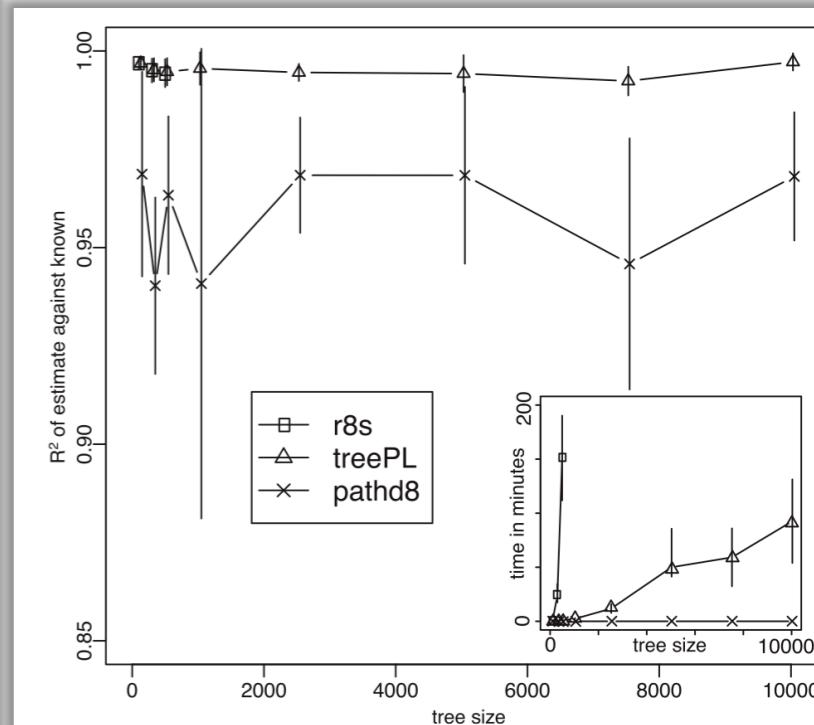
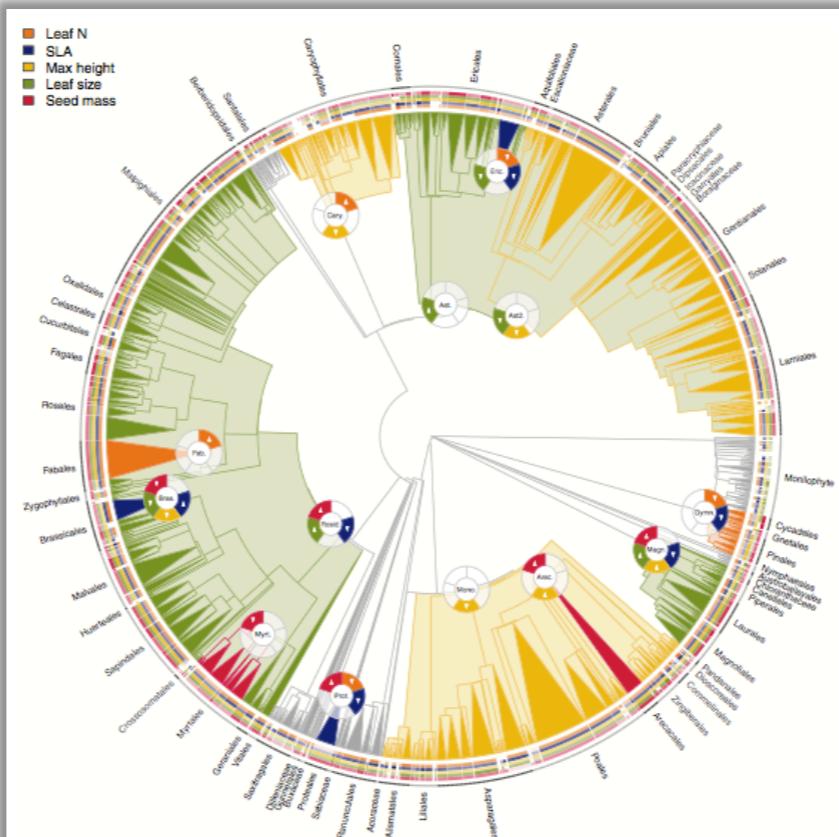
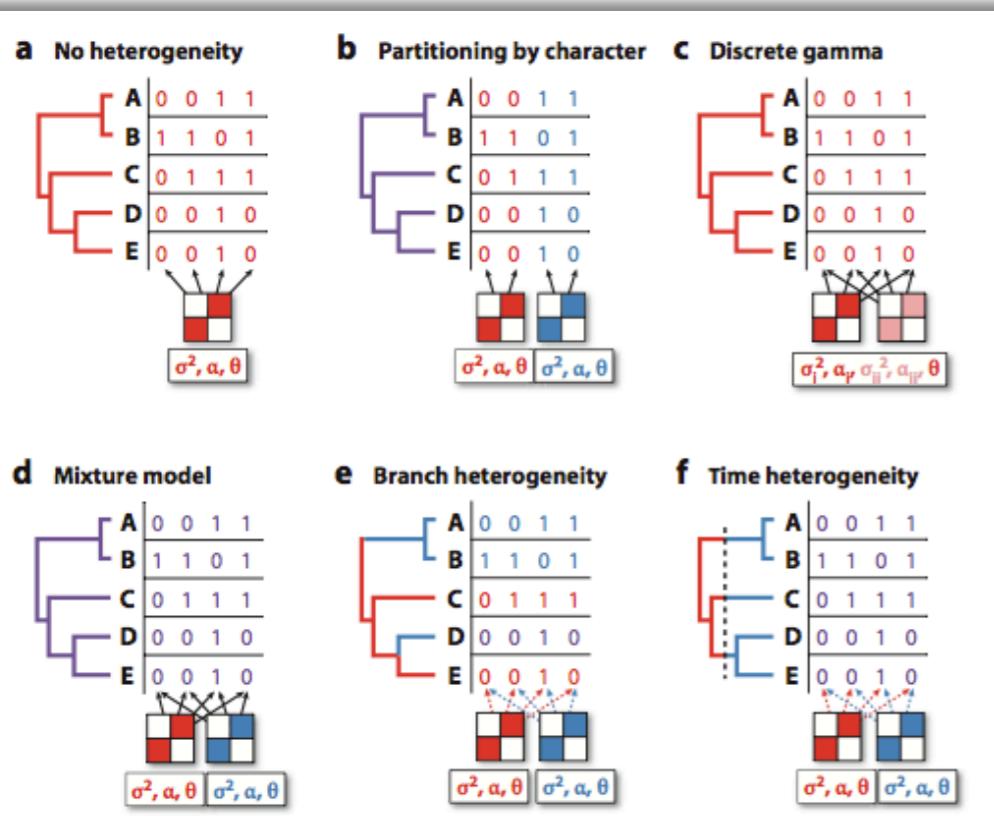


Developing and applying tools to answer outstanding biological questions using phylogenies, II



