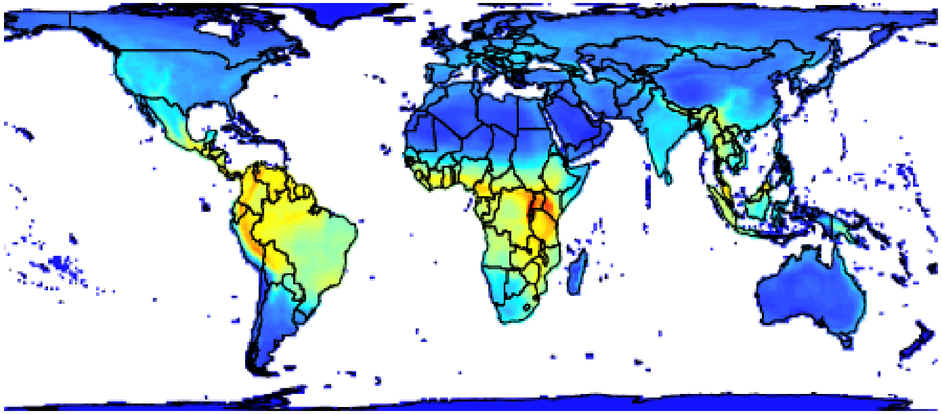
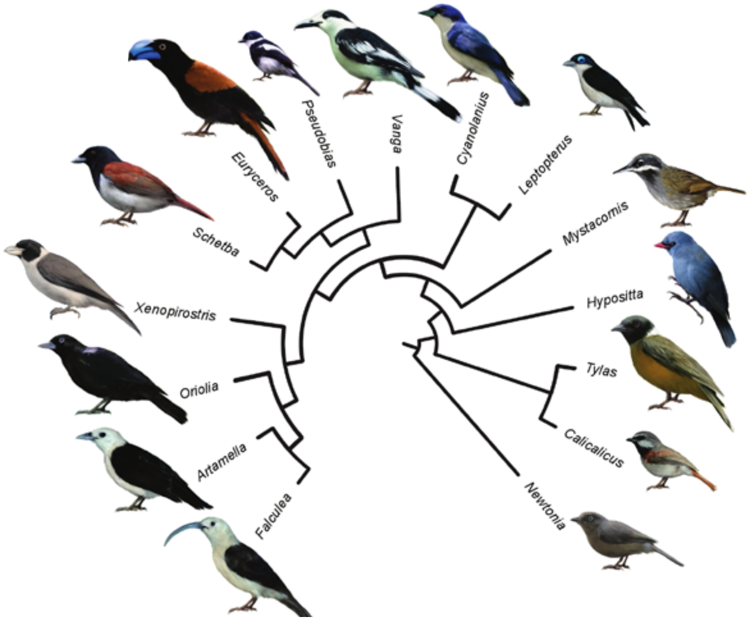
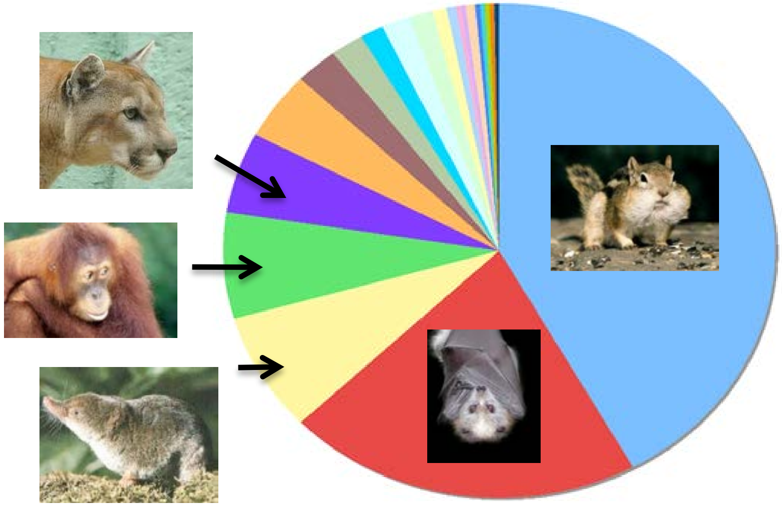
Understanding global biodiversity patterns using the Tree of Life



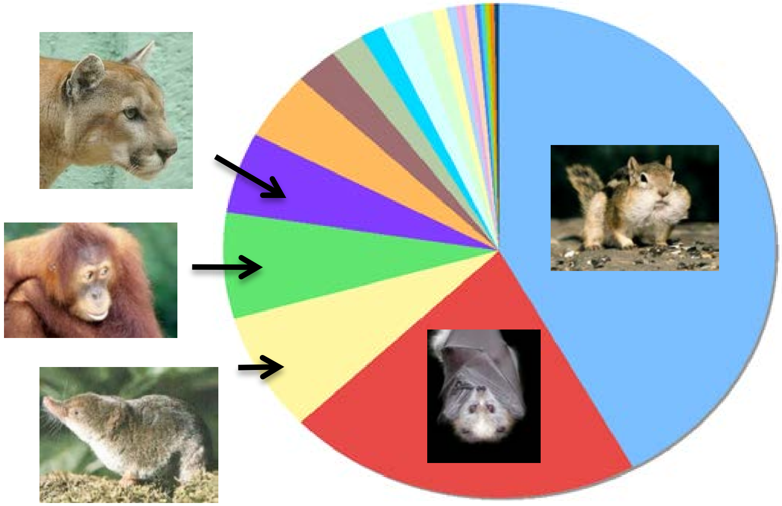


Hélène Morlon
Ecole Normale Supérieure

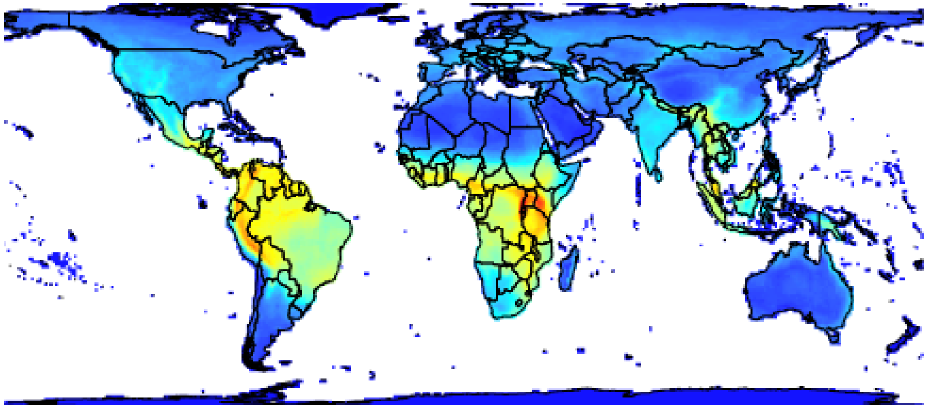
What explains species diversity across groups?



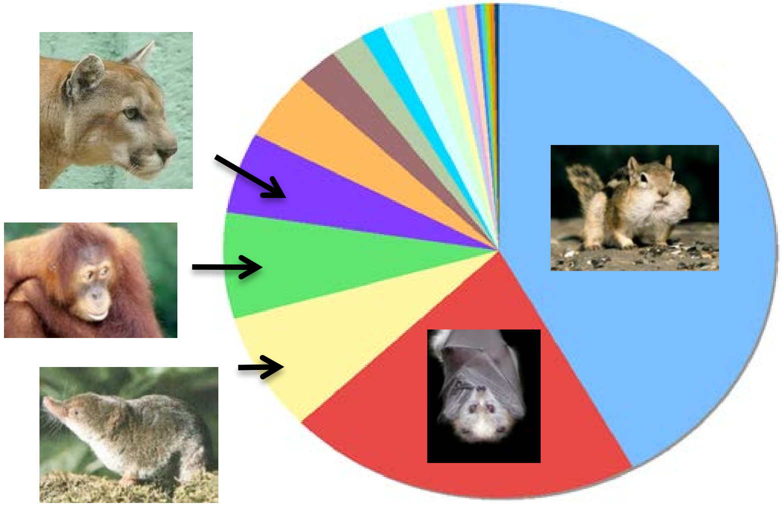
What explains species diversity across groups?



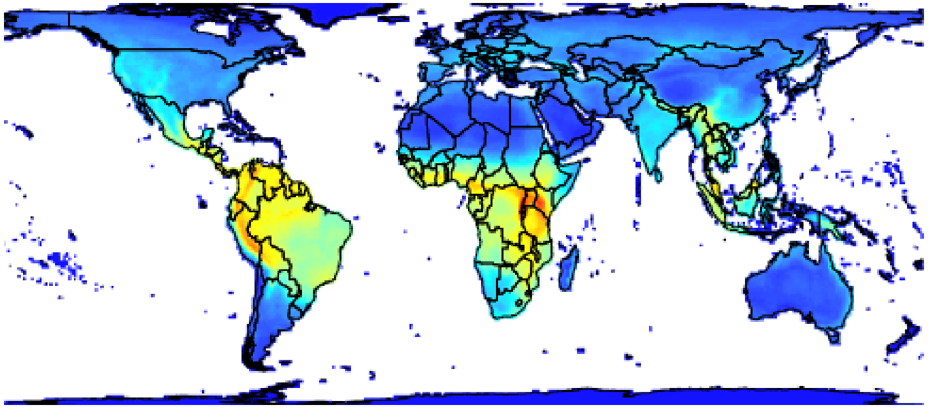
What explains species diversity across regions?



What explains species diversity across groups?



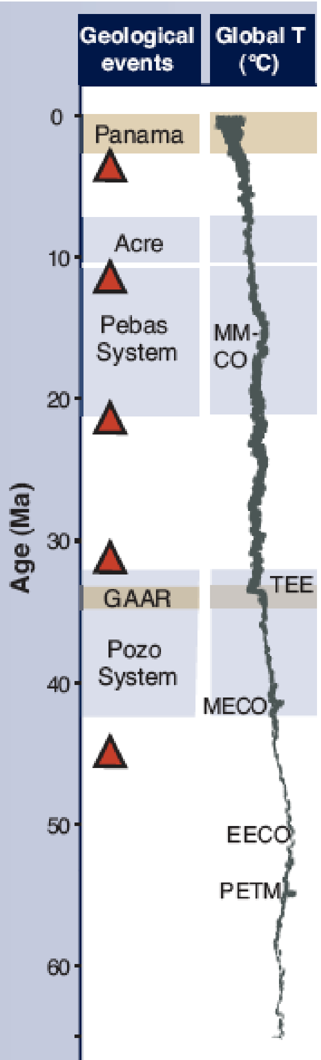
What explains species diversity across regions?



What explains phenotypic diversity across groups and regions?

Species richness results from speciation and extinction events, themselves influenced by various ecological and evolutionary processes

Abiotic factors



Biotic factors

competition

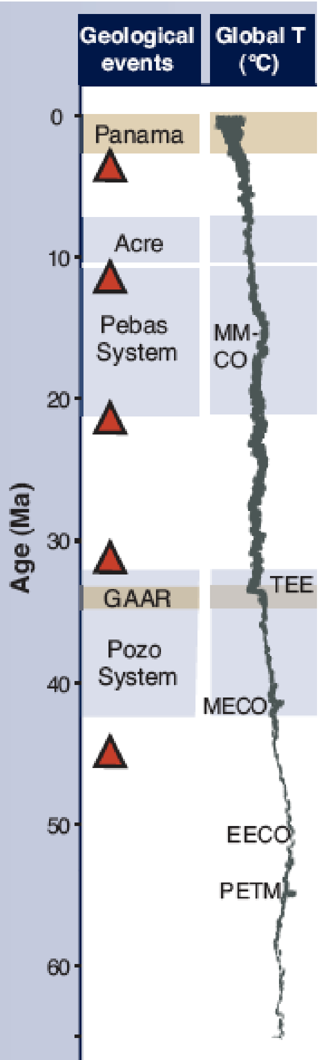
predation

parasitism

mutualism

Phenotypic diversity results from character evolution, itself influenced by various ecological and evolutionary processes

Abiotic factors



Biotic factors

competition

predation

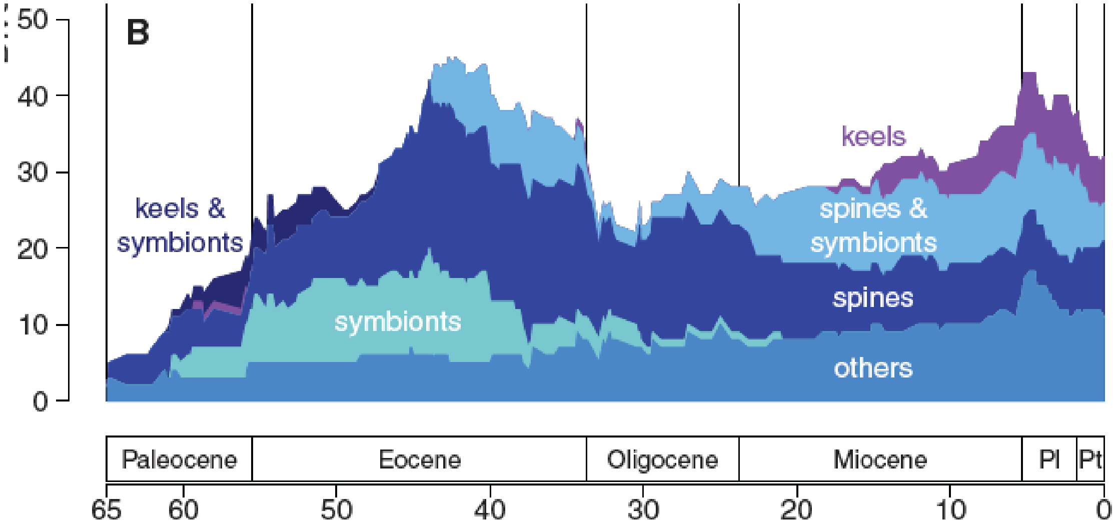
parasitism

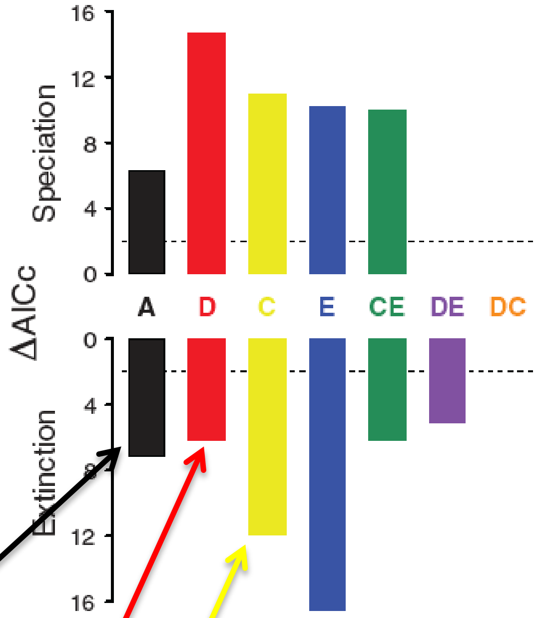
mutualism

Estimating rates of speciation, extinction, dispersal and trait evolution

Understanding how and why they vary across time, geographic regions, habitats, and taxonomic groups

Fossil approaches for understanding diversification and trait evolution





species age

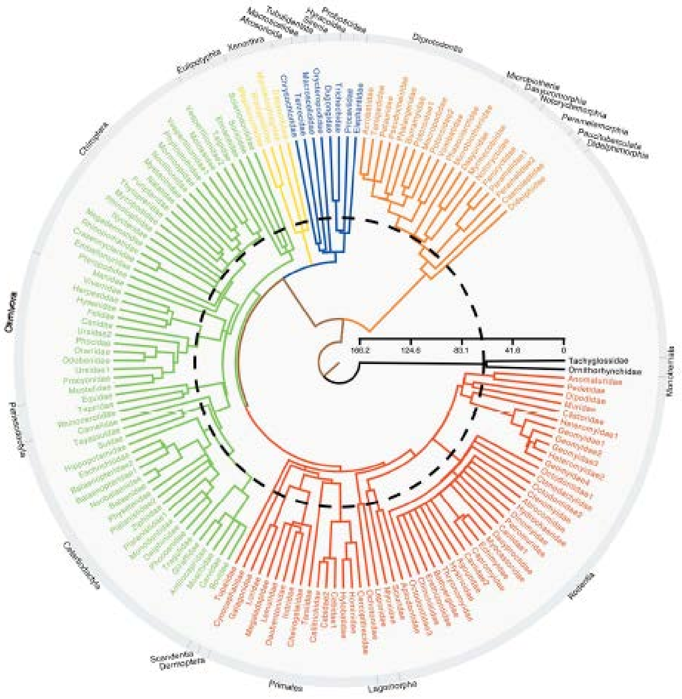
diversity

climate

species ecology

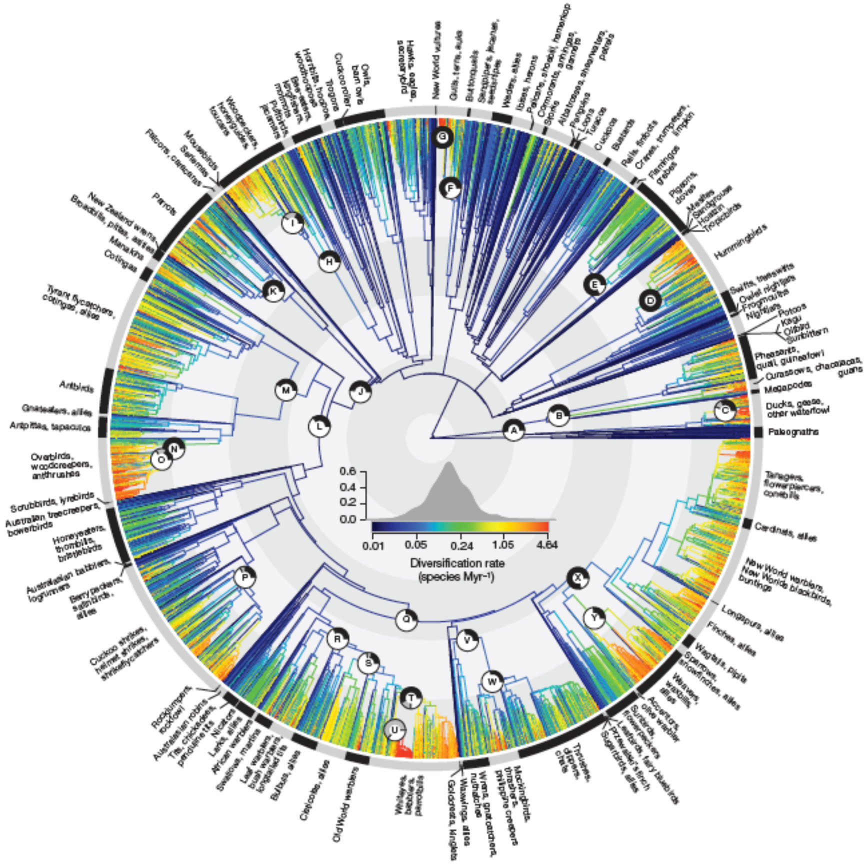
Ezard *et al.* Science 2011

Phylogenetic approaches for understanding diversification and trait evolution



4 510 mammal species

Bininda-Edmond *et al. Nature* 2007

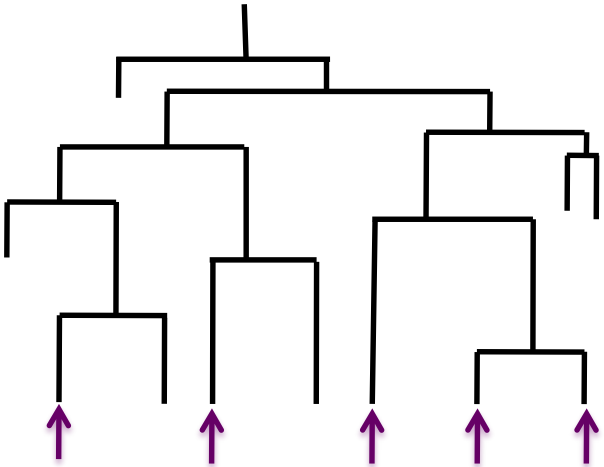


10 000 bird species

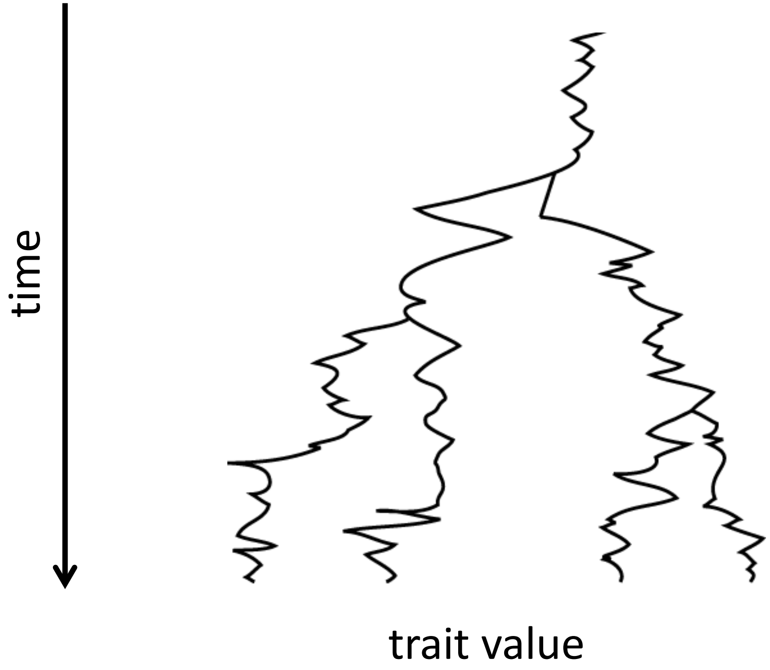
Jetz *et al. Nature* 2012

Phylogenetic approaches for understanding diversification and trait evolution

Stochastic models of cladogenesis



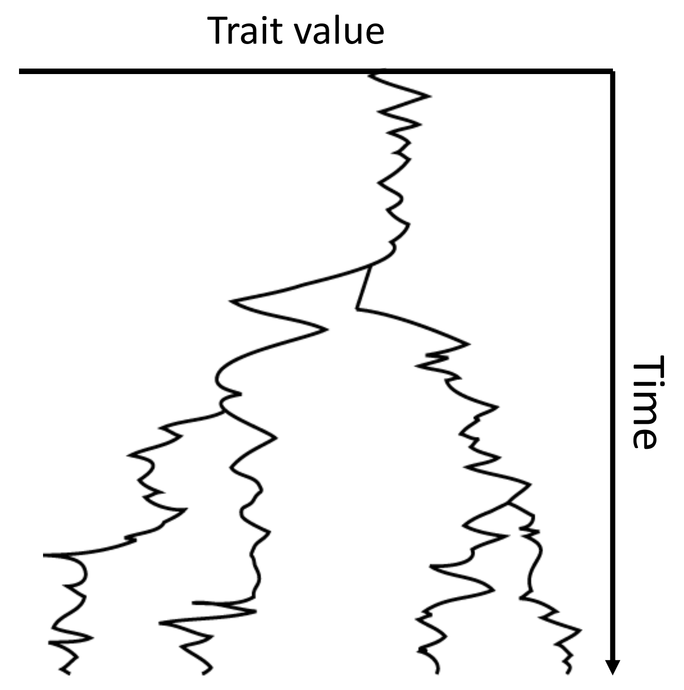
Stochastic models of trait evolution



We assume the phylogeny is known

Fit of models to data allows testing alternative scenarios of diversification and trait evolution and estimating relevant parameters

Stochastic models of trait evolution



Choosing models, estimating parameters

- Likelihoods of continuous models are based on the multivariate normal distribution
  - Result of a continuous-time Markov process is a sum of multiple independent events ➡ central limit theorem

$$L = \frac{\exp\left\{-\frac{1}{2}[\mathbf{X} - \mathrm{E}(\mathbf{X})]'(\mathbf{V}^{-1})[\mathbf{X} - \mathrm{E}(\mathbf{X})]\right\}}{\sqrt{(2\pi)^{N} * \det(\mathbf{V})}}$$

Where:

X = vector of data

E(**X**) = vector of expected values (all the same in this case)

V = *variance-covariance matrix*

Specific models

Brownian motion

- Named after Robert Brown, who described the motion of pollen grains in water in 1827
- First proposal for comparative analyses by Felsenstein (1985)
- Simplest model of character evolution
- Widely used (assumed) model for all types of analyses

Specific models

Brownian motion

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

$dX(t)$ = change in $X(t)$ in an instant of time

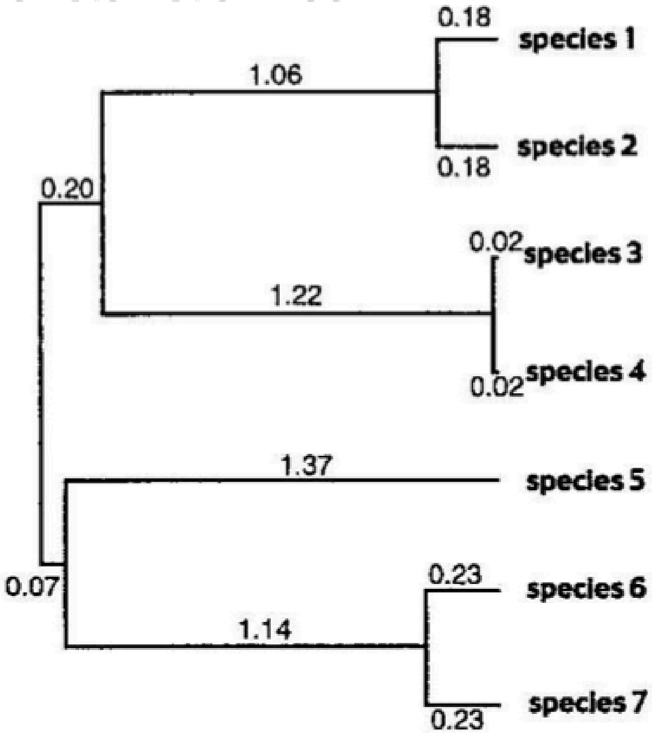
σ = scale of change in $X(t)$

$dB(t)$ = random variable of change in $X(t)$, distributed as $dB(t) \sim N(0,dt)$

