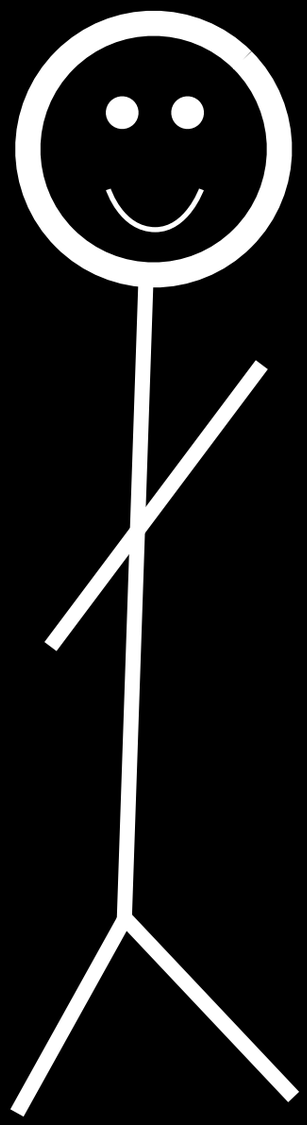
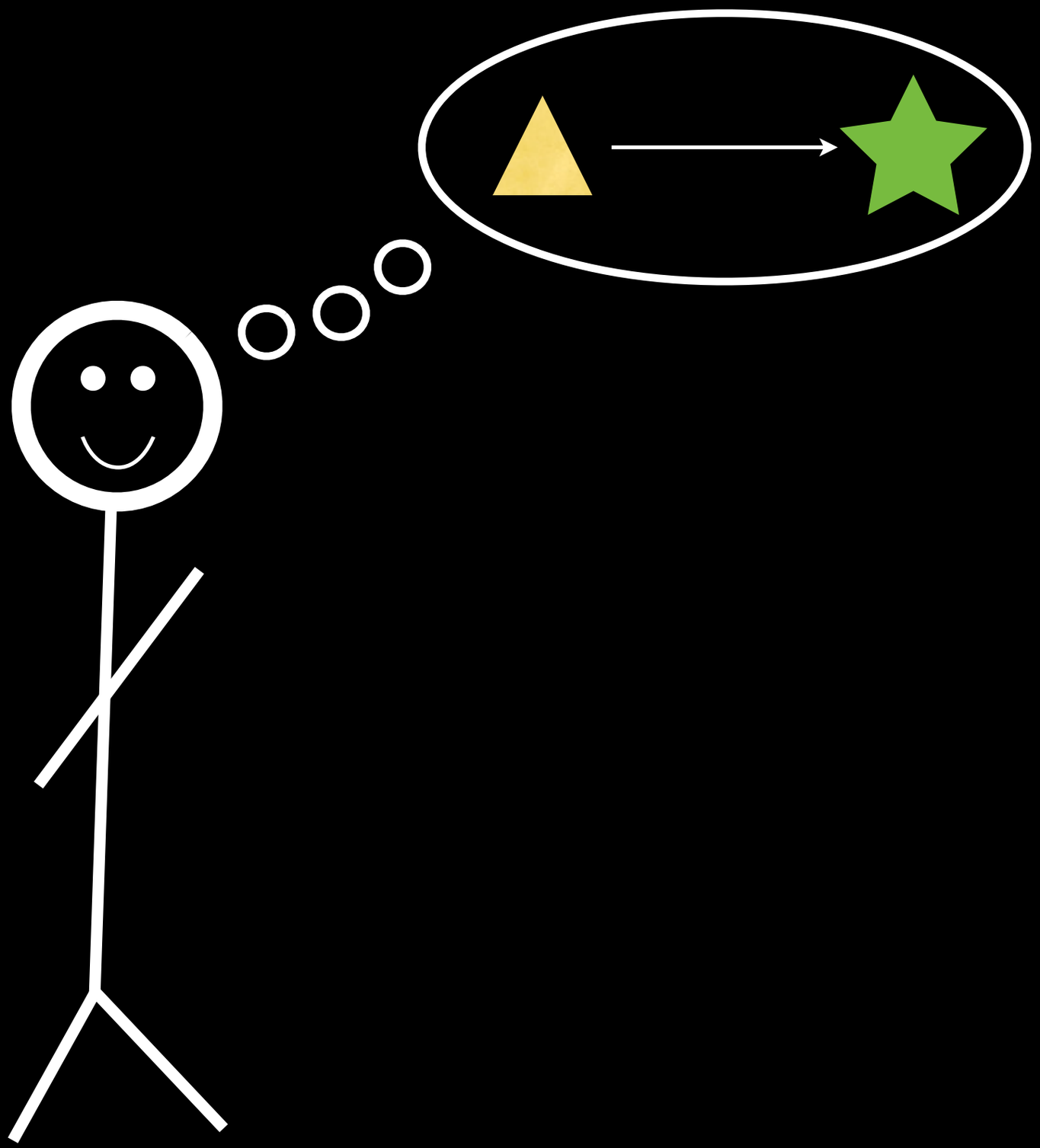
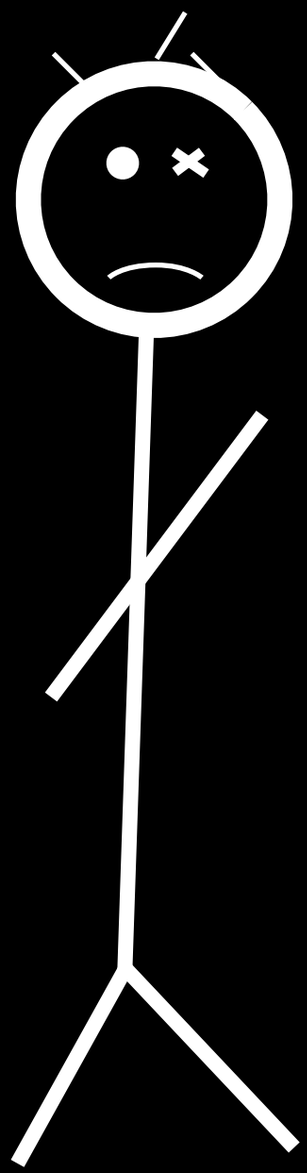
New frontiers for the comparative analysis of adaptive radiation