Brian O'Meara
brianomeara.info
 UT Knoxville



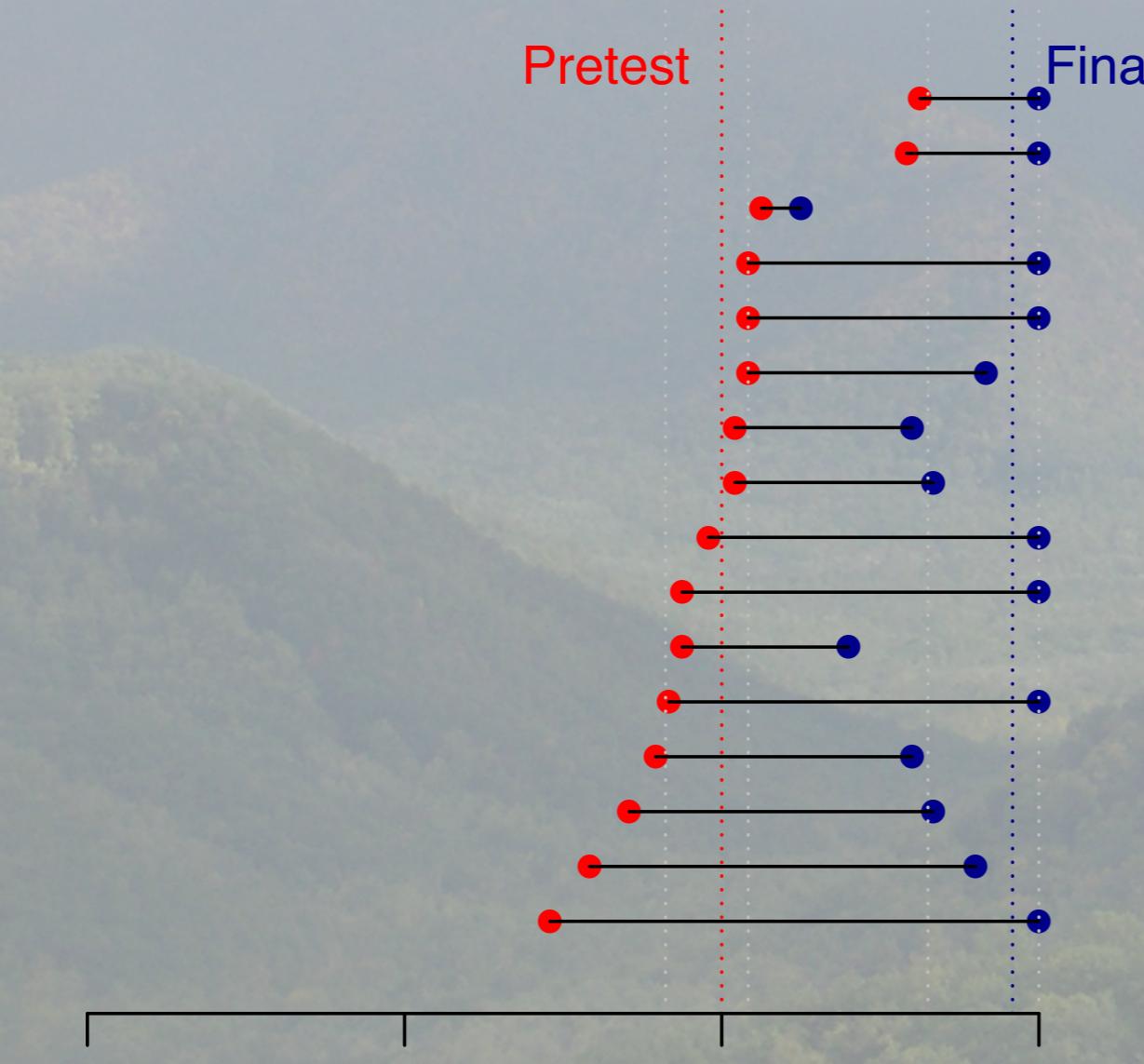
Teaching

| | 2014-15 | 2013-14 | 2012-13 | 2011-12 | 2010-11 | 2009-10 |
|----------------------|---------|---------|---------|---------|---------|---------|
| Speciation | 2 | 1 | | | | 1 |
| Macroevolution | 1 | 1 | 1 | 1 | 1 | 1 |
| Core: Evolution* | 1 | 1 | 1 | 1 | 1 | 1 |
| HOFF* | 2 | 2 | 2 | 2 | | |
| Bio130: Biodiversity | | 1 | | 1 | | |
| Seminar | | | | | 1 | |

- High performance computing for phylogenetics, NIMBioS tutorial. Organizer
- Species delimitation course, Gothenburg, Sweden. Instructor
- eFlower summer school, Vienna, Austria. Instructor
- Evolutionary quantitative genetics, NESCent. Instructor
- Markov processes, Lausanne, Switzerland. Instructor
- Computing in the cloud, NIMBioS tutorial. Co-organizer
- Evolutionary quantitative genetics, NIMBioS tutorial. Instructor

Teaching

Assessment



Innovation

Lampyr

Welcome to Lampyr. For more information, see our [website](#). There are 128,604 georeferenced species and 8,703,452 points in the database, so it may take a minute to search once you hit the button below.

Find closest species

Options (scroll down) Use only species with interpret, but fewer species

The 25 closest species:

- Selurus motacilla Louisiana waterthrush 0.2 mi ENE
- Schistocerca damnifica Carolina locust 0.4 mi NE
- Nycticorax nycticorax black-crowned night-heron 0.5 mi WSW
- Cyprinella galactura whitetail shiner 0.8 mi ENE
- Dendroica pensylvanica chestnut-sided warbler 2.3 mi WSW

Feedback to Brian

This is a general feedback form allowing other long-term interaction. It is another second question is required.

* Required

Interaction

- Macroevolution course
- EEB graduate core
- Research in the lab
- Bio130
- Phylogenetics discussion group
- Other: _____

Number of species to return: 25

Home Videos Playlists Channels About

Evidence

2013 Macroevolution EEB464

by Brian O'Meara • 32 videos • 138 views • 24 hours

Play all Share Save

1 Macroevolution: Evidence, 28 Aug 2013 Brian O'Meara

2 Macroevolution: Taphonomy, 30 Aug 2013 Brian O'Meara

3 Macroevolution: Jargon, 4 Sept 2013 Brian O'Meara

4 Macroevolution: Phylogenetics, 6 Sept 2013 Brian O'Meara

5 Macroevolution: Empirical Distributions, 9 Sept 2013 Brian O'Meara

6 Macroevolution: Biogeography and Phylogeography, 11 Sept 2013 Brian O'Meara

Teaching

- Bio130: Greatest contribution to learning: “The open dialogue we had in every lecture”
- Macroevolution: “I found this class wonderfully stimulating and I really appreciated that Prof. O’Meara would stop in the middle of his lecture to answer any and all questions without it bothering him”
- Core: “The subject is a difficult one, but O’Meara communicated complex topics in a very understandable way. In short, he is a great teacher with many great qualities (organized, attentive, intelligent but relatable)”

People

Students

Sam Borstein

Jenn Bosco

Katie Massana

Orlando Schwery

People

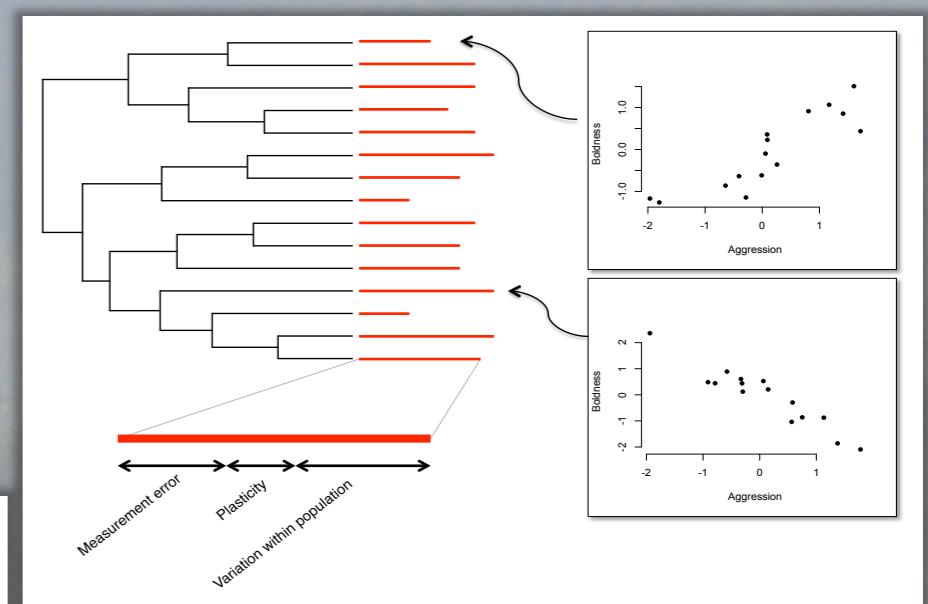
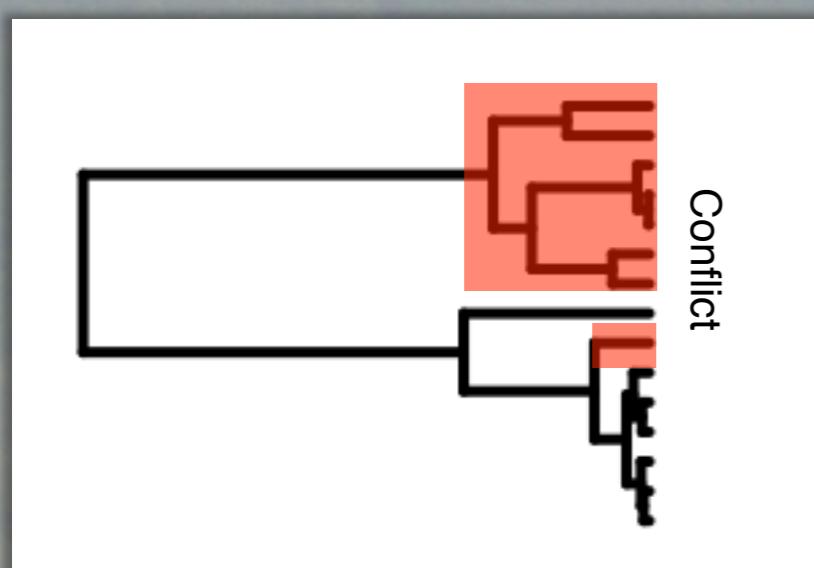
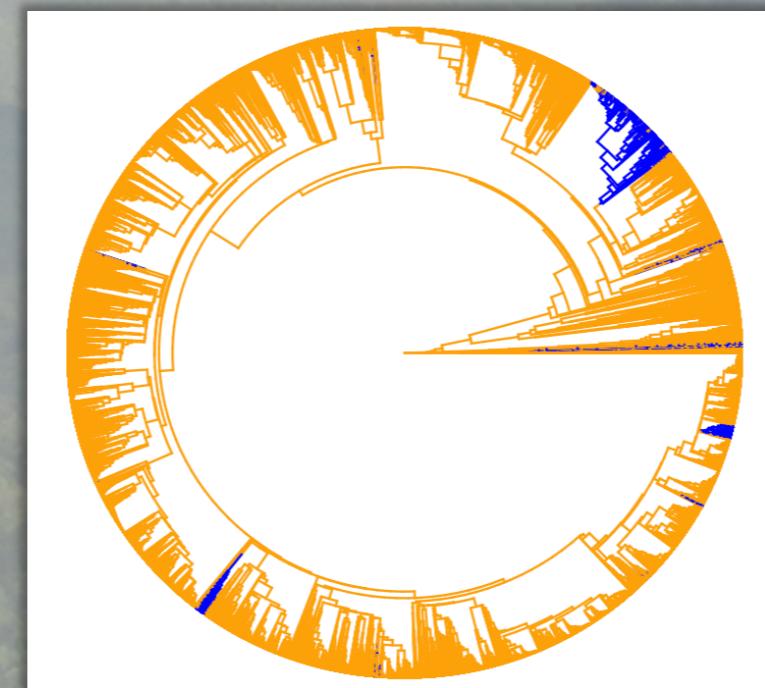
Students