Hansen and Martins 1996 *Evolution*

Brownian motion, phylogeny, and (co)variance

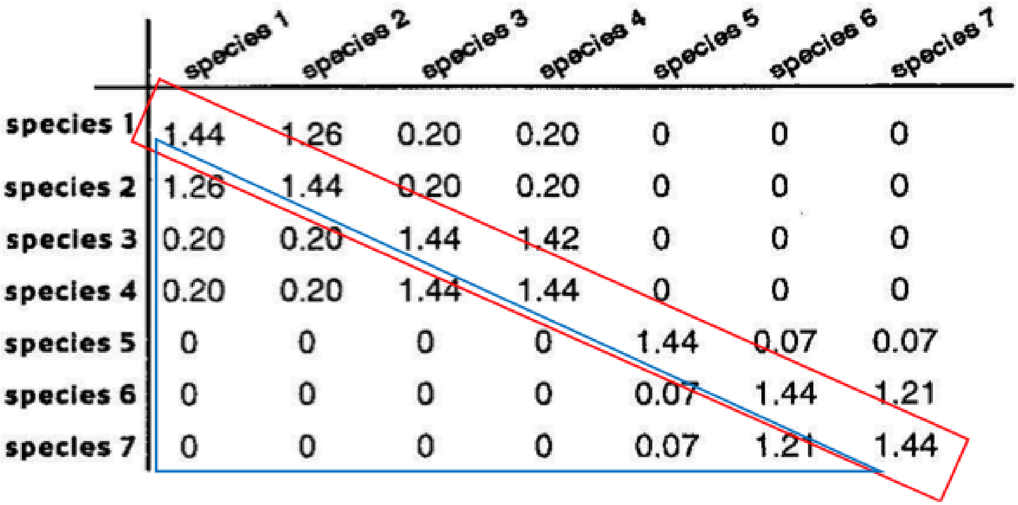
Freckleton et al. 2002



Format: branch lengths are proportional to…

-Expected variance on diagonal

-Expected covariance on off-diagonal



	species 1	species 2	species 3	species 4	species 5	species 6	species 7
species 1	1.44	1.26	0.20	0.20	0	0	0
species 2	1.26	1.44	0.20	0.20	0	0	0
species 3	0.20	0.20	1.44	1.42	0	0	0
species 4	0.20	0.20	1.44	1.44	0	0	0
species 5	0	0	0	0	1.44	0.07	0.07
species 6	0	0	0	0	0.07	1.44	1.21
species 7	0	0	0	0	0.07	1.21	1.44

Specific models

Brownian motion: summary

- “The” model of comparative biology, up to now
- What does this model mean in terms of our expected evolutionary model?
    - Drift: genetic or shifting selection optimum
- Does it actually work?
    - Most comparative datasets fit this model well (Freckleton et al. 2002, Blomberg et al. 2003)
    - Ancestral-state estimates based on this model fit well with known fossils (Polly 2001)

Specific models

Ornstein-Uhlenbeck (OU)

- A process of drift towards an “optimum”
- First introduced for comparative methods by Hansen and Martins (1996), though its incorporation has been very slow
- Simplest model of selection (stabilizing) for modeling evolution along a phylogeny

Specific models

Ornstein-Uhlenbeck (OU): the “rubber-band” model

$$dX(t) = \underbrace{\boxed{\alpha[\theta\text{-}X(t)]dt}}_{\text{Selection component}} + \underbrace{\boxed{\sigma dB(t)}}_{\text{Drift (BM) component}}$$

where

$\alpha =$ strength of "selection"

$\theta =$ adaptive optimum

➡ When $\alpha = 0$, this collapses to Brownian motion

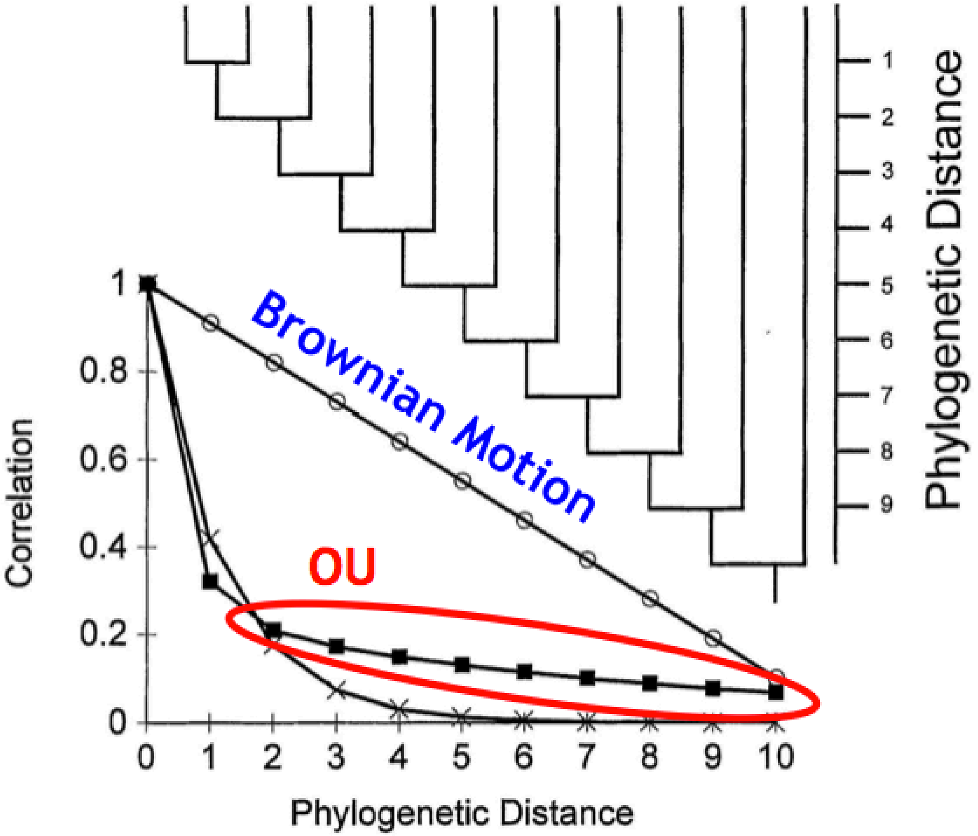
Ornstein-Uhlenbeck (OU): summary

(1) Covariance: decays exponentially with time

$$V_{ij} = \frac{\sigma^2}{2\alpha} e^{-2\alpha(T-s_{ij})}(1 - e^{-2\alpha s_{ij}})$$

Where:

T = max phylo. distance
s_{ij} = shared phylo. distance between species *i* and *j*



(2) Can apply multiple evolutionary optima (θ)

Hansen and Martins, 1996, Evolution

Specific models

Early-burst / ACDC

- Proposed by Blomberg et al. (2003), though actually very similar to an earlier idea (Pagel 1999)
- General idea: rate (σ) of change either accelerates (AC) or decelerates (DC) – previous models have assumed constant σ
- Later authors have used this to test for an early burst of evolution during adaptive radiation (i.e., deceleration of rate over time)

installed.

Specific models

Early-burst / ACDC

- Effects on covariance
  - Acceleration (AC) : covariance increases more over time than under BM
  - Deceleration (DC) : covariance increases less over time than under BM

$$V_{ij} = \int_{0}^{s_{ij}} \sigma_0^2 e^{rt} \, dt$$

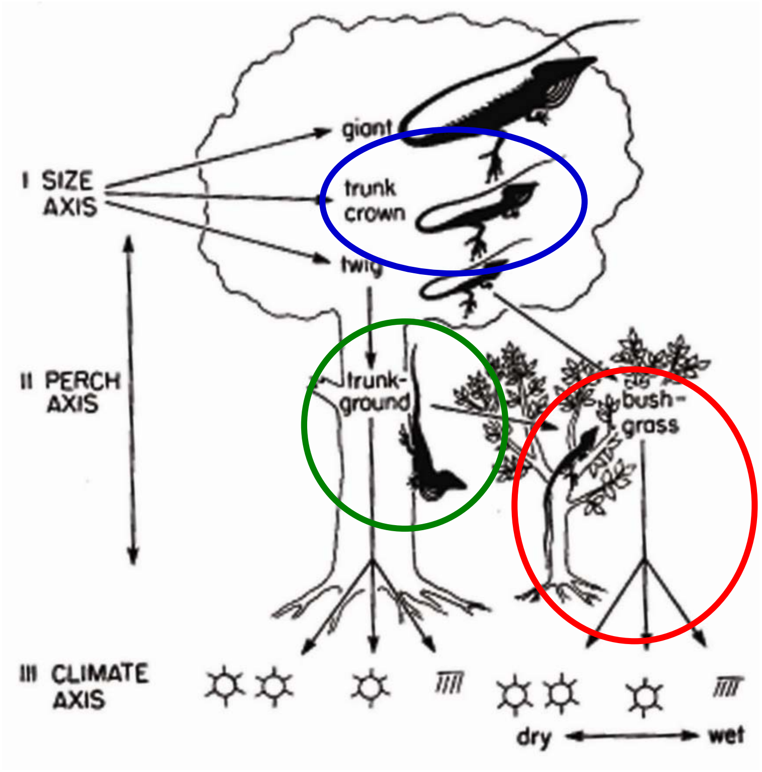
Where:

$\sigma^2{}_0$ = base rate
s_{ij} = shared phylo. distance between species *i* and *j*
r = *ACDC parameter*

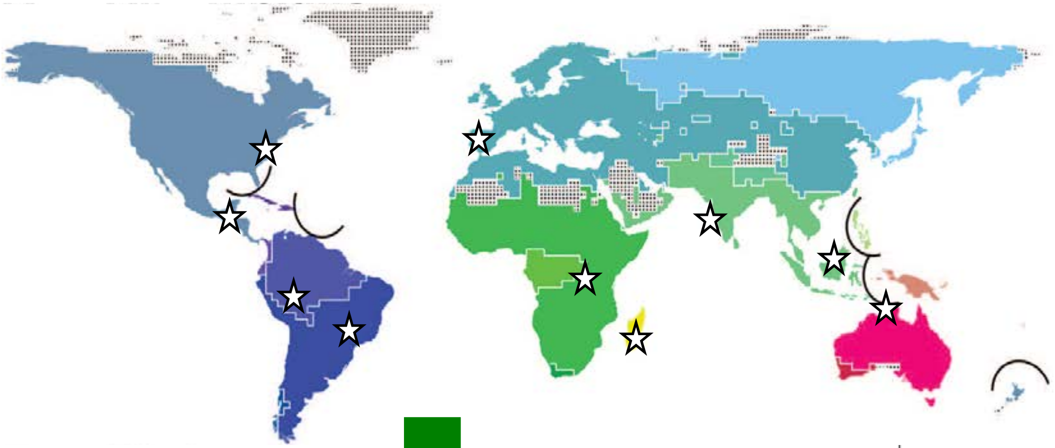
What drives phenotypic diversity?

What is the role of shared ancestry versus local adaptation?

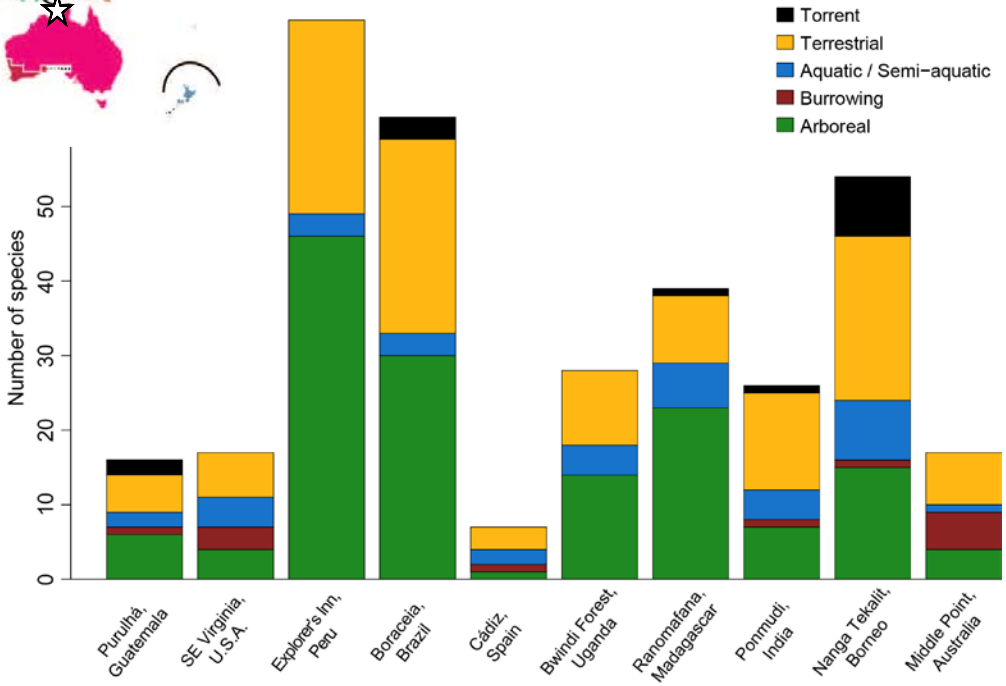
Anolis lizards in the Caribbean



Williams 1983 Book chapter



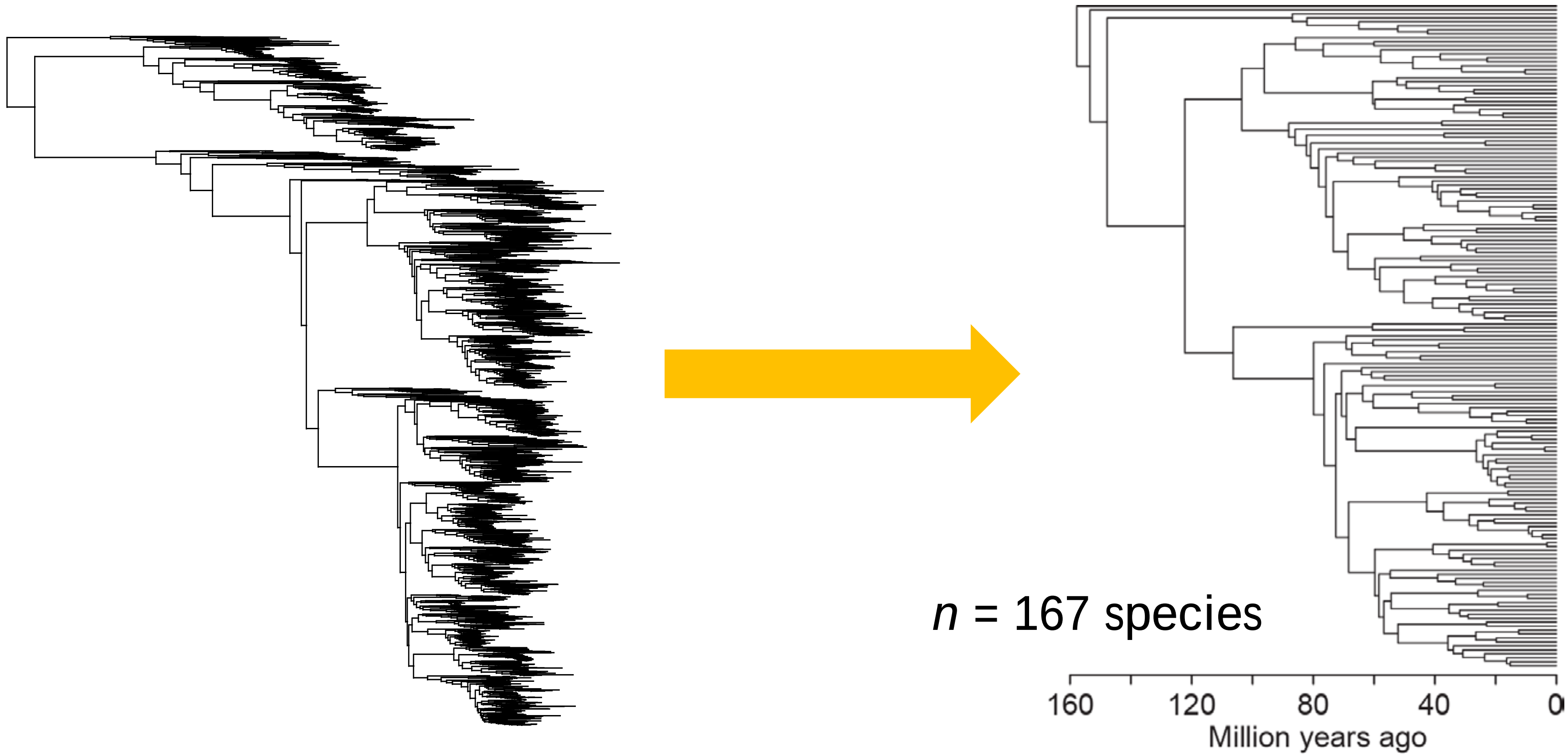
?



Question 1: Have there been many independent microhabitat transitions in frogs?

Phylogeny

- Topology: Pyron and Wiens 2011 *Mol. Phylogenet. Evol.*
- Branch lengths: BEAST (Drummond and Rambaut 2007 *BMC Evol. Biol.*)

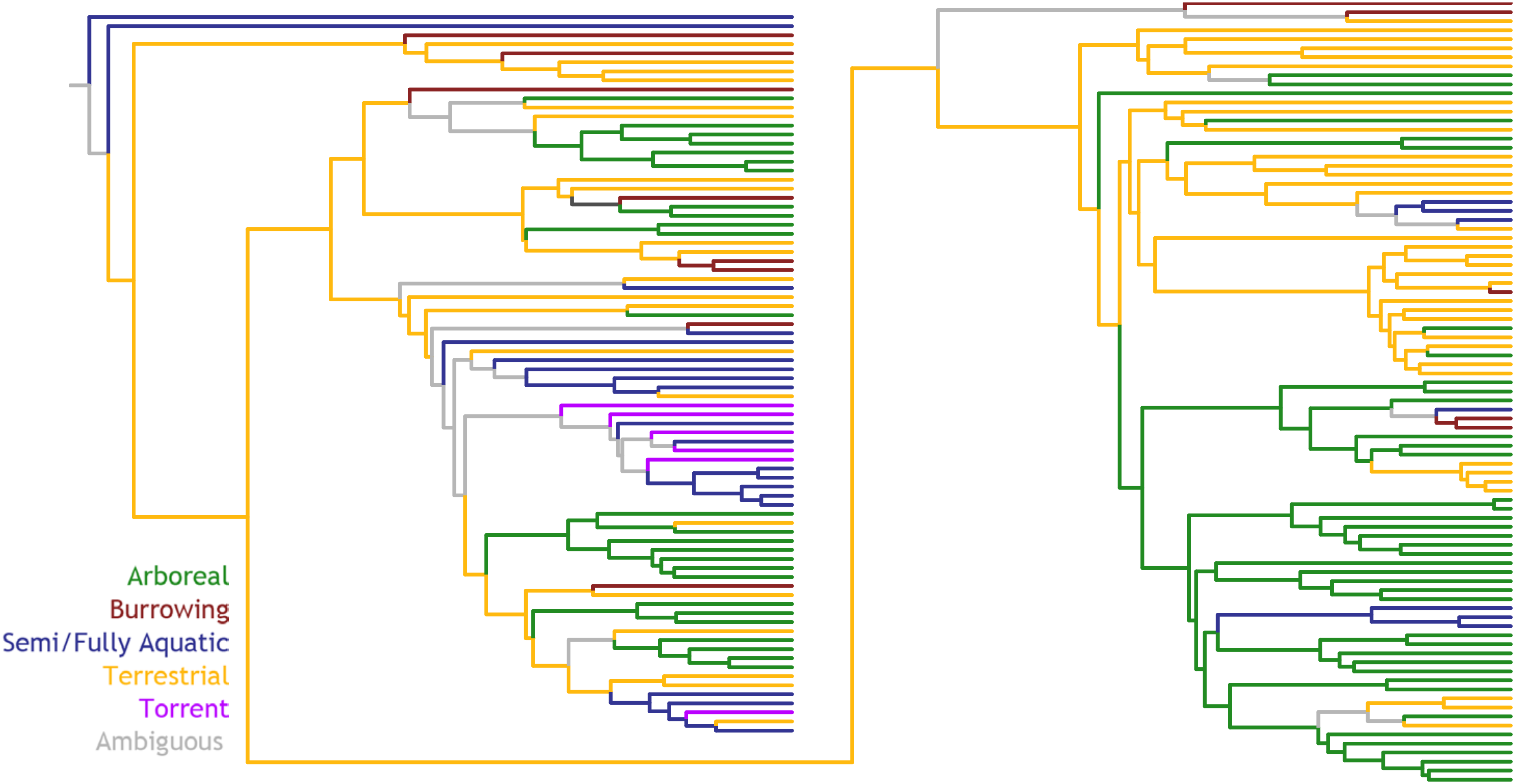


n = 167 species

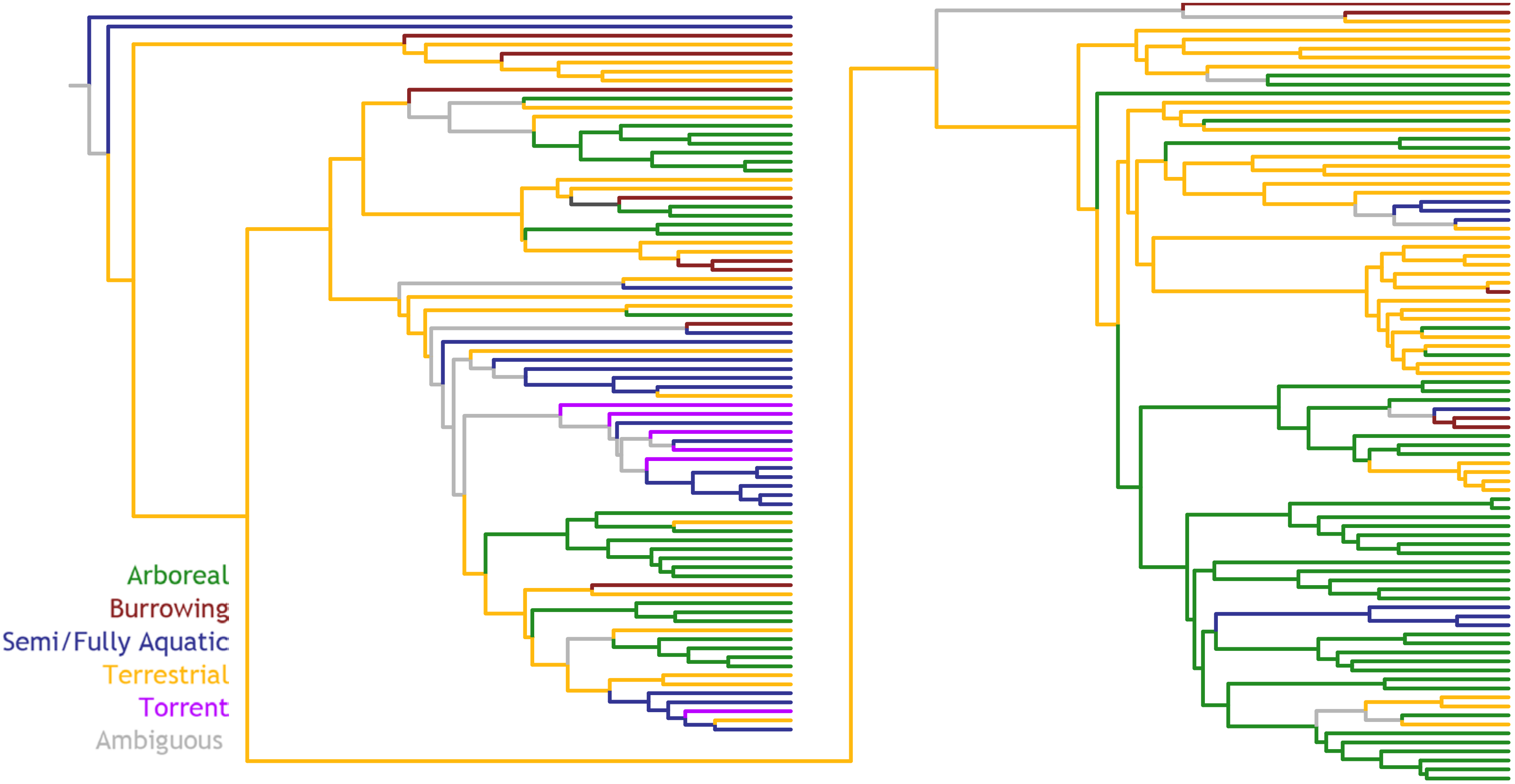
We find many transitions:

11 Arboreal
8 Semi/Fully Aquatic
9 Burrowing

> 2 Torrent
~ 5 Terrestrial

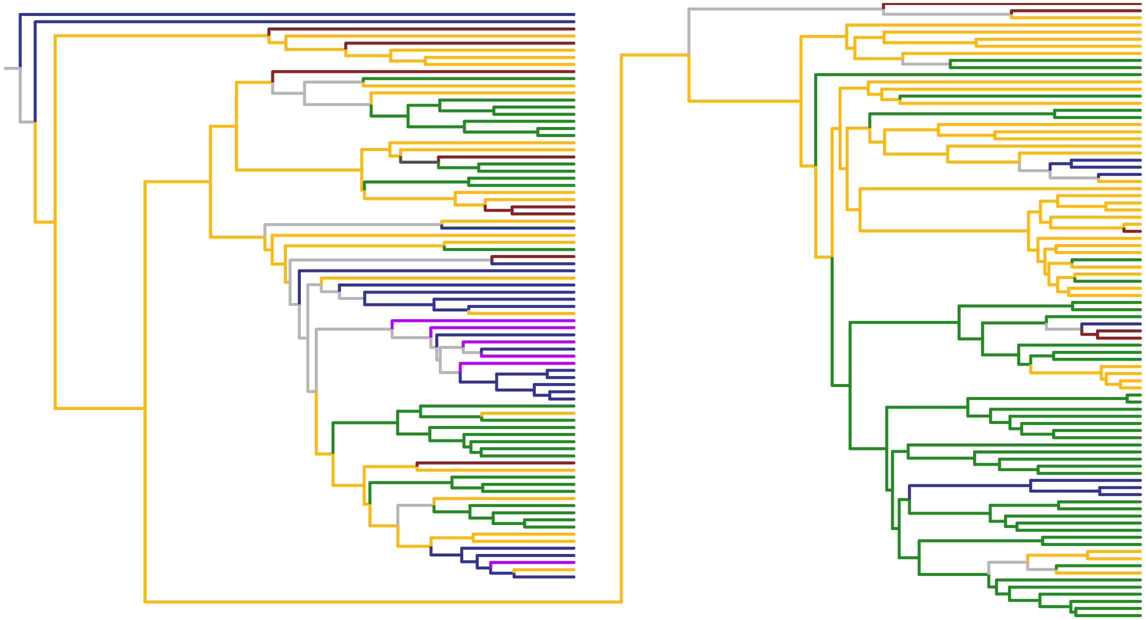


How repeatable is evolution? Might we see some convergent evolution but also a "footprint" of history?