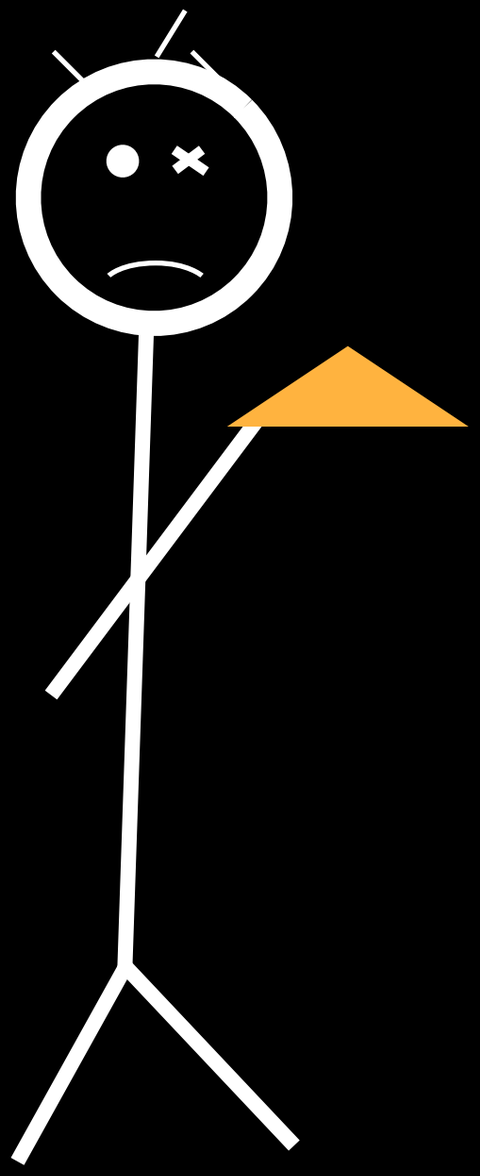
Luke J. Harmon
University of Idaho

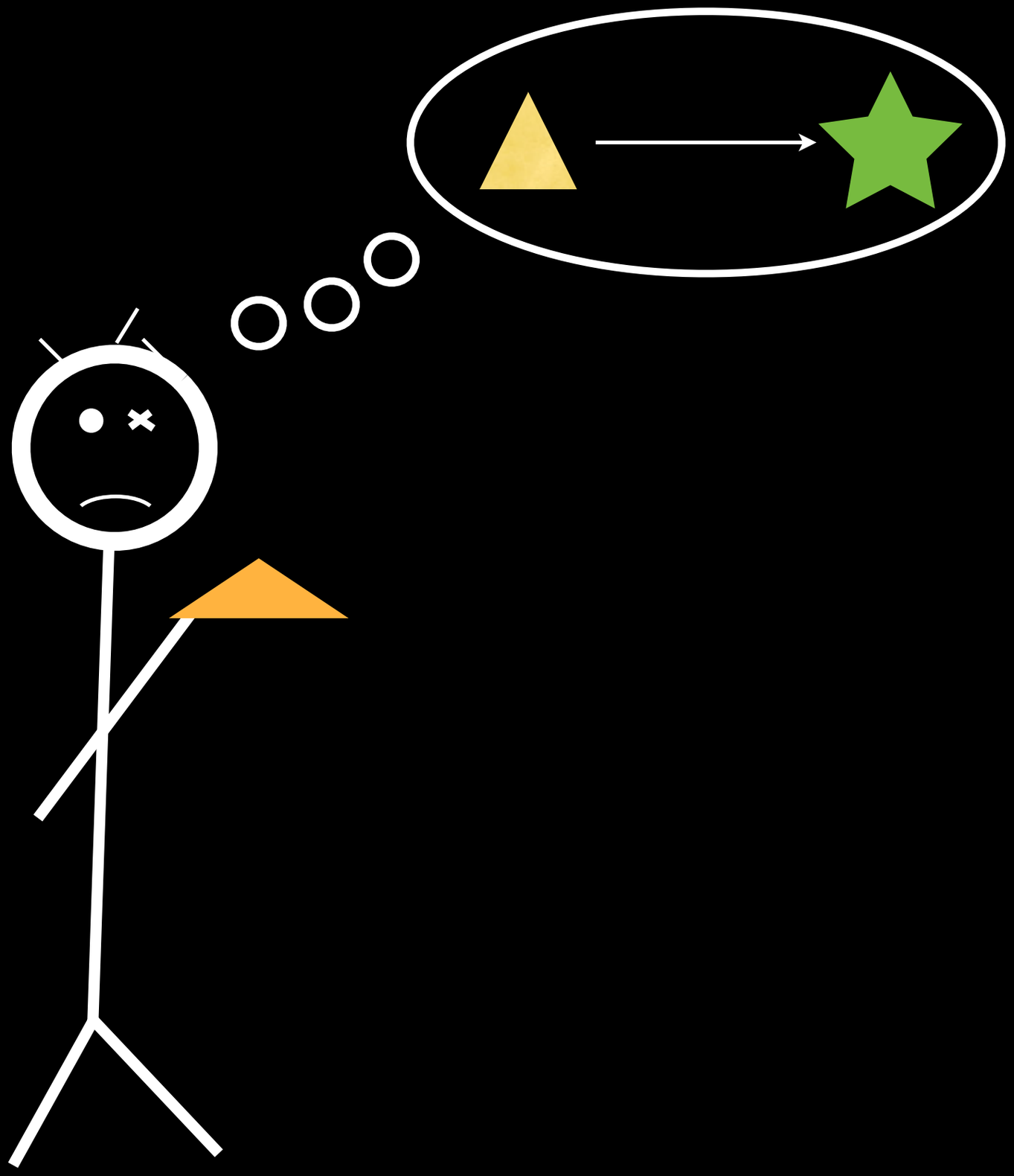




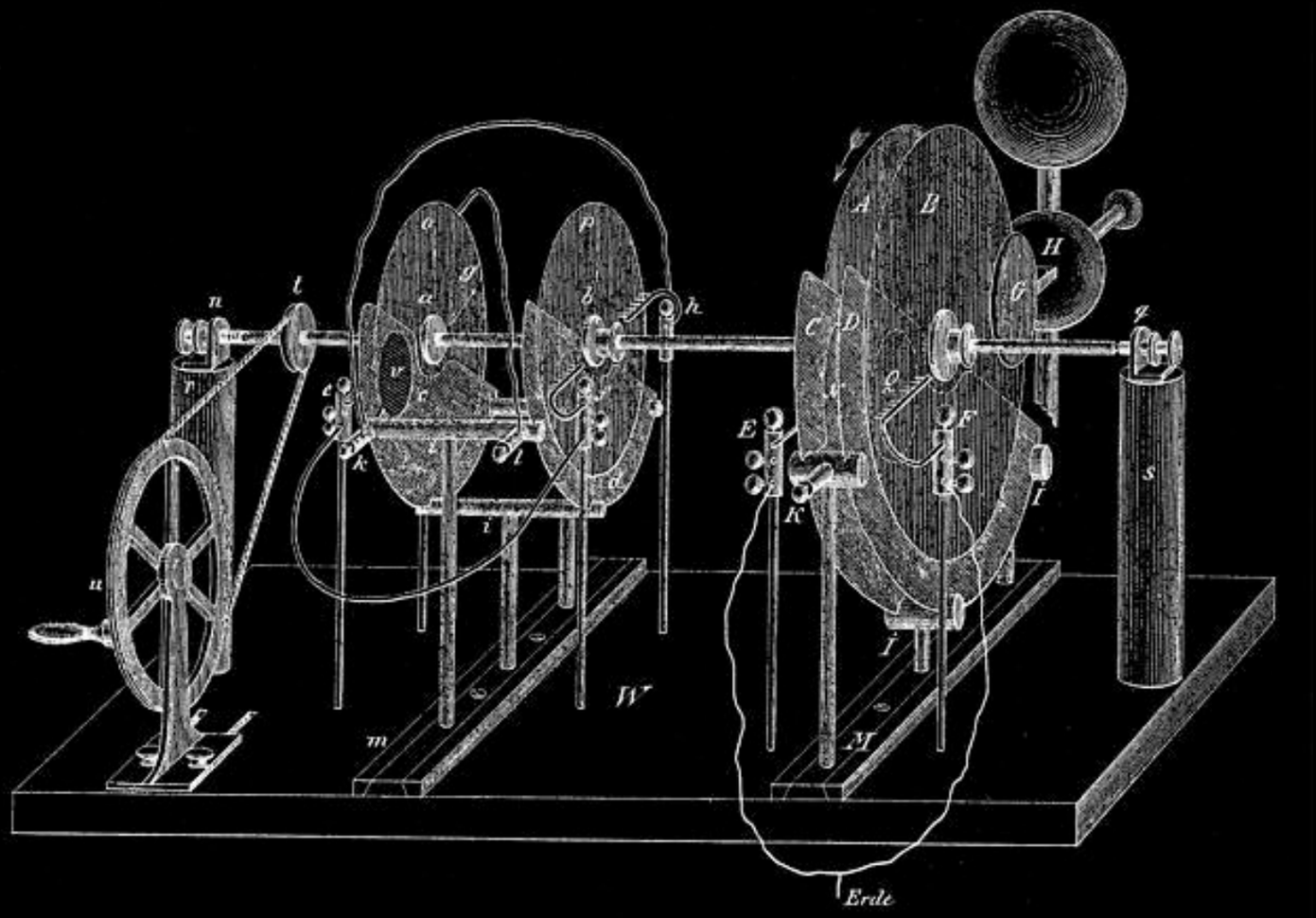
Tuesday, February 15, 2011



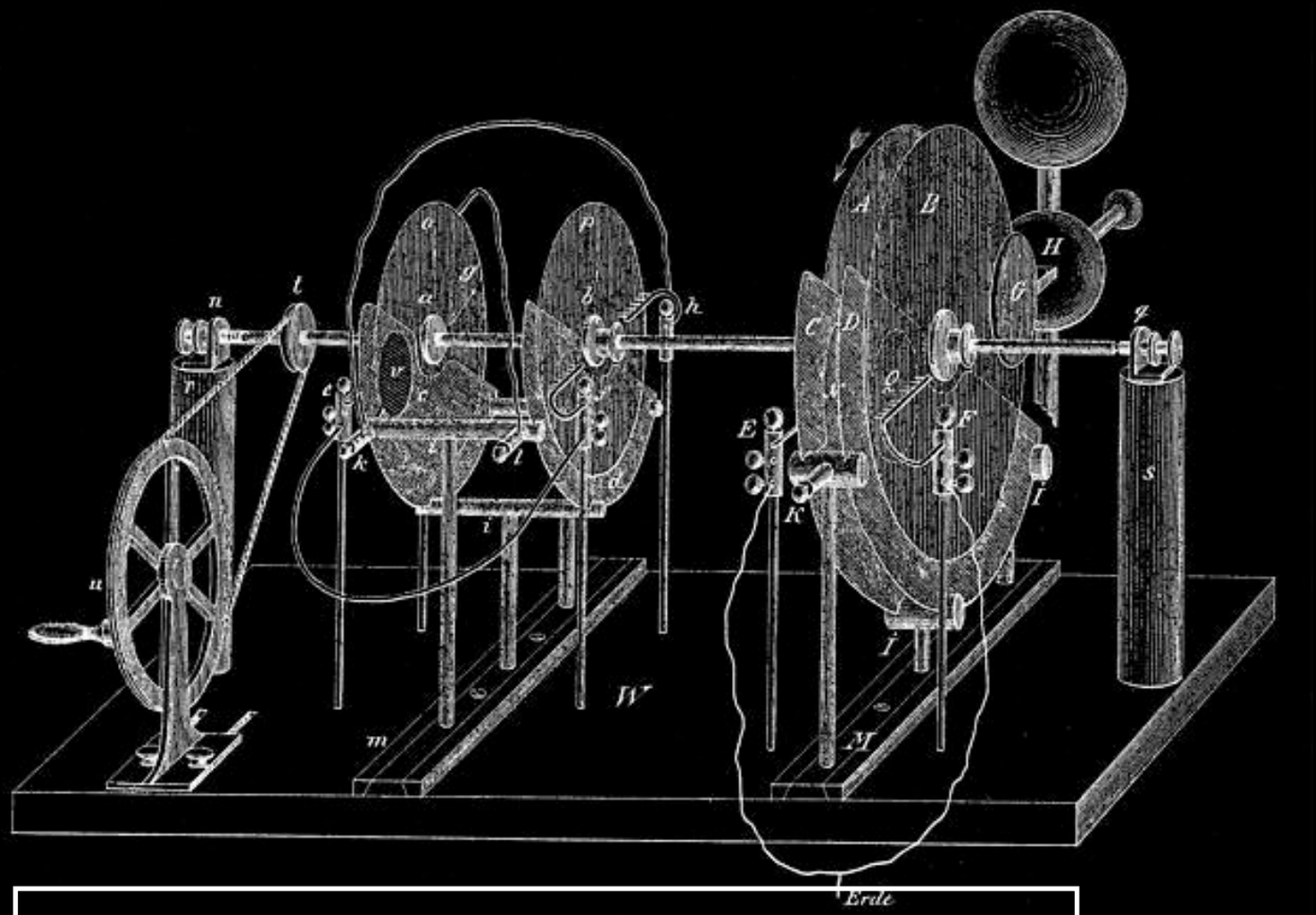


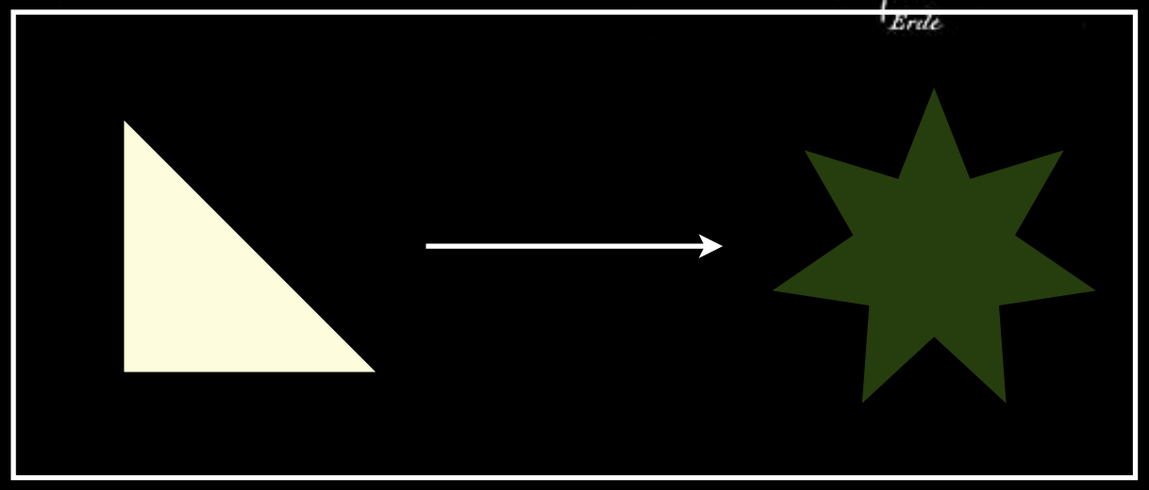


Statistical comparative methods machine

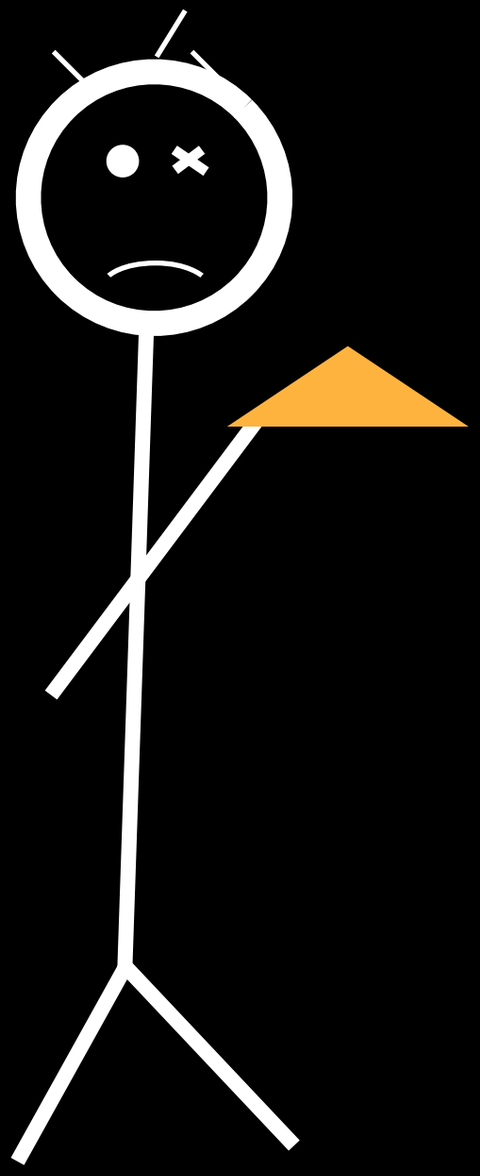


Statistical comparative methods machine





How comparative methods work:



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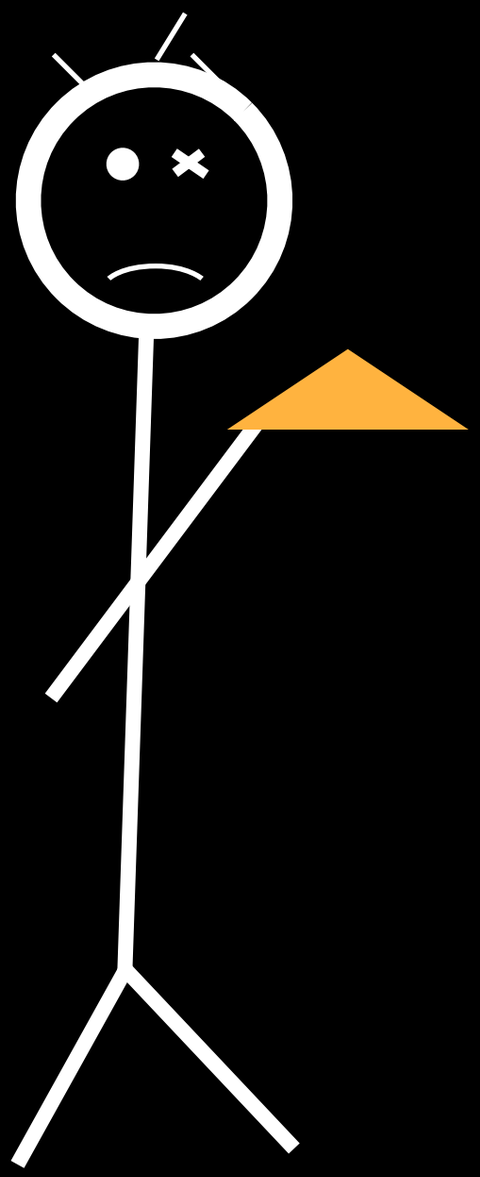

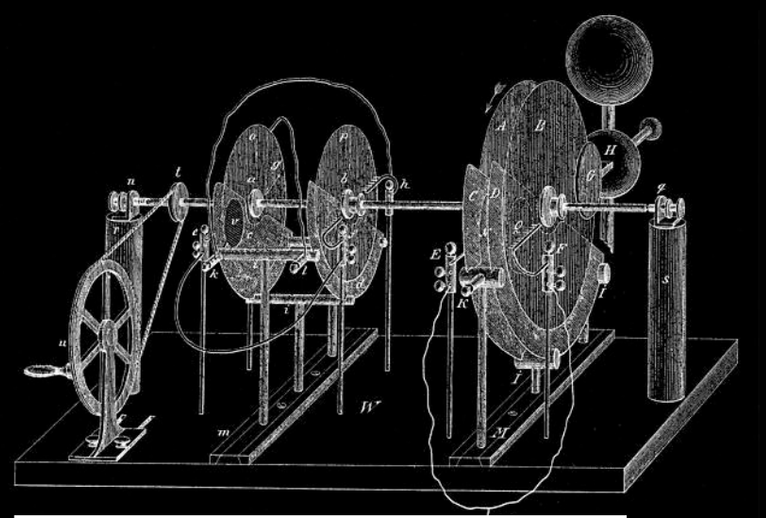

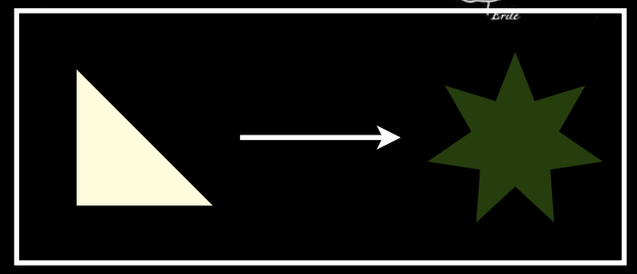

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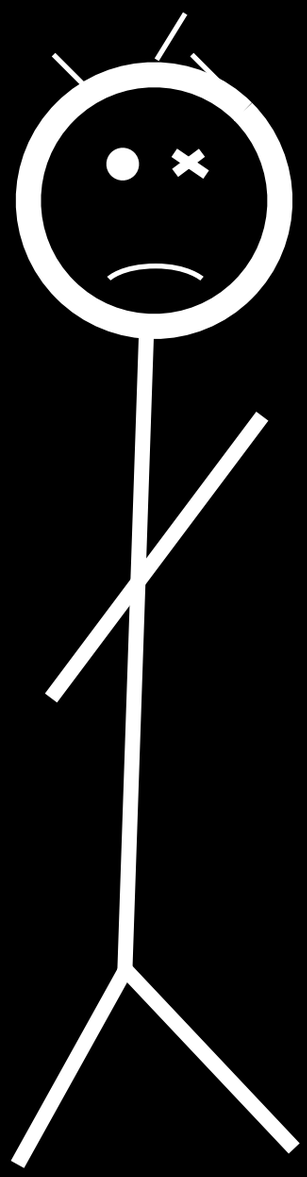

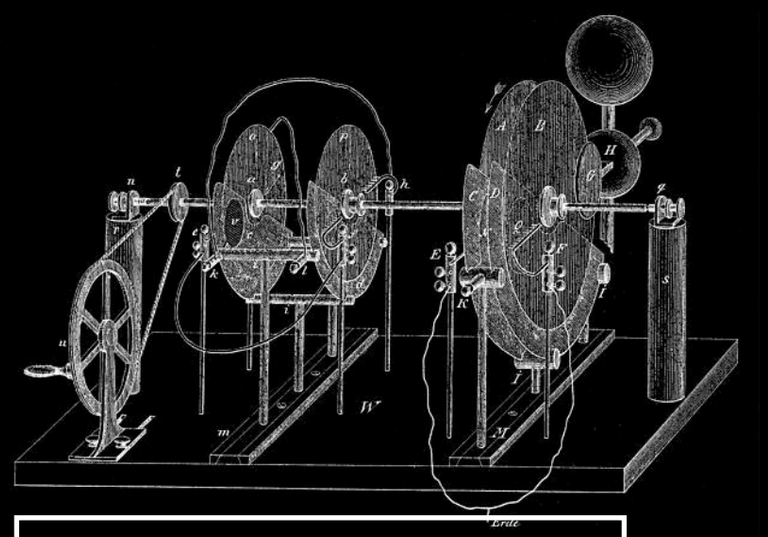

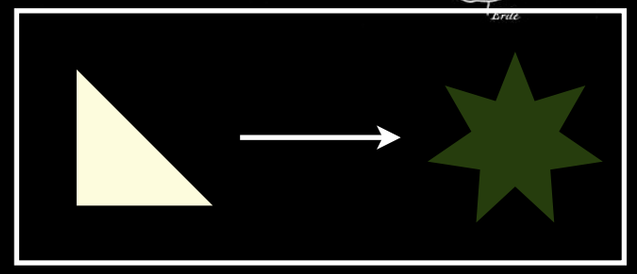

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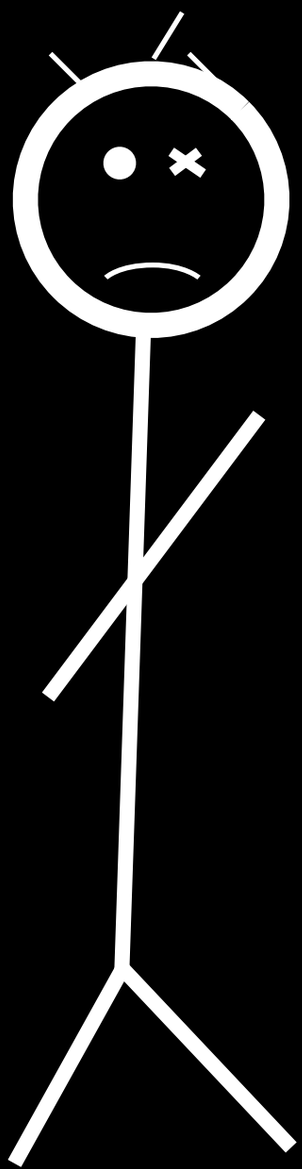

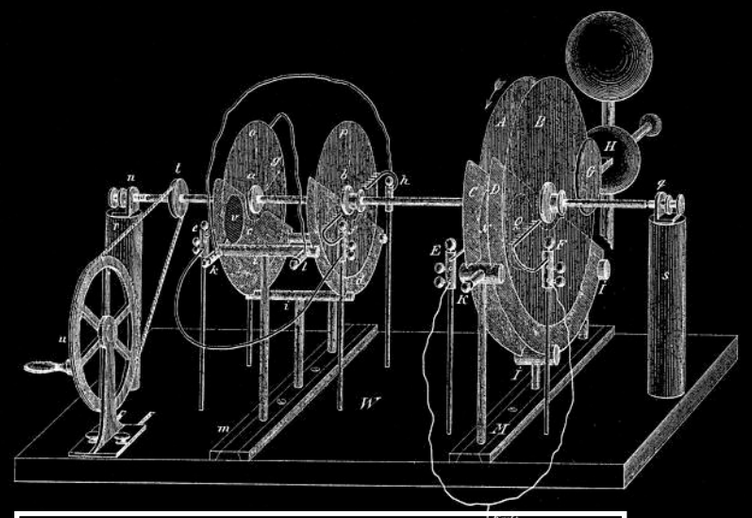

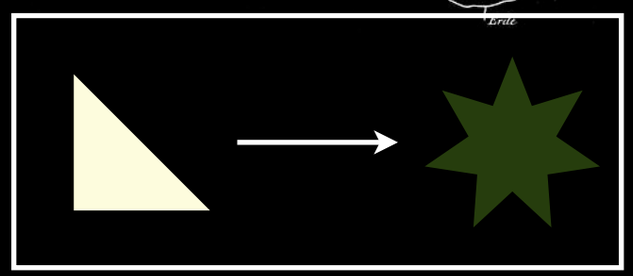

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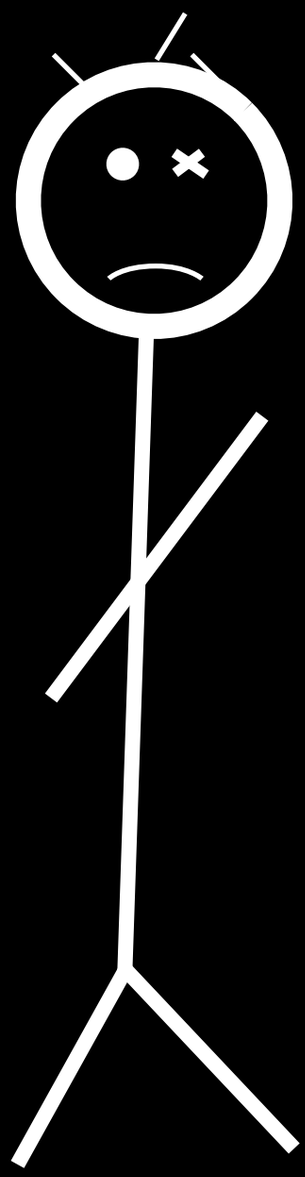
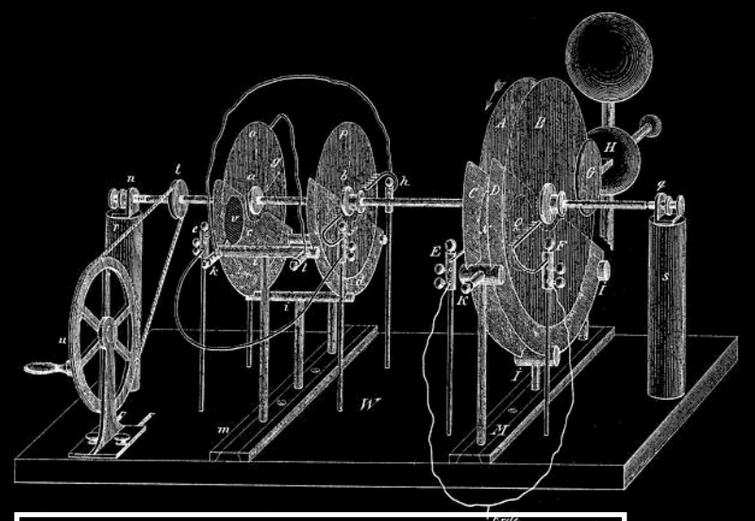
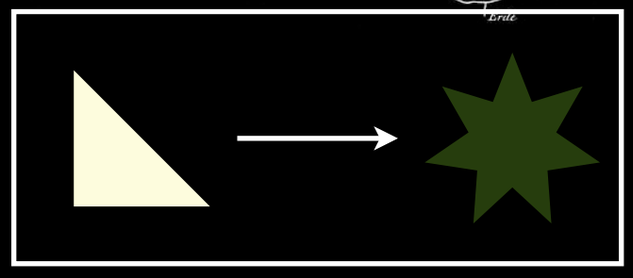
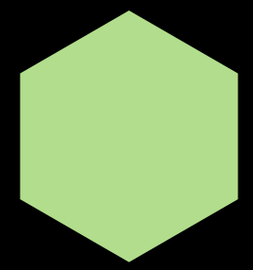
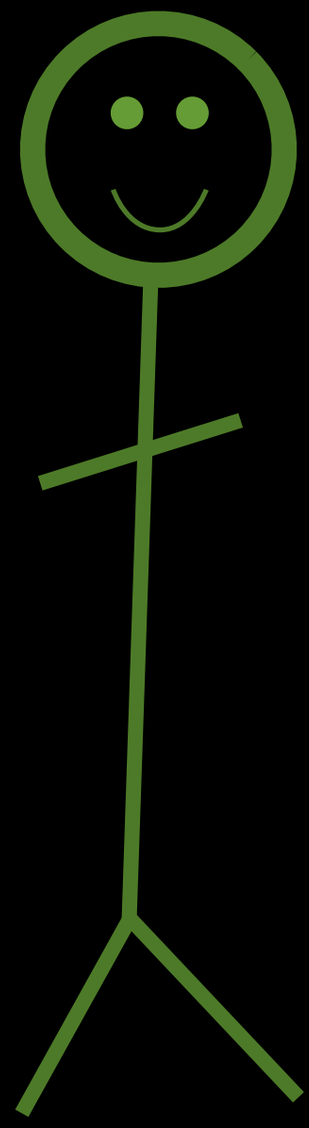