Sam Borstein

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Orlando Schwery



People

Students

Sam Borstein

Jenn Bosco

Katie Massana

Orlando Schwery

Postdocs

Hugo Alamillo

Barb Banbury

Jeremy Beaulieu*

JJ Chai*

Nathan Jackson

Tony Jhwueng*

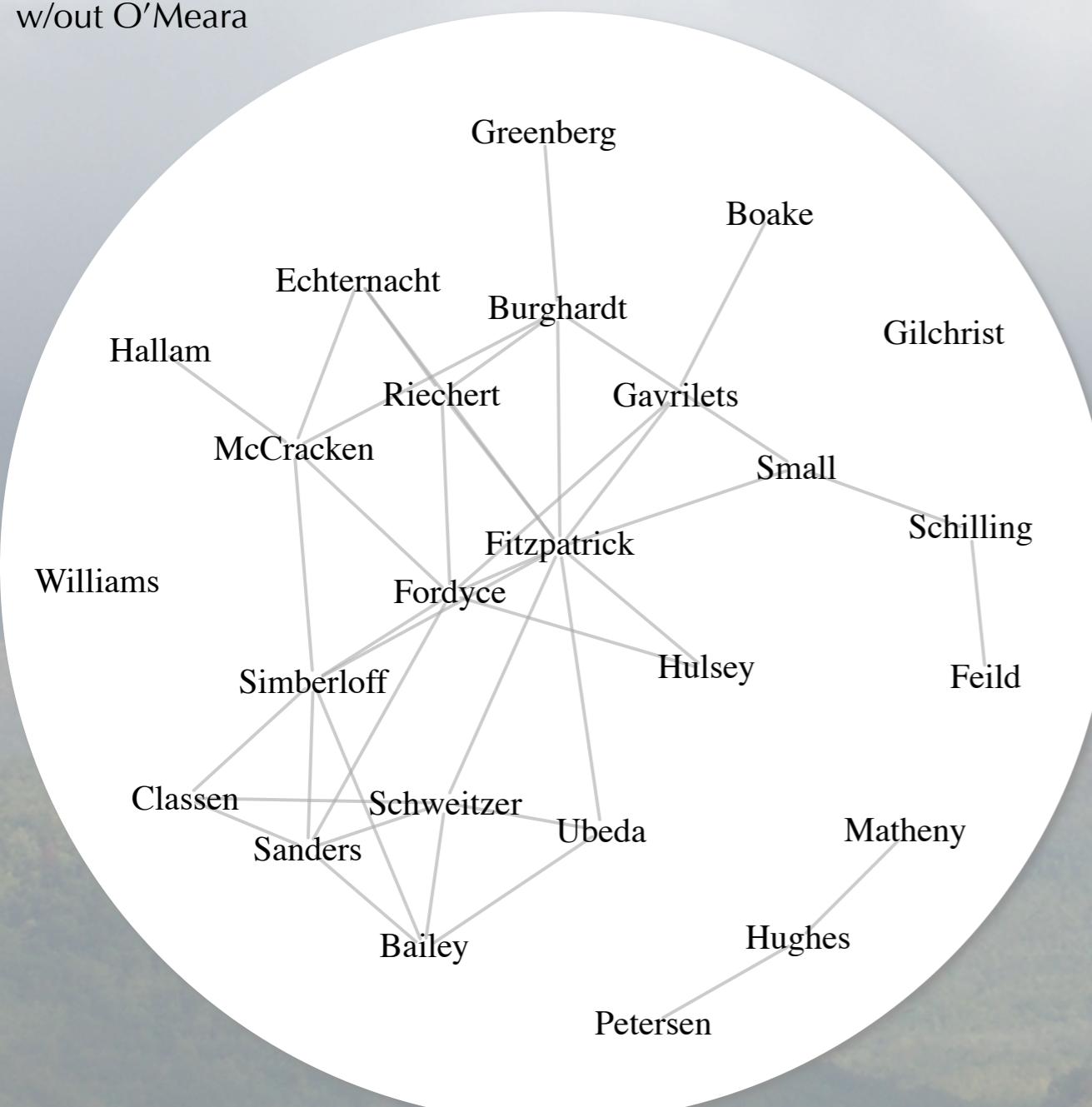
Sandy Kawano*

Michelle Lawing*

Ryan Martin*

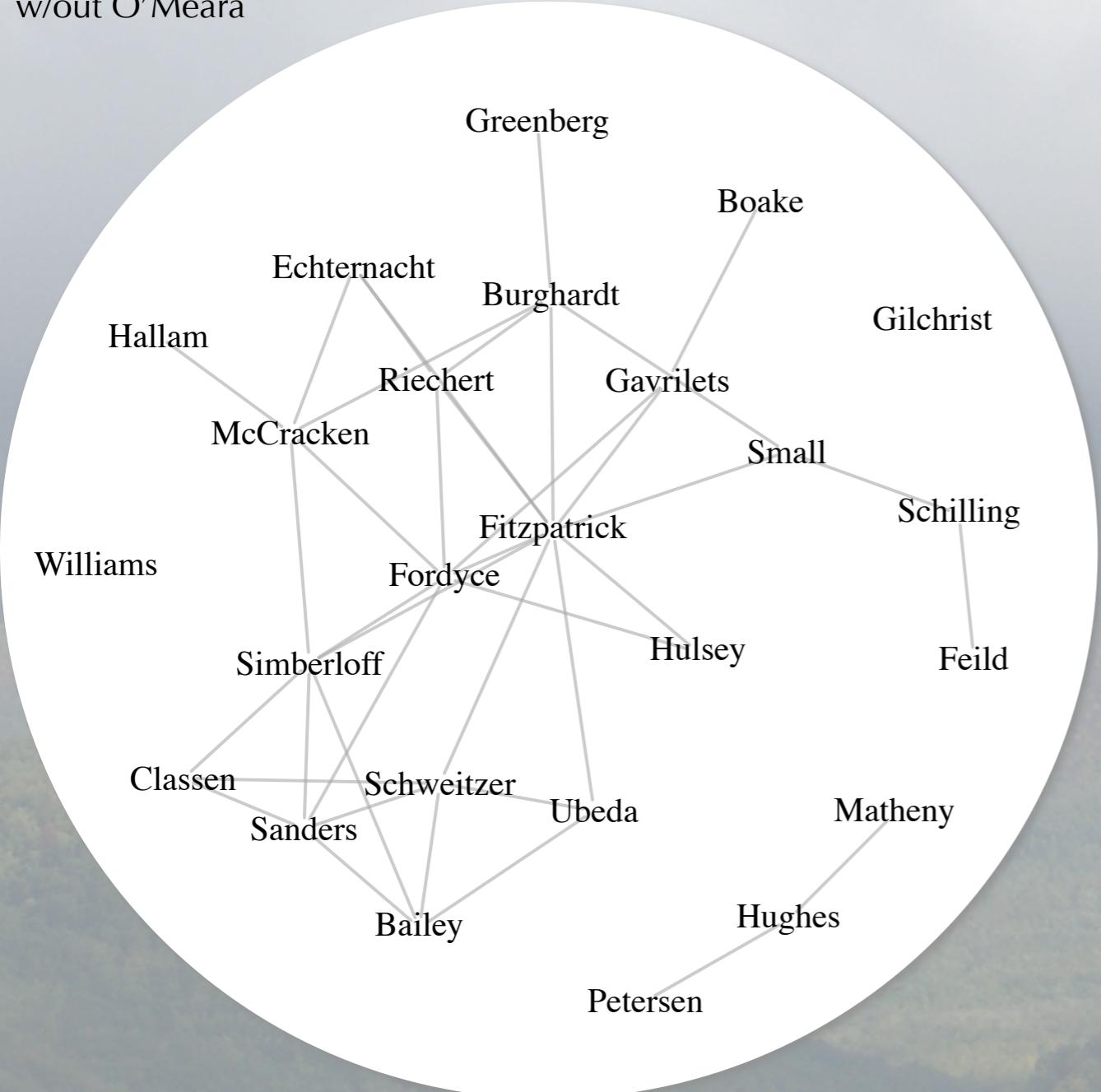
Nick Matzke*

EEB Network,
w/out O'Meara

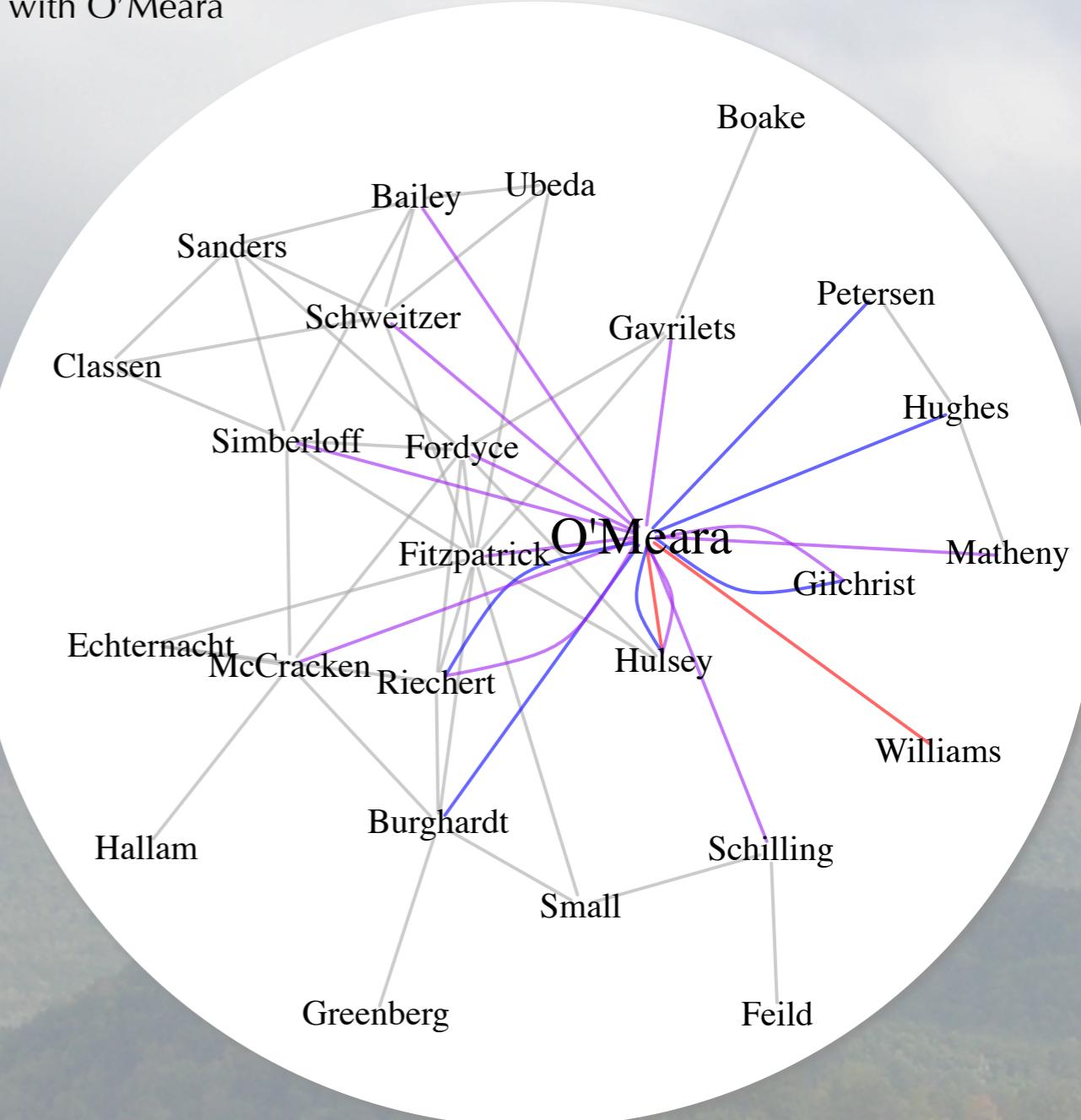


Networks includes all EEB faculty from 2008 – present who
are connected to at least one other member on a network

EEB Network,
w/out O'Meara



EEB Network,
with O'Meara



- Coauthorship
- Coauthorship with me
- Grant proposal with me
- Serving on the committee of another's student

Networks includes all EEB faculty from 2008 – present who are connected to at least one other member on a network



Service & Outreach

- Co-Organizer, Evolution 2014 (2000 participants)
- Lightning talk organizer, Evolution 2013
- Phylotastic Leadership Team (hackathons)
- iEvoBio Leadership (satellite conference)
- Elected member of Society of Systematic Biologists council



Service & Outreach

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- iEvoBio Leadership (satellite conference)
- Elected member of Society of Systematic Biologists council
- Darwin Day Tennessee advisor
- Applications Editor, *Methods in Ecology and Evolution*
- Reviewer for *Science*, NSF, *Systematic Biology*, and numerous other journals
- Maintainer of CRAN Task View for Phylogenetics in R
- EEB Dept. web committee, head search committee, undergrad affairs, grad admissions, Dean's Advisory Council, many grad student committees in four departments

Service & Outreach

- Co-organized Women in Science seminar series in first year at UTK, got funds from Haines-Morris and buy-in from multiple departments

Service & Outreach

- Co-organized Women in Science seminar series in first year at UTK, got funds from Haines-Morris and buy-in from multiple departments
- Highlighted twice in *Science Careers* for work helping grad students prepare for NSF proposals during federal shutdown