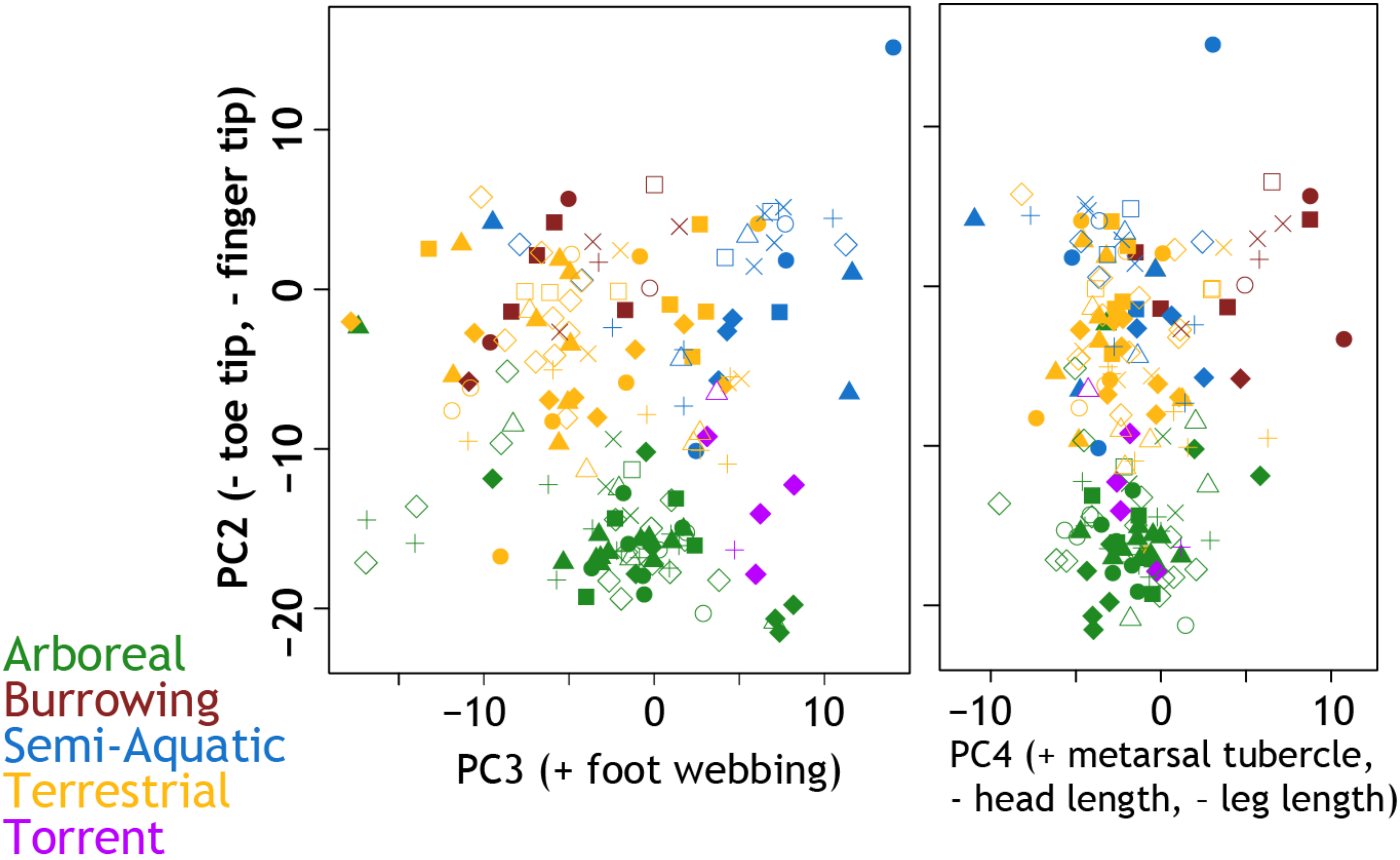


How repeatable is evolution? Might we see some convergent evolution but also a "footprint" of history?

→ Collected additional data on functional morphology from 167 species across 10 sites

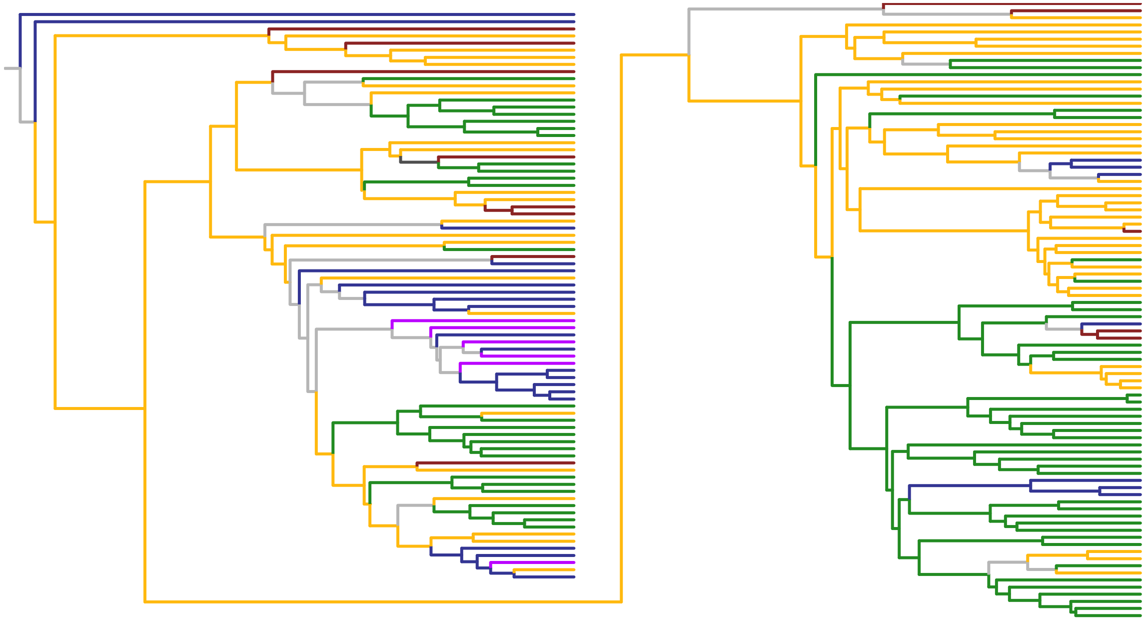


Species (generally) cluster by microhabitat type

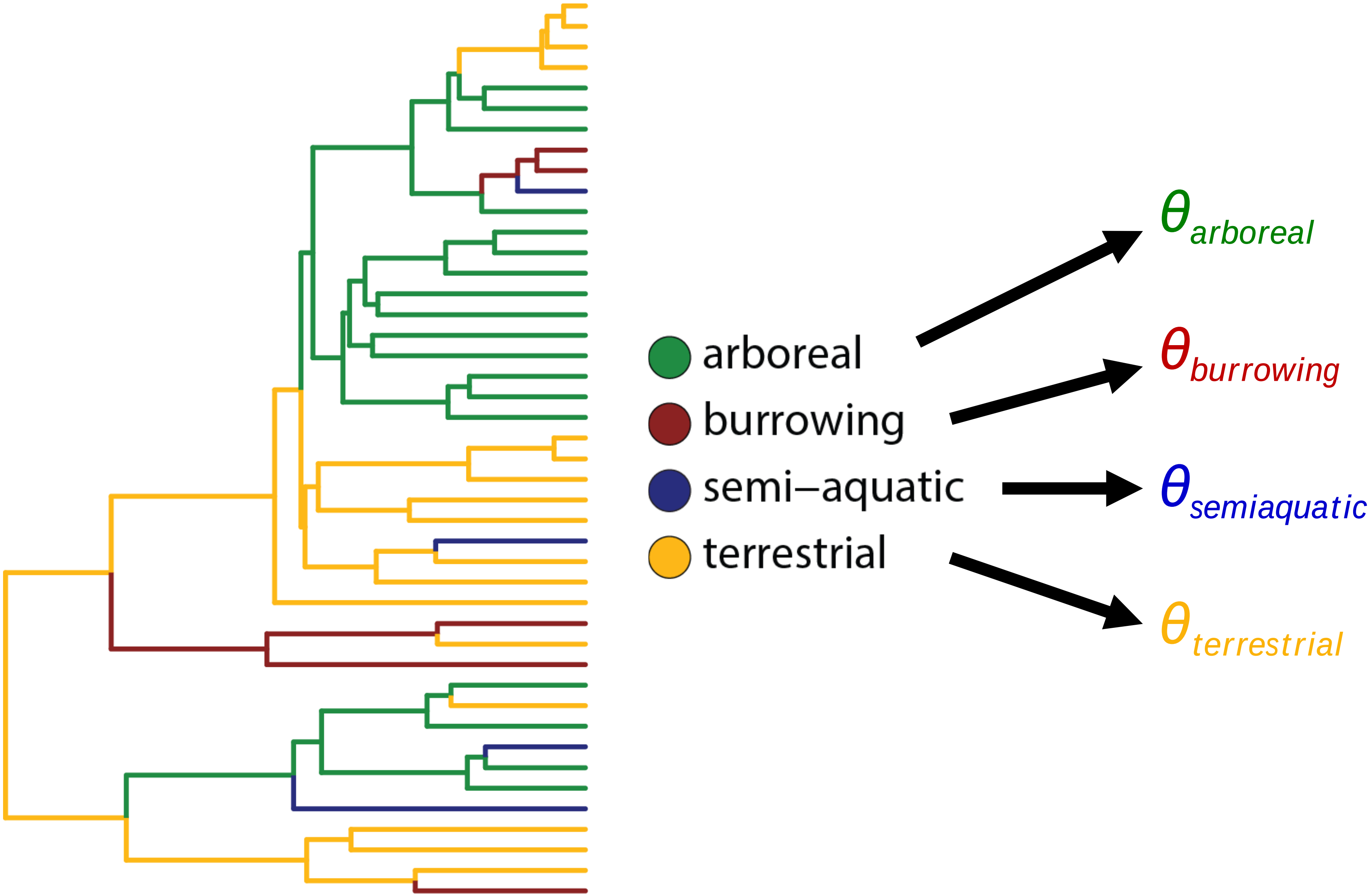


How repeatable is evolution? Might we see some convergent evolution but also a "footprint" of history?

- Collected additional data on functional morphology from 167 species over 10 sites
- Developed novel tests of the effect of past adaptation to previous environments



Ornstein-Uhlenbeck models of adaptation



🟢 arboreal → $\theta_{arboreal}$

🔴 burrowing → $\theta_{burrowing}$

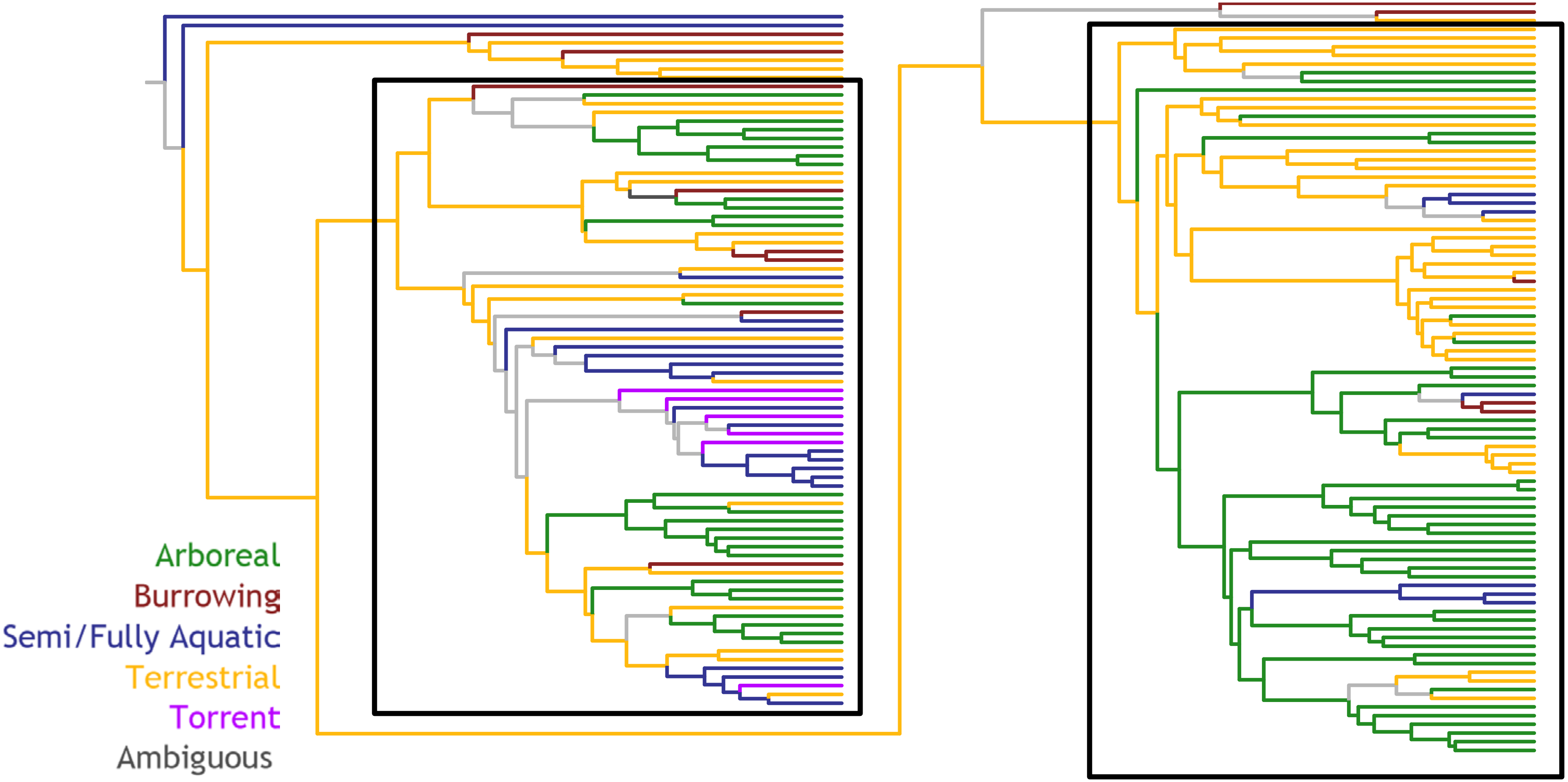
🔵 semi–aquatic → $\theta_{semiaquatic}$

🟡 terrestrial → $\theta_{terrestrial}$

Tests of history versus convergent adaptation

Do different origins of similar microhabitat use lead to different morphology?

(A) Major clade?

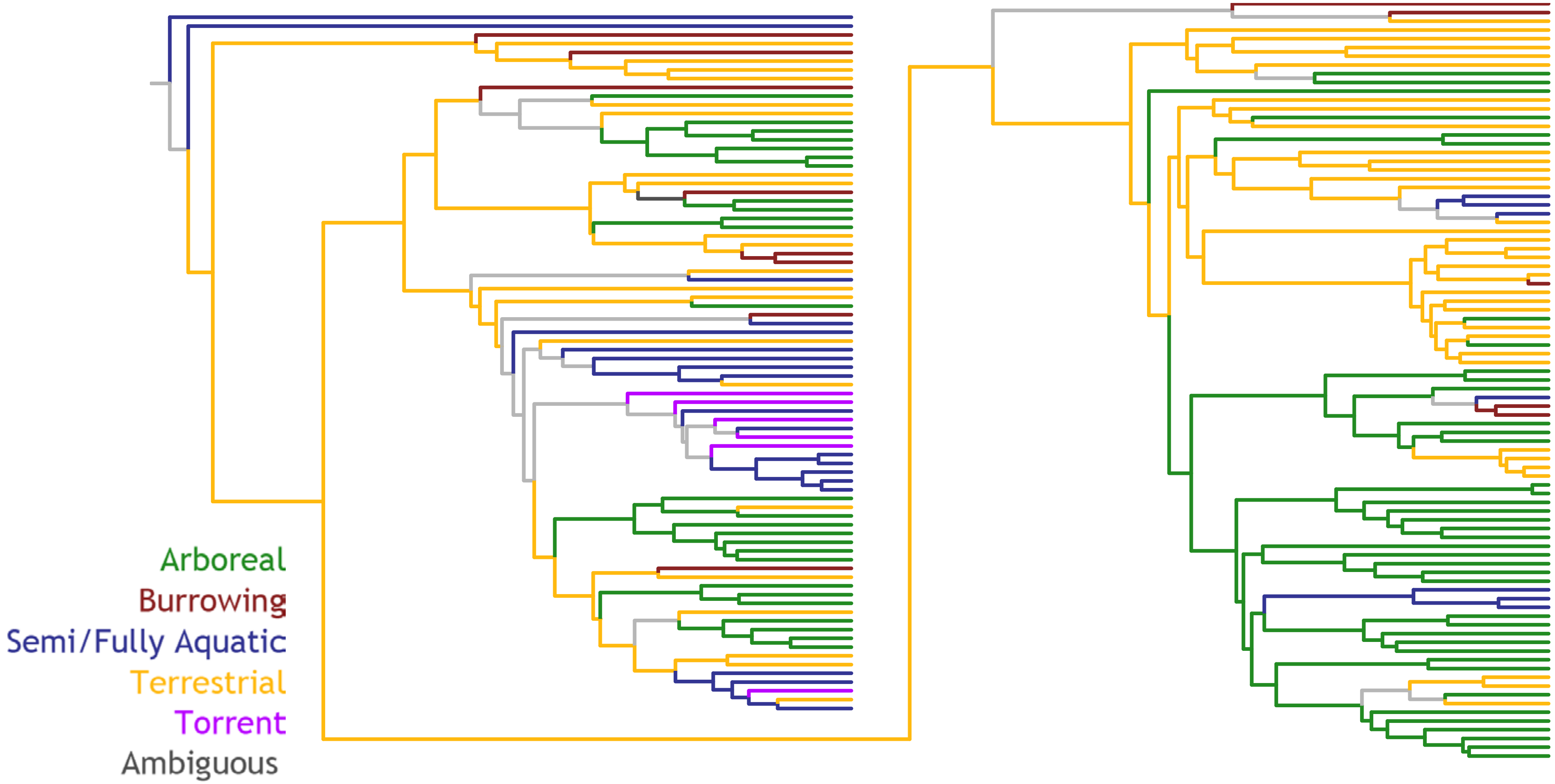


Tests of history versus convergent adaptation

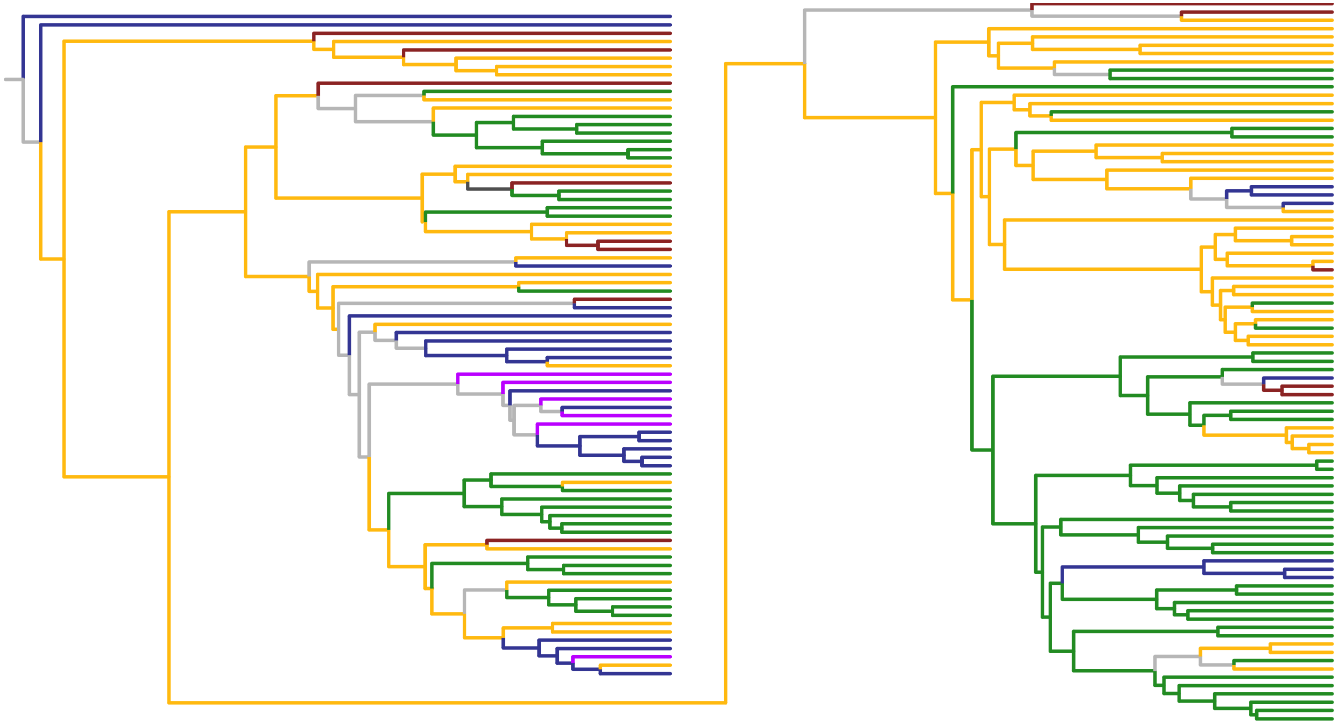
Do different origins of similar microhabitat use lead to different morphology?

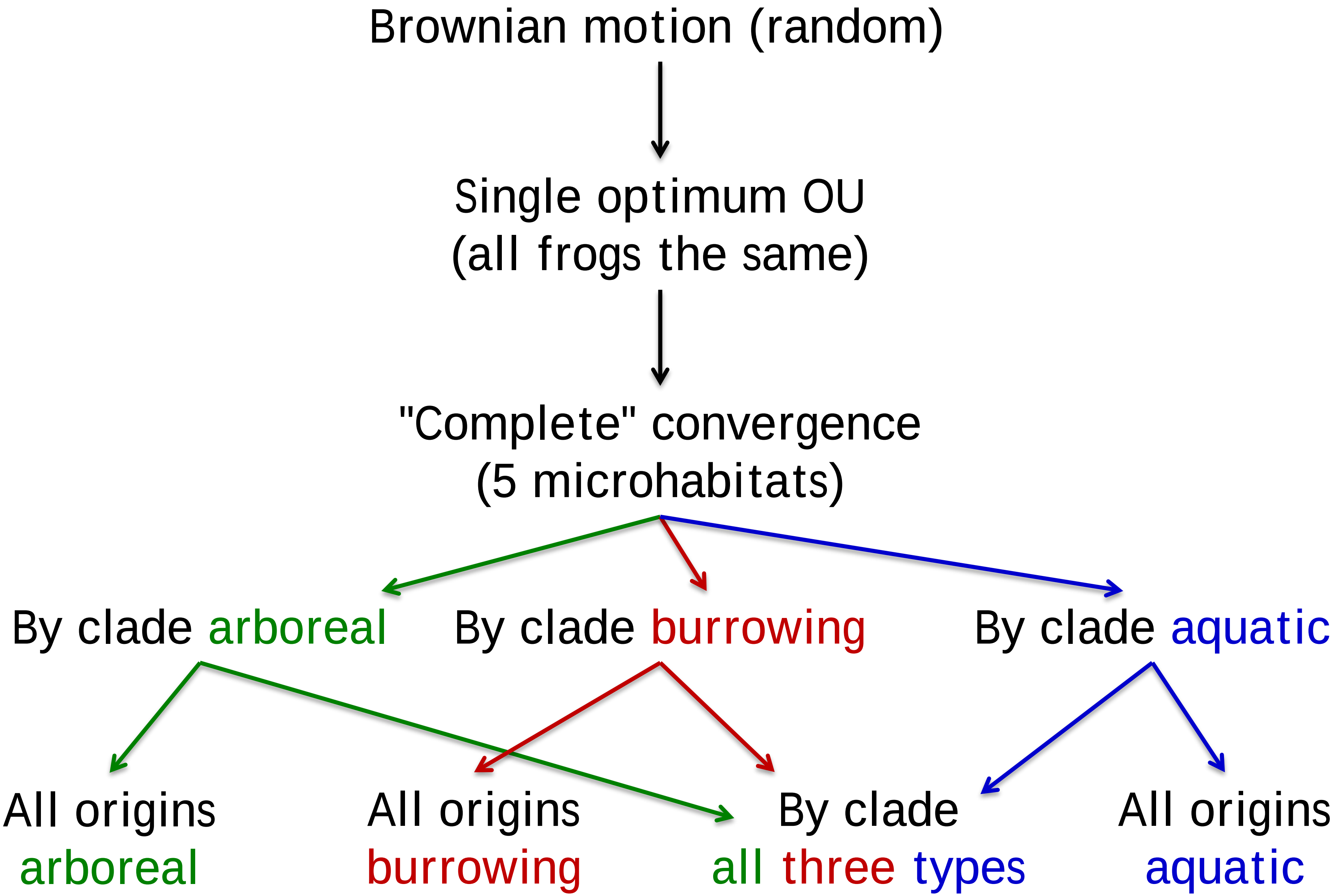
(A) Major clade?

(B) All independent origins?



"Complete" convergence model





Brownian motion (random)

Single optimum OU
(all frogs the same)

"Complete" convergence
(5 microhabitats)

By clade arboreal

By clade burrowing

By clade aquatic

All origins
arboreal

All origins
burrowing

By clade
all three types

All origins
aquatic

What drives phenotypic diversity?