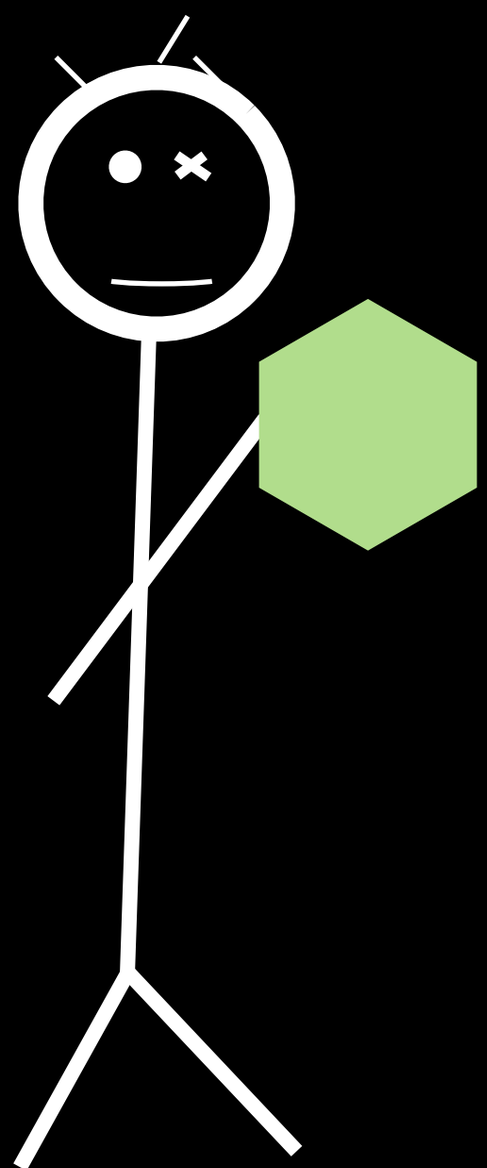


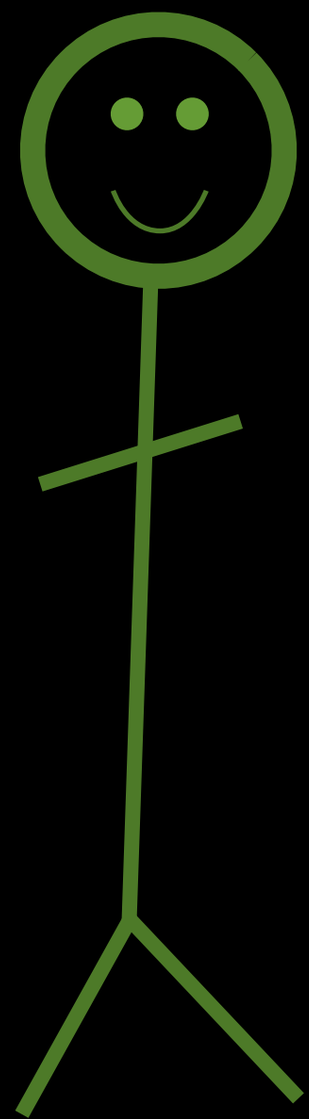






Dr. So-and-so





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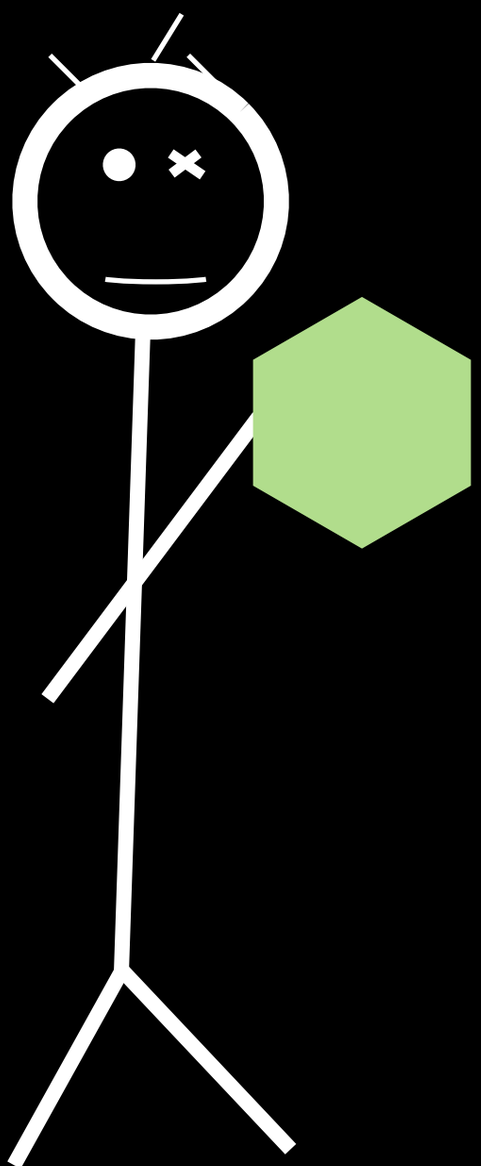
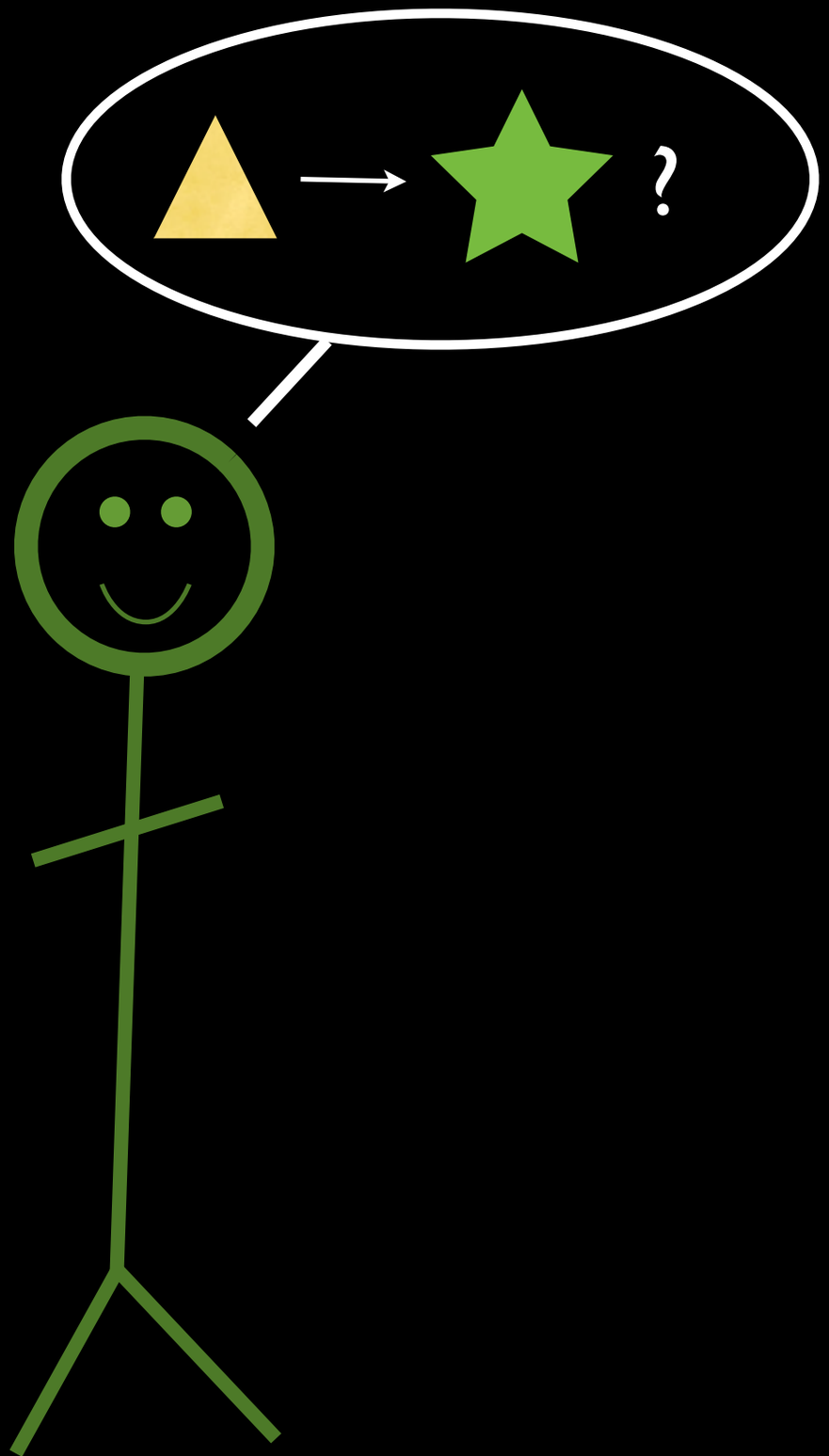
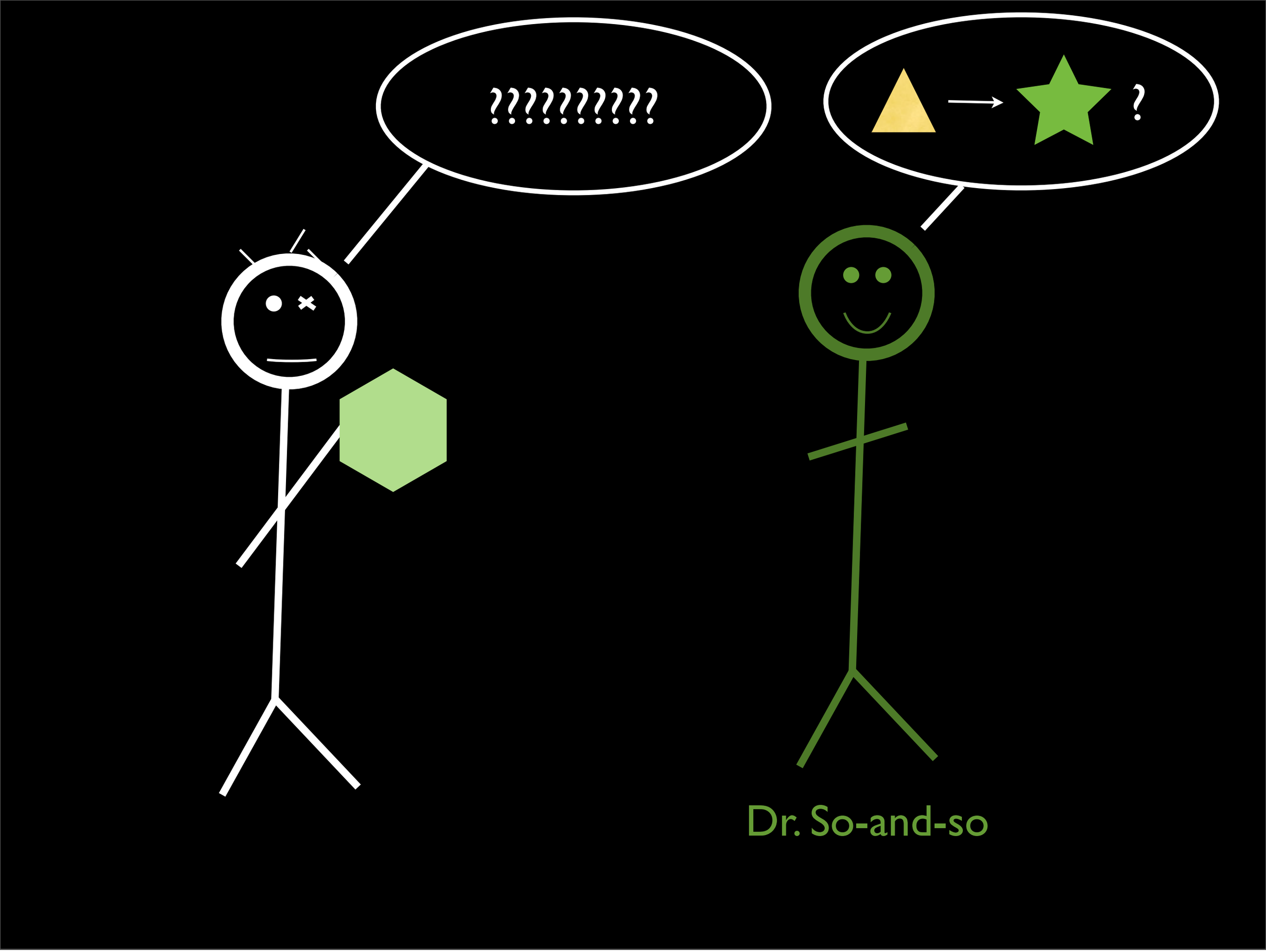




Dr. So-and-so

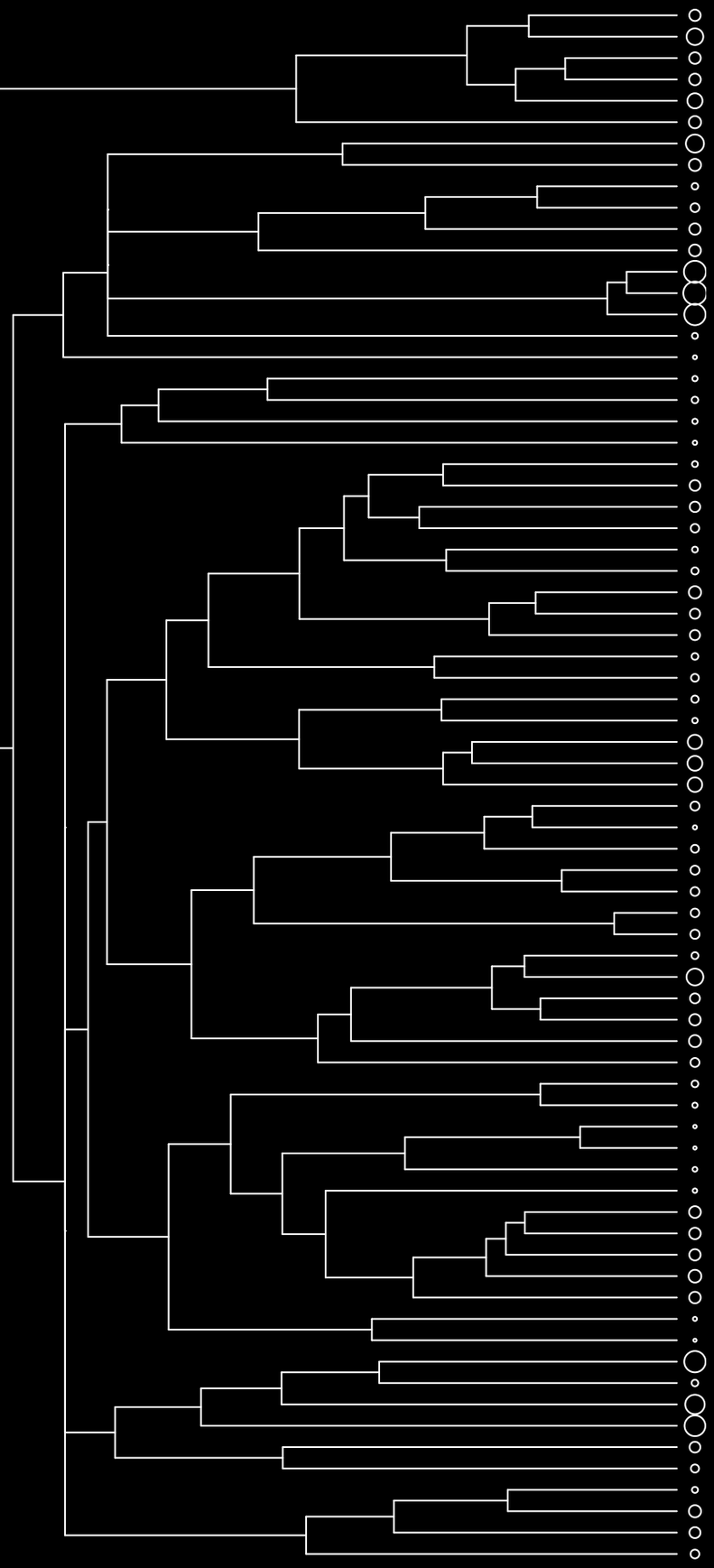

??????????
?
Dr. So-and-so

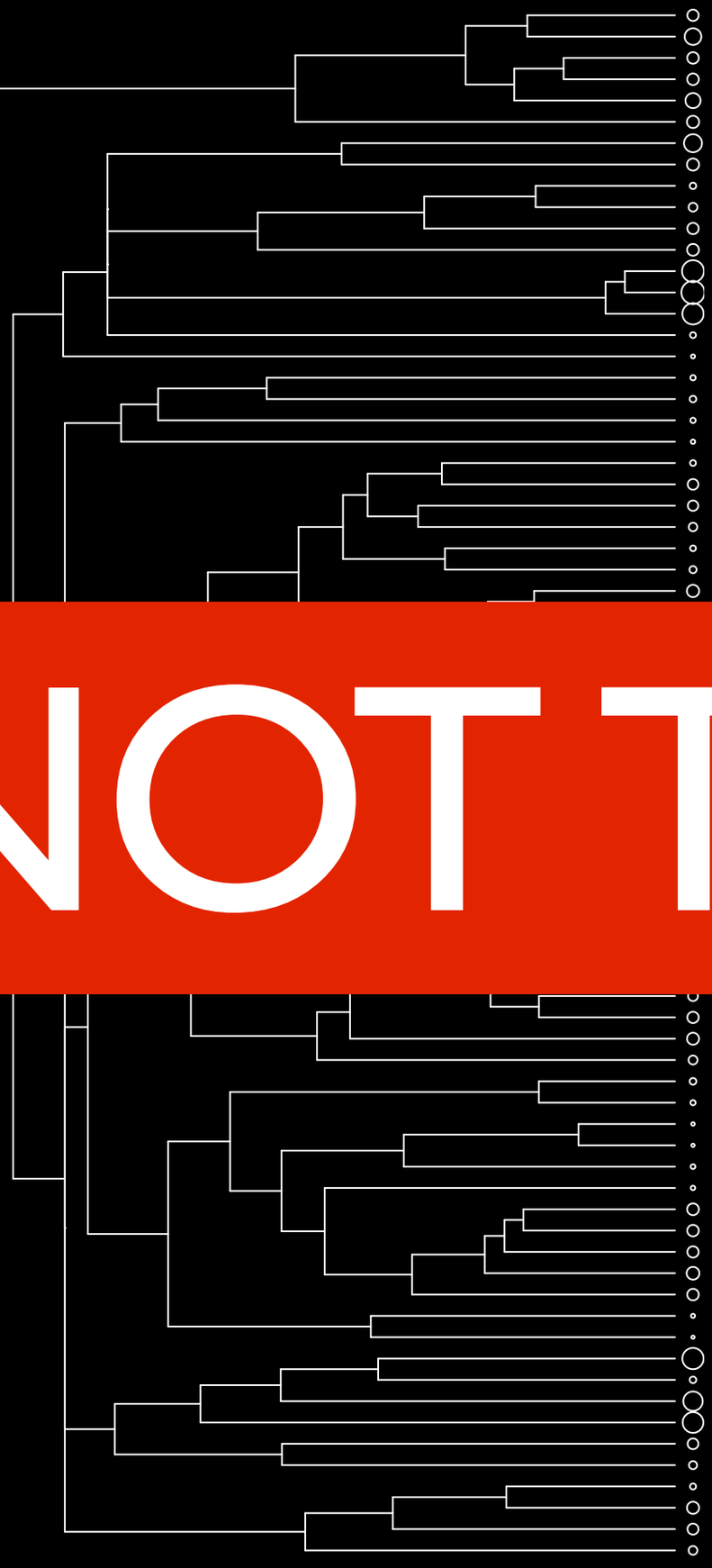
Tuesday, February 15, 2011

Goal:

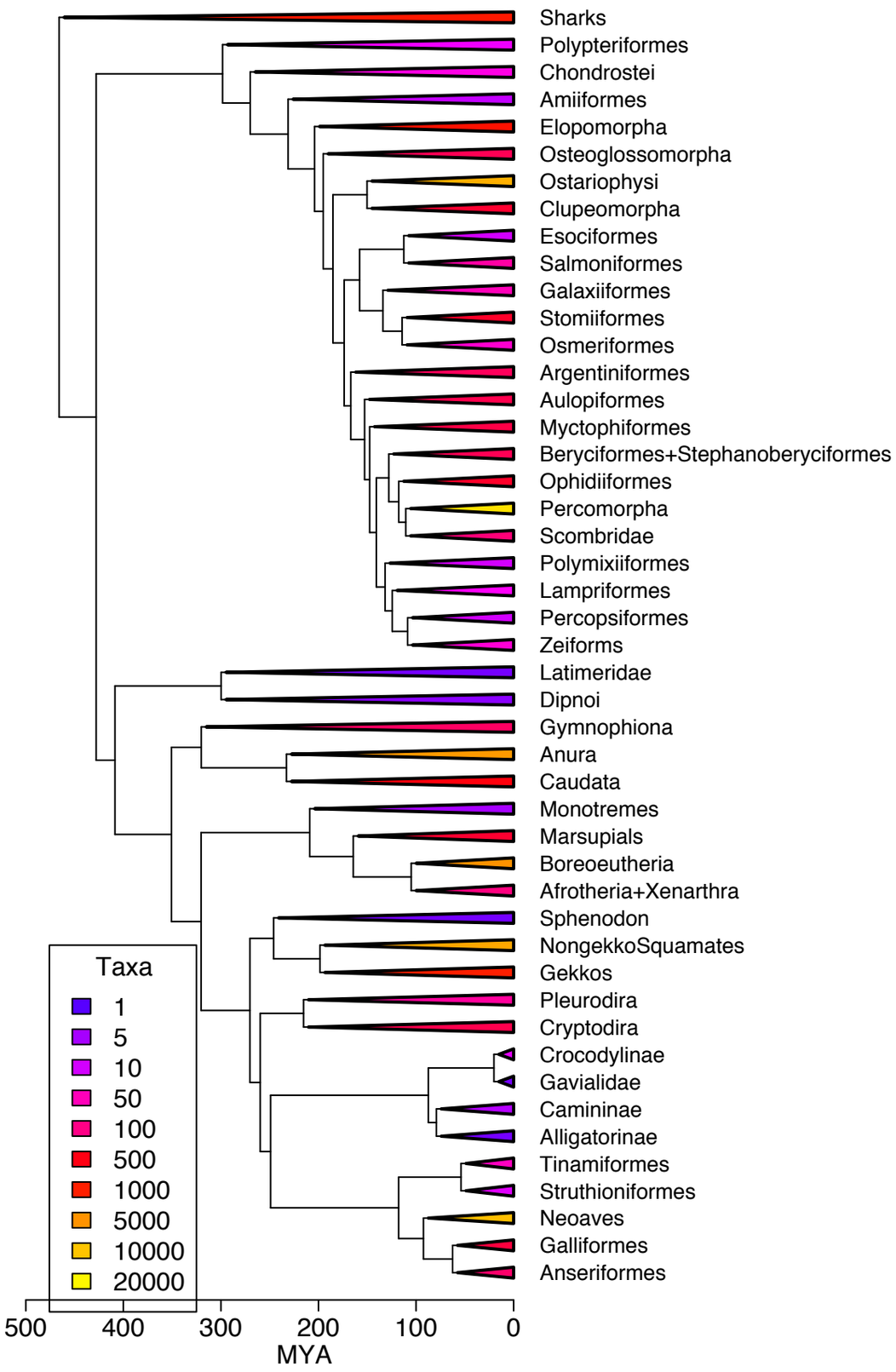
- Create methods that analyze the data that people actually have to estimate things that they really want to know

What data do people actually have?

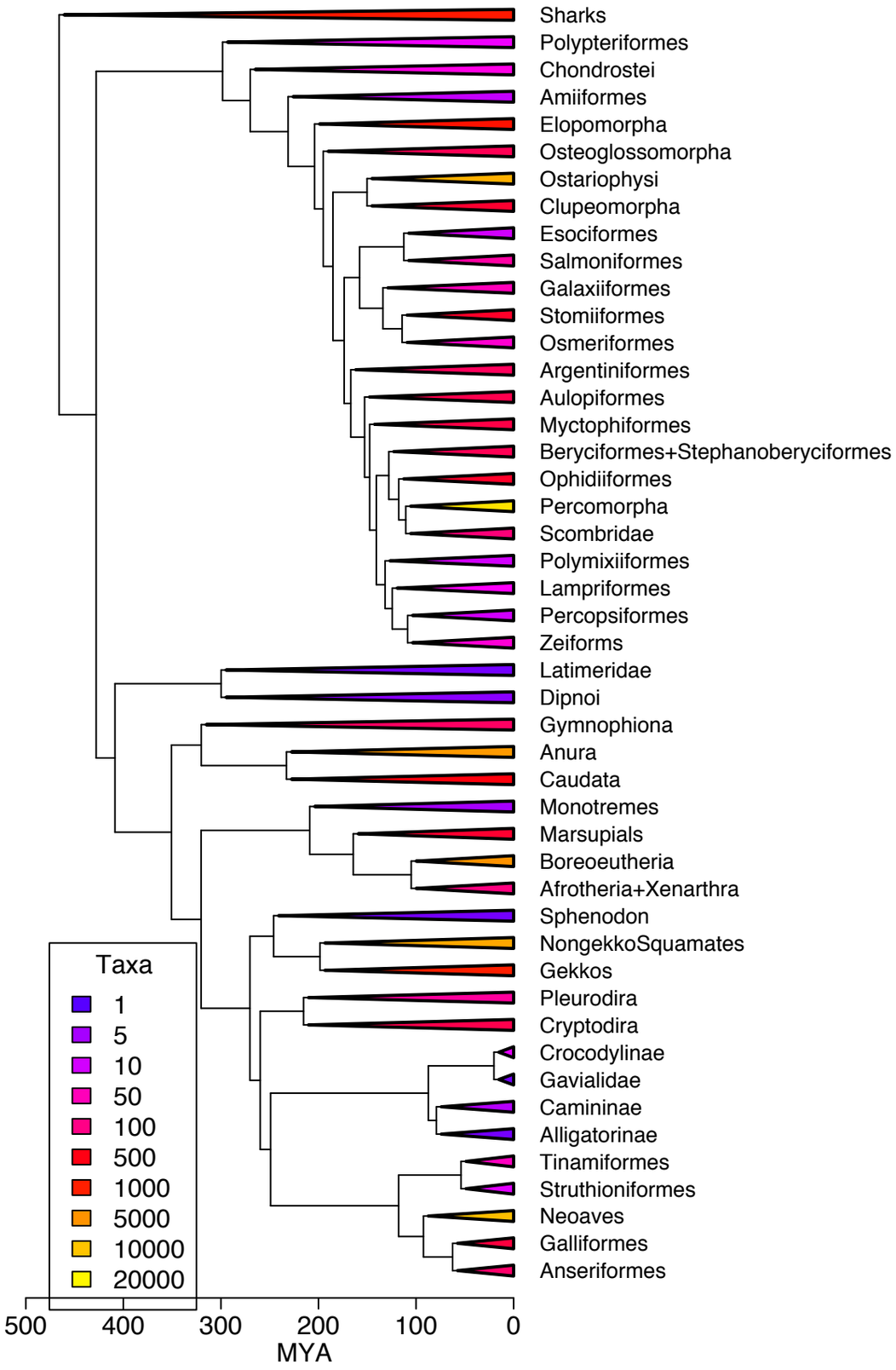




NOT TYPICAL



More common to have incomplete trees where tips represent unsampled clades


Sharks
Polypteriformes
Chondrostei
Amiiformes
Elopomorpha
Osteoglossomorpha
Ostariophysi
Clupeomorpha
Esociformes
Salmoniformes
Galaxiiformes
Stomiiformes
Osmeriformes
Argentiniformes
Aulopiformes
Myctophiformes
Beryciformes+Stephanoberyciformes
Ophidiiformes
Percomorpha
Scombridae
Polymixiiformes
Lampriformes
Percopsiformes
Zeiforms
Latimeridae
Dipnoi
Gymnophiona
Anura
Caudata
Monotremes
Marsupials
Boreoeutheria
Afrotheria+Xenarthra
Sphenodon
NongekkoSquamates
Gekkos
Pleurodira
Cryptodira
Crocodylinae
Gavialidae
Camininae
Alligatorinae
Tinamiformes
Struthioniformes
Neoaves
Galliformes
Anseriformes
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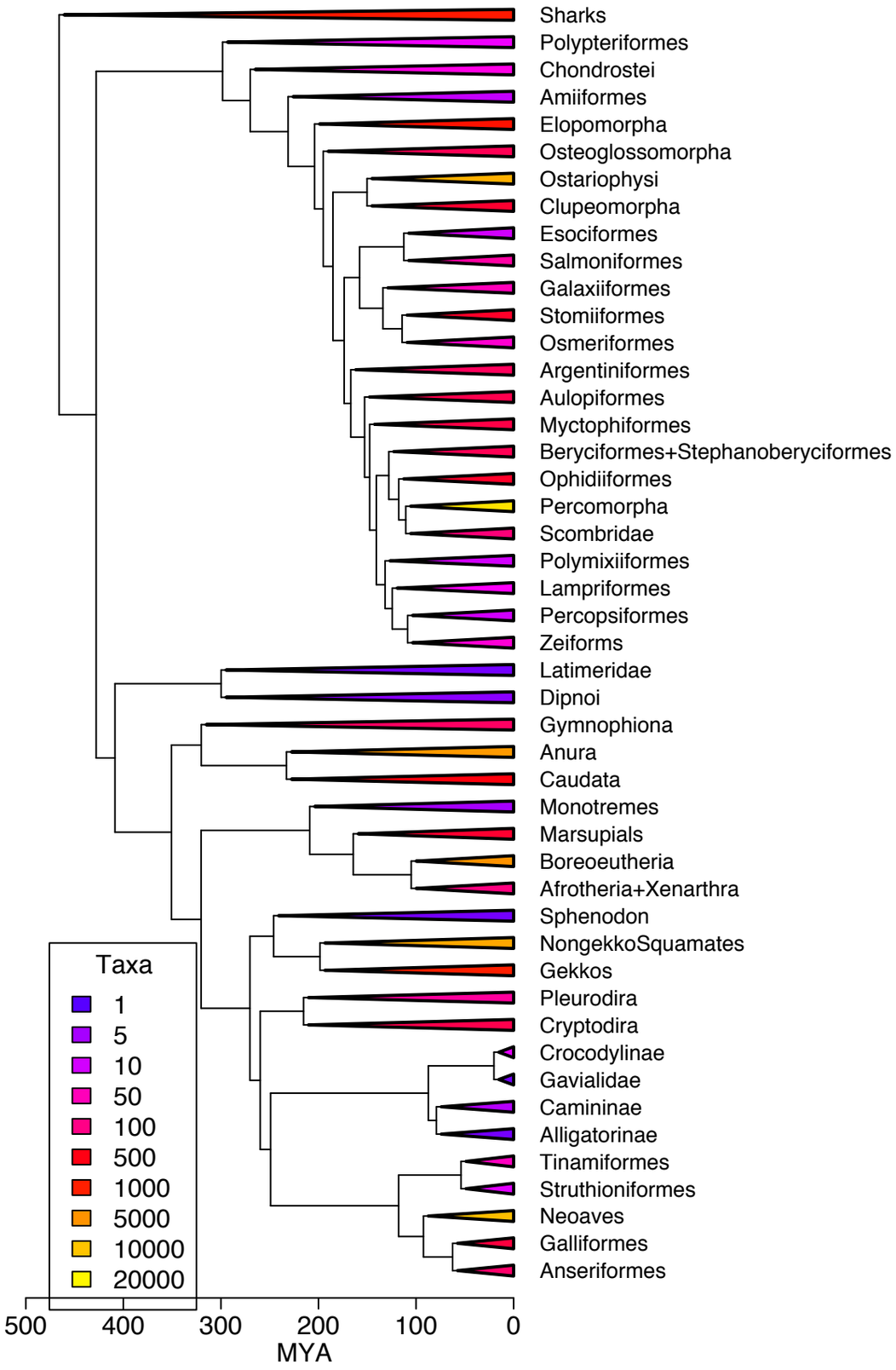
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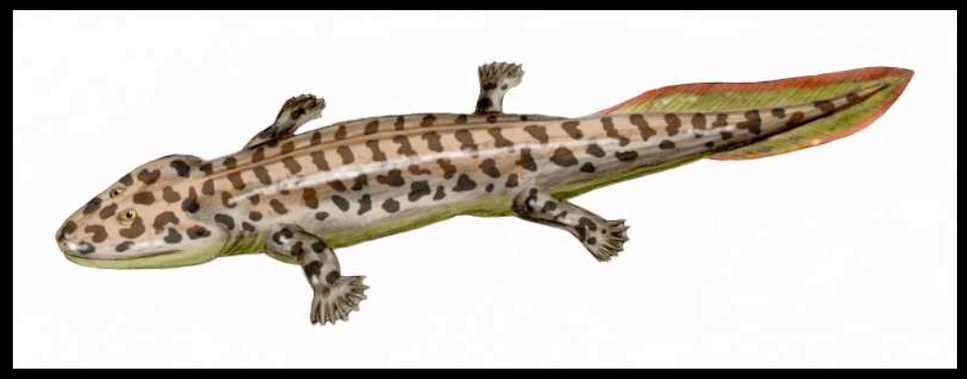