The screenshot shows the Science Careers website with a red header. The main navigation bar includes links for AAAS, NEWS, SCIENCE JOURNALS, CAREERS, MULTIMEDIA, and COLLECTIONS. Below the header, there's a sub-navigation for Science Careers, including Career Magazine, My Science Career, Find A Job, Graduate Programs, Tools & Tips, Forum, and For Employers. The main content area features a large image of a building with a "CLOSED" sign. The title of the article is "The Latest Shutdown Information for NIH- and NSF-Funded Researchers (UPDATE)". The author is Jim Austin, and the date is September 30, 2013. The article discusses the impact of the shutdown on researchers funded by NIH and NSF. It includes a sidebar with social media sharing options (Facebook, Twitter, RSS, LinkedIn) and a "Search Articles" bar. At the bottom, there's a section for "Related Articles" and a "Print Article" link.

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Fortunately, there are workarounds. Start at [the Web site of Brian O'Meara](#), an assistant professor at the University of Tennessee, Knoxville, in the Department of Ecology and Evolutionary Biology. O'Meara has located and stashed away some NSF forms likely to be in frequent demand: NSF's [Grant Proposal Guide](#); the program solicitation for Directorate for Biological Sciences [Doctoral Dissertation Improvement Grants](#) (Due date: 10 October); and the program solicitation for the crosscutting [Graduate Research Fellowship Program](#), which has due dates in early November.


Government Shutdown
The Latest Shutdown Information for NIH- and NSF-Funded Researchers (UPDATE)
By Jim Austin
September 30, 2013
[Email Article](#) [Email Editor](#) [Discuss in Forum](#) [Related Articles](#) [Print Article](#) [Free Newsletter](#) [BOOKMARK](#)

GREDIT: Diniydown, distributed under a CC-BY 3.0 license (Wikimedia Commons)

Do you have new shutdown-related information that's relevant to NSF- or NIH-funded investigators or those seeking funding from the major agencies? [Send us an email](#).