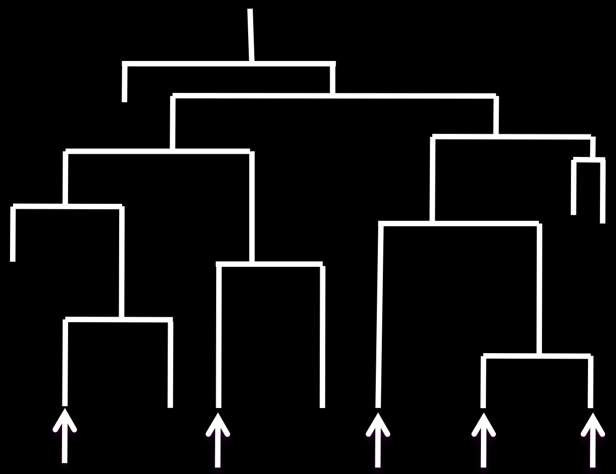
Frog communities around the world converge towards similar evolutionary optima

… except burrowers for which different clades each have their own optimum

Moen, Morlon & Wiens, *in press*

Stochastic models of cladogenesis

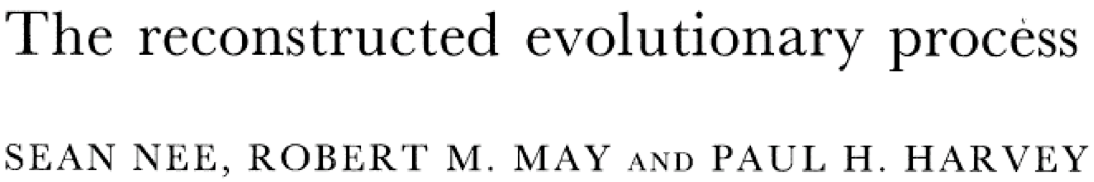
1. the bases



Phylogenetic approaches to diversification

Stochastic birth-death process

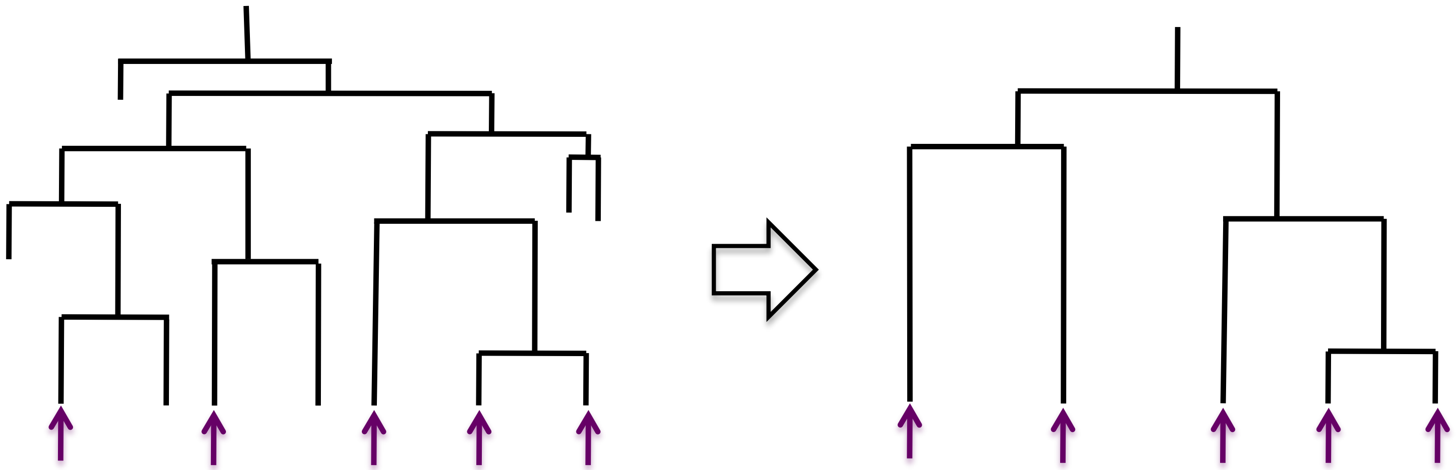
Reconstucted phylogeny



The reconstructed evolutionary process

SEAN NEE, ROBERT M. MAY AND PAUL H. HARVEY

PTB 1994



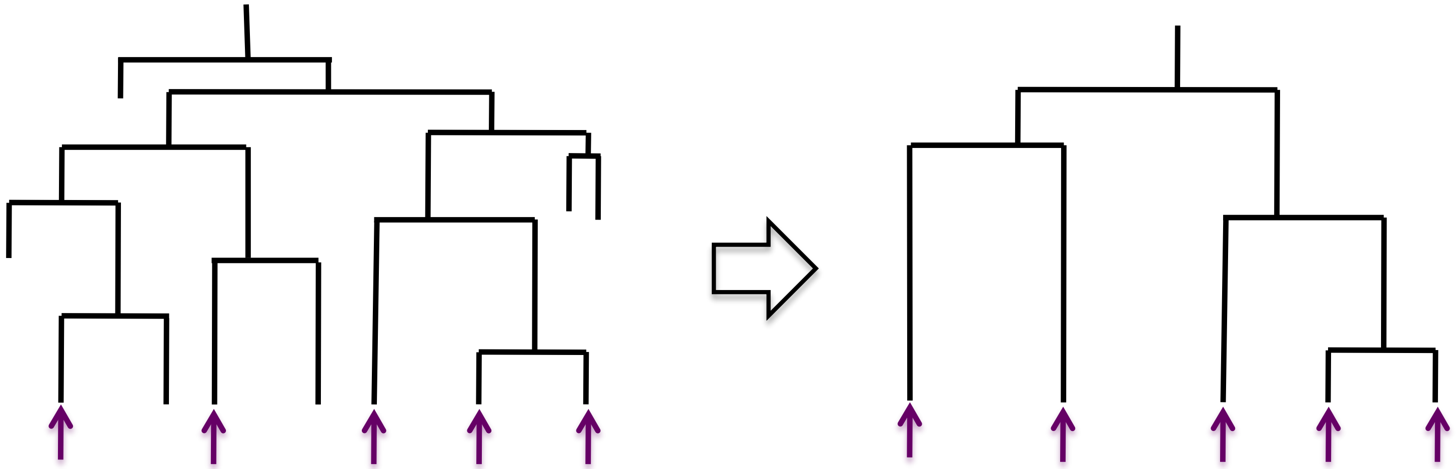
Phylogenetic approaches to diversification

Stochastic birth-death process

Reconstucted phylogeny

1. compute the likelihood of the reconstructed phylogeny

2. apply maximum likelihood or bayesian methods to fit the model to empirical data



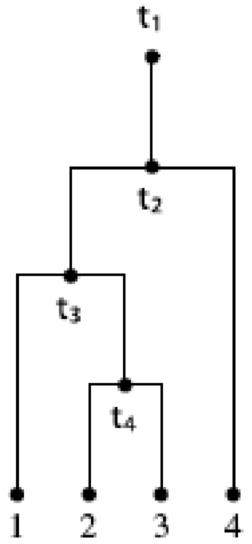
Calculating the likelihood of a reconstructed phylogeny

birth-death model

stem age t_1
speciation rate λ
extinction rate μ

+

λ and μ can vary over time
sampling fraction f



$$\mathcal{L}(t_1, \ldots, t_n) = \frac{f^n \Psi(t_2, t_1) \prod_{i=2}^{n} \lambda(t_i) \Psi(s_{i,1}, t_i) \Psi(s_{i,2}, t_i)}{1 - \Phi(t_1)},$$

Morlon *et al. PNAS* 2011

Calculating the likelihood of a reconstructed phylogeny

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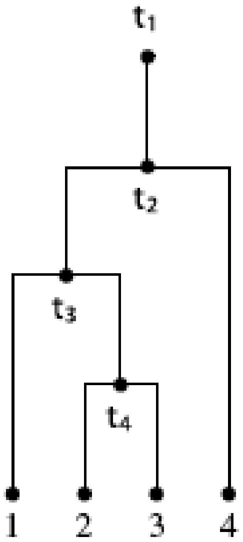

probability that n species are sampled today

$$\mathcal{L}(t_1,\ldots,t_n) = \frac{f^n \Psi(t_2,t_1)\prod_{i=2}^{n}\lambda(t_i)\Psi(s_{i,1},t_i)\Psi(s_{i,2},t_i)}{1-\Phi(t_1)},$$

Morlon *et al.* *PNAS* 2011

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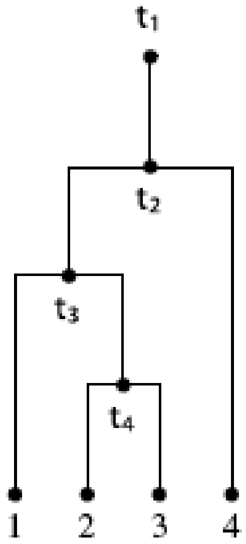

probability that a lineage survives from t_1 to t_2 and leaves no descendant in the sample

$$\mathcal{L}(t_1, \ldots, t_n) = \frac{f^n \Psi(t_2, t_1) \prod_{i=2}^{n} \lambda(t_i) \Psi(s_{i,1}, t_i) \Psi(s_{i,2}, t_i)}{1 - \Phi(t_1)},$$

Morlon *et al. PNAS* 2011

Calculating the likelihood of a reconstructed phylogeny

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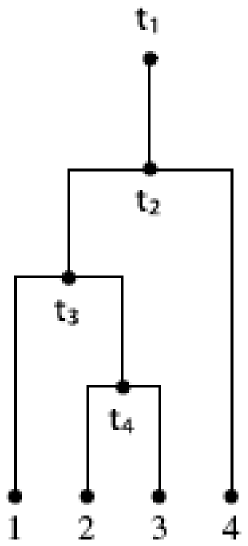

probability that a lineage survives from t_1 to t_2 and lives no descendant in the sample

$$\mathcal{L}(t_1,\ldots,t_n) = \frac{f^n \Psi(t_2,t_1)\prod_{i=2}^{n}\lambda(t_i)\Psi(s_{i,1},t_i)\Psi(s_{i,2},t_i)}{1-\Phi(t_1)},$$

probability of a speciation event at time t_i

Morlon *et al. PNAS* 2011

Calculating the likelihood of a reconstructed phylogeny

birth-death model

stem age t_1
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extinction rate μ

+

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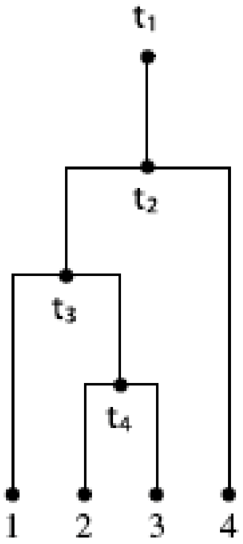


$$\mathcal{L}(t_1,\ldots,t_n) = \frac{f^n \Psi(t_2,t_1)\prod_{i=2}^{n}\lambda(t_i)\Psi(s_{i,1},t_i)\Psi(s_{i,2},t_i)}{1-\Phi(t_1)},$$

probability that a lineage alive at time t_1 has no descendant in the sample

Morlon *et al. PNAS* 2011

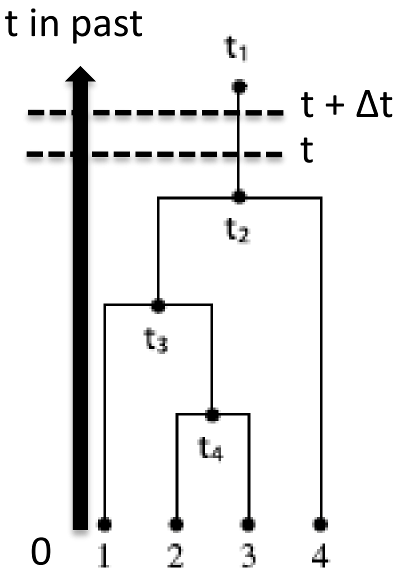
Calculating the likelihood of a reconstructed phylogeny

birth-death model

stem age t_1
speciation rate λ
extinction rate μ

+

λ and μ can vary over time
sampling fraction f



$\Phi(t) = \mathbb{P}\{\text{a lineage is } \textit{not} \text{ in the sample} | \text{it was alive at the time } t\}$

$$\begin{aligned}\Phi(t+\Delta t) = {} & \mu(t)\Delta t \\ & + (1-\mu(t)\Delta t)\lambda(t)\Phi^2(t) \\ & + (1-\mu(t)\Delta t)(1-\lambda(t)\Delta t)\Phi(t) \\ & + o(\Delta t)\end{aligned}$$

$\Delta t \to 0$

$$\frac{d\Phi}{dt} = \mu(t) - (\lambda(t)+\mu(t))\Phi(t) + \lambda(t)\Phi^2(t)$$

$$\boxed{\Phi(t) = 1 - \frac{e^{\int_0^t \lambda(u)-\mu(u)du}}{\frac{1}{f} + \int_0^t e^{\int_0^s \lambda(u)-\mu(u)du}\lambda(s)ds}}$$

Calculating the likelihood of a reconstructed phylogeny

birth-death model

stem age t_1
speciation rate λ
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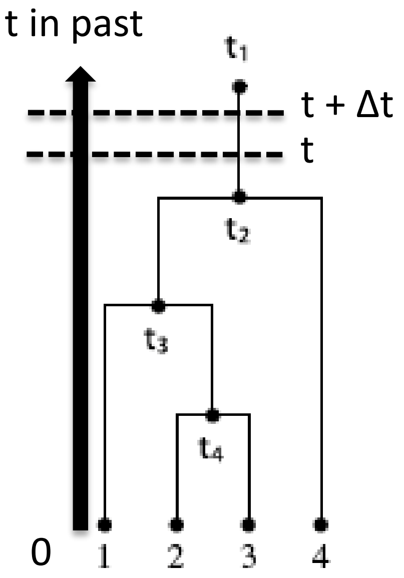
λ and μ can vary over time
sampling fraction f



$\Psi(s,\ t)$ **probability that a lineage survives from t to s and lives no descendant in the sample**

$$\Psi(s,t) = e^{\int_s^t \lambda(u)-\mu(u)du}\left[1+\frac{\int_s^t e^{\int_0^\tau \lambda(\sigma)-\mu(\sigma)d\sigma}\lambda(\tau)d\tau}{\frac{1}{f}+\int_0^s e^{\int_0^\tau \lambda(\sigma)-\mu(\sigma)d\sigma}\lambda(\tau)d\tau}\right]^{-2}$$

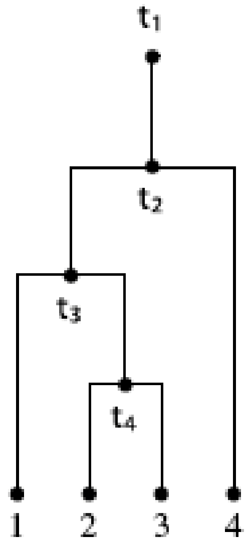
Calculating the likelihood of a reconstructed phylogeny

birth-death model

stem age t_1
speciation rate λ
extinction rate μ

+

λ and μ can vary over time
sampling fraction f



$$\mathcal{L}(t_1,\ldots,t_n) = \frac{f^n \Psi(t_2,t_1)\prod_{i=2}^{n}\lambda(t_i)\Psi(s_{i,1},t_i)\Psi(s_{i,2},t_i)}{1-\Phi(t_1)},$$

Morlon *et al. PNAS* 2011

Support for a 4-shift rate model in the cetacean phylogeny

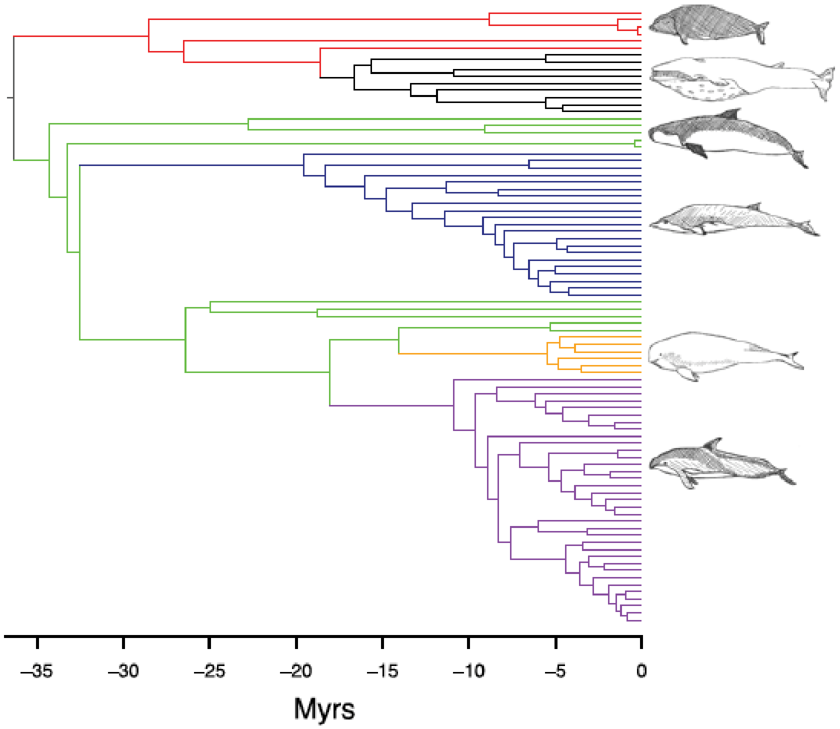
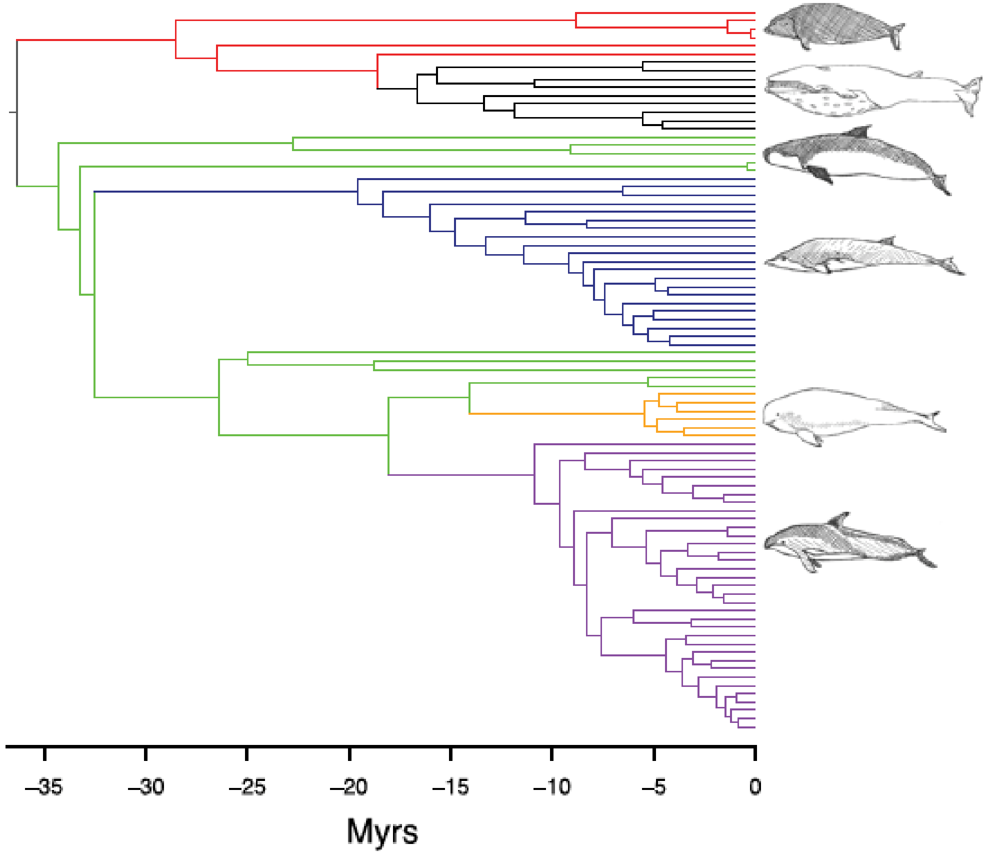
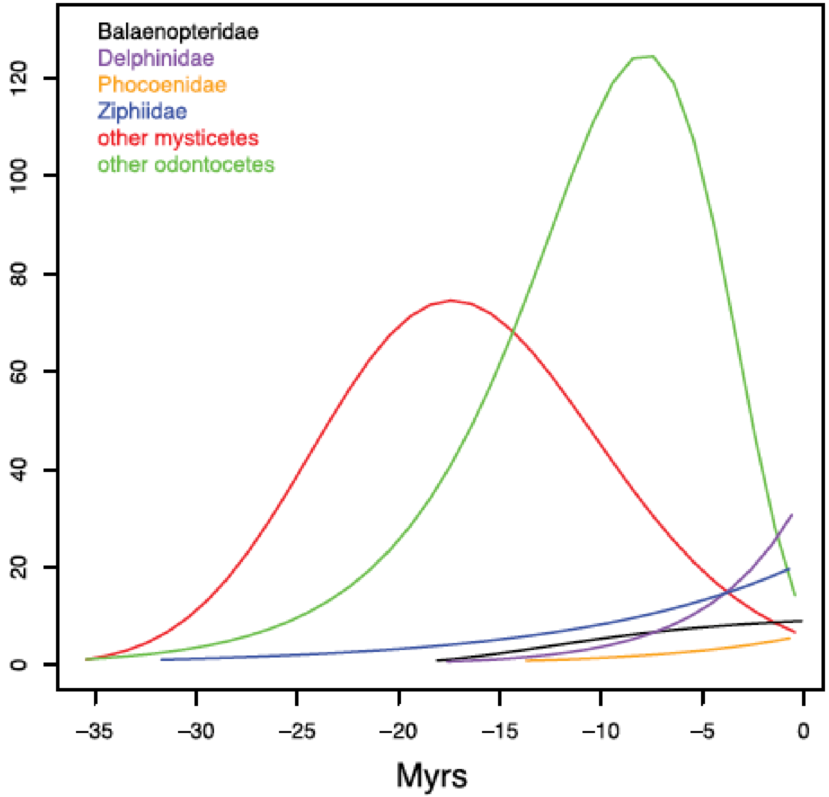


Table S2. Statistical support for rate shifts in the cetacean phylogeny

Model	nb	Description	LogL	AIC_c
No shift	1	Best fit model	−279.03	560.08
One shift	5	Best fit model: shift in the Delphinidae	−262.93*	536.22
Two shifts	6	Best fit model: shifts in the Delphinidae and Phocoenidae	−260.17†	532.85
Three shifts	7	Best fit model: shifts in the Delphinidae, Phocoenidae and Ziphiidae	−256.13‡	526.94
Four shifts	**8**	**Best fit model: shifts in the Delphinidae, Phocoenidae, Ziphiidae, and Balaenopteridae**	**−250.13**	**517.14**

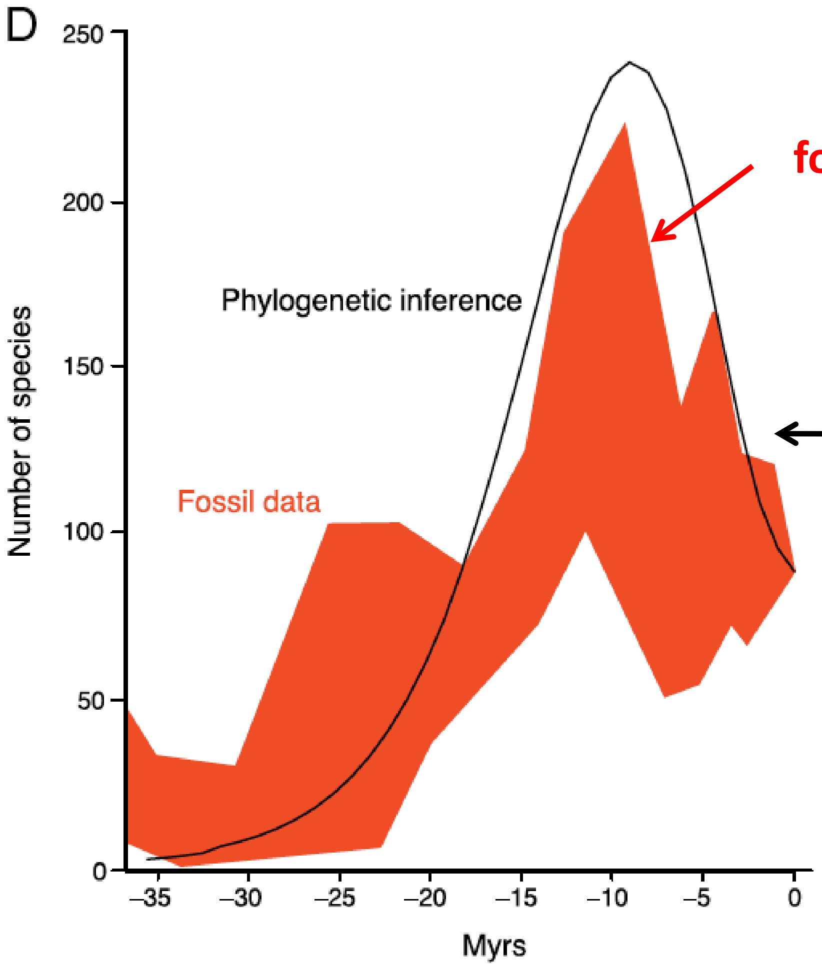
The resulting diversity curves show boom-then-bust diversity dynamics