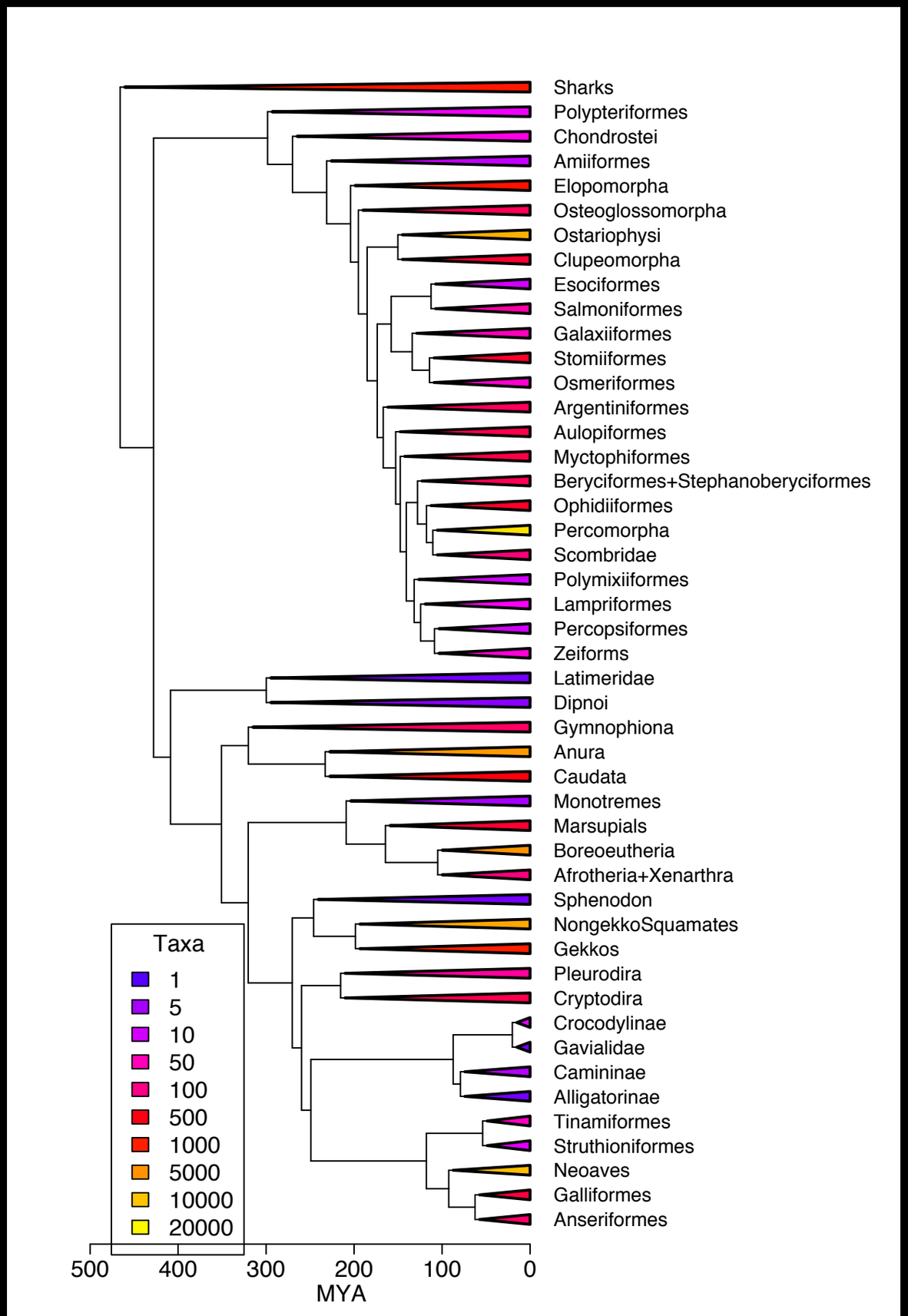
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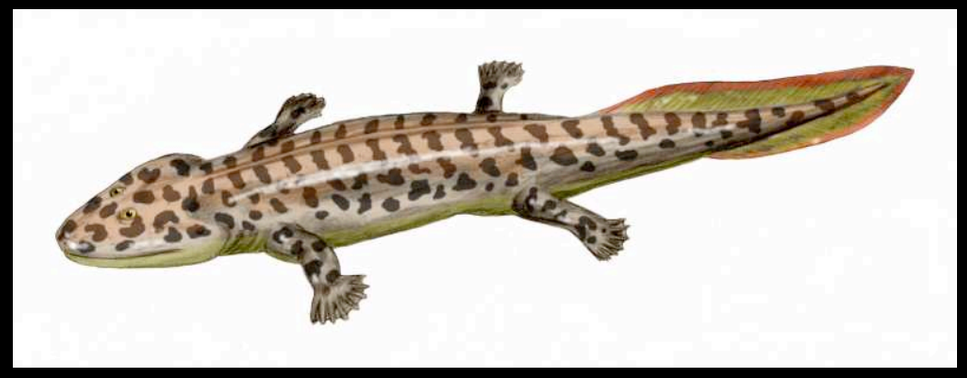
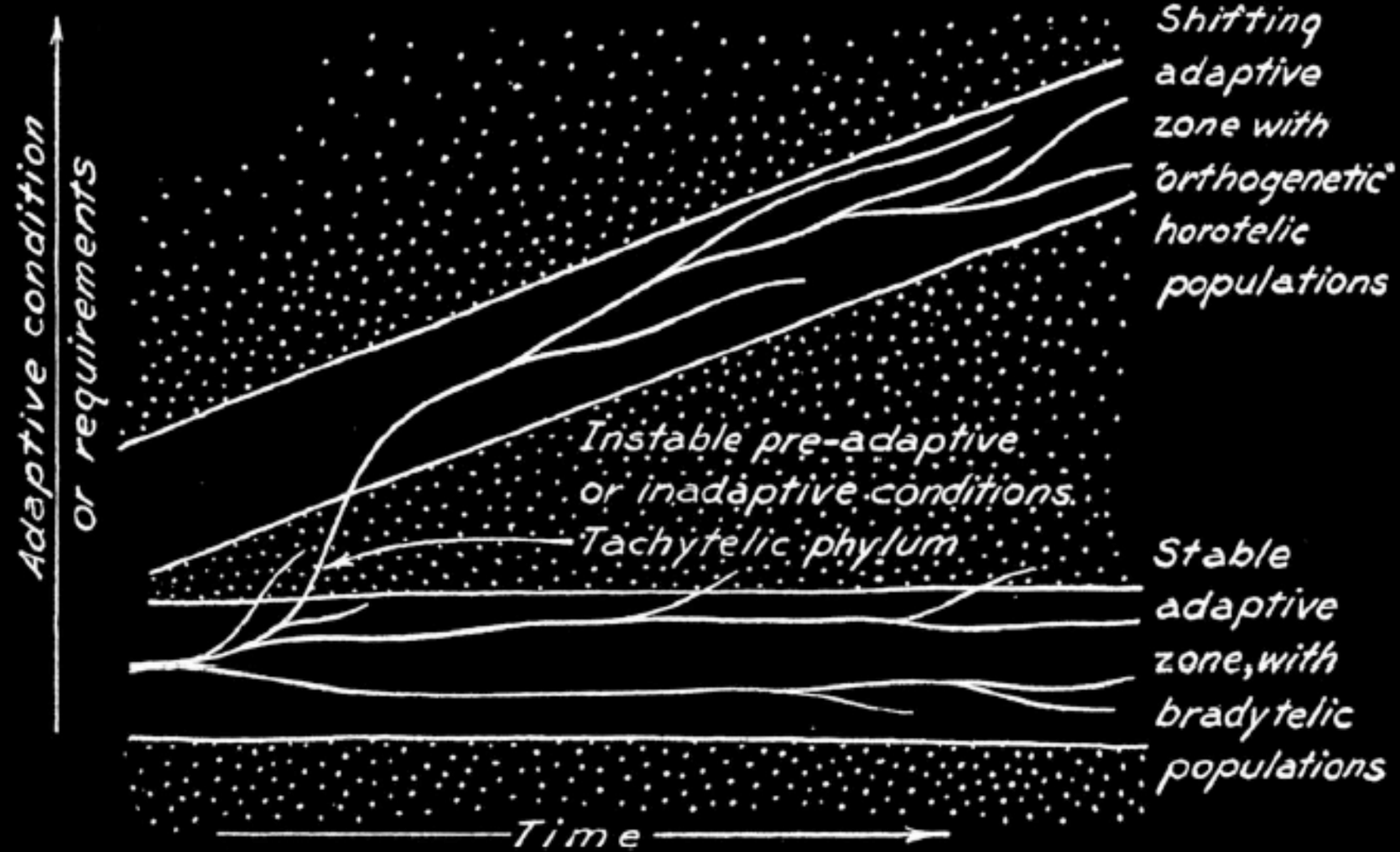


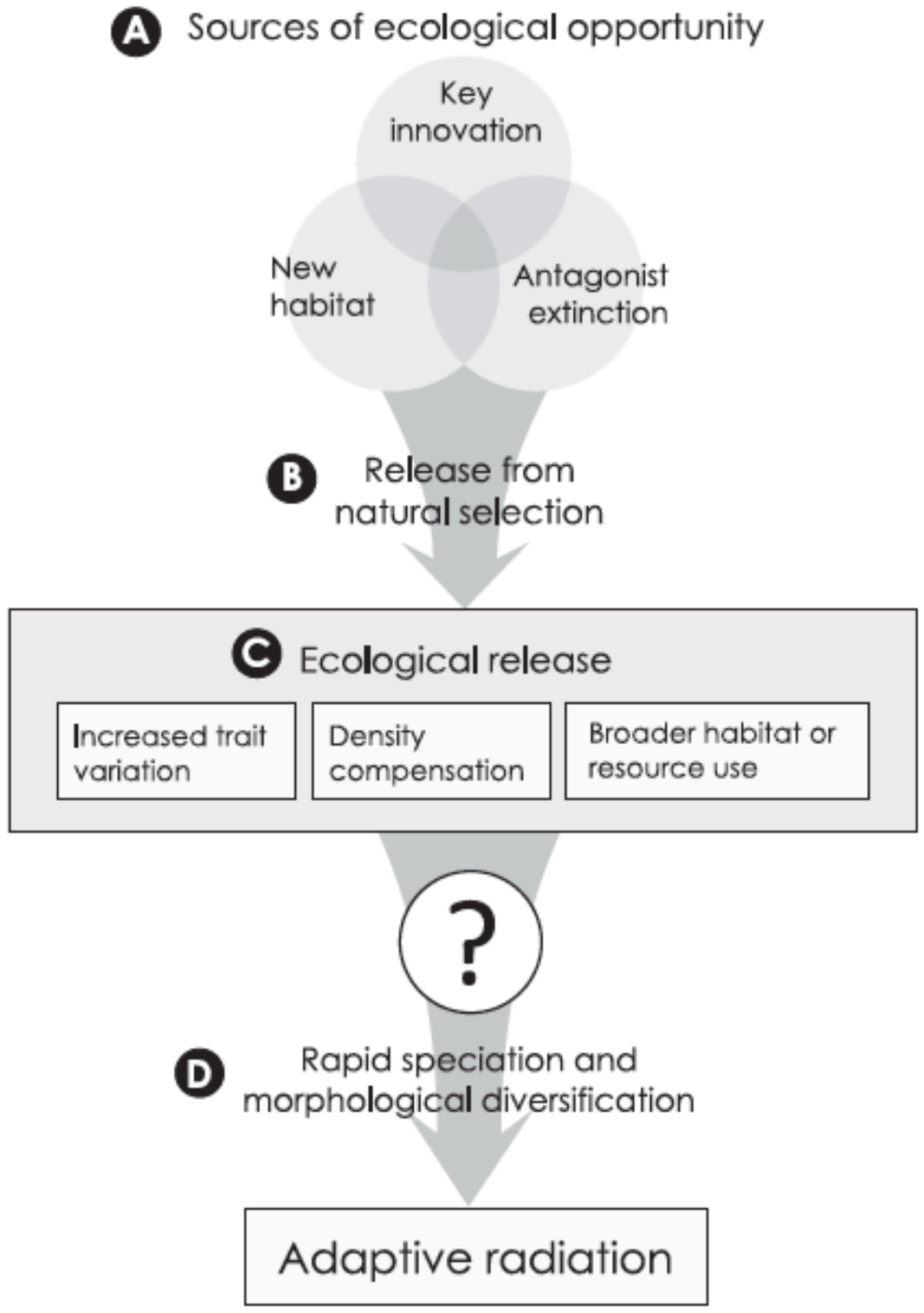
What do people really want to know?

Adaptive Radiation



Simpson 1953

Yoder et al. 2010

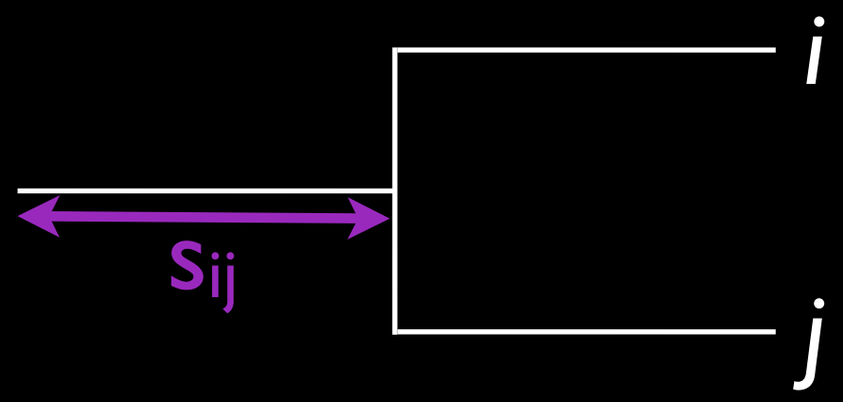


Brownian motion

- Two parameters: starting value (μ) and rate (σ^2)

$$dX(t) = \sigma dB(t)$$

$$V_{ij} = \sigma^2 s_{ij}$$



No current comparative methods look very much like Simpson's vision!

Goal:

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Three vignettes

- Fossil MEDUSA
- Reversible-jump MCMC
- MECCA

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- Fossil MEDUSA
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Joseph Brown
Harmon lab post-doc

Nine exceptional radiations plus high turnover explain species diversity in jawed vertebrates

Michael E. Alfaro[a,1], Francesco Santini[a], Chad Brock[b], Hugo Alamillo[b], Alex Dornburg[c], Daniel L. Rabosky[d,e], Giorgio Carnevale[f], and Luke J. Harmon[g]

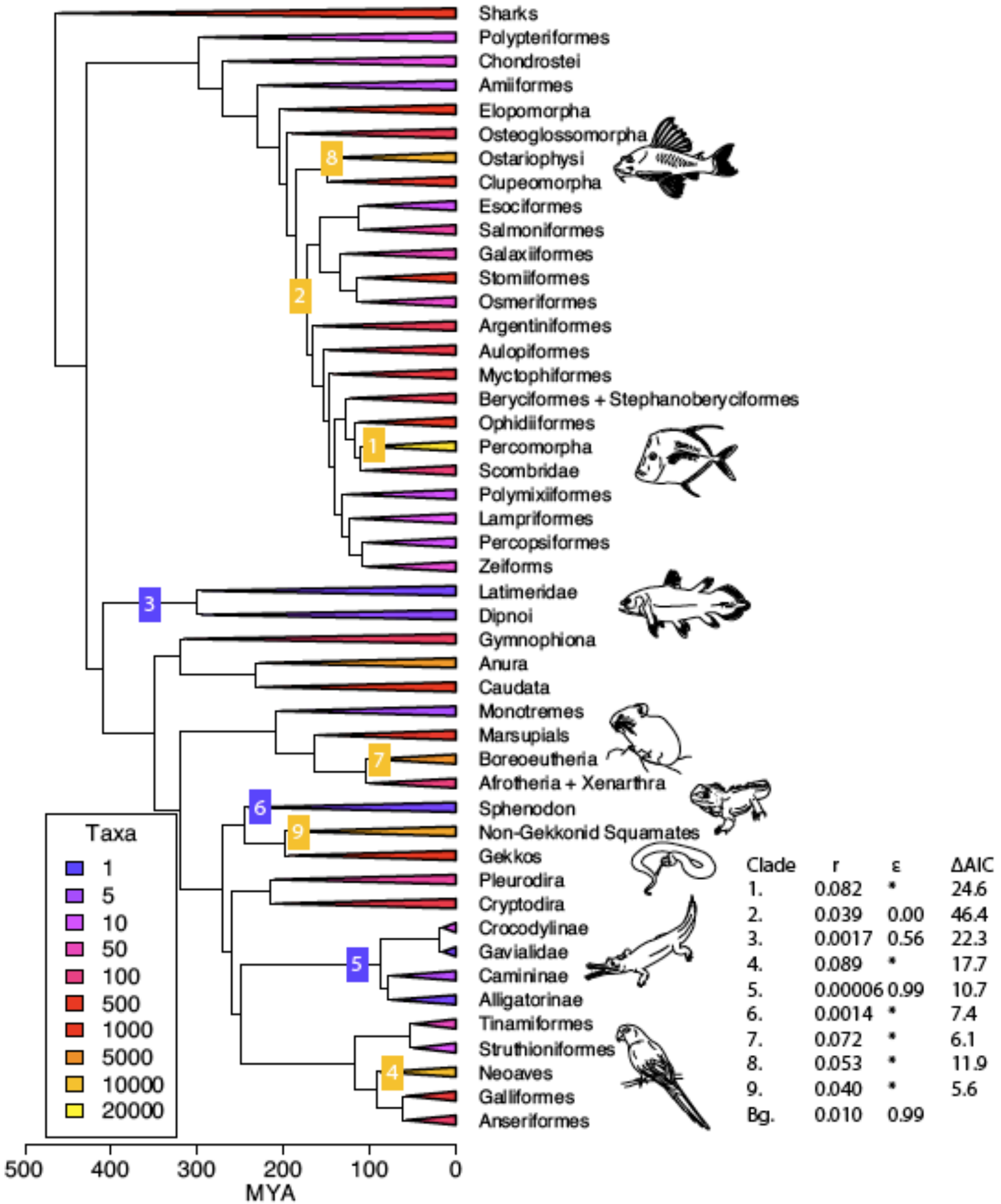
[a]Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA 90095; [b]School of Biological Sciences, Washington State University, Pullman, WA 99164; [e]Department of Ecology and Evolutionary Biology and [d]Cornell Laboratory of Ornithology, Cornell University, Ithaca, NY 14850; [f]Dipartimento di Scienze della Terra and Museo di Storia Naturale e del Territorio, Università di Pisa, Pisa, 56100 Italy; [g]Department of Biology, University of Idaho, Moscow, ID 83843; and [c]Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT 06520

Edited by David M. Hillis, University of Texas, Austin, TX, and approved June 12, 2009 (received for review November 2, 2008)

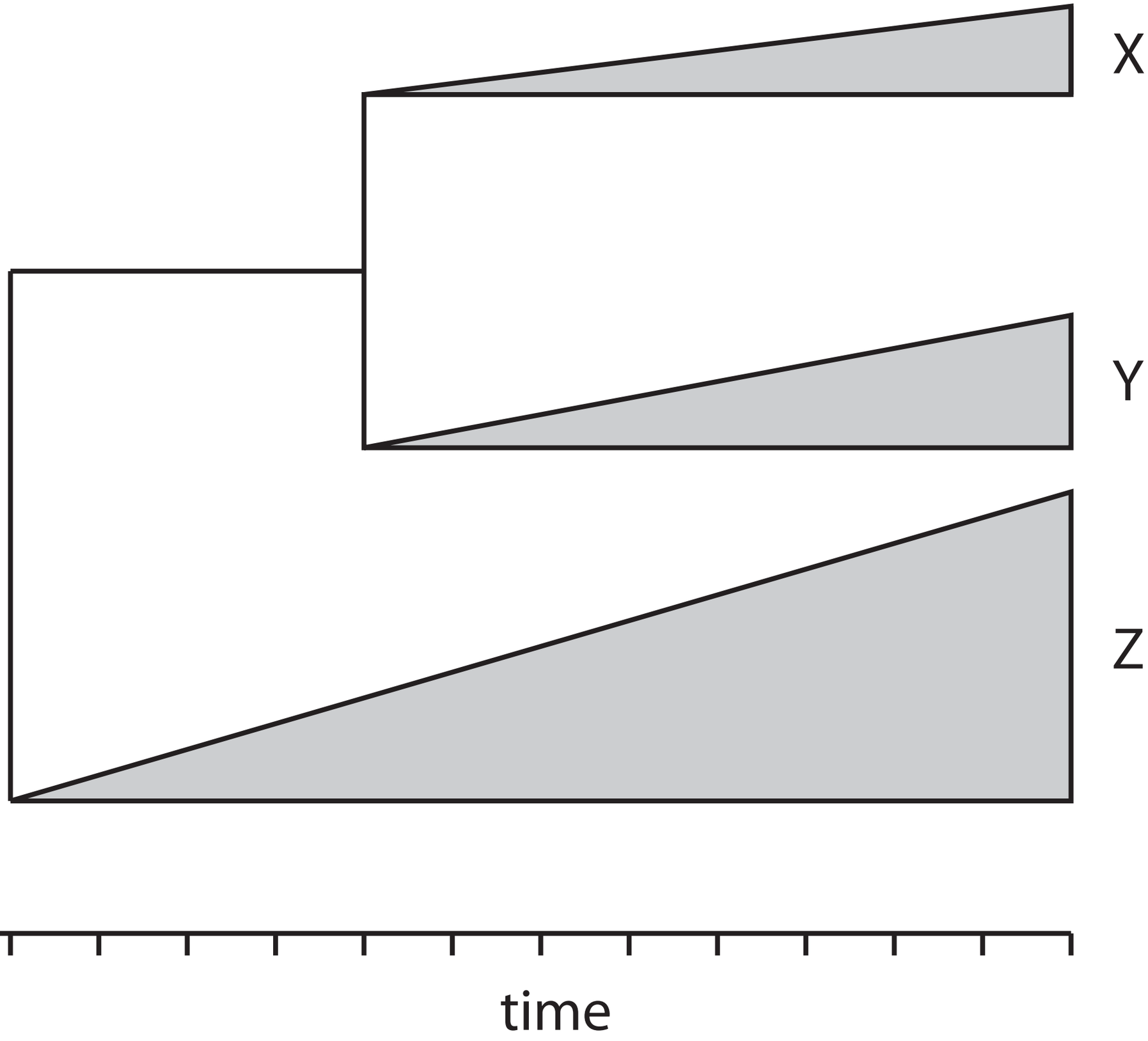
The uneven distribution of species richness is a fundamental and unexplained pattern of vertebrate biodiversity. Although species richness in groups like mammals, birds, or teleost fishes is often attributed to accelerated cladogenesis, we lack a quantitative conceptual framework for identifying and comparing the exceptional changes of tempo in vertebrate evolutionary history. We develop MEDUSA, a stepwise approach based upon the Akaike information criterion for detecting multiple shifts in birth and death rates on an incompletely resolved phylogeny. We apply MEDUSA incompletely to a diversity tree summarizing both evolutionary relationships and species richness of 44 major clades of jawed vertebrates. We identify 9 major changes in the tempo of gnathostome diversification; the most significant of these lies at

Comparative methods like SymmeTREE (10, 11) are an exception to some degree, because they can deal with missing taxa through random resolution of tip clades. However, this approach quickly becomes impractical as the number of unsampled taxa grows.