On Friday, 27 September, we described the likely impact on scientists funded by the National Institutes of Health (NIH) and the National Science Foundation (NSF) if the government entered a period of partial shutdown. That indeed came to pass the following Monday, at midnight. Here's what we've learned since then:

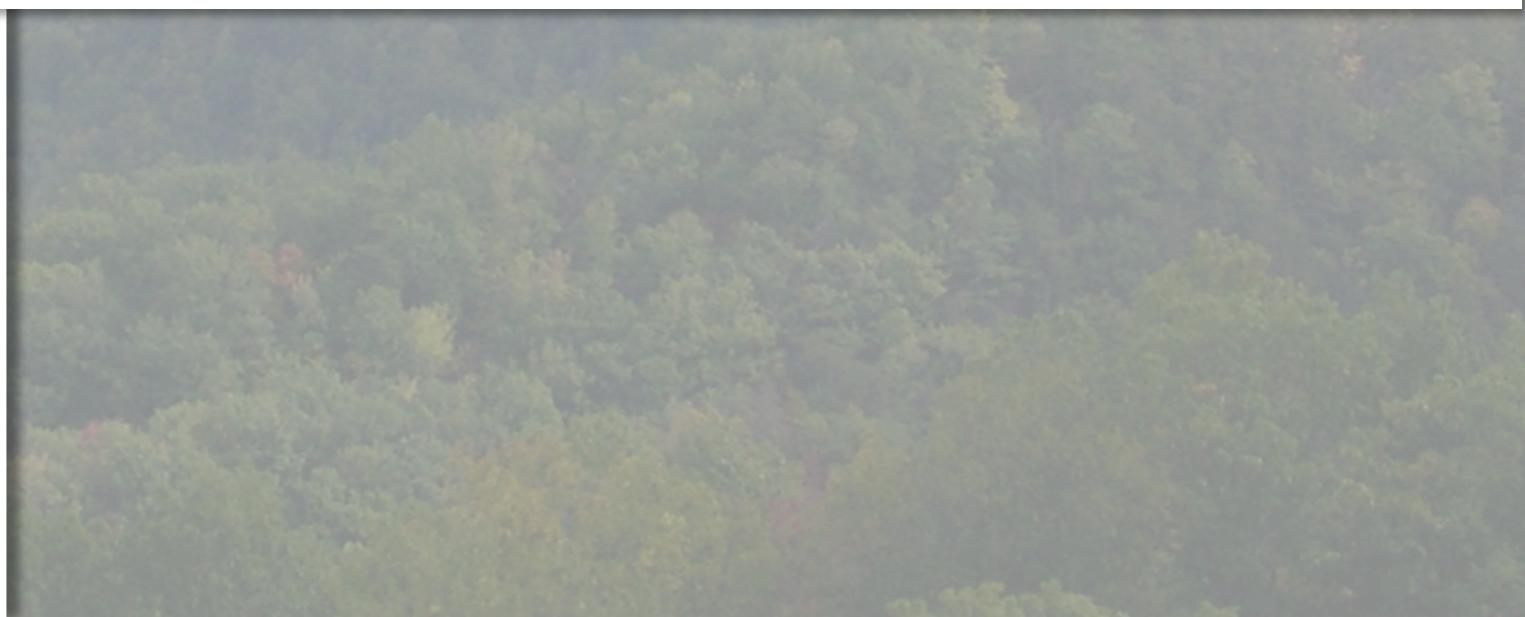
10/06/2013

- More on accessing information from NSF's Web site--this via Twitter from Brian O'Meara, who, as we mentioned on Wednesday, had archived some critical files on his Web site. O'Meara tweets,

Internet Archive to the rescue: [@SciCareerEditor #shutdown .@NSF](http://t.co/MSvmF5A6gj)

— Brian O'Meara (@omearabrian) [October 5, 2013](#)

You may need to be patient because it's slow, but that should get you to most of what you need from NSF. (I've been using the Wayback Machine forever, so I'm surprised I didn't think of that earlier. Thanks Brian!)



Service & Outreach

- Co-organized Women in Science seminar series in first year at UTK, got funds from Haines-Morris and buy-in from multiple departments
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Service & Outreach

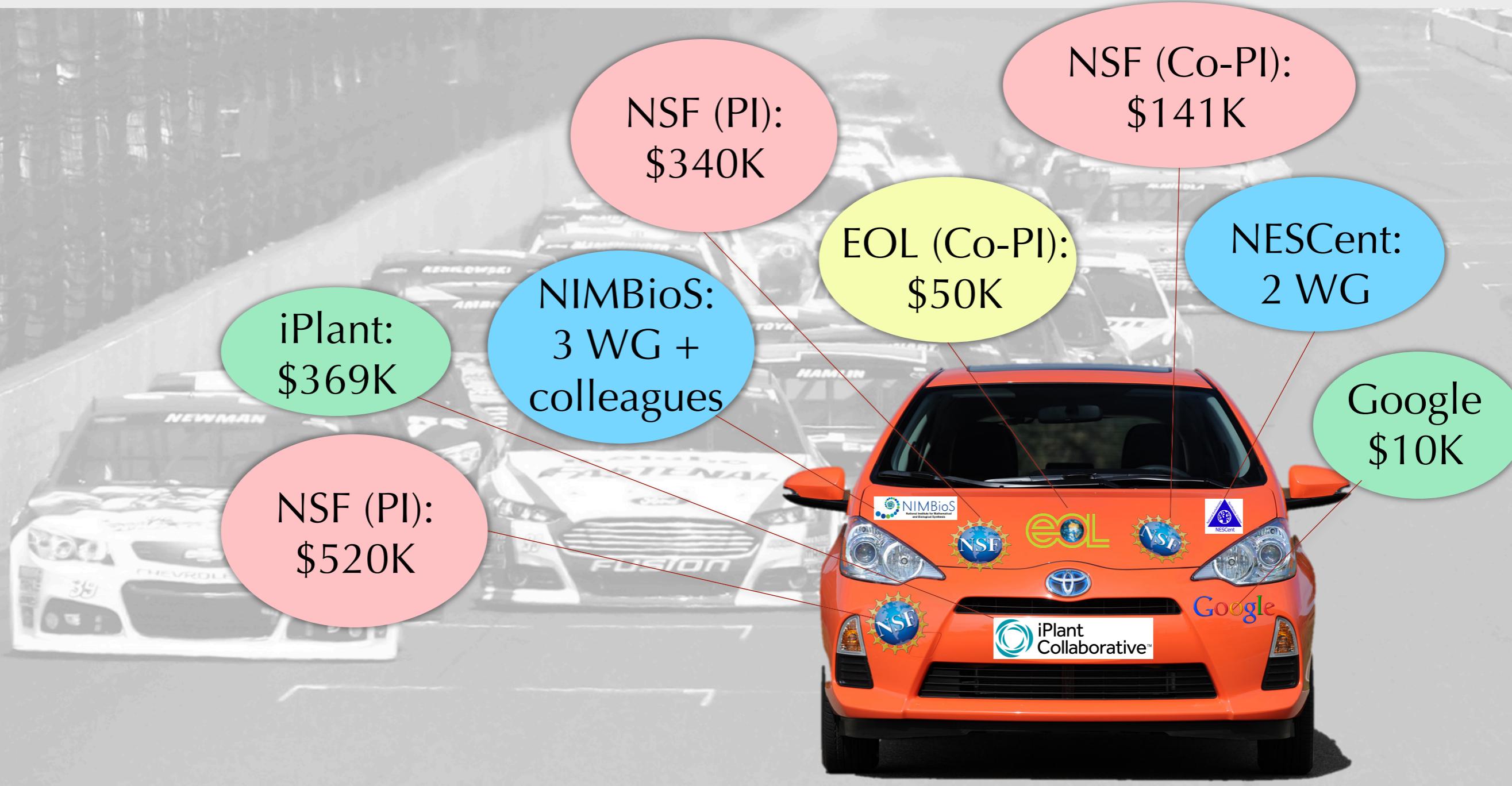
- Co-organized Women in Science seminar series in first year at UTK, got funds from Haines-Morris and buy-in from multiple departments
- Highlighted twice in *Science Careers* for work helping grad students prepare for NSF proposals during federal shutdown
- A representative from SSB on joint *American Society of Naturalists*, *Society for the Study of Evolution*, and *Society of Systematic Biologists* group to help gather data for proposal to improve representation of women in those societies
- Co-organizer of symposium at Evolution 2015 on “Women in Science: Pairing Advances in the Theory and Application of Phylogenetic Methods”
- Outreach via social media and web (i.e., Google “Akaike weight”)



