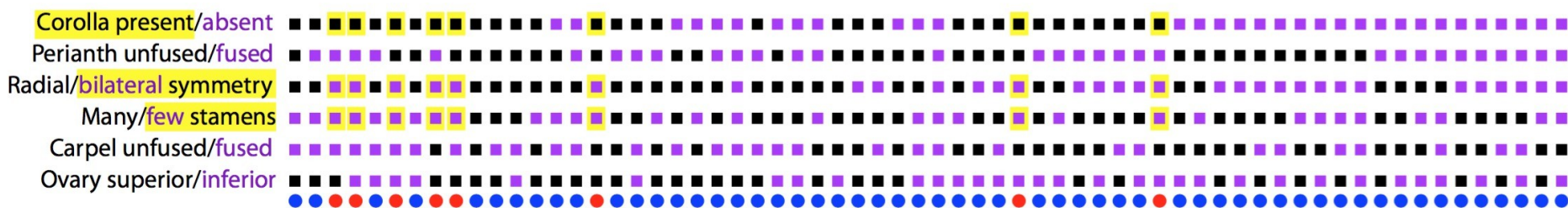
speciation₁

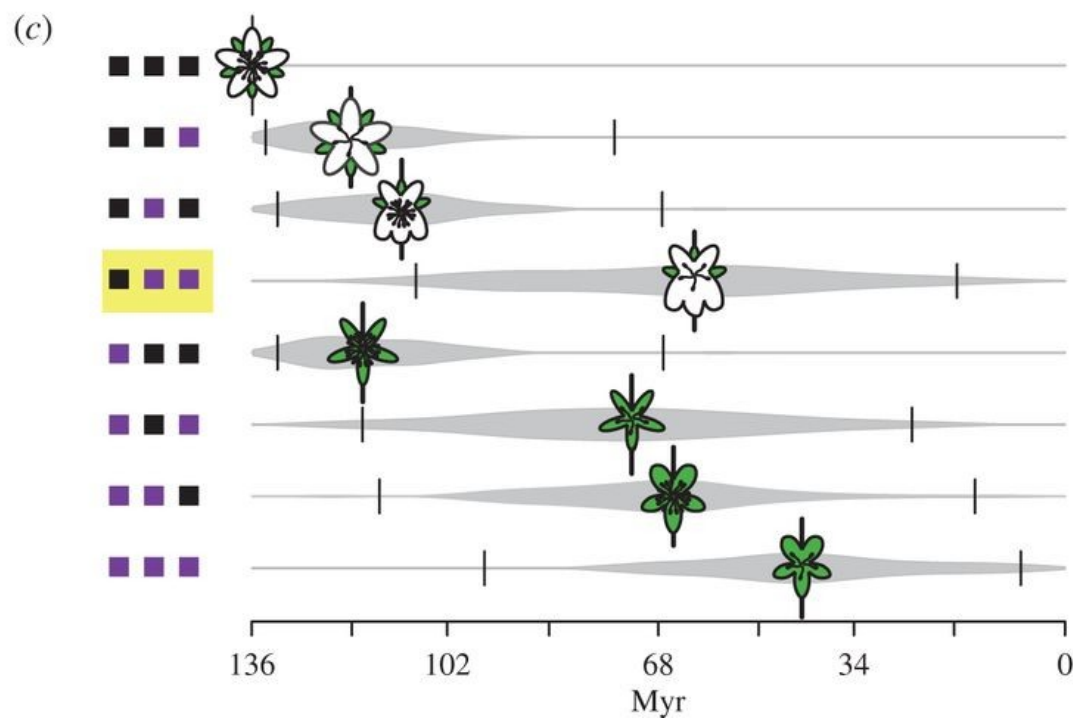
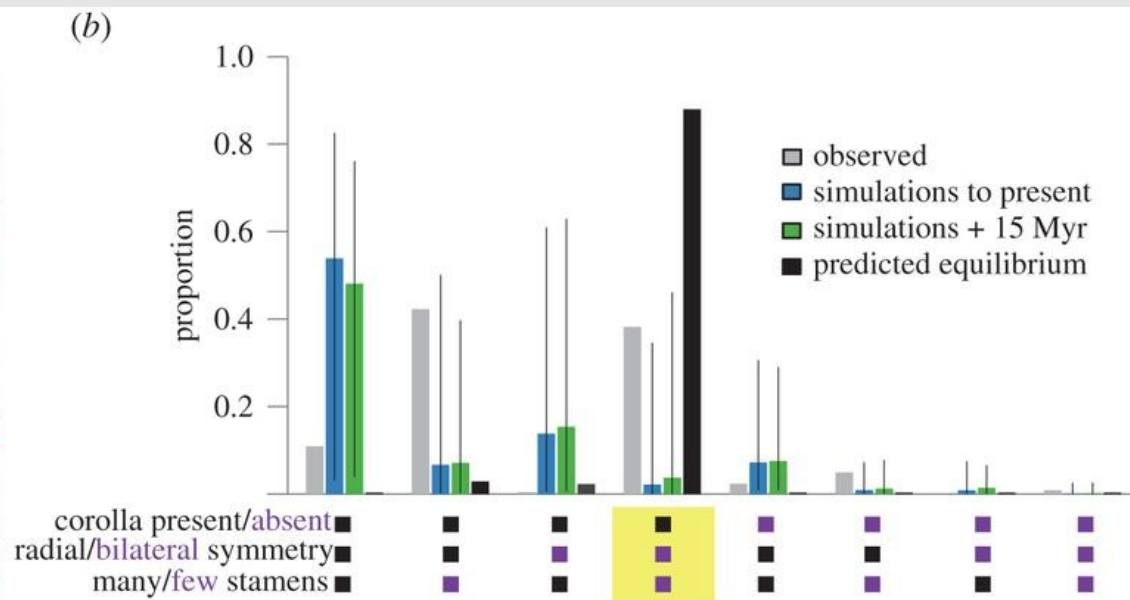
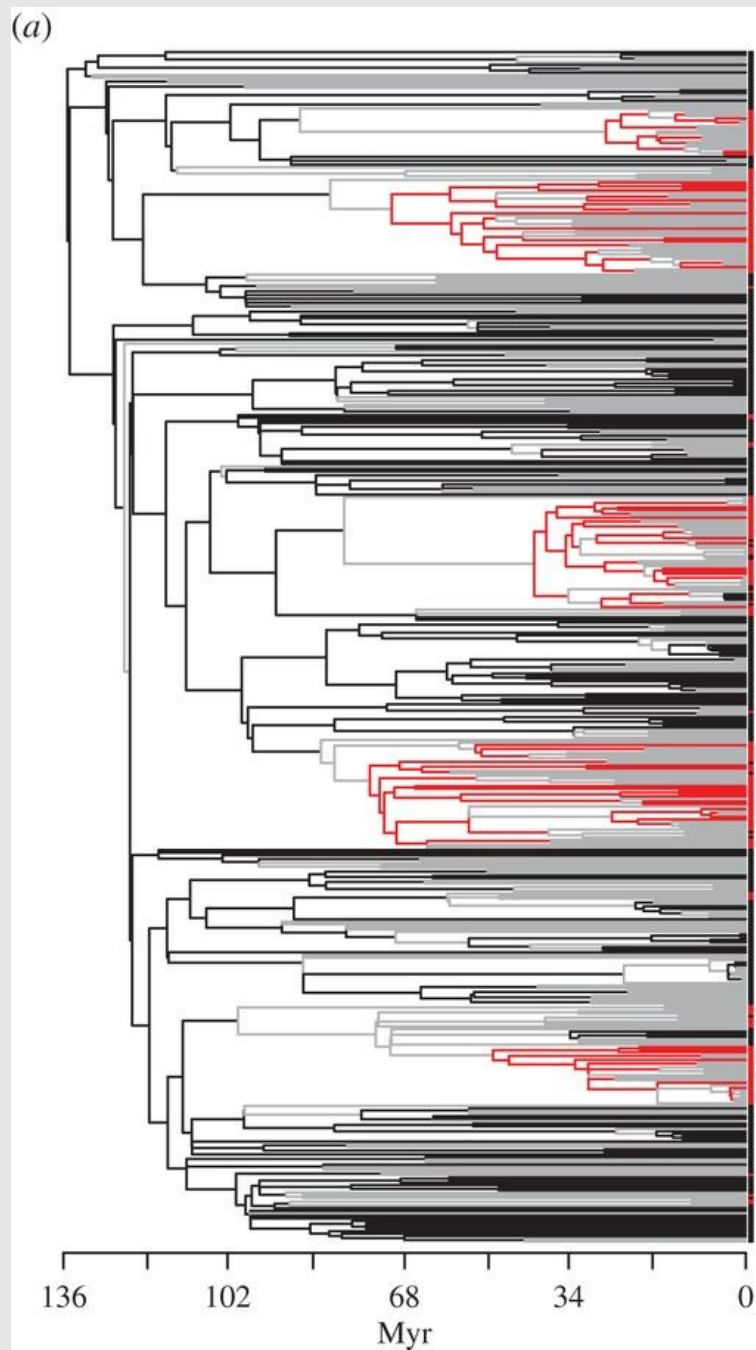