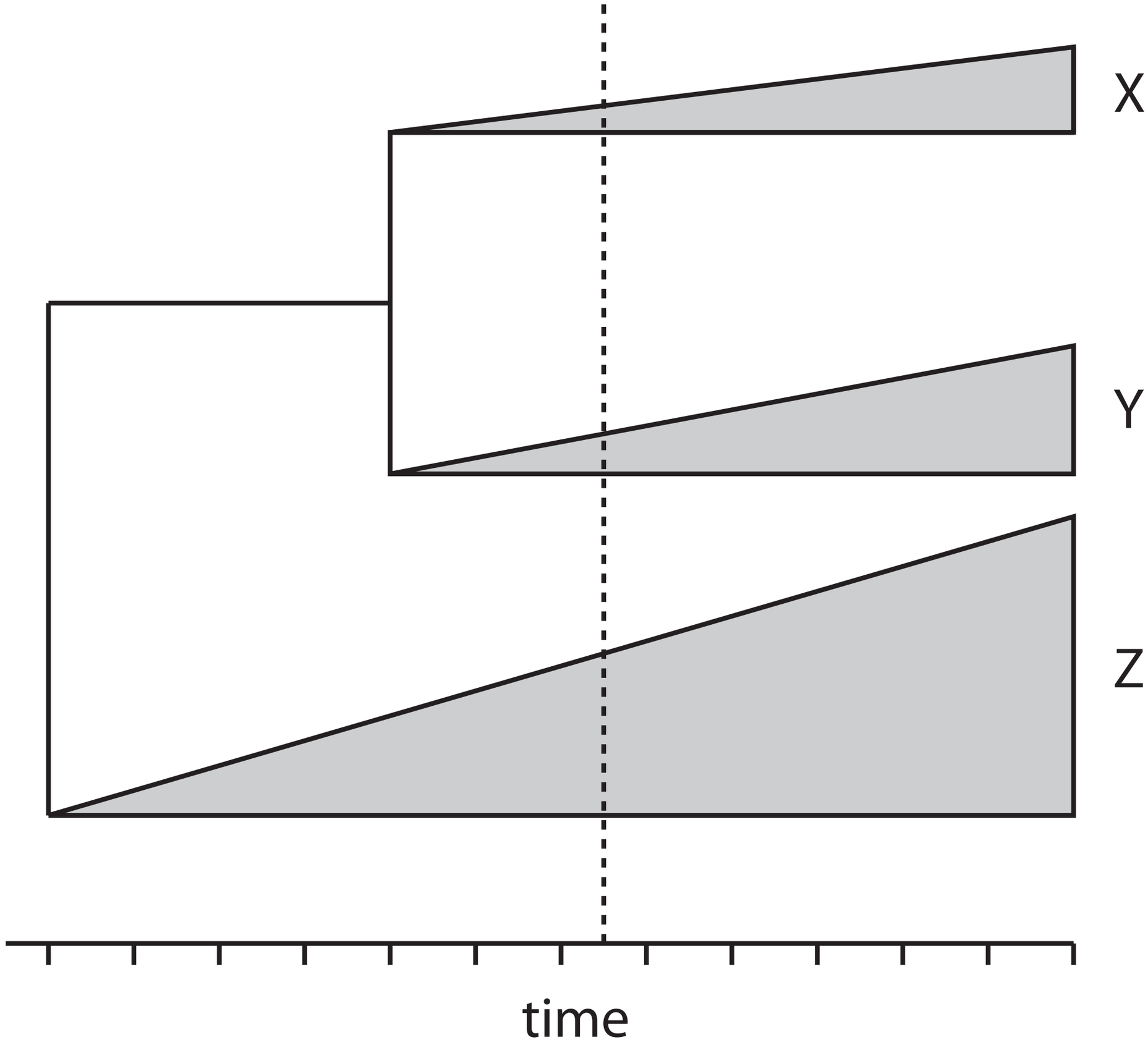
Here, we analyze a phylogenetic dataset with exemplars of 47 major vertebrate lineages using a comparative method that integrates both phylogenetic and taxonomic information to ask two general questions about the patterns of diversification across the vertebrate tree of life: (*i*) What is the background tempo of vertebrate diversification; and (*ii*) which, if any, vertebrate lineages have patterns of extant richness that are too species-rich or -poor to be outcomes of the background diversification rate?



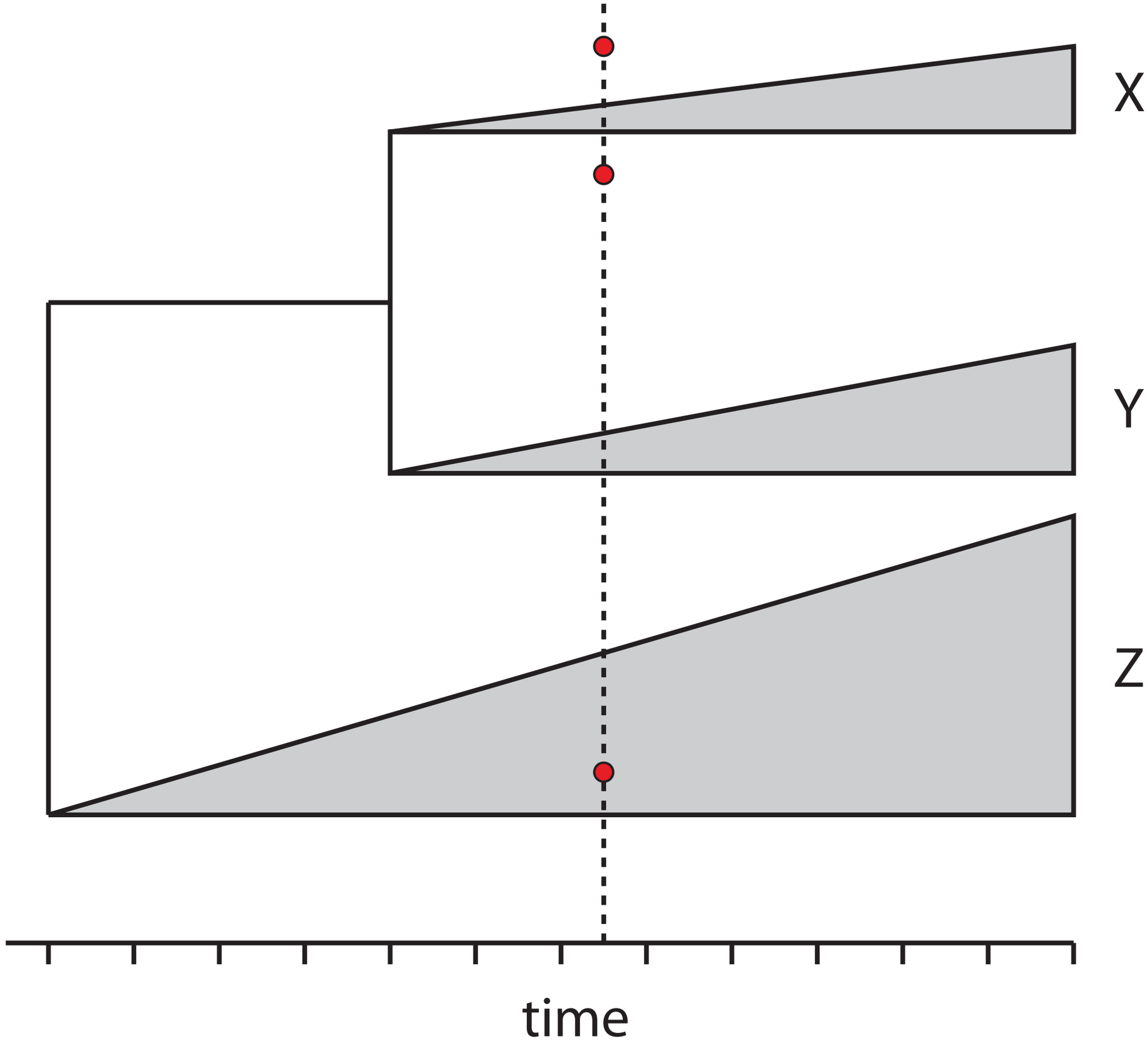
Clade	r	ε	ΔAIC
1.	0.082	*	24.6
2.	0.039	0.00	46.4
3.	0.0017	0.56	22.3
4.	0.089	*	17.7
5.	0.00006	0.99	10.7
6.	0.0014	*	7.4
7.	0.072	*	6.1
8.	0.053	*	11.9
9.	0.040	*	5.6
Bg.	0.010	0.99	


X
Y
Z
time

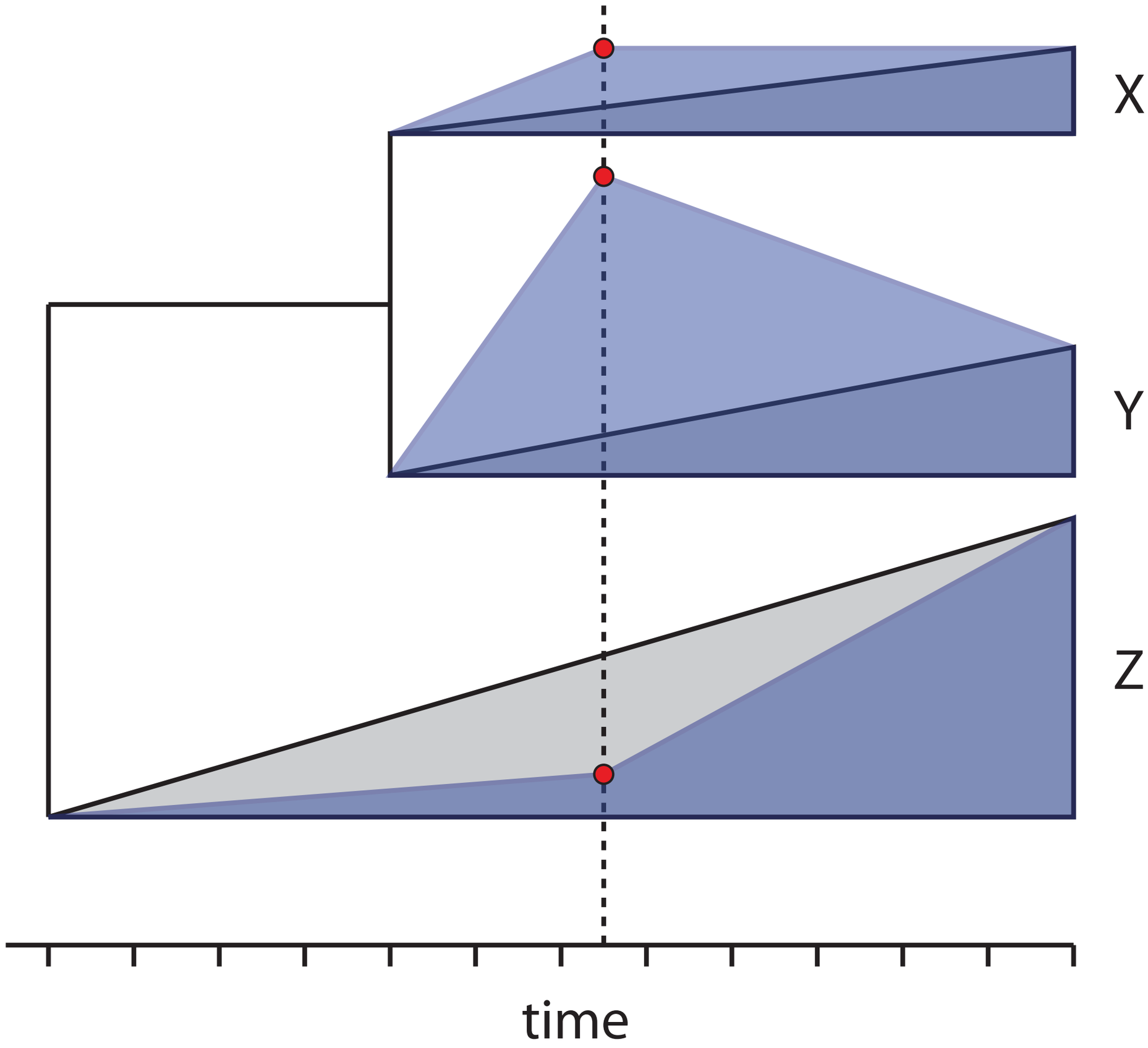
Taking a time-slice...



...of fossil richnesses...



...can reveal diversification dynamics unobservable from molecular phylogenies.



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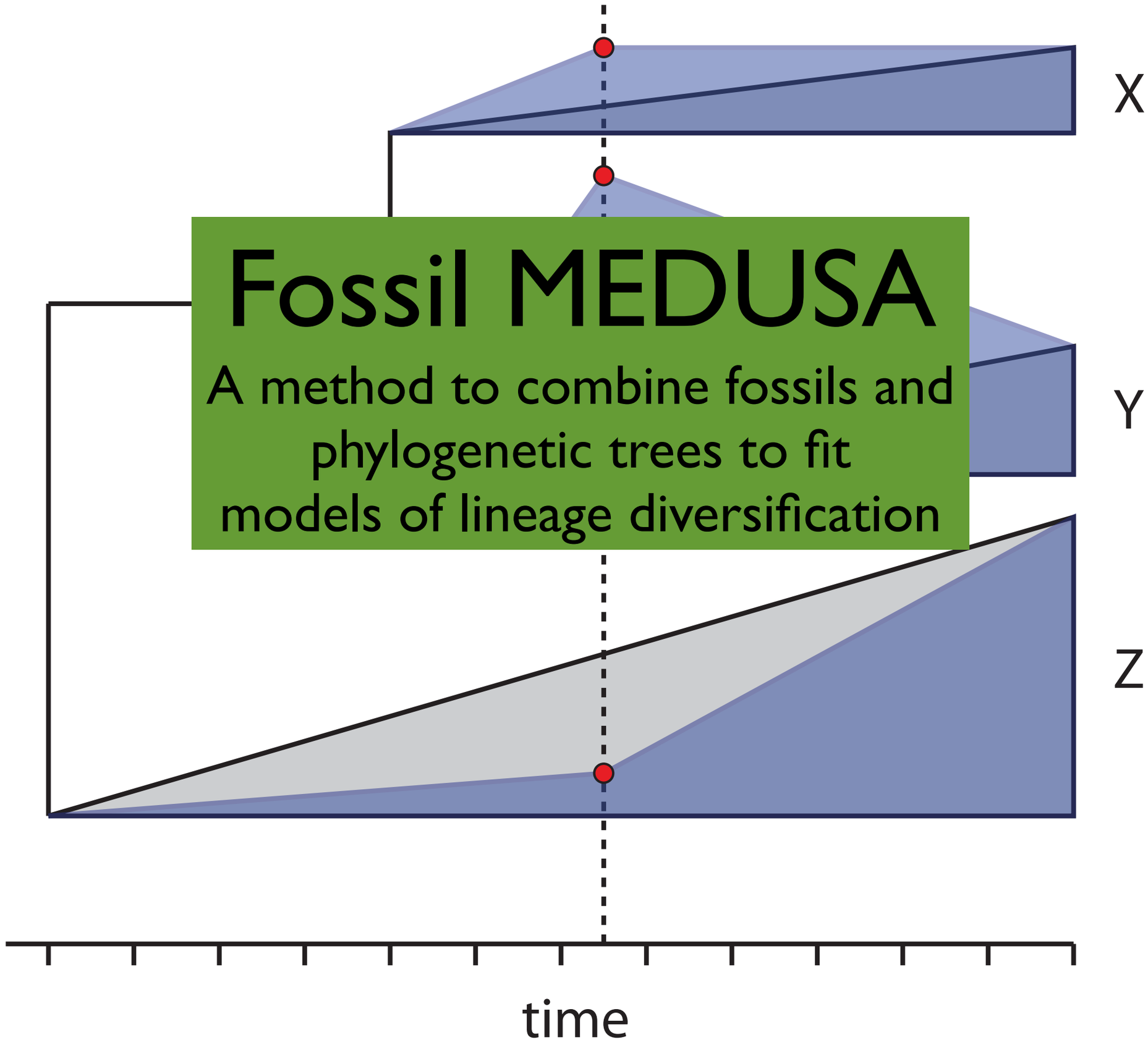