Research: Acknowledgments



Research: Acknowledgments



Continuous trait evolution

384

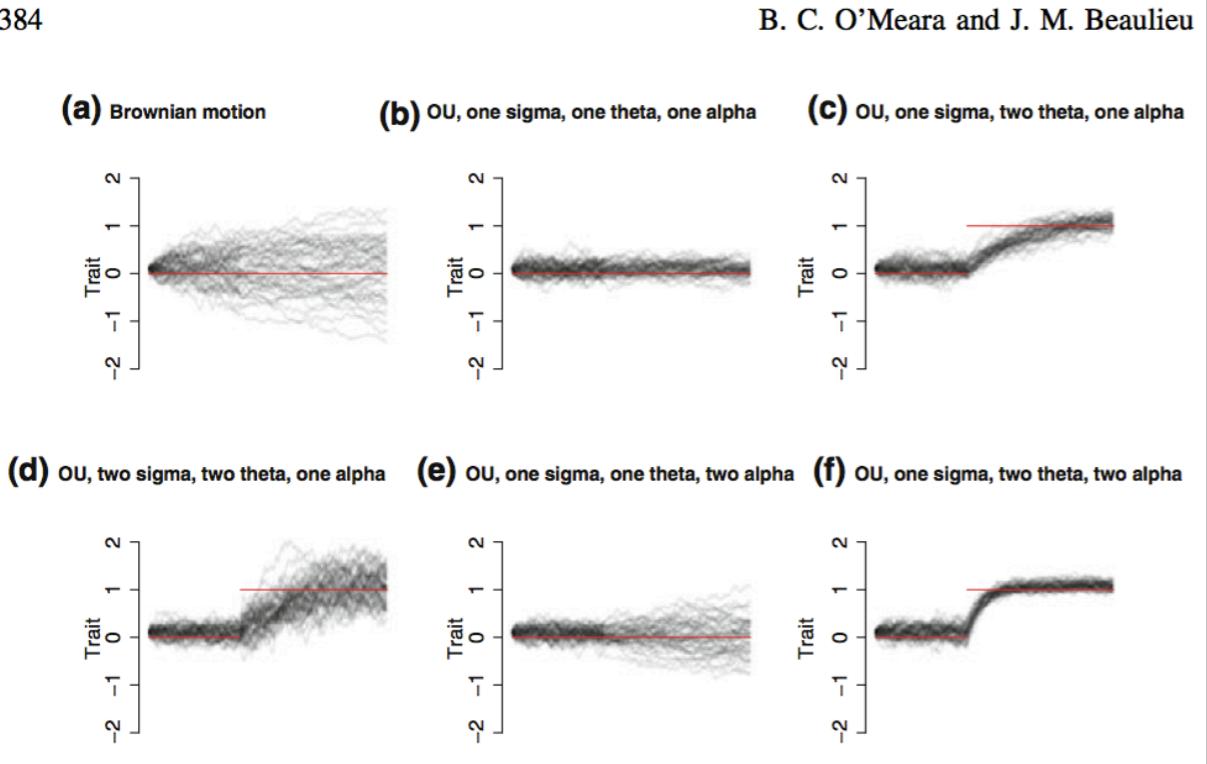


Table 2. The fit of alternative models of genome size evolution in monocots. The best model, based on ΔAIC and Akaike weights, was the OU_{MVA} , which estimated a separate θ , α , and σ^2 for woody and herbaceous monocot lineages.

| Model | -lnL | AIC | ΔAIC | w_i |
|-------------------|--------|-------|--------------------|-------|
| BM1 | -227.6 | 459.1 | 156.2 | <0.01 |
| BMS | -203.0 | 412.0 | 109.1 | <0.01 |
| OU1 | -160.0 | 326.1 | 23.2 | <0.01 |
| OU _M | -159.2 | 326.5 | 23.6 | <0.01 |
| OU _{MV} | -147.3 | 304.6 | 1.7 | 0.290 |
| OU _{MA} | -159.2 | 328.5 | 25.6 | <0.01 |
| OU _{MVA} | -145.3 | 302.9 | 0.0 | 0.678 |

Cited 249 times

Evolution, 60(5), 2006, pp. 923–933

TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD

BRIAN C. O'MEARA,¹ CÉCILE ANÉ,² MICHAEL J. SANDERSON,^{3,4} AND PETER C. WAINWRIGHT^{3,5}
¹Center for Population Biology, University of California, Davis, One Shields Avenue, Davis, California 95616
E-mail: brian@popbio.ucdavis.edu
²Department of Statistics, University of Wisconsin-Madison, Media Science Center, 1300 University Avenue, Madison, Wisconsin 53706-1532
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³Section of Evolution and Ecology, University of California, Davis, One Shields Avenue, Davis, California 95616
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Abstract. Rates of phenotypic evolution have changed throughout the history of life, producing variation in levels of morphological, functional, and ecological diversity among groups. Testing for the presence of these rate shifts is key to comparing evolutionary models and generalizing about the causes of changes in phenotypic diversity as a function of evolutionary history and rates are developed, and tests are derived to evaluate rate changes. Simulations show that these tests are more powerful than existing tests using standardized contrasts. The new approaches are distributed in an application called *Brownie* and in *r8s*.

Keywords: Brownian motion, *Brownie*, comparative method, continuous characters, disparity, morphological evolution, rate.

Received March 8, 2005. Accepted March 4, 2006.

All five extant flamingo species are long-legged filter feeders, whereas their sister group, consisting of twenty species of grebes (Van Tuinen et al., 2001; Chubb 2004; Mayr 2004), feed on prey ranging from fish and insects to marine mammals. Figure 1 shows the distribution of body and bill shapes. Methods to test whether the differences in species number between flamingos and grebes arose by chance or reflects differences in diversification rates have been developed (Slowinski and Guyer 1989; Nee et al. 1992; Hey 1992; Harvey et al. 1994). These methods are aimed at discovering factors associated with diversification. But there are also many other ways that lead to the difference in variability of ecologically important traits within these two groups. This paper is concerned with hypotheses about factors that lead to differences between groups in phenotypic and biological diversity, as opposed to species richness.

Received March 8, 2005. Accepted March 4, 2006.

In this paper, we develop and implement new methods to make inferences regarding these questions. Basic results concerning character evolution on trees are presented. Our methods are illustrated using an example of genome size evolution in angiosperms.

SOME BASIC PROPERTIES OF CHARACTER EVOLUTION ON TREES

Disparity is commonly measured as variance of the states of the taxa (so higher disparity means the taxa are less similar for that particular character). The observed disparity is a function of many factors, such as the rate of phenotypic evolution, the amount of time the group has been evolving, and the relationships of the taxa. To examine any one factor, such as the rate of phenotypic evolution, it is necessary to control for other factors, such as the phylogeny. A reasonable model to use in the case of phenotypic evolution is Brownian motion (BM). This is the standard model for continuous character evolution, used in independent contrasts (Felsenstein 1985) and estimation of ancestral states (Schlüter et al. 1997). In Brownian motion, at each point in time the state of a character is determined by the rate of growth of genome size evolution. Thus, invasion of a new, competing, free-living taxon may increase the rate of evolution of feeding structures. These hypotheses all attempt to relate a change in some aspect of the biology of the lineage with a change of the rate of evolution of a continuous character based on an idea about how evolution works. Hypotheses can also be generated from several sets of pairwise comparisons of related characters based on a mechanism. Grebes appear to have more interspecific variation in bill dimensions than flamingos: this may reflect a faster rate of bill evolution, or perhaps the grebe species have been evolving independently for more time than the flamingo species.

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JOURNAL COMPILATION © 2006 EUROPEAN SOCIETY FOR EVOLUTIONARY BIOLOGY

Habitat use affects morphological diversification in dragon lizards

D. C. COLLAR*, J. A. SCHULTE II†, B. C. O'MEARA‡ & J. B. LOSOS*

*Department of Organismic and Evolutionary Biology and Museum of Comparative Zoology, Harvard University, Cambridge, MA, USA
†Department of Biology, Clarkson University, Potsdam, NY, USA
‡Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN, USA

Keywords:
Agamidae;
Brownian motion;
ecomorphology;
iguania;
locomotion;
phylogenetic comparative method.

Abstract
Habitat use may lead to variation in diversity among evolutionary lineages because habitats differ in the variety of ways they allow for species to make a living. Here, we show that structural habitats contribute to differential diversification of limb and body form in dragon lizards (Agamidae). Based on phylogenetic comparative methods, we find that multiple lineages have independently adopted each of four habitat use types: rock-dwelling, terrestrial, semi-arboreal and arboreal. Given these reconstructions, we fit models of evolution to species' morphological trait values and find that rock-dwelling and arboreality limit diversification relative to terrestrial and semi-arboreality. Models preferred by Akaike information criterion infer slower rates of size and shape evolution in lineages inferred to occupy rocks and trees, and model-averaged rate estimates are slowest for these habitat types. These results suggest that ground-dwelling facilitates ecomorphological differentiation and that use of trees or rocks impedes diversification.

Introduction

One of the great questions in evolutionary biology concerns the causes of differences in diversity among clades. Ecological factors are often implicated to explain this pattern because the ecological circumstances available to the members of a lineage contribute to the mode of evolution. For example, environmental gradients may facilitate means for microbial specialization or local adaptation. Other habitats may impose stringent functional constraints that lead to strong selection resisting ecological and phenotypic divergence away from an adaptive peak (Butler & King, 2004; Collar et al., 2009). Habitat types may also contribute differently to diversification rates and patterns in the timing and type of species interactions they provide, such as the presence or absence of predators (McPeek & Brown, 2000). In addition, some habitats may provide opportunities for them to vary across space in the strength of species interactions (McPeek, 1996) or in their functional demands.