Morlon *et al. PNAS* 2011

The resulting diversity curve is consistent with the fossil record



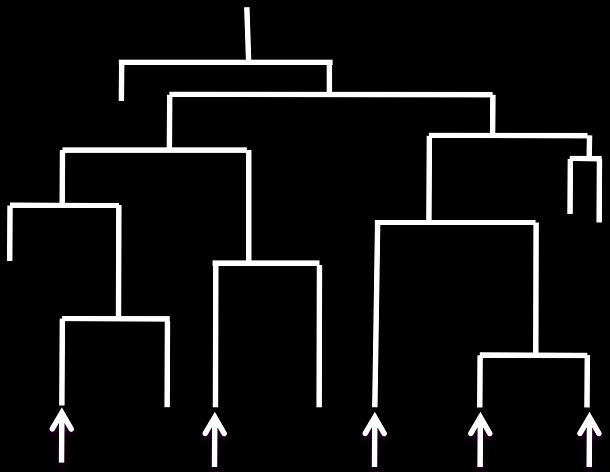
fossil record

phylogenetic inference,
obtained by summing
individual diversity curves

Morlon *et al.* *PNAS* 2011

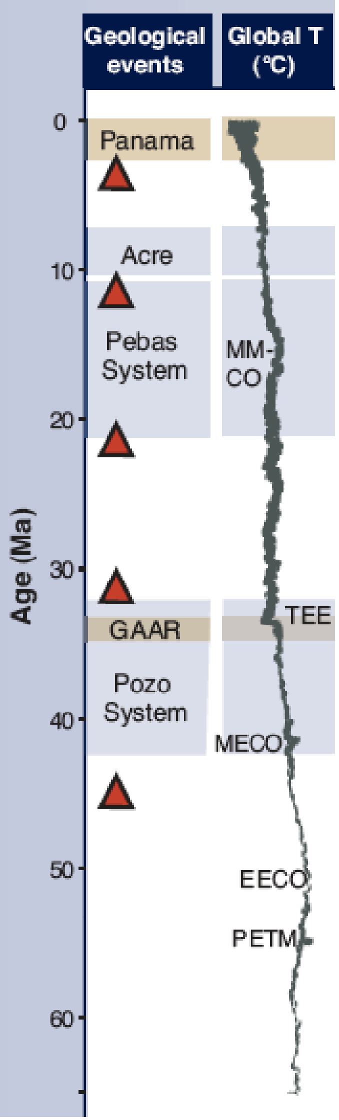
Stochastic models of cladogenesis

2. environmental dependence

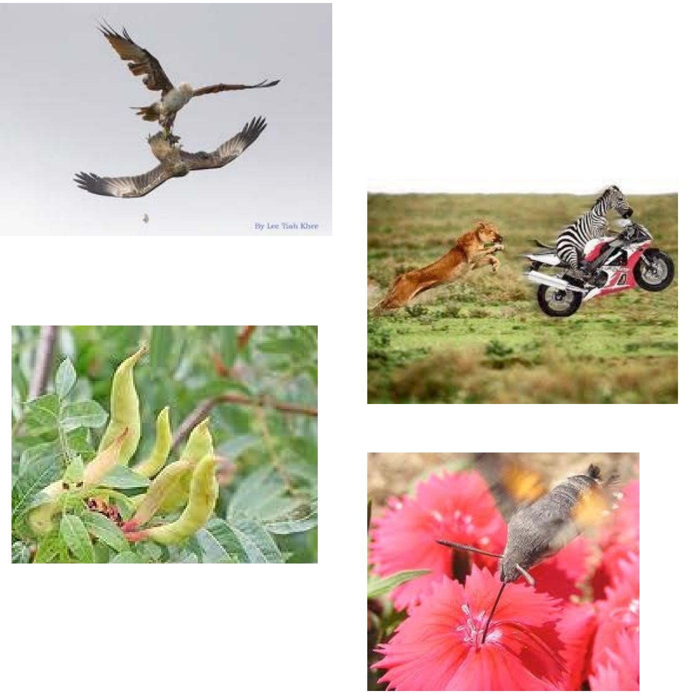


Species richness results from speciation and extinction events, themselves influenced by various biotic and abiotic processes

Abiotic factors

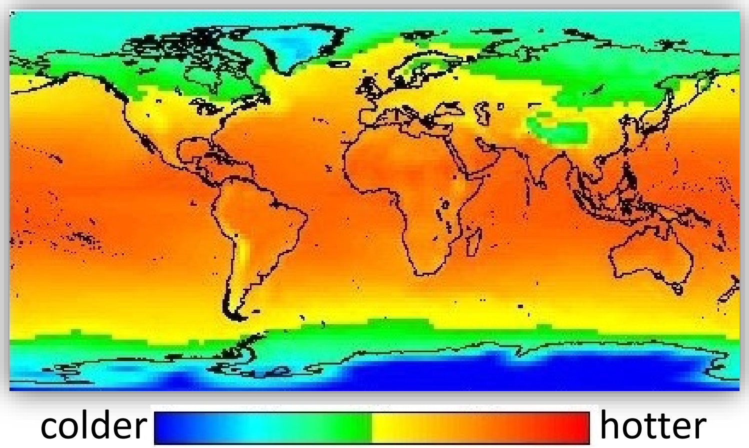


Biotic factors

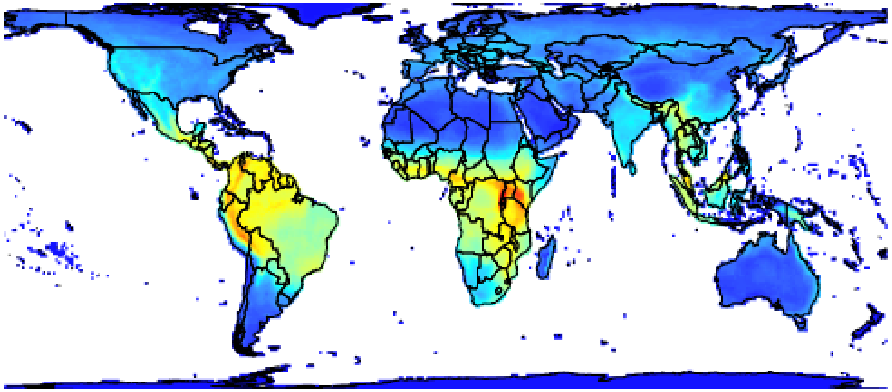


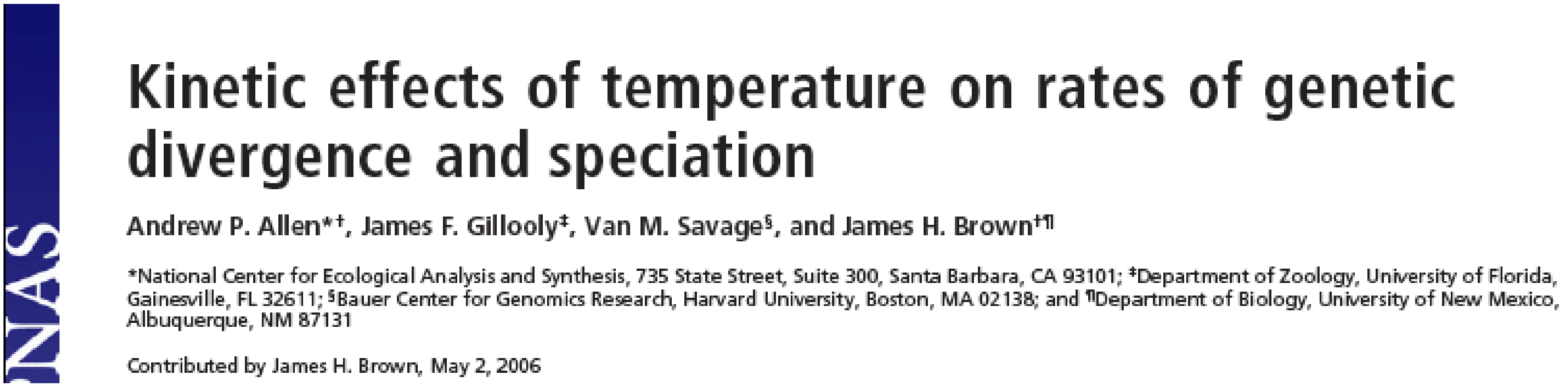
Climate has been proposed as a major driver of diversification

Global surface temperature distribution



Diversity gradients





Kinetic effects of temperature on rates of genetic divergence and speciation

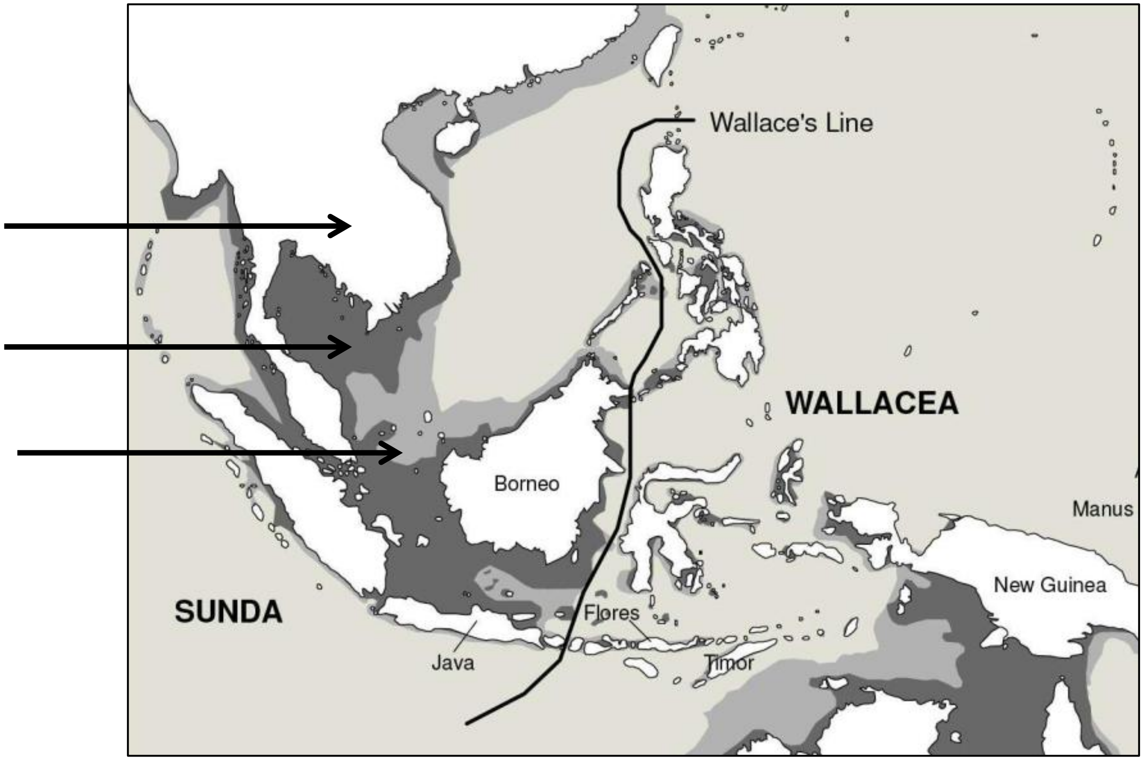
Andrew P. Allen*†, James F. Gillooly‡, Van M. Savage§, and James H. Brown†¶

*National Center for Ecological Analysis and Synthesis, 735 State Street, Suite 300, Santa Barbara, CA 93101; ‡Department of Zoology, University of Florida, Gainesville, FL 32611; §Bauer Center for Genomics Research, Harvard University, Boston, MA 02138; and ¶Department of Biology, University of New Mexico, Albuquerque, NM 87131

Contributed by James H. Brown, May 2, 2006

Sea level may be a major determinant of diversity dynamics

Indonesia



Current level

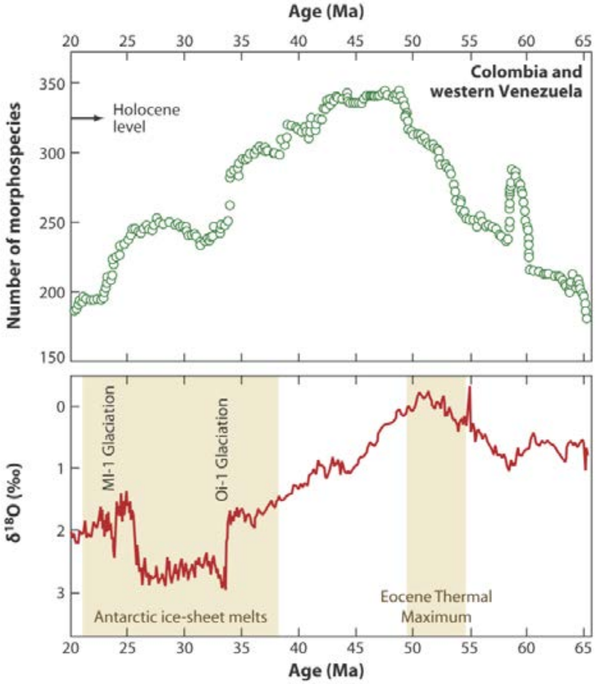
-65 m

-120 m

Macroevolutionary perspectives to environmental change

Condamine, Rolland & Morlon *Ecology Letters* (2013)

How can we test the effect of abiotic factors on diversity dynamics using paleoenvironmental and phylogenetic data?



Macroevolutionary perspectives to environmental change

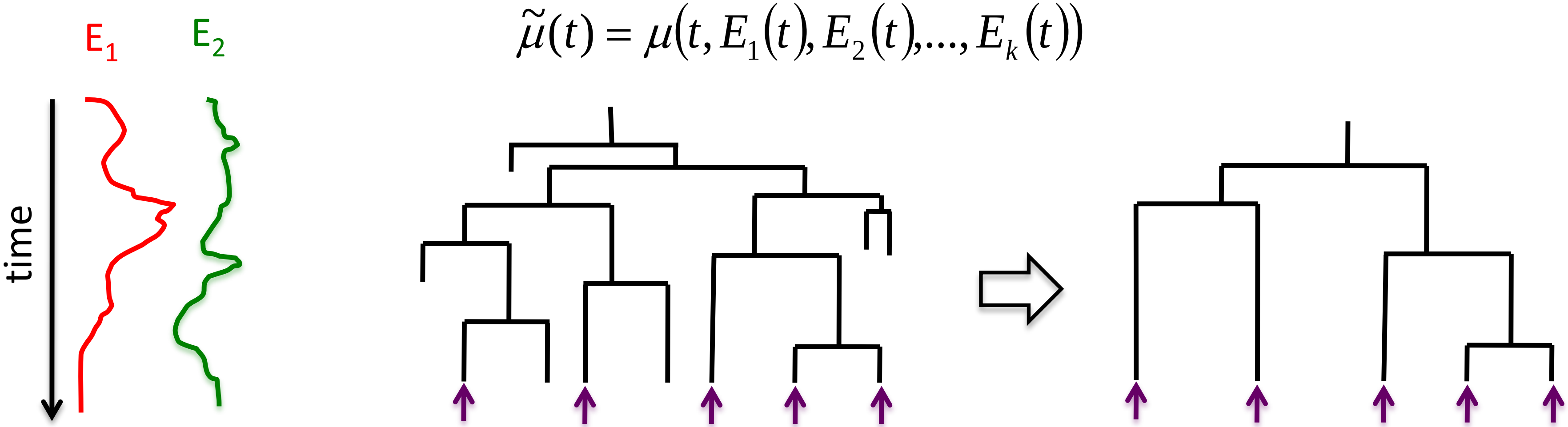
Condamine, Rolland & Morlon *Ecology Letters* (2013)

We derived the likelihood corresponding to a birth-death process in which:

the speciation rate λ can vary over time, lineages, and measured environmental variables E(t)
the extinction rate μ can vary over time, lineages, and measured environmental variables E(t)
the extinction rate can exceed the speciation rate (periods of diversity decline)
only a fraction f of extant species are sampled

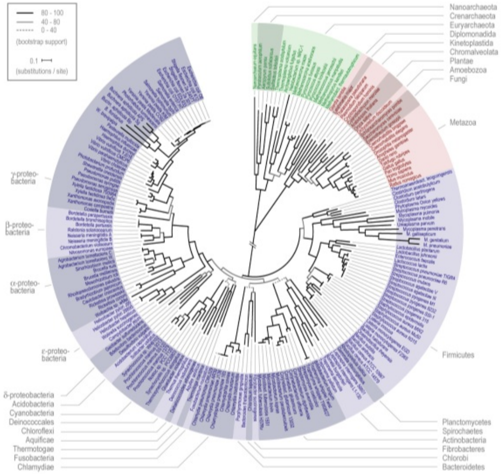
$$\tilde{\lambda}(t) = \lambda(t, E_1(t), E_2(t), \ldots, E_k(t))$$

$$\tilde{\mu}(t) = \mu(t, E_1(t), E_2(t), \ldots, E_k(t))$$



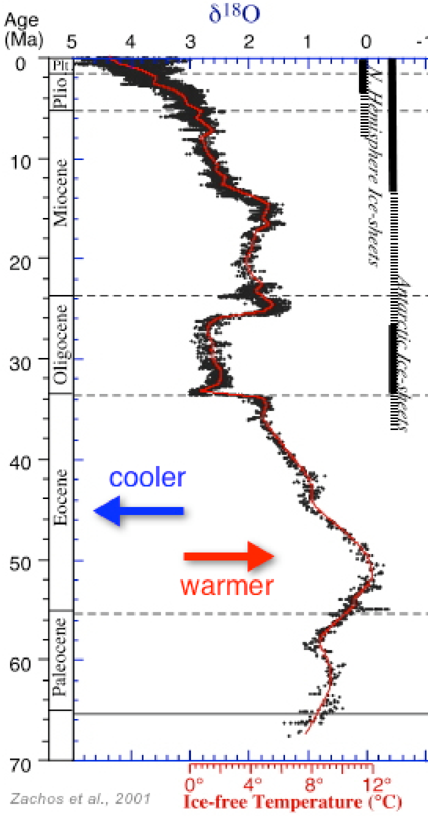
Empirical application… under way

- Phylogenetic trees spanning most of the tree of life
    - Amphibians
    - Angiosperms
    - Birds
    - Gymnosperms
    - Insects
    - Mammals
    - Reptiles



- Paleoclimatic records from the Cenozoic (Zachos et al. 2001)

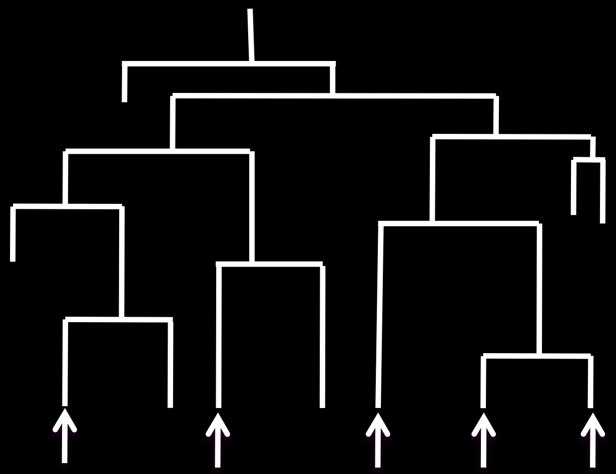
suggests the influence of temperature on diversification may explain the diversification slowdown observed in molecular phylogenies



Zachos et al., 2001

Stochastic models of cladogenesis

3. diversity- dependence



PROCEEDINGS
OF
THE ROYAL
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B

Proc. R. Soc. B (2012) **279**, 1300–1309
doi:10.1098/rspb.2011.1439
Published online 12 October 2011

Diversity-dependence brings molecular phylogenies closer to agreement with the fossil record

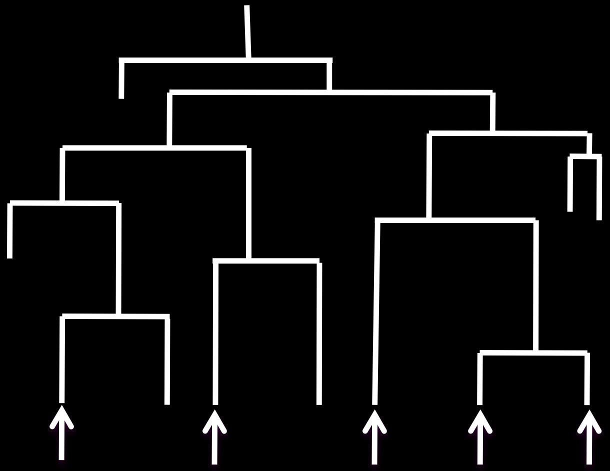
Rampal S. Etienne[1,*], Bart Haegeman[2], Tanja Stadler[3], Tracy Aze[4], Paul N. Pearson[4], Andy Purvis[5] and Albert B. Phillimore[5]

[1]*Community and Conservation Ecology, Centre for Ecological and Evolutionary Studies,*

Louis DU PLESSIS tomorrow!

Stochastic models of cladogenesis

4. testing hypotheses of equilibrium dynamics



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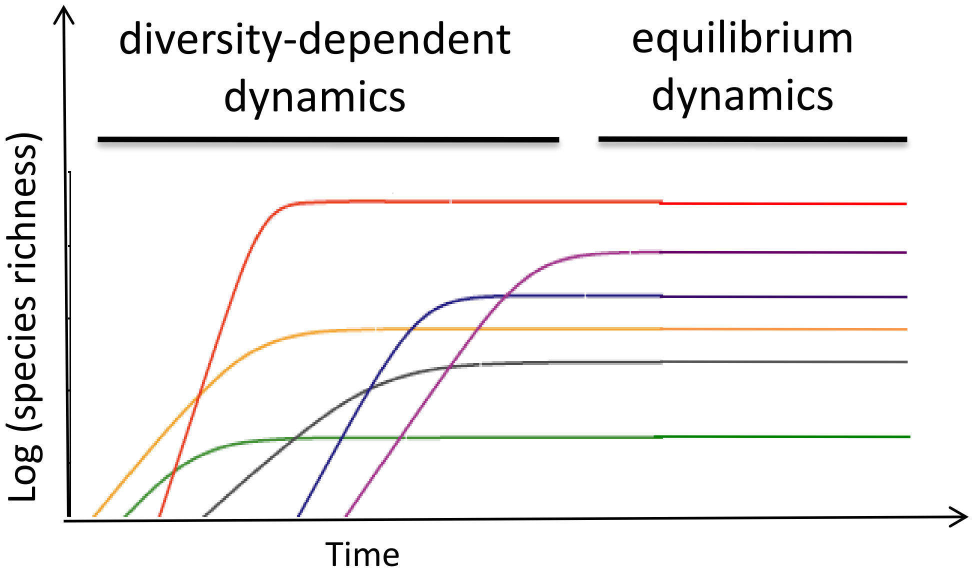
PLoS BIOLOGY

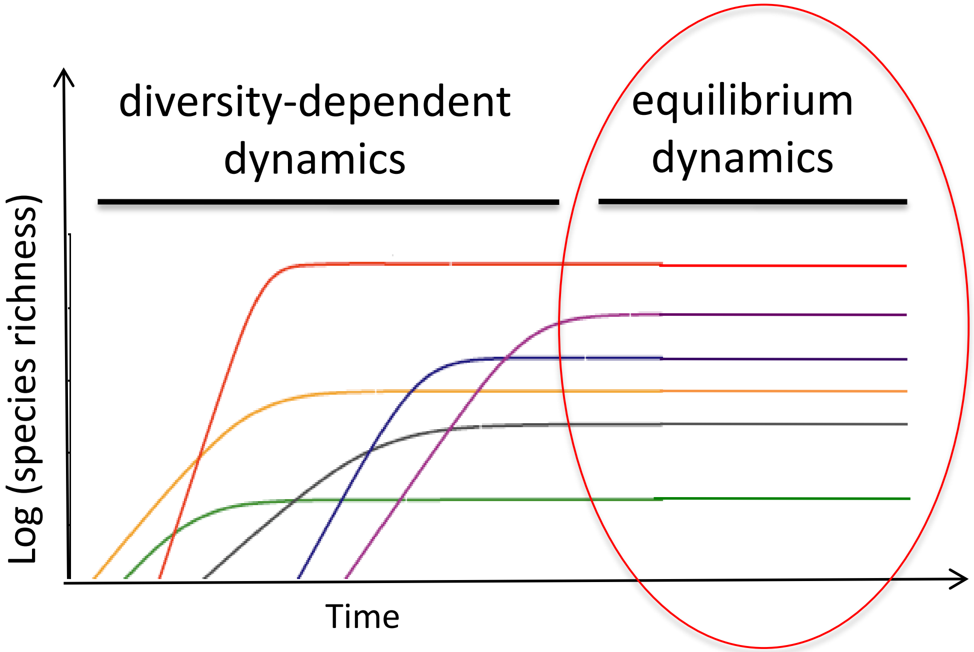
Inferring the Dynamics of Diversification: A Coalescent Approach

Hélène Morlon[1]*, Matthew D. Potts[2], Joshua B. Plotkin[1]*

Is present-day species richness constrained by current ecological limits?