Fossil MEDUSA

A method to combine fossils and phylogenetic trees to fit models of lineage diversification

FOSSILMEDUSA

- Fit piecewise birth-death models:

1. Without fossil information
2. Assuming fossil richnesses as exact
3. Treating fossil counts as minimum richnesses

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- MECCA

Jon Eastman
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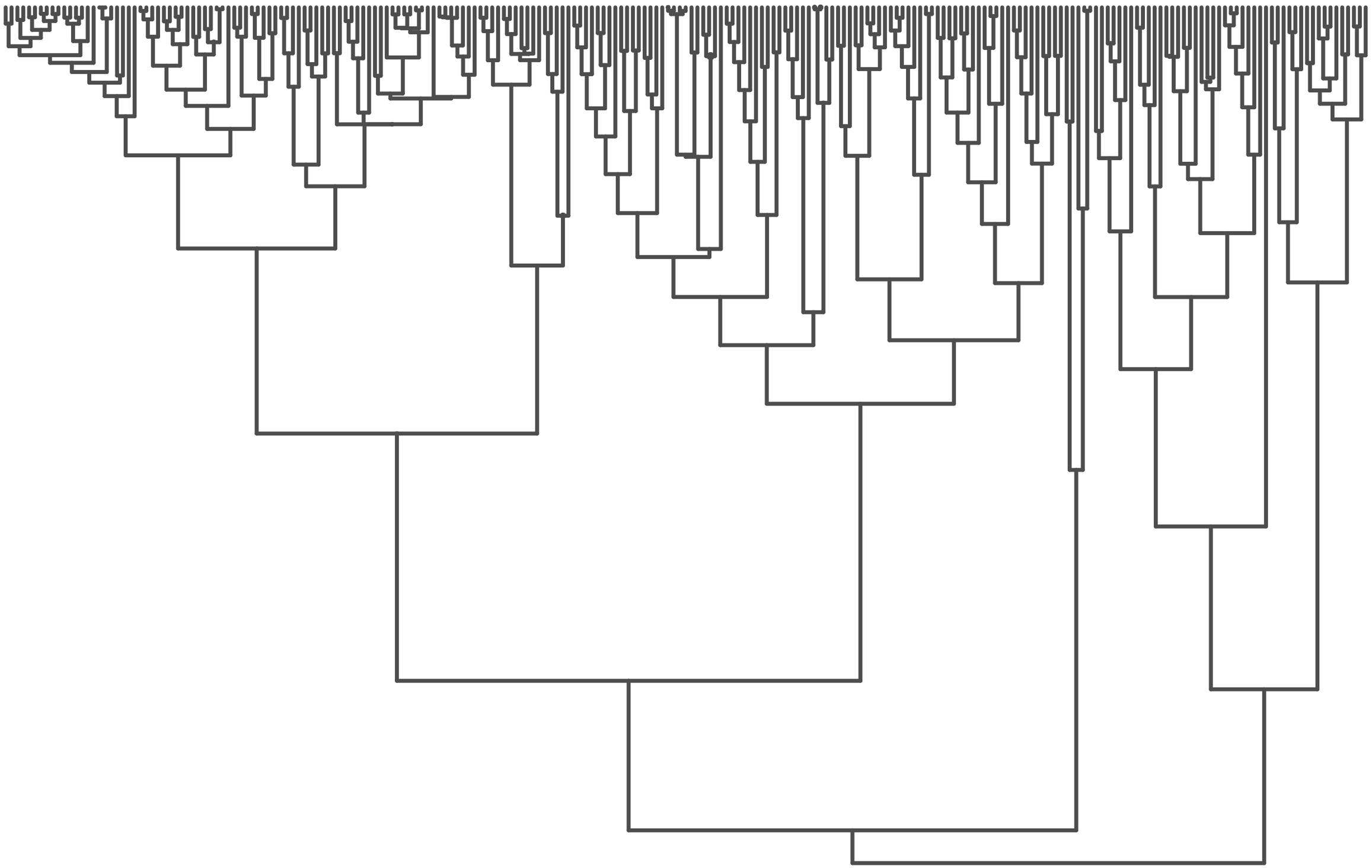
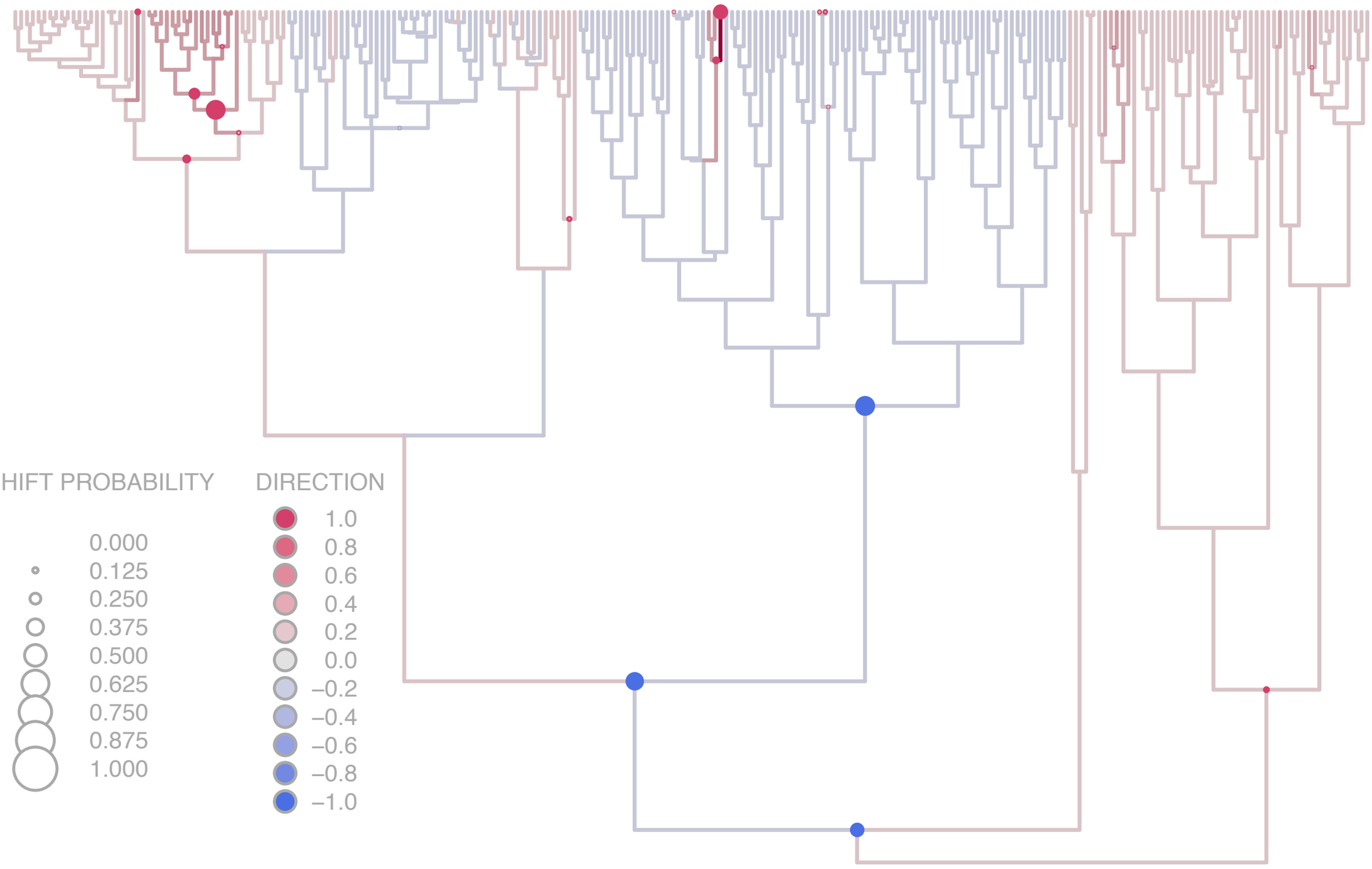
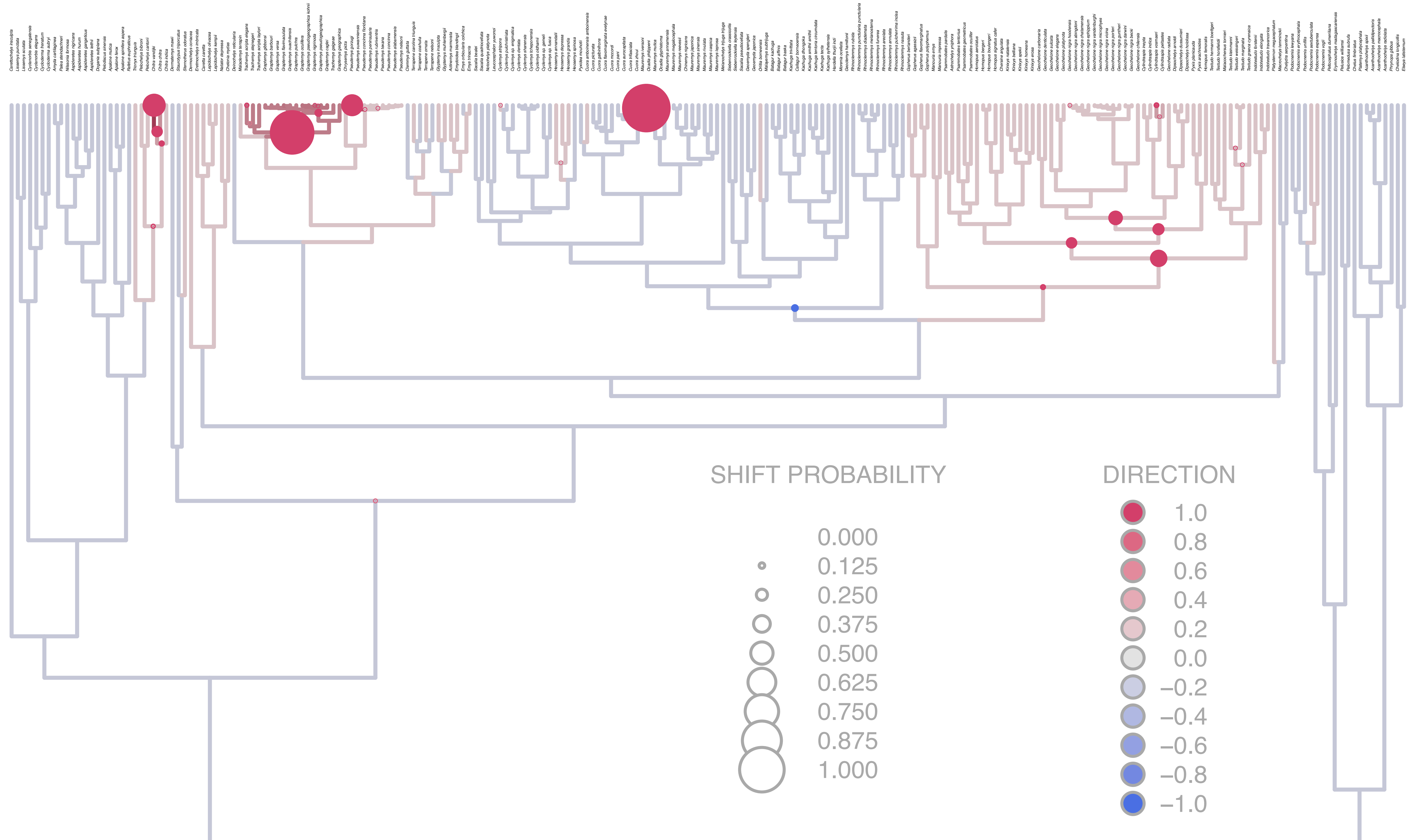
PRIMATES



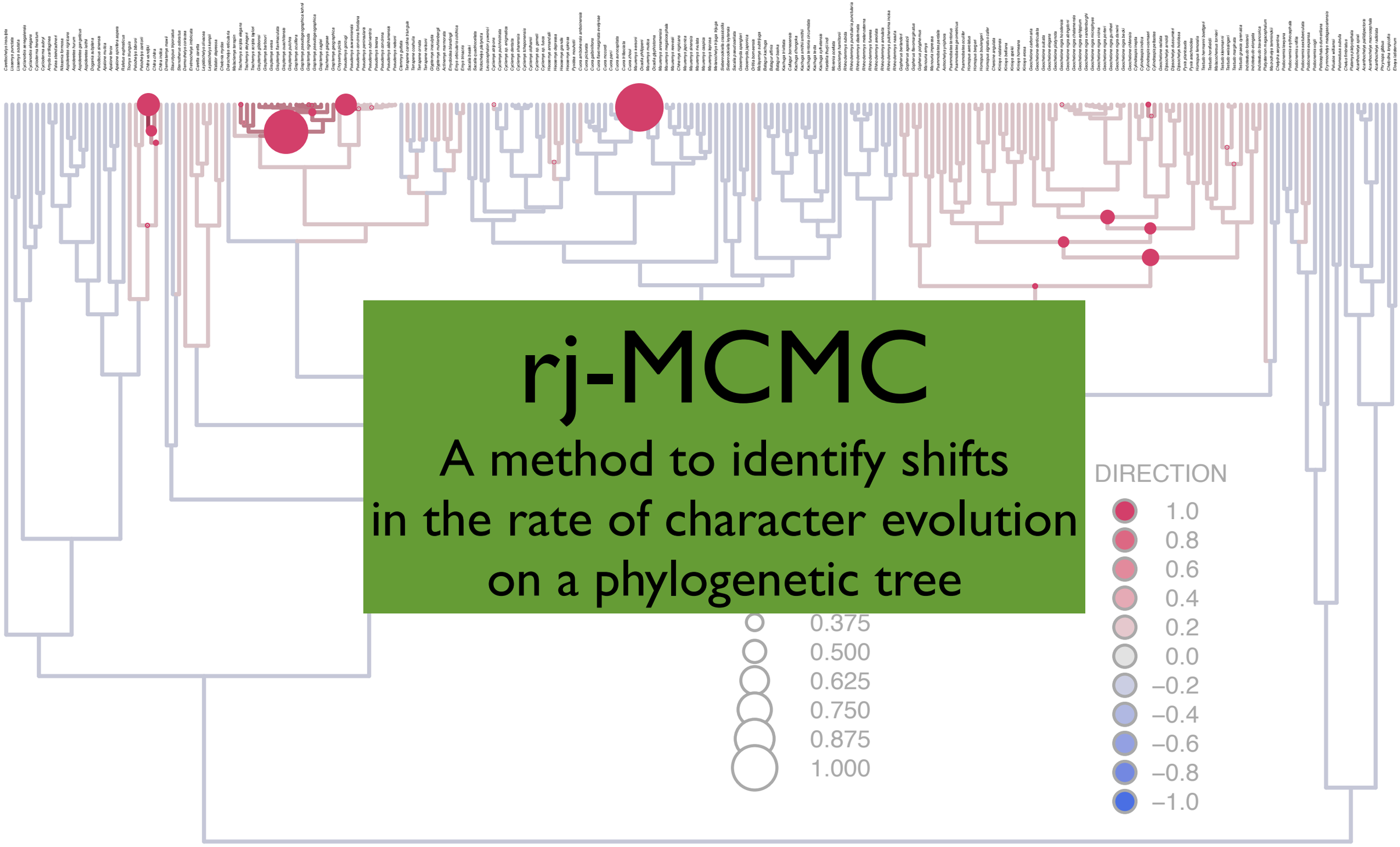
PRIMATES


SHIFT PROBABILITY
0.000
0.125
0.250
0.375
0.500
0.625
0.750
0.875
1.000
DIRECTION
1.0
0.8
0.6
0.4
0.2
0.0
–0.2
–0.4
–0.6
–0.8
–1.0

TESTUDINES


SHIFT PROBABILITY
0.000
0.125
0.250
0.375
0.500
0.625
0.750
0.875
1.000
DIRECTION
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0

TESTUDINES


rj-MCMC
A method to identify shifts
in the rate of character evolution
on a phylogenetic tree
0.375
0.500
0.625
0.750
0.875
1.000
DIRECTION
1.0
0.8
0.6
0.4
0.2
0.0
–0.2
–0.4
–0.6
–0.8
–1.0

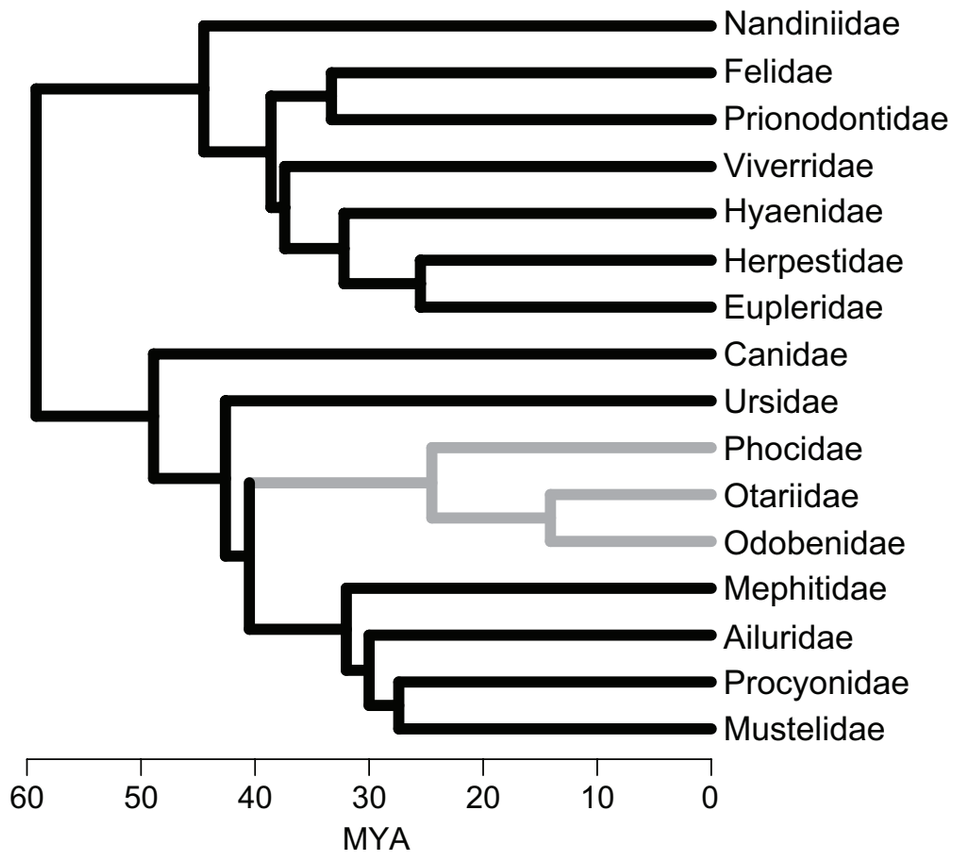
Three vignettes

- Fossil MEDUSA
- Reversible-jump MCMC
- MECCA

Data on body size in carnivores

(a)