The consequences of habitat use for diversification have been investigated primarily in the context of

Cited 63 times

ORIGINAL ARTICLE



MODELING STABILIZING SELECTION: EXPANDING THE ORNSTEIN-UHLENBECK MODEL OF ADAPTIVE EVOLUTION

JEREMY M. BEAULIEU,^{1,2} DWUENG-CHUAN JHUWANG,^{3,4} CARL BOETTLIGER,⁵ AND BRIAN C. O'MEARA⁶
¹Department of Ecology and Evolutionary Biology, Yale University, P.O. Box 208106, New Haven, Connecticut 06520-8106
E-mail: jeremy.beaulieu@yale.edu
²National Institute for Mathematical and Biological Synthesis, 1534 White Ave, University of Tennessee, Knoxville, Tennessee, 37996-1527
³Department of Statistics, Feng-Chia University, Taichung, Taiwan 40724, R.O.C.
⁴Center for Population Biology, University of California, Davis, 1 Shields Avenue, Davis, California, 95616
⁵Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, Tennessee, 37996-1610

Received September 2, 2011
Accepted February 6, 2012

Comparative methods used to study patterns of evolutionary change in a continuous trait on a phylogeny range from Brownian motion processes to models where the trait is assumed to evolve according to an Ornstein–Uhlenbeck (OU) process. Although these models have proved useful in a variety of contexts, they still do not cover all the scenarios biologists want to examine. For models based on the OU process, model complexity is restricted in current implementations by assuming that the rate of stochastic motion and the strength of selection do not vary among selective regimes. Here, we expand the OU model of adaptive evolution to include models that variously relax the assumption of a constant rate and strength of selection. In its most general form, the methods described here can assign each selective regime a separate trait optimum, a rate of stochastic motion parameter, and a parameter for the strength of selection. We use simulations to show that our models can detect meaningful differences in the evolutionary process, especially with larger sample sizes. We also illustrate our method using an empirical example of genome size evolution within a large flowering plant clade.

KEY WORDS: Brownian motion, comparative method, continuous characters Hansen model, Ornstein–Uhlenbeck.

Single-rate Brownian motion works reasonably well as a model for evolution of traits. It models drift, drift-mutation balance, and even stabilizing selection toward a moving optimum (Hansen and Martins 1996). However, a single parameter model can certainly not explain the evolution of traits across all life. There have been extensions to the model, such as a single Ornstein–Uhlenbeck (OU) process that has a constant pull toward an optimum value, a multiple mean OU process with different possible means for different groups (Hansen 1997; Butler and King 2004), and multiple OU processes allowing different rates of evolution on different branches (O'Meara et al. 2006; Thomas et al. 2006). These models, while useful, still do not cover all the scenarios biologists want to examine. For example, existing models with a value toward which species are being pulled have a fixed

Chapter 15 Modelling Stabilizing Selection: The Attraction of Ornstein–Uhlenbeck Models

BRIAN C. O'MEARA AND JEREMY M. BEAULIEU

Abstract Ornstein–Uhlenbeck models are a generalization of Brownian motion models that allow trait values to evolve to follow optima. They have become broadly popular in evolutionary studies due to their ability to better fit empirical data as well as for the biological conclusions which can be drawn based on their parameter estimates, especially optimum trait values. We include a survey of available software implementing these models in phylogenetics as well as cautions regarding the use of this software.

15.1 Introduction

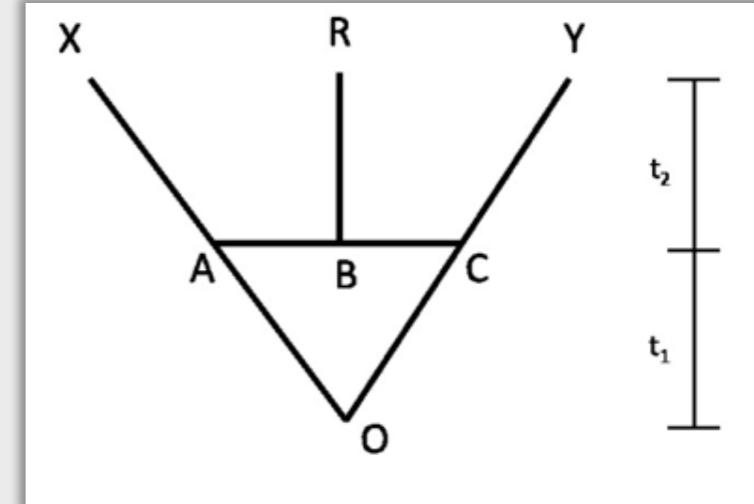
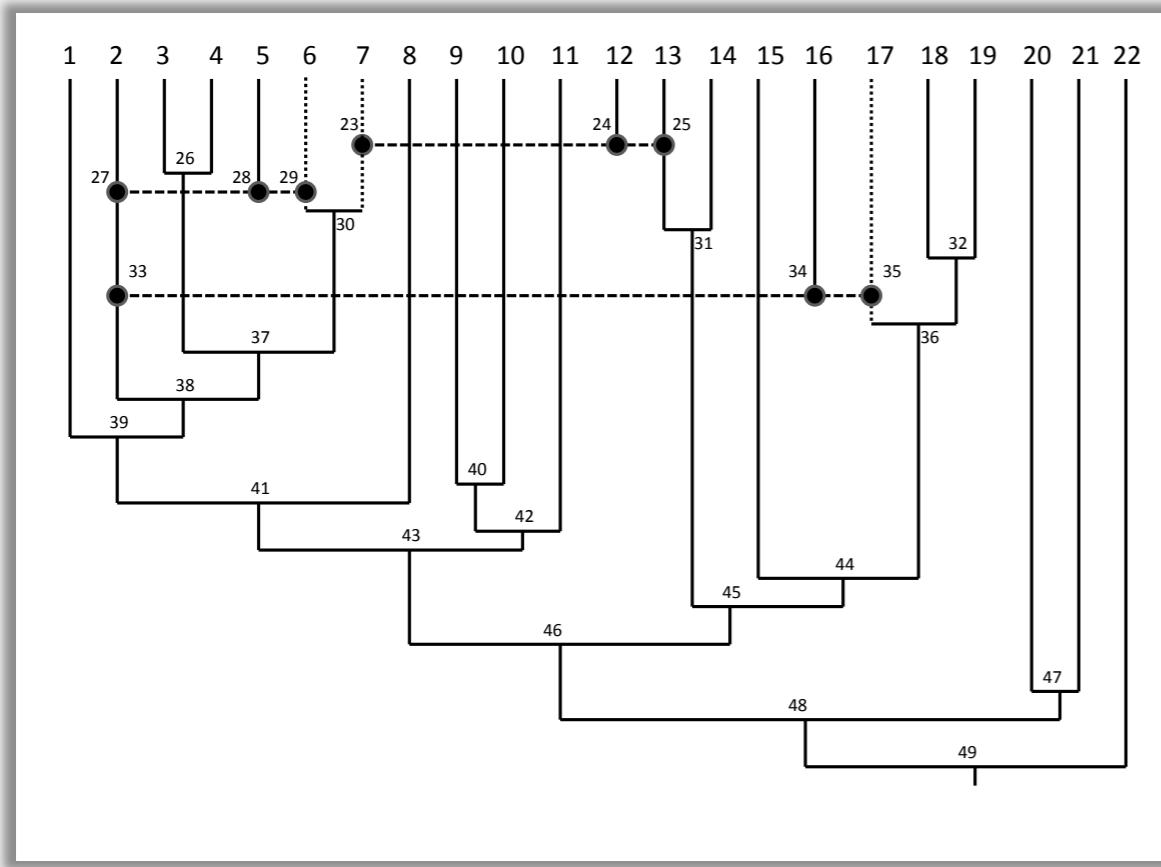
The mean value of a trait in a species is affected by multiple factors: physical constraints on evolution, lack of variation, change due to finite population size, and trade-offs between different optima. From one generation to the next, a trait value could change due to processes such as genetic drift, selection towards an optimum, or mutational pressure. If these movements are independent and identically distributed and have an additive effect through time, by the central limit theorem, evolution will fit a Brownian motion process (if the movements have a multiplicative effect through time, the log of the trait value will be evolving under Brownian motion). An Ornstein–Uhlenbeck (OU) process would better describe the process if these movements tended to be in the direction of a particular trait value (such that species with a trait value larger tend to evolve a smaller trait value).