We derived the likelihood of a reconstructed phylogeny corresponding to equilibrium dynamics

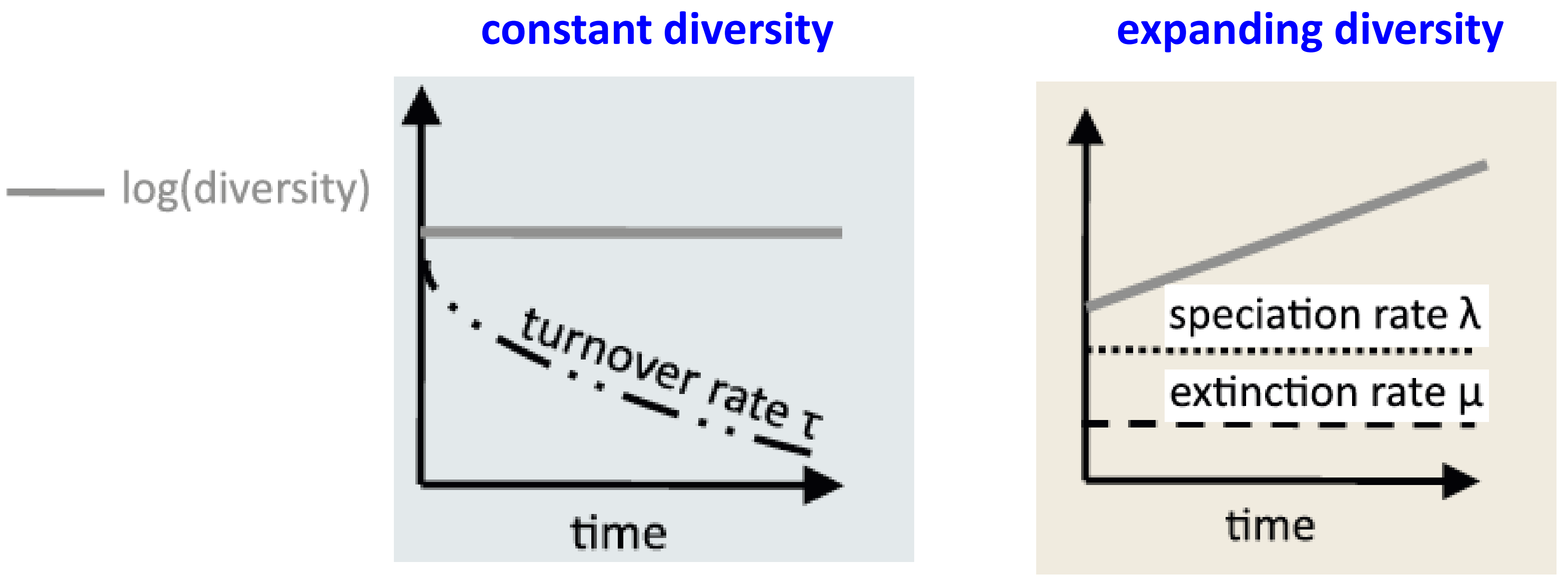


Morlon *et al. PloS B* 2010

Likelihood derived from the coalescent process from population genetics

Likelihood of internode distances for the phylogeny of k randomly sampled species:

$$\Lambda(t_1,t_2,\ldots,t_{k-1}) = \sum_{i=1}^{k-1} \log L(t_i) \qquad L(t_i) = \frac{i(i+1)}{2}\,\frac{2\lambda(v_i)}{N(v_i)}\exp\left[-\frac{i(i+1)}{2}\int_{v_i-t_i}^{v_i}\frac{2\lambda(t)}{N(t)}\,dt\right]$$



Morlon *et al.* *PloS B* 2010

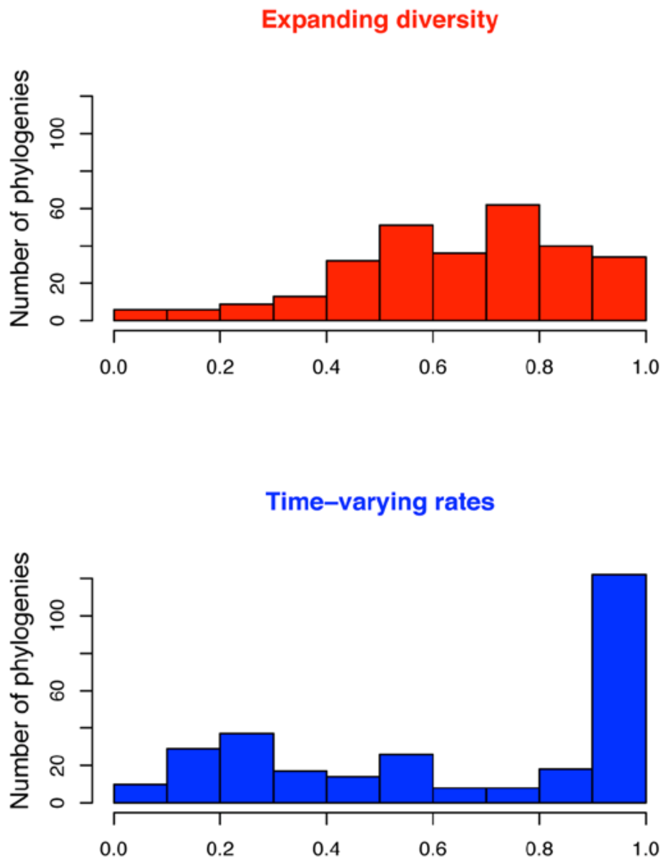
We used this likelihood to test the support for equilibrium dynamics across a wide range of phylogenies (289)

Morlon *et al. PloS B* 2010

McPeek *AmNat* 2008

Phillimore & Price *PloSB* 2008

Most phylogenies are consistent with the hypothesis that diversity is expanding with time- varying diversification rates

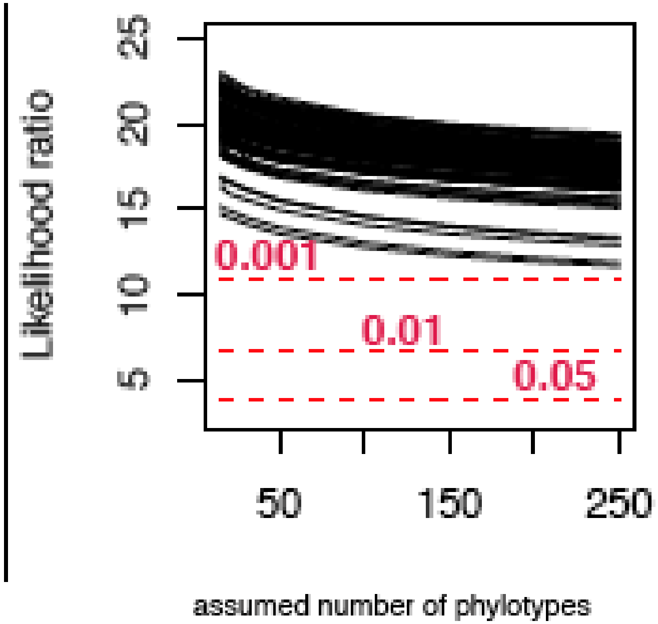


Model probability (Akaike weight)

Morlon *et al. PloS B* 2010

Consistent result for a bacterial clade

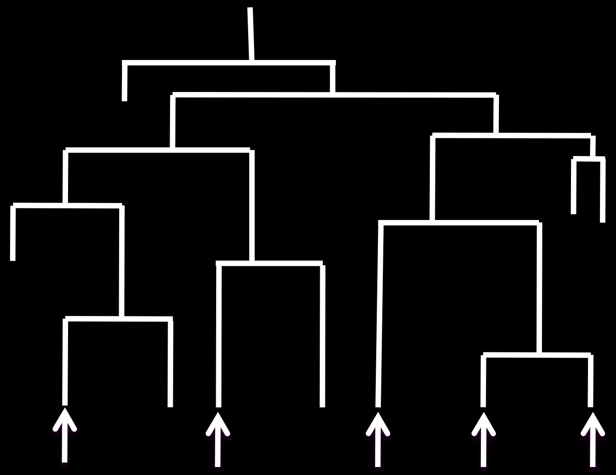
Borrelia burgdorferi sensu lato



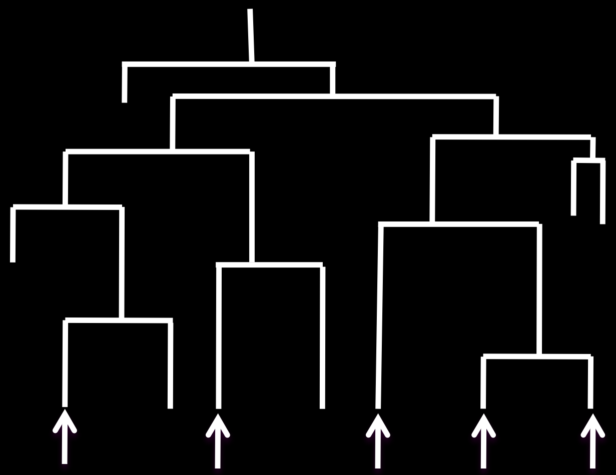
Stochastic models of cladogenesis

5. protracted speciation (Rampal!)

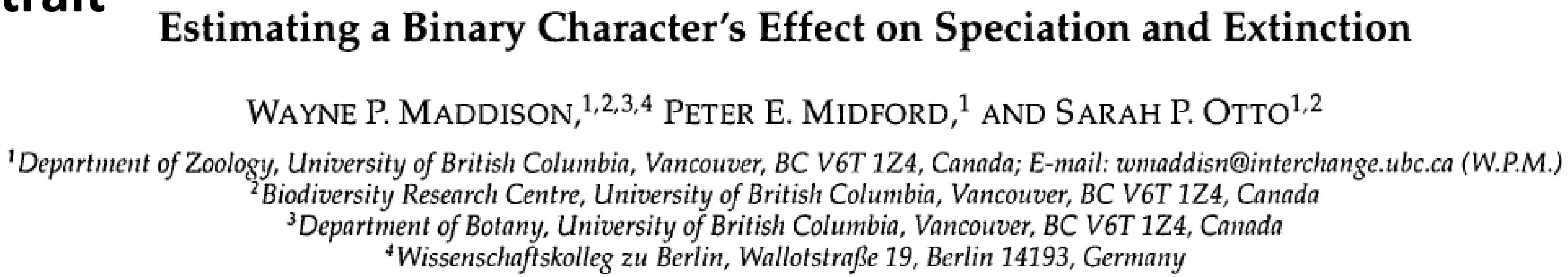
6. age dependence



Combining models of trait evolution with models of cladogenesis : character-dependent diversification



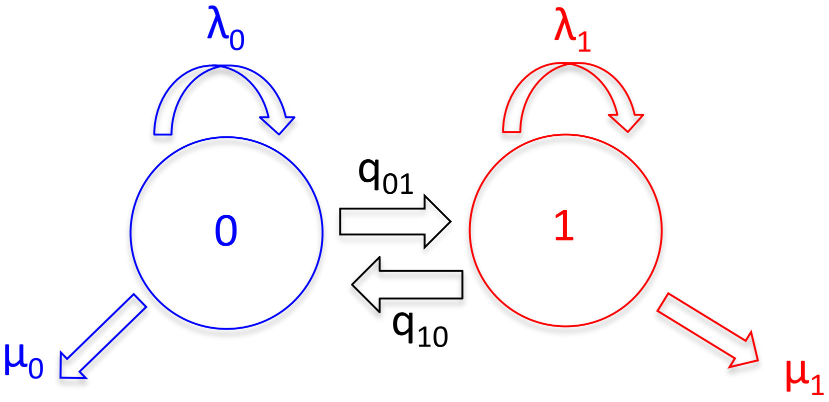
Binary trait



Estimating a Binary Character's Effect on Speciation and Extinction

WAYNE P. MADDISON,[1,2,3,4] PETER E. MIDFORD,[1] AND SARAH P. OTTO[1,2]

[1]Department of Zoology, University of British Columbia, Vancouver, BC V6T 1Z4, Canada; E-mail: wmaddisn@interchange.ubc.ca (W.P.M.)
[2]Biodiversity Research Centre, University of British Columbia, Vancouver, BC V6T 1Z4, Canada
[3]Department of Botany, University of British Columbia, Vancouver, BC V6T 1Z4, Canada
[4]Wissenschaftskolleg zu Berlin, Wallotstraße 19, Berlin 14193, Germany



Quantitative trait

DOI:10.1093/sysbio/syq053

Quantitative Traits and Diversification

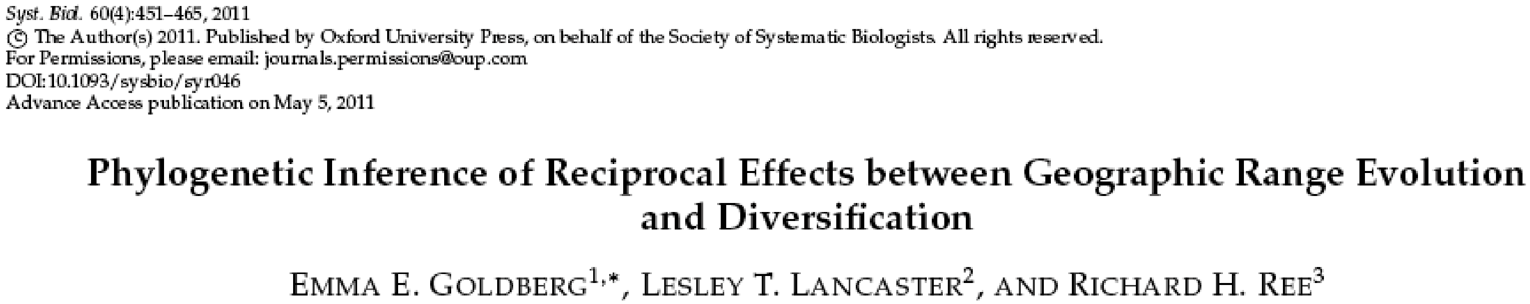
RICHARD G. FITZJOHN*

Department of Zoology and Biodiversity Research Centre, University of British Columbia, Vancouver, BC V6T 1Z4, Canada
**Correspondence to be sent to: Department of Zoology, University of British Columbia, Vancouver, BC V6T 1Z4, Canada; E-mail: fitzjohn@zoology.ubc.ca.*

Received 24 December 2009; reviews returned 28 February 2010; accepted 9 August 2010
Guest Associate Editor: Daniel Rabosky

Abstract.—Quantitative traits have long been hypothesized to affect speciation and extinction rates. For example, smaller

Geographic trait

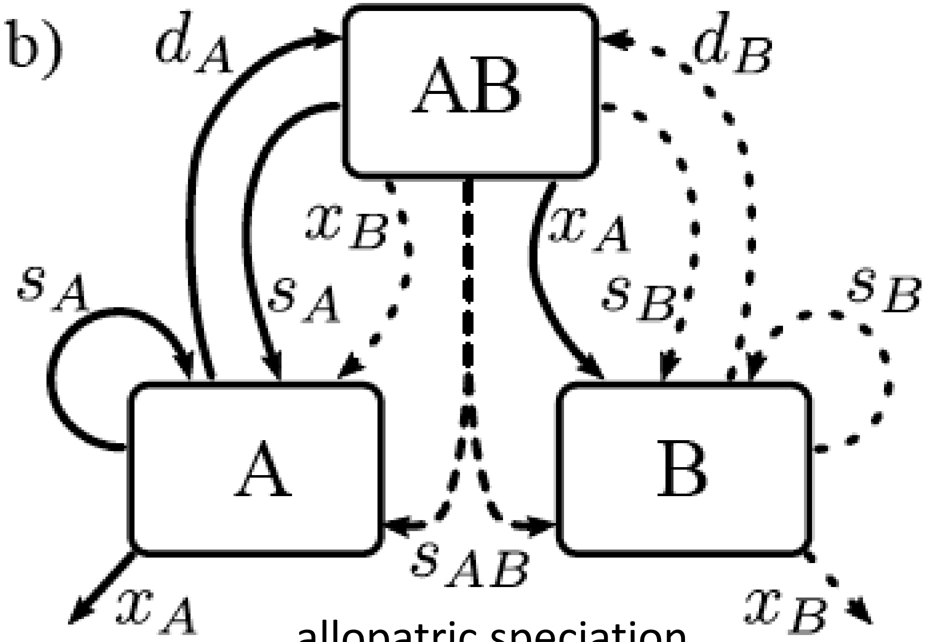


Syst. Biol. 60(4):451–465, 2011

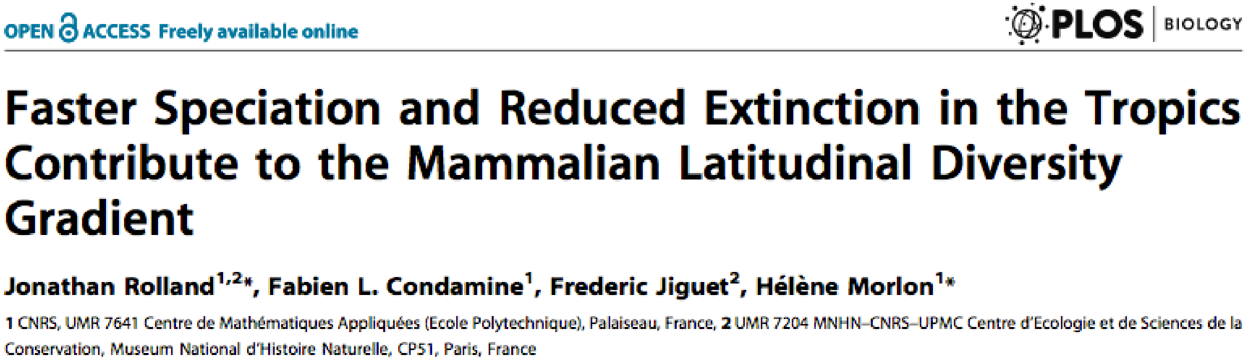
DOI:10.1093/sysbio/syr046
Advance Access publication on May 5, 2011

Phylogenetic Inference of Reciprocal Effects between Geographic Range Evolution and Diversification

EMMA E. GOLDBERG[1,*], LESLEY T. LANCASTER[2], AND RICHARD H. REE[3]



allopatric speciation



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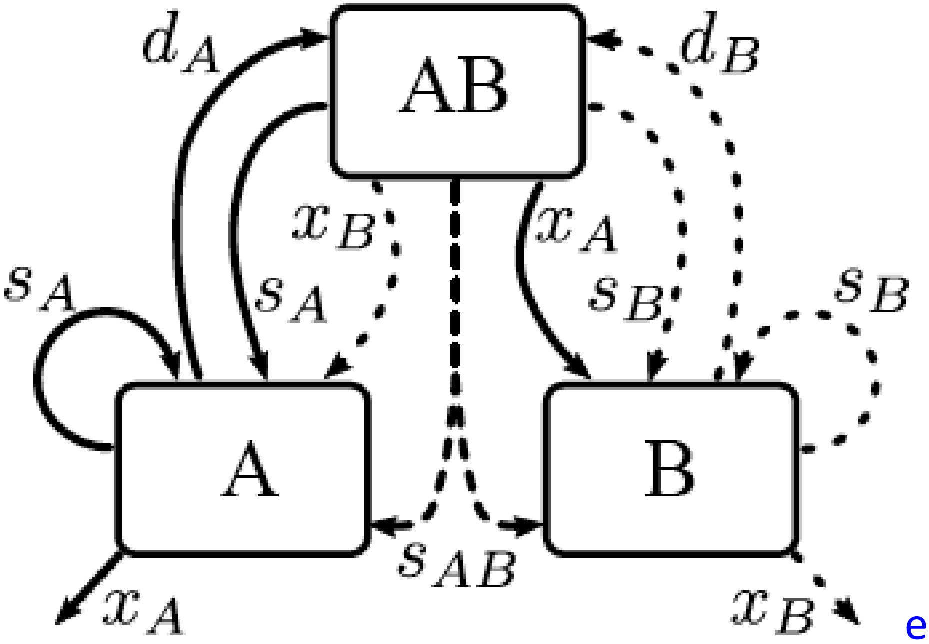
PLOS | BIOLOGY

Faster Speciation and Reduced Extinction in the Tropics Contribute to the Mammalian Latitudinal Diversity Gradient

Jonathan Rolland[1,2]*, Fabien L. Condamine[1], Frederic Jiguet[2], Hélène Morlon[1]*

1 CNRS, UMR 7641 Centre de Mathématiques Appliquées (Ecole Polytechnique), Palaiseau, France, 2 UMR 7204 MNHN–CNRS–UPMC Centre d'Ecologie et de Sciences de la Conservation, Museum National d'Histoire Naturelle, CP51, Paris, France



range expansion
into temperate regions

range expansion
into tropical regions

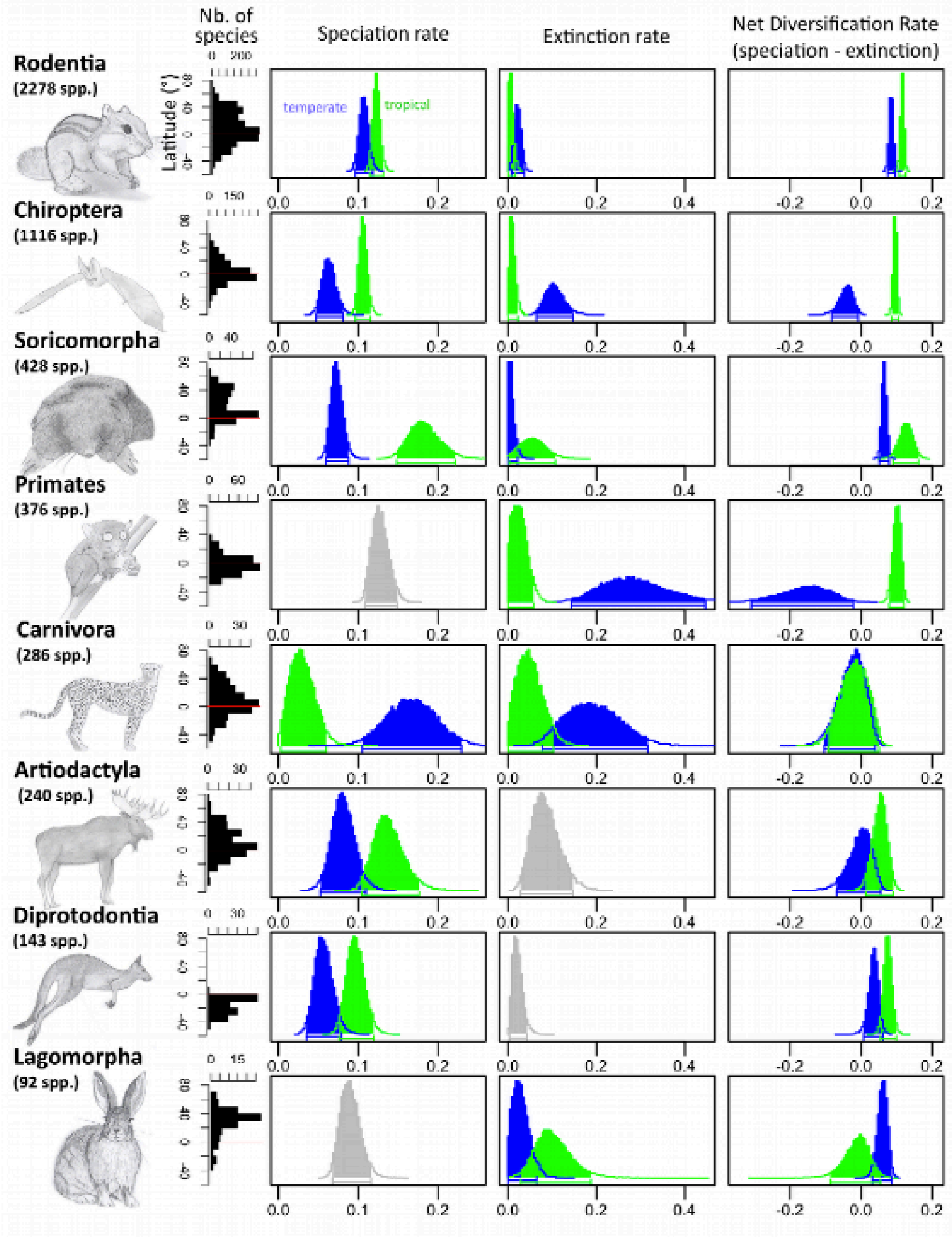
speciation rate
in the tropics

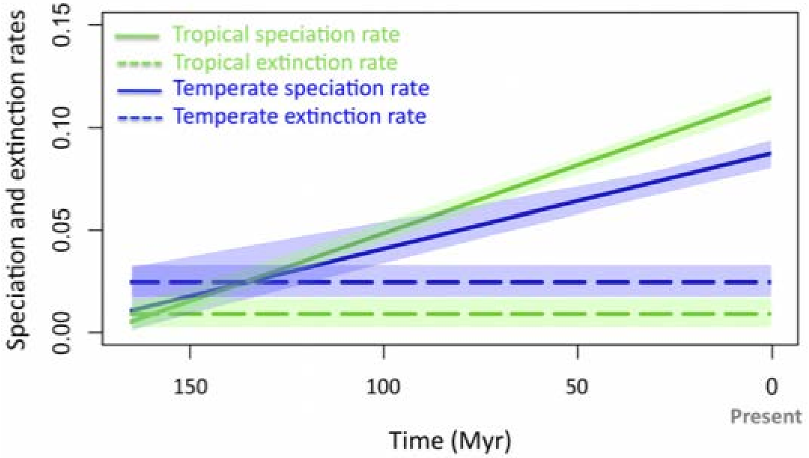
speciation rate
in temperate regions

extinction rate
in the tropics

extinction rate
in temperate regions

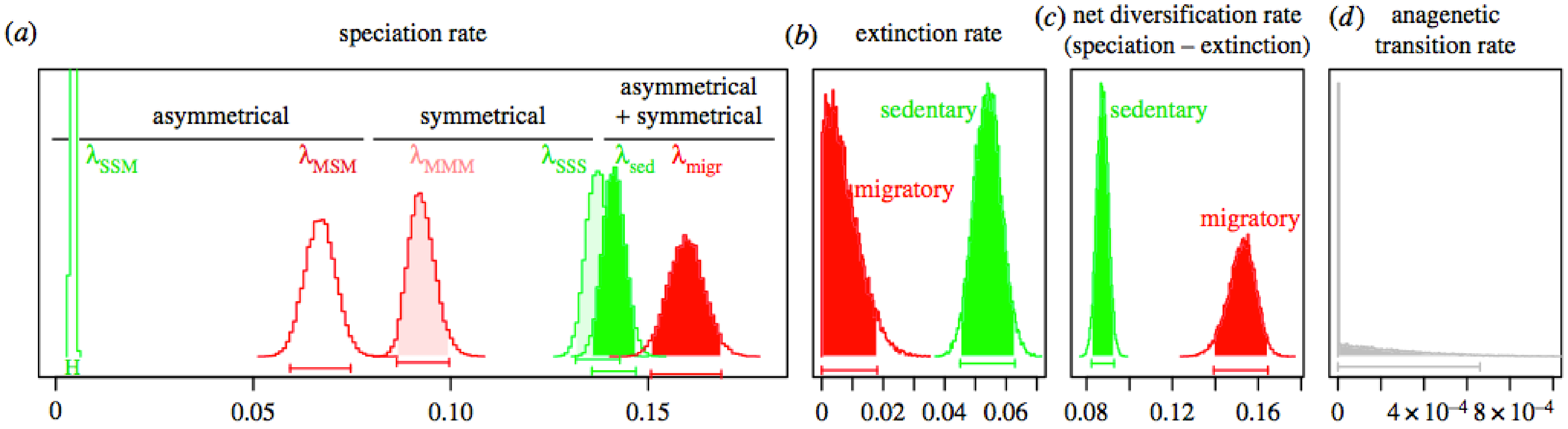
speciation of
widespread species
by
biome divergence

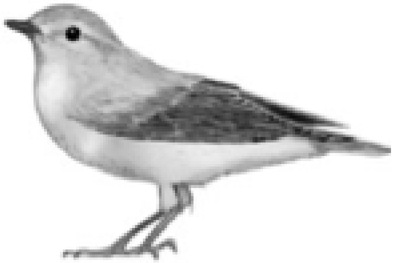




Rolland, Condamine, Jiguet & Morlon *PloS B* (2014)