extinction₀

extinction₁







Why are some traits and trait combinations exceptionally common across the tree of life, whereas others are vanishingly rare? The distribution of trait diversity across a clade at any time depends on the ancestral state of the clade, the rate at which new phenotypes evolve, the differences in speciation and extinction rates across lineages, and whether an equilibrium has been reached. Here we examine the role of transition rates, differential diversification (speciation minus extinction) and non-equilibrium dynamics on the evolutionary history of angiosperms, a clade well known for the abundance of some trait combinations and the rarity of others. **Our analysis reveals that three character states (corolla present, bilateral symmetry, reduced stamen number) act synergistically as a key innovation, doubling diversification rates for lineages in which this combination occurs. However, this combination is currently less common than predicted at equilibrium because the individual characters evolve infrequently.** Simulations suggest that angiosperms will remain far from the equilibrium frequencies of character states well into the future. Such non-equilibrium dynamics may be common when major innovations evolve rarely, allowing lineages with ancestral forms to persist, and even outnumber those with diversification-enhancing states, for tens of millions of years.

O'Meara, Smith, et al. 2016.

Diversification, speciation, extinction

- Which matters more in structuring what we see: speciation or extinction? [Speciation = 1, Ext=2]
- Can speciation and extinction rates evolve? Why or why not? [Yes = 1, No = 2]
- Why study diversification, not just speciation and extinction?
- $\text{Div.} = \text{Spec.} - \text{Ext.}$. Are there other parameters to describe the process that might be informative?