(b)



Family	richness	mean log(g)	variance	sample size
Nandiniidae	1	7.68	0	1
Felidae	40	9.18	1.59	33
Prionodontidae	2	6.78	0.13	2
Viverridae	34	7.89	0.66	27
Hyaenidae	4	10.30	0.80	4
Herpestidae	33	7.18	0.48	29
Eupleridae	8	7.24	0.92	8
Canidae	35	8.58	0.68	32
Ursidae	8	11.75	0.30	8
Phocidae	19	12.24	0.75	19
Otariidae	16	11.69	0.38	14
Odobenidae	1	13.86	0	1
Mephitidae	12	7.26	0.57	10
Ailuridae	1	8.55	0	1
Procyonidae	14	7.65	0.53	13
Mustelidae	59	7.45	2.26	49

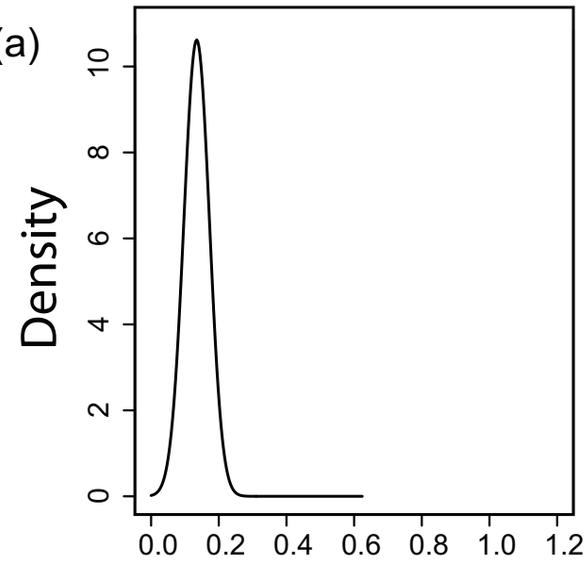
MECCA

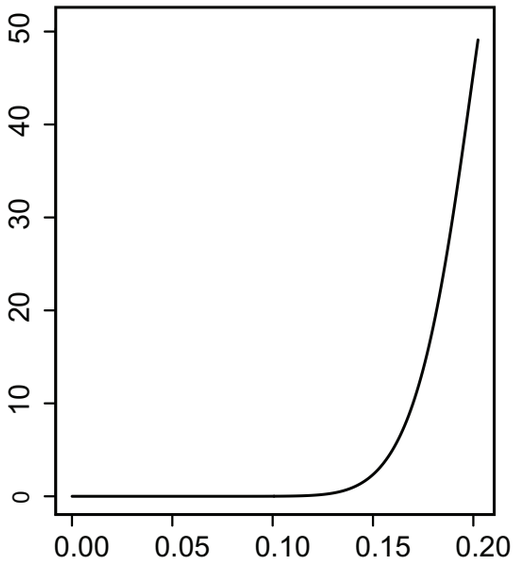
- Modeling evolution of continuous characters using ABC
- ABC = approximate Bayesian computation
- ABC is a method for calculating Bayesian posterior distributions WITHOUT likelihoods

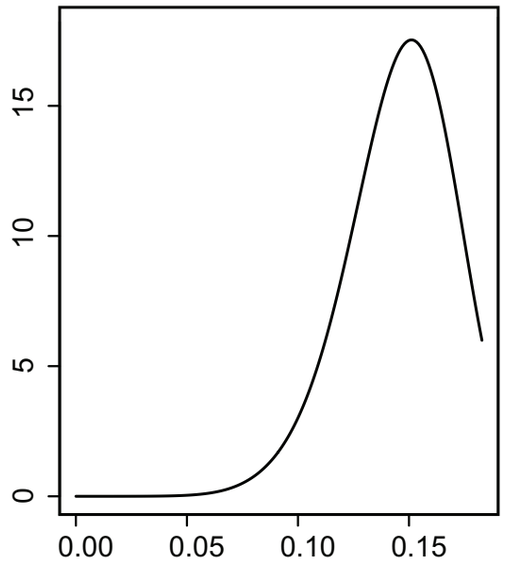
MECCA

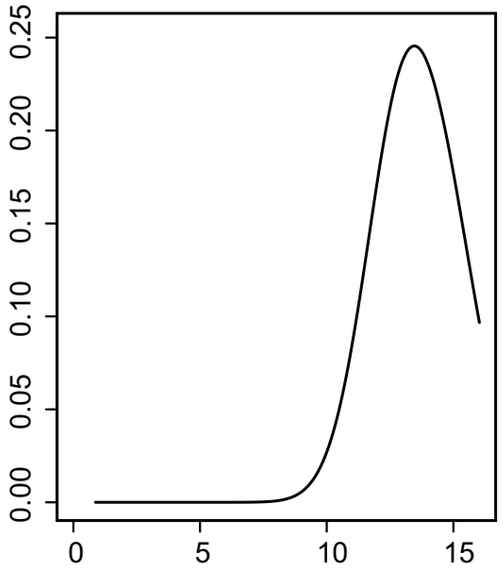
- We assume:
  - Trees grow under a birth-death model (parameters: λ, μ)
  - Traits evolve by Brownian motion (parameters: σ^2, θ)
- Use ABC to calculate posterior distribution of all four parameters given priors & the data

(a)



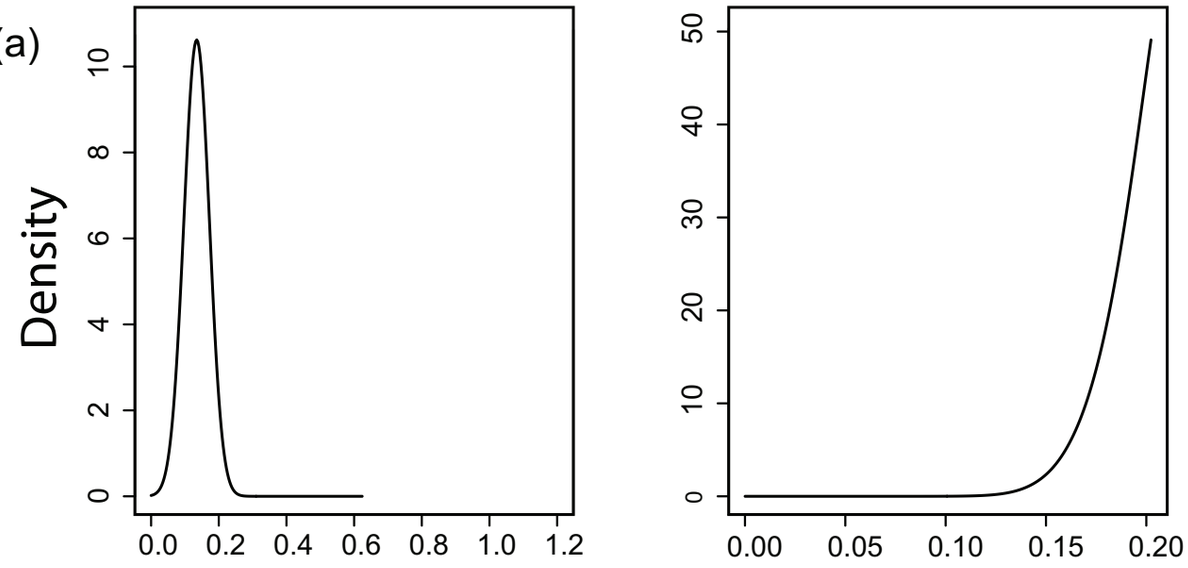




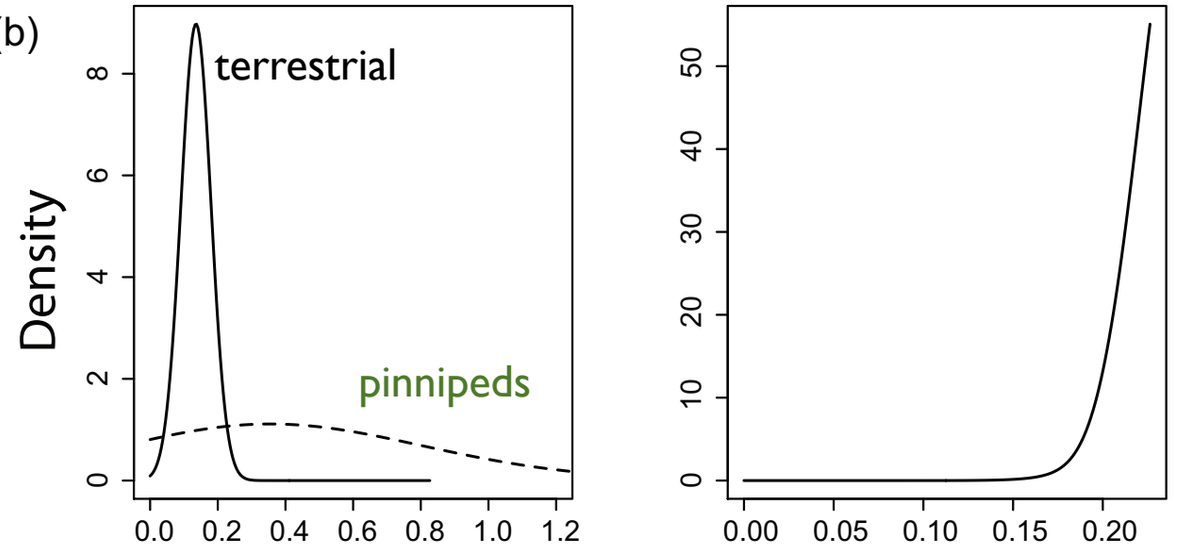


σ^2 λ μ θ

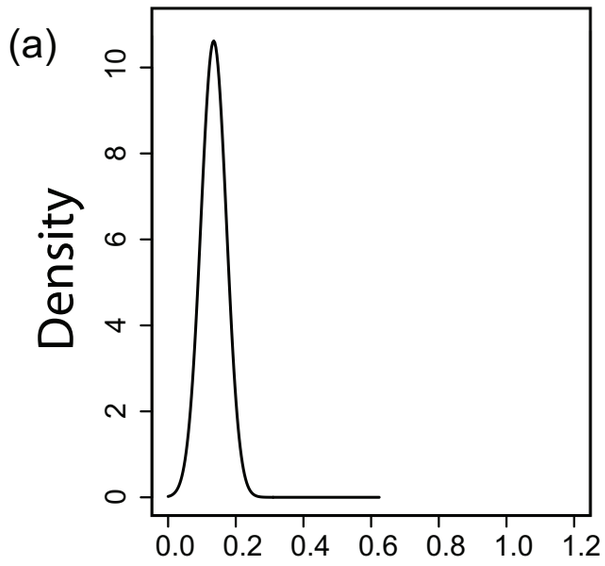
(a)

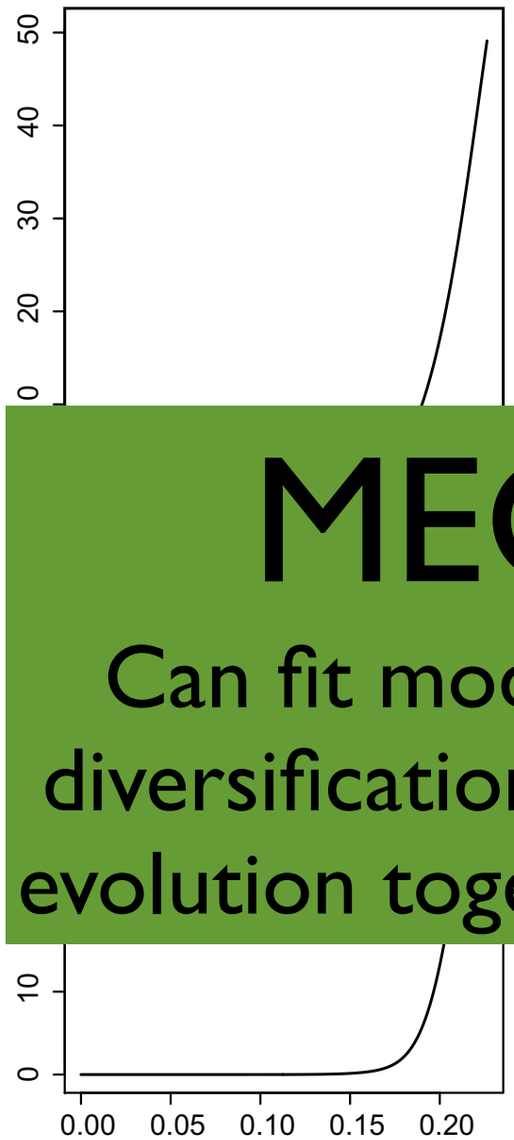


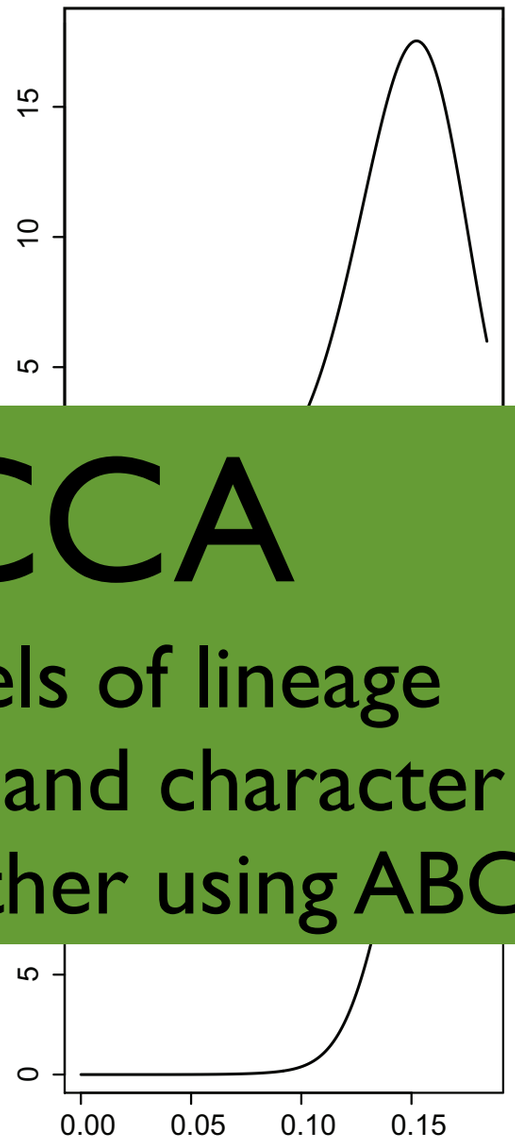
(b)

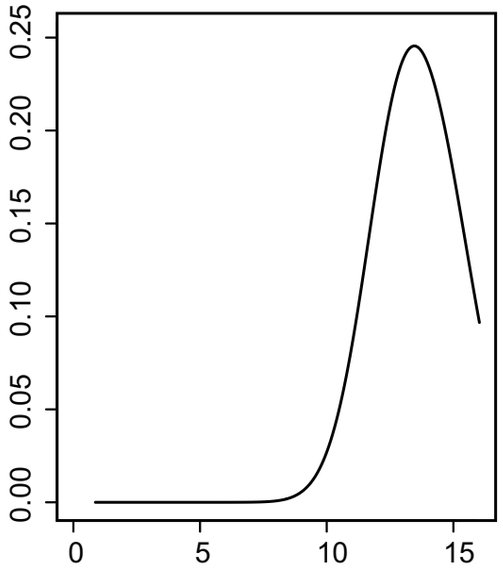


σ^2 λ μ θ



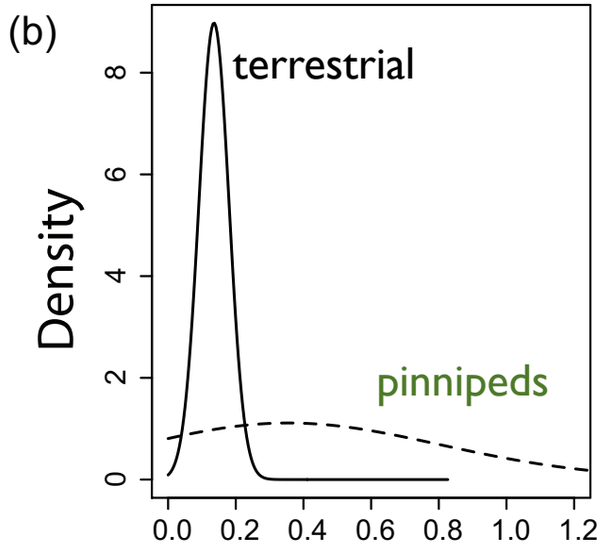


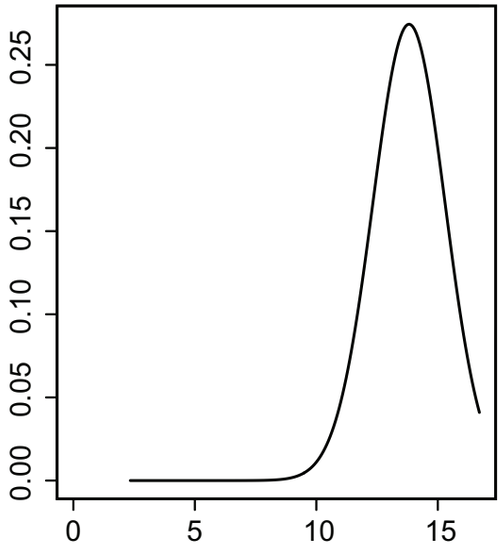




MECCA

Can fit models of lineage diversification and character evolution together using ABC





σ^2 λ μ θ

Goal:

- Create methods that analyze the data that people actually have to estimate things that they really want to know