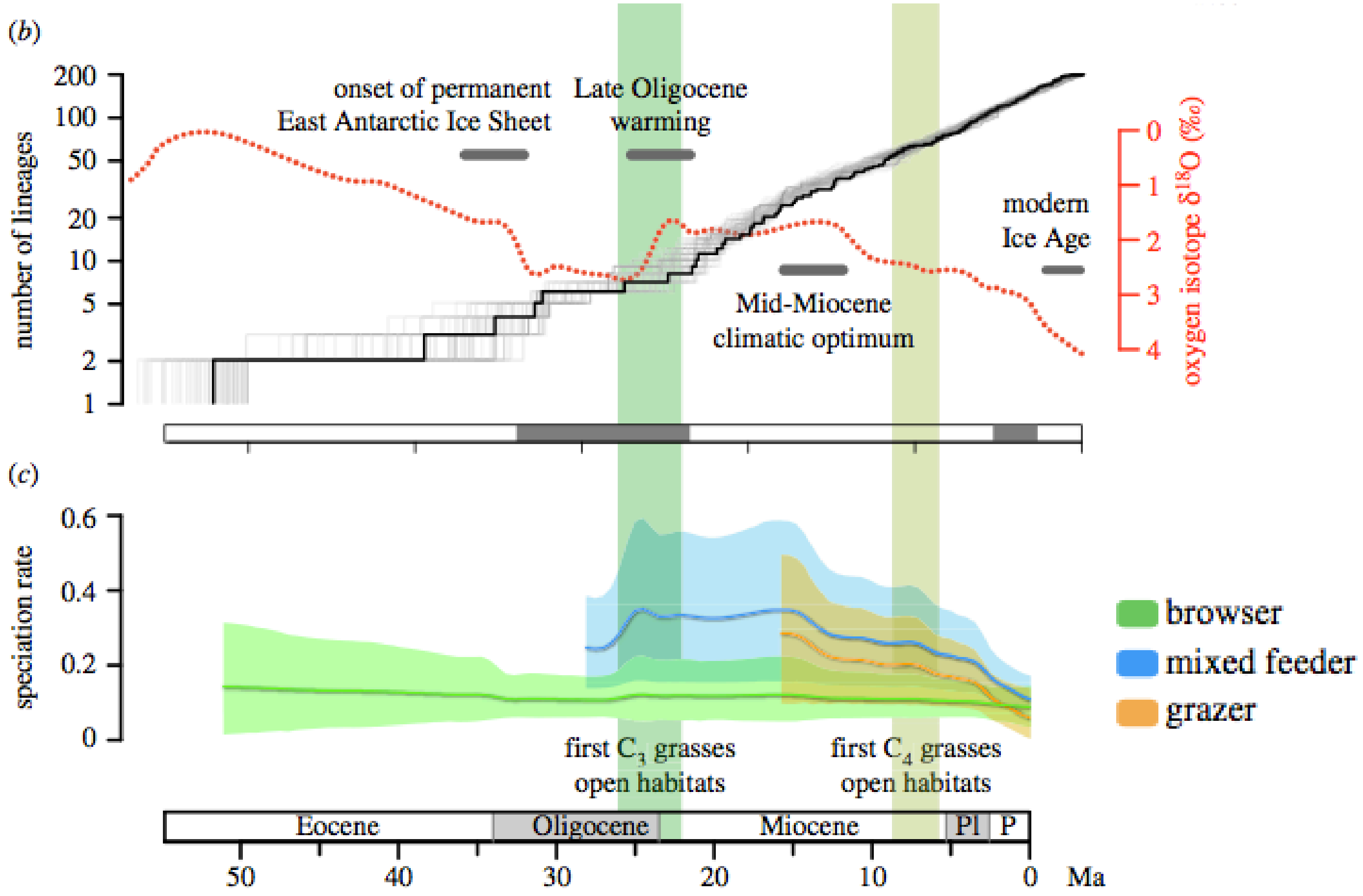
Trait change at cladogenetic event (Goldberg & Igic Evolution 2012)





Rolland, Jiguet, Jonsson, Condamine & Morlon *PRSB* (2014)

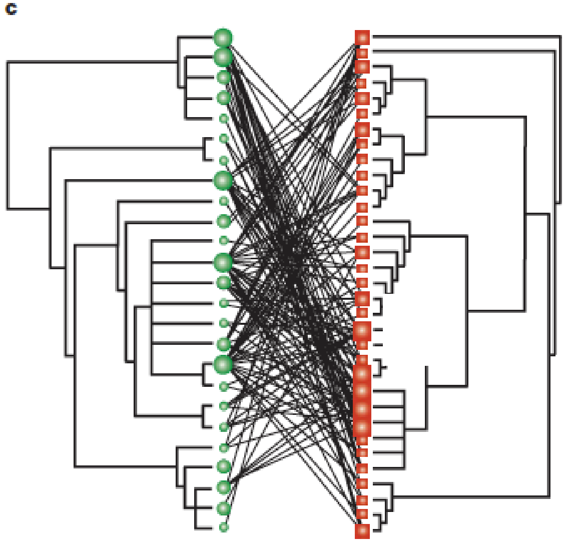
Character + environmental dependence



Cantalapiedra *et al. PRSB* 2013

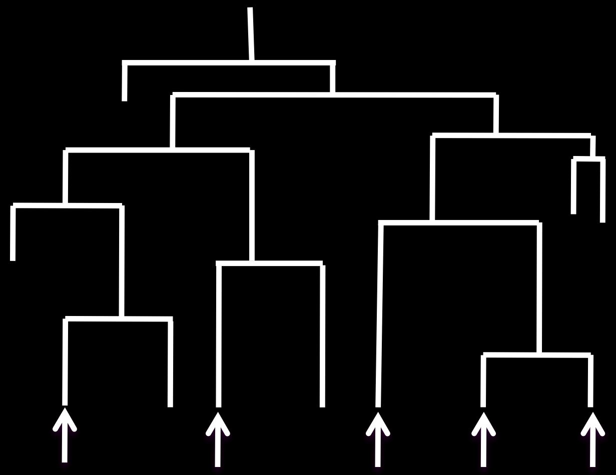
Developments under way

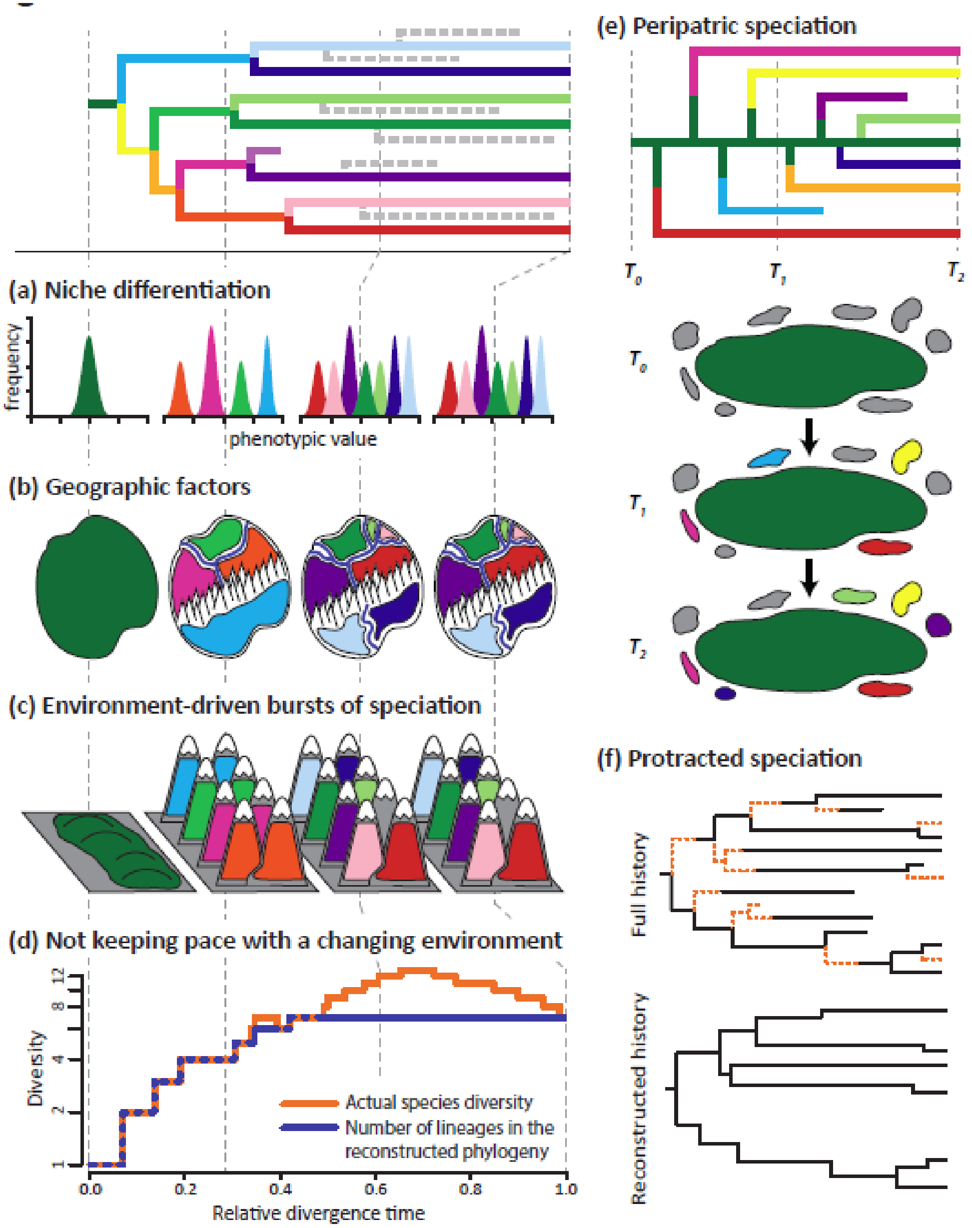
Testing the effect of biotic interactions on diversification



Stochastic models of cladogenesis:

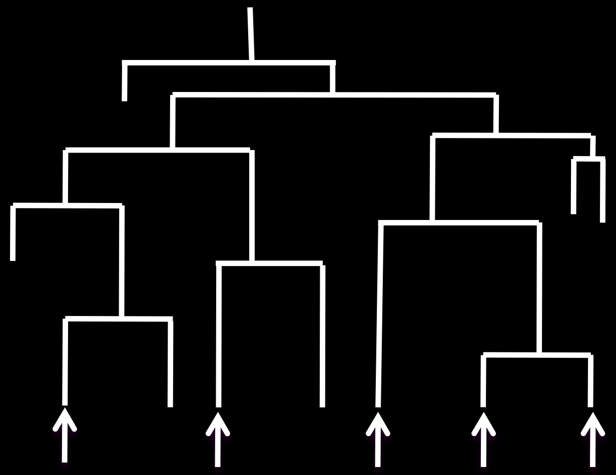
Do we need a different approach?

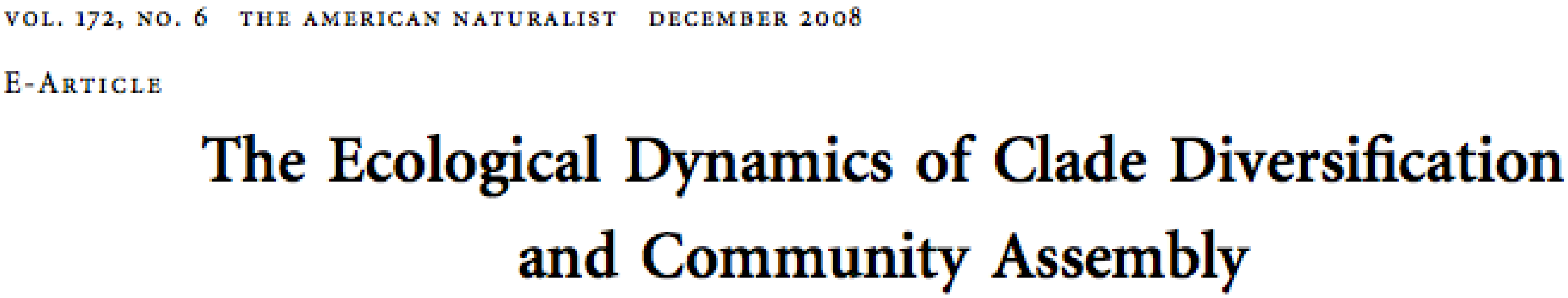



(a) Niche differentiation
frequency
phenotypic value
(b) Geographic factors
(c) Environment-driven bursts of speciation
(d) Not keeping pace with a changing environment
Diversity
1
2
4
8
12
Actual species diversity
Number of lineages in the reconstructed phylogeny
0.0
0.2
0.4
0.6
0.8
1.0
Relative divergence time
(e) Peripatric speciation
T_0
T_1
T_2
T_0
T_1
T_2
(f) Protracted speciation
Full history
Reconstructed history

Stochastic models of cladogenesis:

Models incorporating community assembly, range dynamics, population dynamics?





VOL. 172, NO. 6 THE AMERICAN NATURALIST DECEMBER 2008

E-ARTICLE

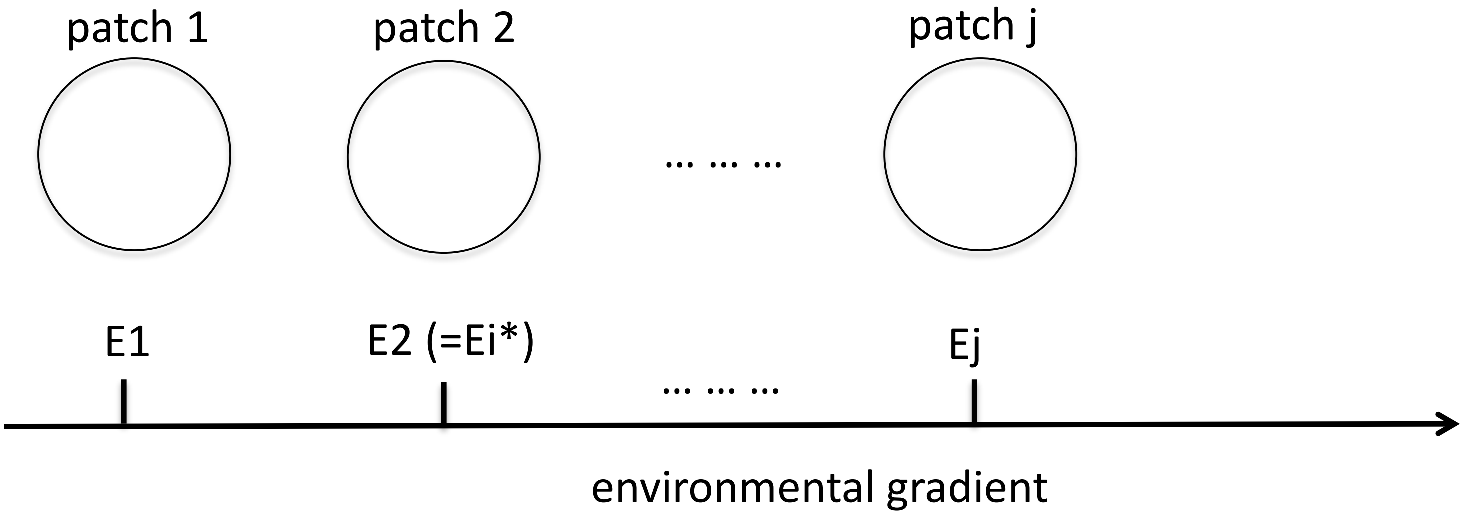
The Ecological Dynamics of Clade Diversification and Community Assembly

Mark A. McPeek*

dynamics of species i in patch j

$$N_{ij}(t+1) = N_{ij}(t)\exp\left(1 - \frac{\Sigma_j N_{ij}(t)}{K_{ij}}\right)$$

$$K_{ij} = K_{\text{opt}}\exp\left[-\left(\frac{E_j - E_i^*}{\omega}\right)^2\right]$$

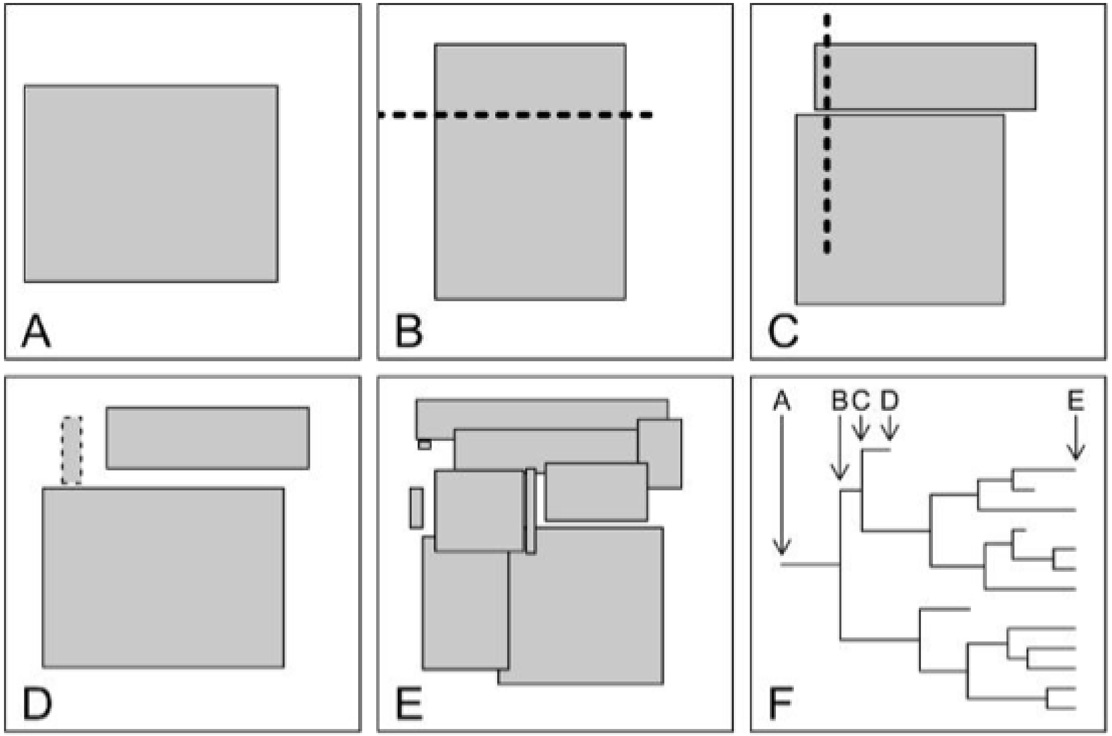


The Shape and Temporal Dynamics of Phylogenetic Trees Arising from Geographic Speciation

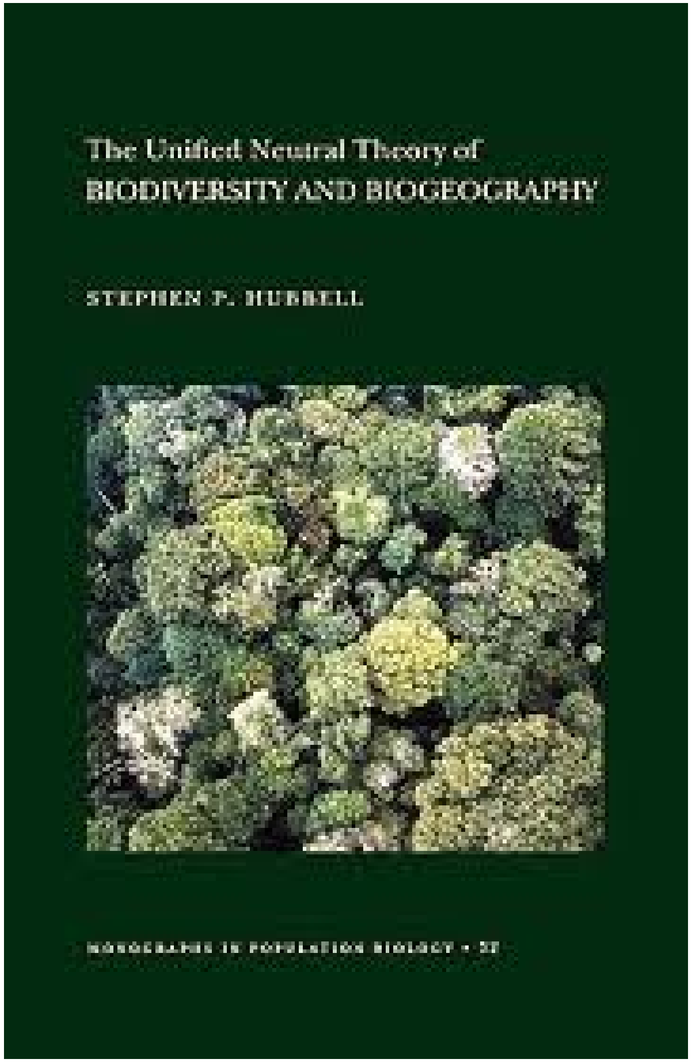
ALEX L. PIGOT[1,2,*], ALBERT B. PHILLIMORE[1,3], IAN P. F. OWENS[1,3], AND C. DAVID L. ORME[1,2]

[1]*Division of Biology, Department of Life Sciences, Imperial College London, Silwood Park, Ascot, Berkshire SL5 7PY, UK;*
[2]*Grantham Institute for Climate Change, Imperial College London, South Kensington, London SW7 2AZ, UK; and* [3]*Natural Environment Research Council Centre for Population Biology, Imperial College London, Silwood Park, Ascot, Berkshire SL5 7PY, UK;*
[*]*Correspondence to be sent to: Division of Biology, Department of Life Sciences, Imperial College London, Silwood Park, Ascot, Berkshire SL5 7PY, UK;*
E-mail: alexander.pigot@imperial.ac.uk.

Syst. Biol. 2010

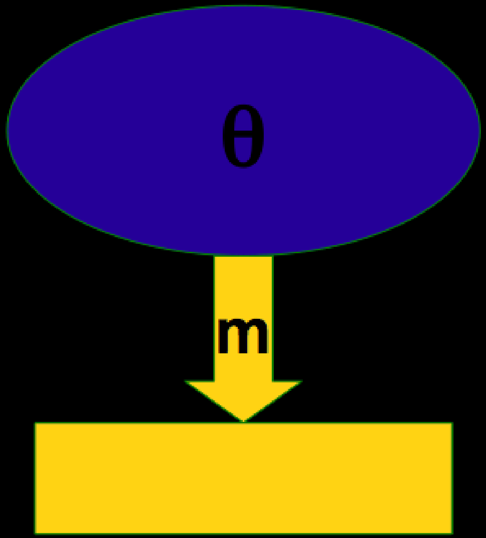


Phylogenies arising from the Neutral Theory of Biodiversity (NTB)



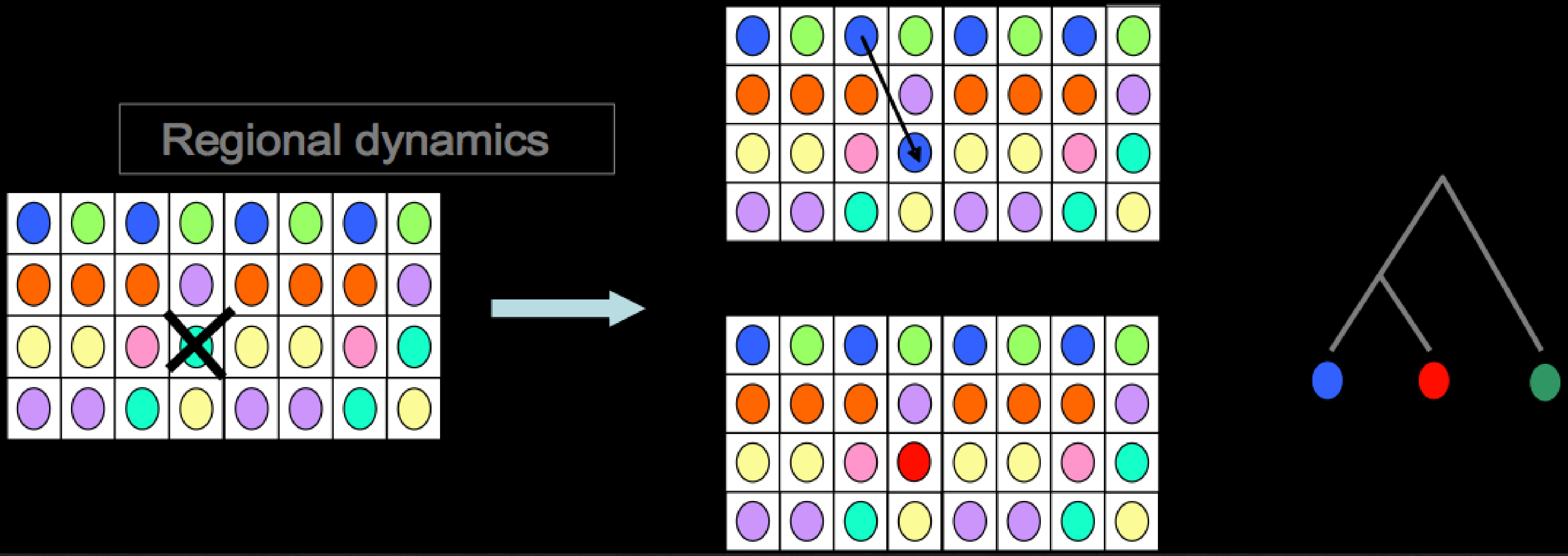
Hubbell 2001

Hubbell's model produces a species phylogeny

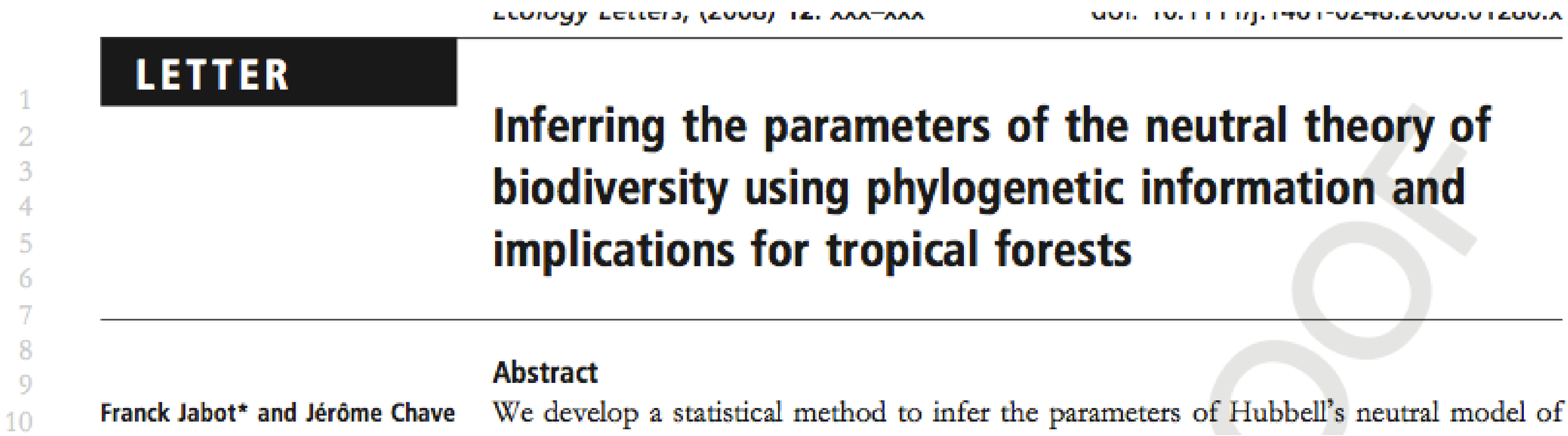


Species Phylogeny

Species Abundance Distribution (SAD)



Regional dynamics



Ecology Letters, (2008) 12: xxx–xxx doi: 10.1111/j.1461-0248.2008.01280.x

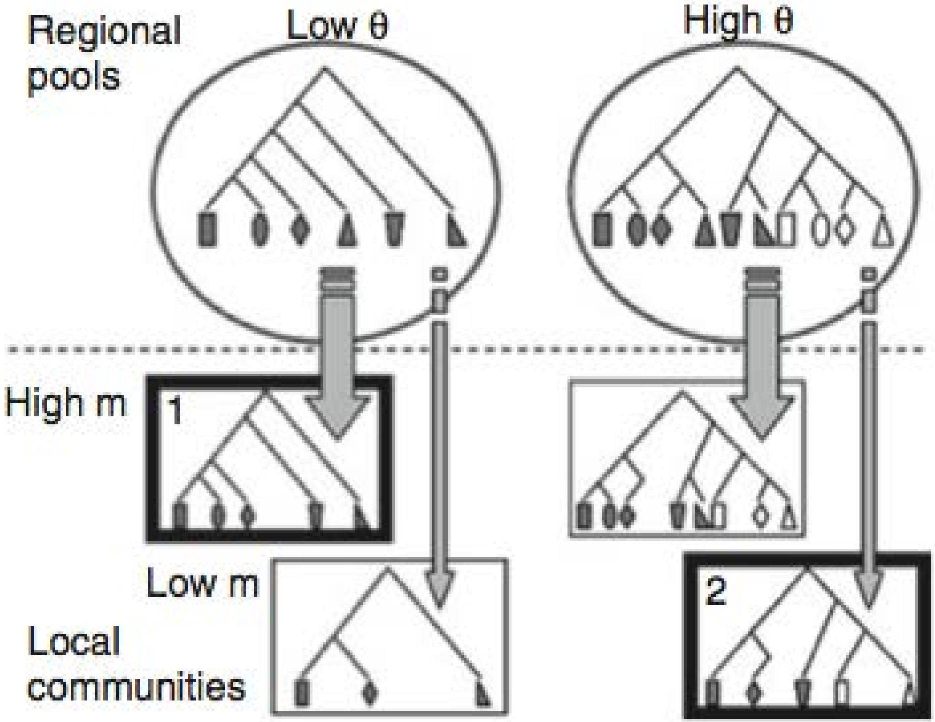
LETTER

Inferring the parameters of the neutral theory of biodiversity using phylogenetic information and implications for tropical forests

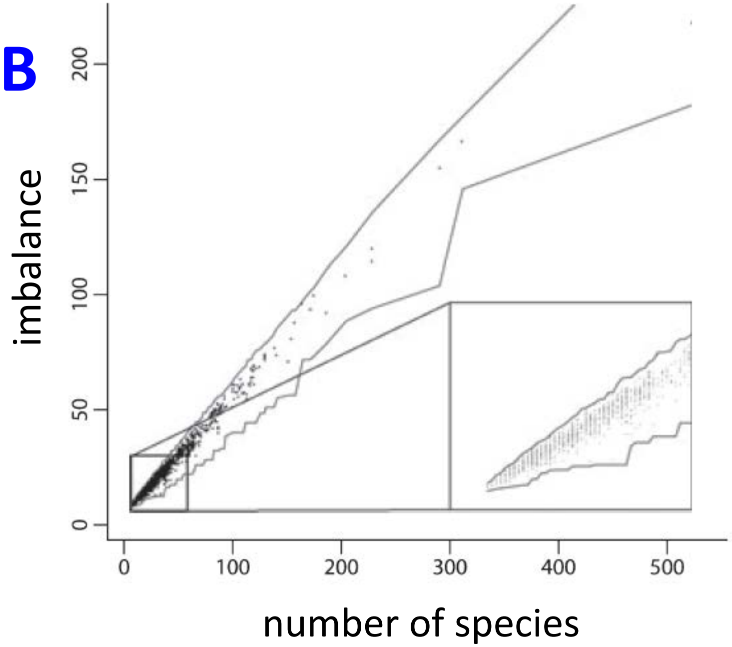
Franck Jabot* and Jérôme Chave

Abstract

We develop a statistical method to infer the parameters of Hubbell's neutral model of

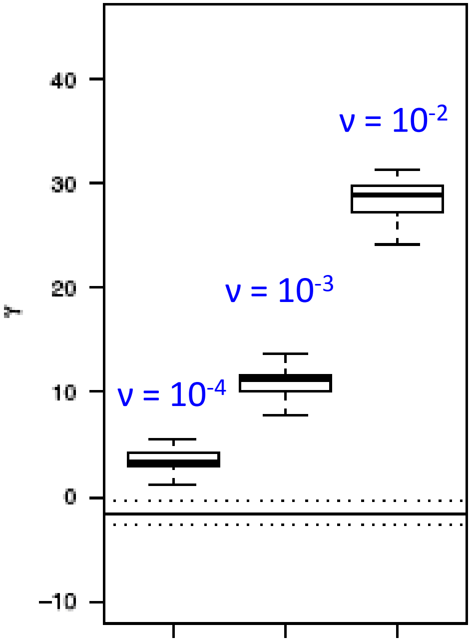


Phylogenies predicted by NTB have realistic imbalance…



Jabot & Chave
Eco. Lett. 2008

… but unrealistic branch-length patterns



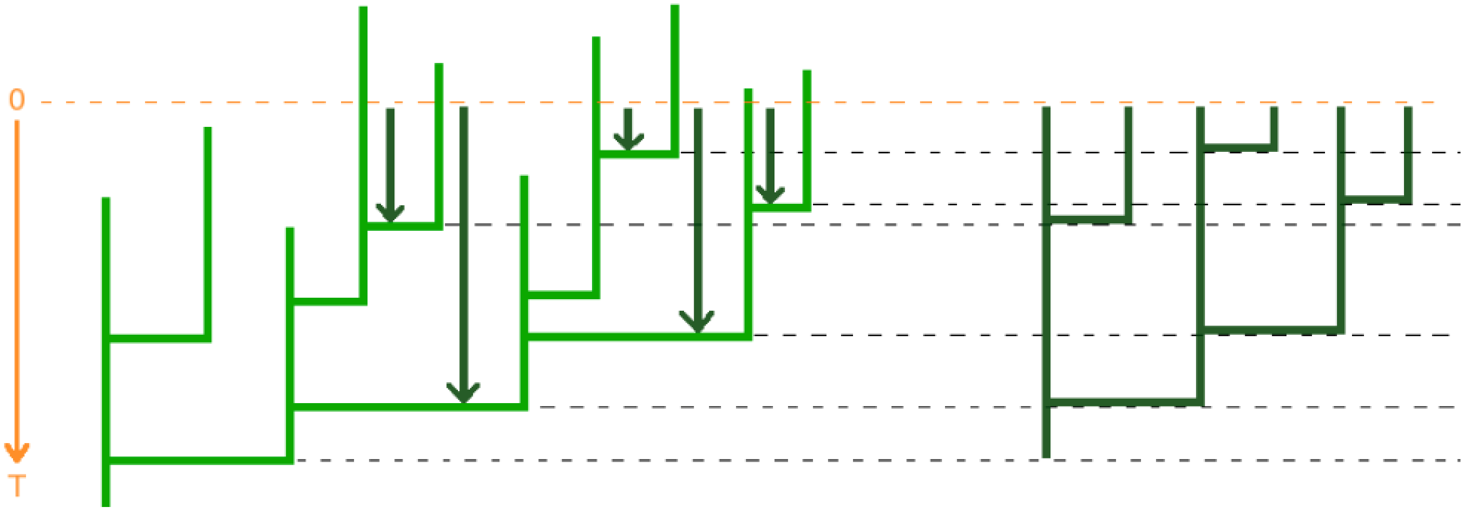
Davies et al.
Evolution **2011**

The model of speciation by genetic differentiation

We relax a first limitation of NTB: constant total population size

We assume individuals give birth with rate *b* and die with rate *d*

b and *d* can vary over time and we can have *b*<*d*

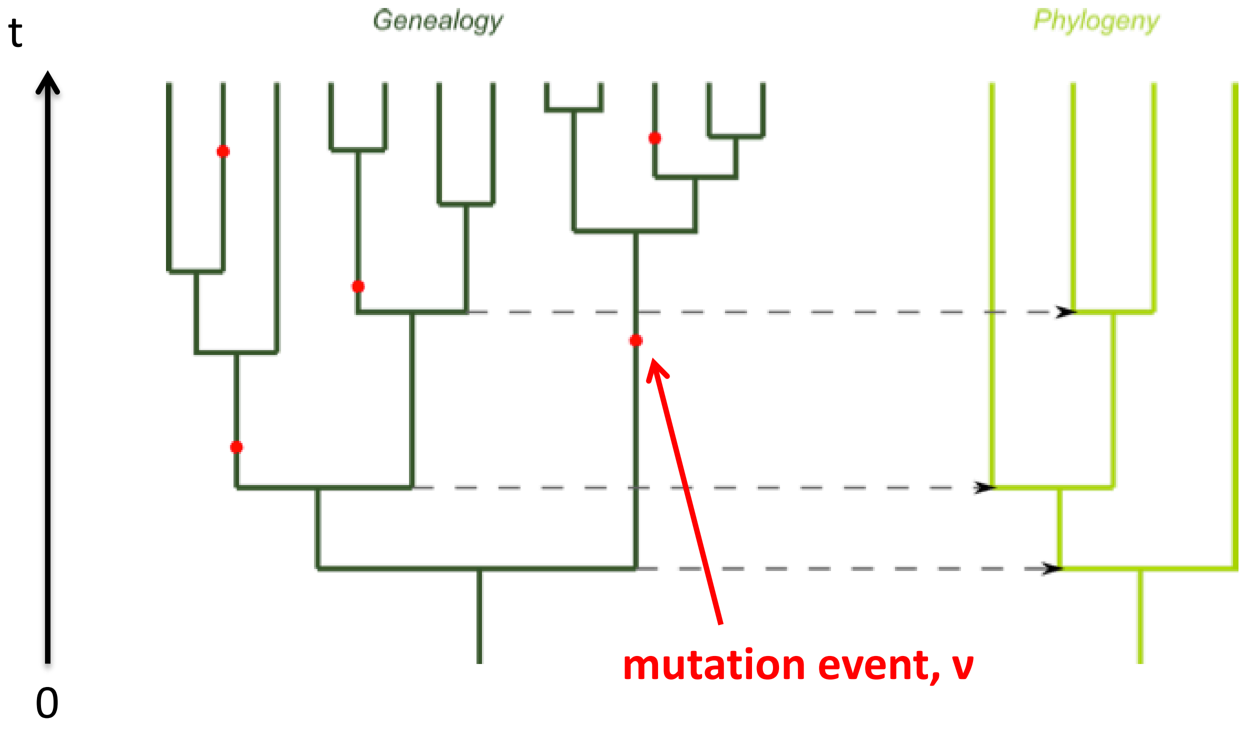


birth-death process

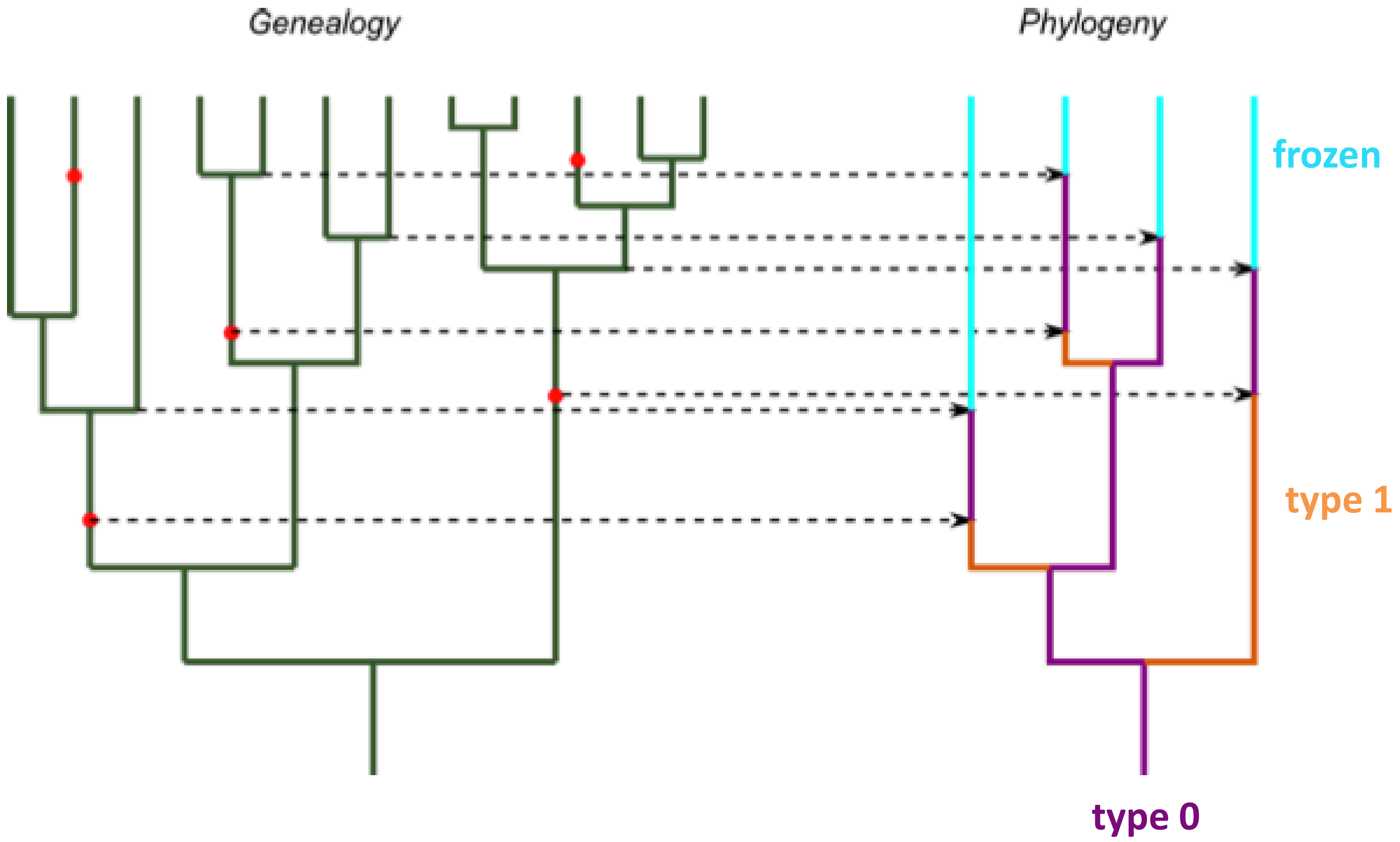
resulting genealogy

We relax a second limitation of NTB: the point mutation mode of speciation

Speciation by genetic differentiation:
A node is a speciation event only if *all individuals*
of the two descendant populations are separated by *at least* one
mutation



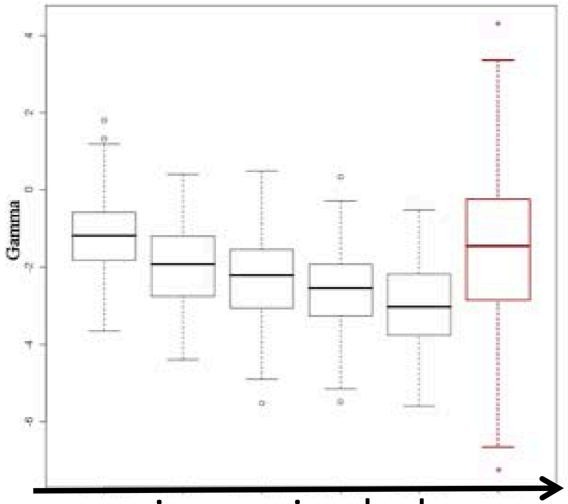
Phylogenies under SGD can be generated by a forward in time time-inhomogeneous branching process with three types



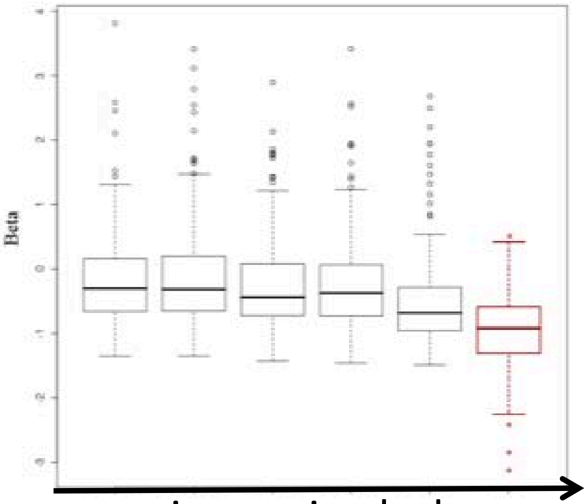
Phylogenies under SGD have realistic branch-lengths and imbalance

branch-length

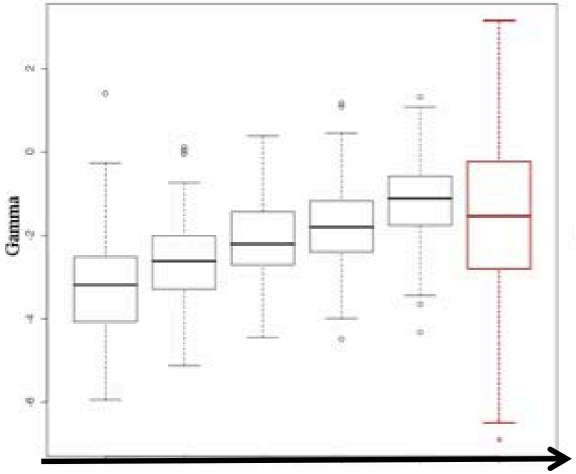
imbalance



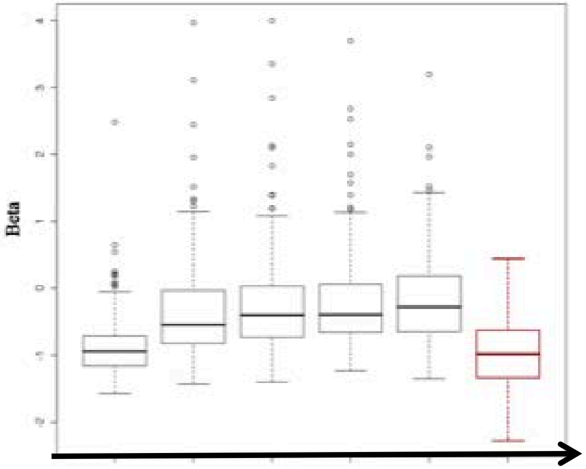
increasing b-d



increasing b-d

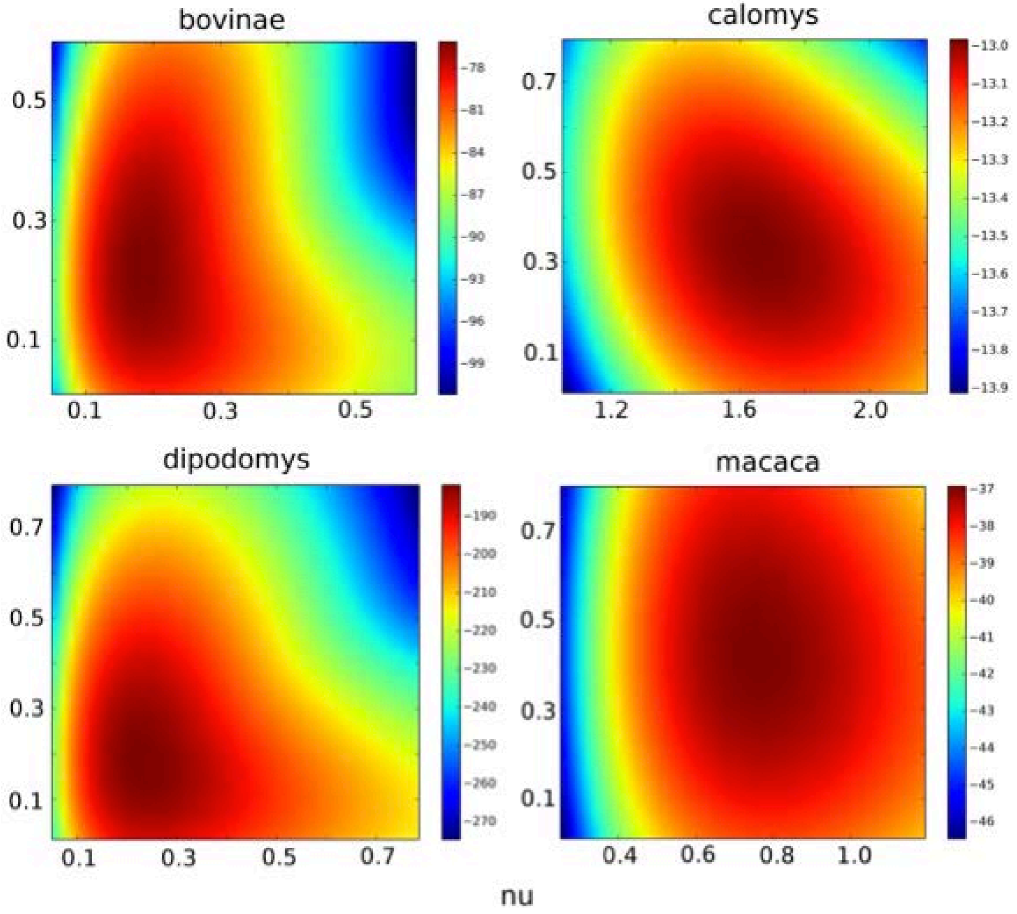


increasing ν



increasing ν

Likelihoods of trees under SGD can be computed efficiently



taxon	p	$\log(b)$	$b-d$	ν
bovinae	1	11.0	0.19	0.16
calomys	0.85	12.3	0.45	1.72
caprinae	0.89	10.7	0.40	0.39
dasyurid	0.92	10.8	0.20	0.23
dipodomys	0.95	11.2	0.05	0.30
duikers	0.83	11.2	0.38	0.30
genets	0.88	11.3	0.36	0.31
gibbon	1	8.8	0.53	0.32
howlerMonkey	0.91	11.5	0.20	0.39
macaca	0.95	6.4	0.42	0.76
microtus	0.69	6.9	1.84	1.05
mustelid	0.85	11.8	0.38	0.22
pikas	0.92	10.5	0.25	0.35
talpa	0.77	10.9	0.16	0.21

Ecology Letters, (2014) doi: 10.1111/ele.12251

REVIEW AND SYNTHESIS

Phylogenetic approaches for studying diversification

Hélène Morlon*

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Abstract

Estimating rates of speciation and extinction, and understanding how and why they vary over evolutionary time, geographical space and species groups, is a key to understanding how ecological and evolutionary processes generate biological diversity. Such inferences will increasingly benefit from phylogenetic approaches given the ever-accelerating rates of genetic sequencing. In the last few years, models designed to understand diversification from phylogenetic data have advanced significantly. Here, I review these approaches and what they have revealed about diversification in the natural world. I focus on key distinctions between different models, and I clarify the conclusions that can be drawn from each model. I identify promising areas for future research. A major challenge ahead is to develop models that more explicitly take into account ecology, in particular the interaction of species with each other and with their environment. This will not only improve our understanding of diversification; it will also present a new perspective to the use of phylogenies in community ecology, the science of interaction networks and conservation biology, and might shift the current focus in ecology on equilibrium biodiversity theories to non-equilibrium theories recognising the crucial role of history.

Keywords

Birth–death models, cladogenesis, diversity dynamics, extinction, speciation, stochastic biodiversity models.

Ecology Letters (2014)

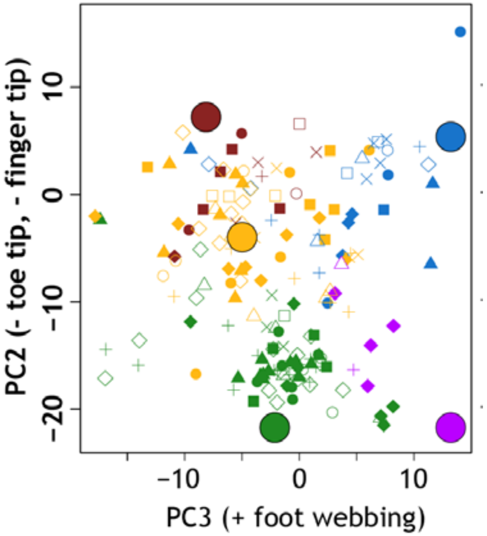
Current and future developments

Testing diversity-dependent effects in trait evolution

Quantifying the role of past adaptation on current morphological diversity

Arboreal
Burrowing
Semi-Aquatic
Terrestrial
Torrent

○ = "optimum" morphology



We develop and use phylogenetic approaches to understand global biodiversity patterns, across the Tree of Life

Fabien Condamine

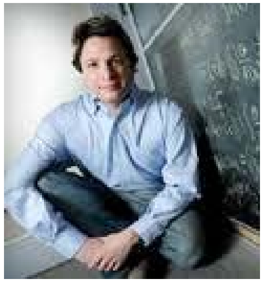
Dan Moen

Jonathan Rolland

Amaury Lambert

Marc Manceau

Frederic Jiguet



Joshua Plotkin

Todd Parsons

erc

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MARIE CURIE ACTIONS

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i “type 0” if it is a lineage from the underlying genealogy that has at least one descendant of same genetic type at present,

ii “type 1” if it is a lineage from the underlying genealogy that has no descendant of same genetic type at present,

iii "frozen" if there exists at least two individuals, one in each of the two subpopulations separated by the descending node in the underlying genealogy, of same genetic type. In this case, all the individuals from the descending nodes are collapsed into a single species, and the lineage is “frozen”, in the sense that no further splitting or extinction events happen to this lineage up to the present.

A lineage of type 1 becomes of type 0 :

$$\rho_{1\to 0}(t) = \frac{\nu(t)m(t)}{(1-m(t))}$$

A lineage of type 1 branches and gives rise to two descendant lineages of type 1 :

$$\rho_{1\to +1}(t) = g(t)(1-m(t))$$

A lineage of type 0 branches and gives rise to one descendant lineage of type 0 and one descendant lineage of type 1 :

$$\rho_{0\to +1}(t) = 2g(t)(1-m(t))$$

A lineage of type 0 “freezes”, giving rise to a terminal branch in the phylogeny :

$$\rho_{0\to\varnothing}(t) = g(t)m(t)$$