B. C. O'Meara (✉)
Department of Ecology and Evolutionary Biology, Knoxville, TN, USA
e-mail: bomearn@utk.edu

J. M. Beaulieu
National Institute for Biological and Mathematical Synthesis, University of Tennessee,

Continuous trait evolution, ongoing

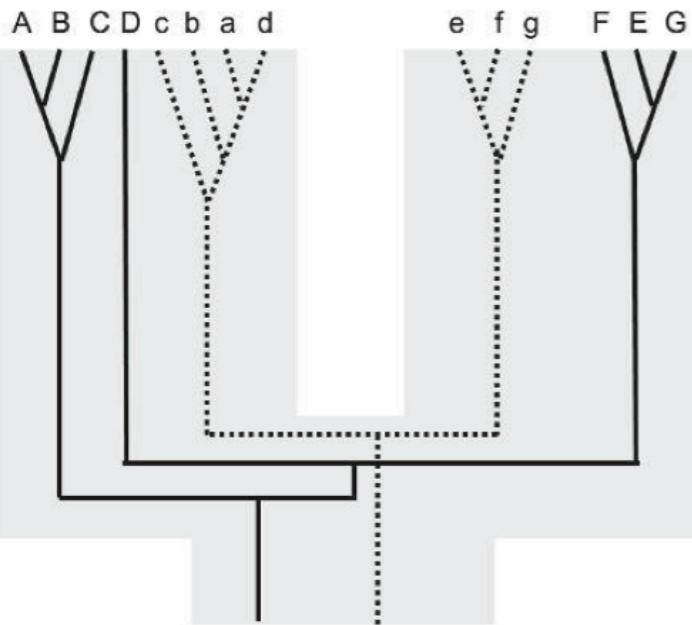
Brownian motion on phylogenetic networks, not trees



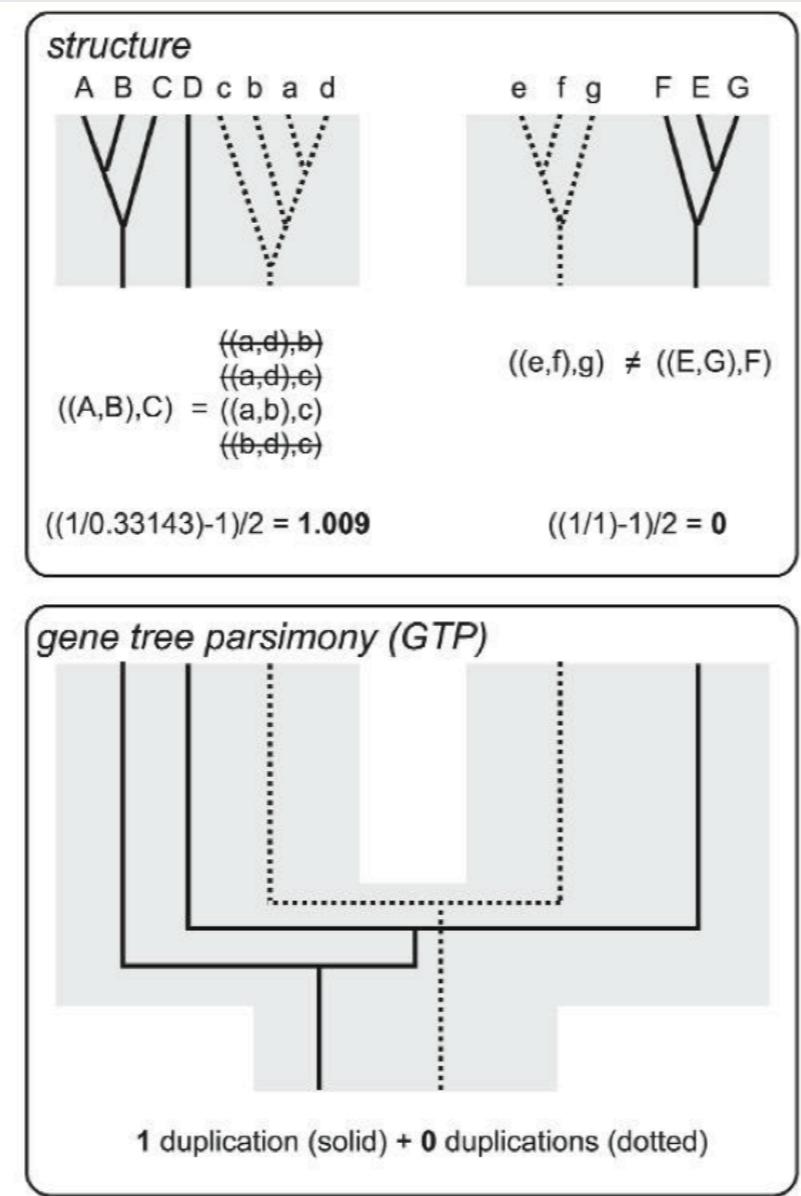
$$\mathbf{V}_R = \begin{bmatrix} X \\ R_1 \\ R_2 \\ Z \end{bmatrix} = \begin{bmatrix} 5\sigma^2 \\ 2\beta_1\sigma^2 \\ 0 \\ 0 \end{bmatrix} \quad \begin{bmatrix} Y \\ R_1 \\ R_2 \\ Z \end{bmatrix} = \begin{bmatrix} 0 \\ (3 + 4\beta_1^2)\sigma^2 + v_{1,H} \\ 2\beta_1\sigma^2 \\ 2\beta_1\beta_2\sigma^2 \end{bmatrix}$$
$$= \begin{bmatrix} 2\beta_1\sigma^2 \\ 2\beta_1\sigma^2 \\ 5\sigma^2 \\ 3\beta_2\sigma^2 \end{bmatrix} \quad \begin{bmatrix} R_2 \\ Z \end{bmatrix} = \begin{bmatrix} 0 \\ (2 + 5\beta_1^2)\sigma^2 + v_{2,H} \end{bmatrix}$$
$$= \begin{bmatrix} 2\beta_1\beta_2\sigma^2 \\ \sigma^2 \end{bmatrix} \quad \begin{bmatrix} Z \end{bmatrix} = \begin{bmatrix} 3\beta_2\sigma^2 \\ 5\sigma^2 \end{bmatrix}$$

Jhwueng & O'Meara, in revision

Species delimitation



$$\begin{aligned} \text{Total cost} &= (1-wt) \cdot \text{GTP cost} + wt \cdot \text{structure} \\ \text{Total cost} &= 0.5 \cdot (1 + 0) + 0.5 \cdot (1.009 + 0) \\ \text{Total cost} &= 1.0045 \end{aligned}$$



Syst. Biol. 59(1):59–73, 2010
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 DOI:10.1093/sysbio/syp077
 Advance Access publication on November 10, 2009

New Heuristic Methods for Joint Species Delimitation and Species Tree Inference

BRIAN C. O'MEARA*

*Department of Ecology & Evolutionary Biology, University of Tennessee, 569 Dabney Hall, Knoxville, TN 37996-1610, USA;
 Correspondence to be sent to: Department of Ecology & Evolutionary Biology, University of Tennessee, 569 Dabney Hall, Knoxville,
 TN 37996-1610, USA; E-mail:bomeara@utk.edu.

Received 14 February 2008; review returned 3 June 2008; accepted 21 September 2009

Associate Editor: L. Lacey Knowles

Abstract.—Species delimitation and species tree inference are difficult problems in cases of recent divergence, especially when different loci have different histories. This paper quantifies the difficulty of jointly finding the division of samples to species and estimating a species tree without constraining the possible assignments a priori. It introduces a parametric and a nonparametric method, including new heuristic search strategies, to do this delimitation and tree inference using individual gene trees as input. The new methods were evaluated using thousands of simulations and 4 empirical data sets. These analyses suggest that the new methods, especially the nonparametric one, may provide useful insights for systematists working at the species level with molecular data. However, they still often return incorrect results. [Brownie; gene tree parsimony; gene tree species tree; speciation; species delimitation.]

Two of the main goals of systematics are dividing the diversity of life into species and discovering the phylogenetic relationships of these species. Both can be difficult to achieve. Processes such as lineage sorting, introgression, and undetected gene duplication may cause gene trees to disagree with the true tree of species, potentially obscuring the species tree signal (Fitch 1970; Goodman et al. 1979; Avise 1983; Tajima 1983; Pamilo and Nei 1988; Doyle 1992; Hudson 1992; Maddison 1997). For species delimitation, a systematist must choose both a species concept and a criterion to apply this species concept to data. Even if speciation itself is effectively instantaneous, the time required for sufficient evolutionary changes to appear to allow 2 distinct lineages to be recognized will not be (De Queiroz 2007). This causes delimitation of species to be difficult.

These two questions are biologically linked but rarely methodologically coupled. If intervals between speciation events were long enough that all species were monophyletic for all their genes, once the species were correctly delimited, any species could be adequately represented by a single individual on a phylogeny. In reality, putatively independently evolving lineages are often not monophyletic (Funk and Omland 2003). The phylogeny of species, unless they are defined under a strict genealogical species concept (GSC; Baum and Shaw 1995; Hudson and Coyne 2002), will have an assortment of independent evolutionary lineages, which will probably include paraphyly for at least some of their genes. Here, I attempt to unite these two questions as the more general one of jointly inferring the species boundaries and the species tree. I calculate the computational complexity of the problem, develop and implement methods for addressing it, and perform simulations and analyses across hundreds of parameter combinations to evaluate the feasibility. I also analyse 4 empirical data sets, *Drosophila* (Machado et al. 2002; Machado and Hey 2003), *Manacus* (Passeriformes) (Brumfield et al. 2008), *Lactarius* fungi (Nuytinck and

Verbeek 2007), and *Melanoplus* grasshoppers (Carstens and Knowles 2007), to evaluate the performance of the new methods.

MATERIALS AND METHODS

Problem Definition

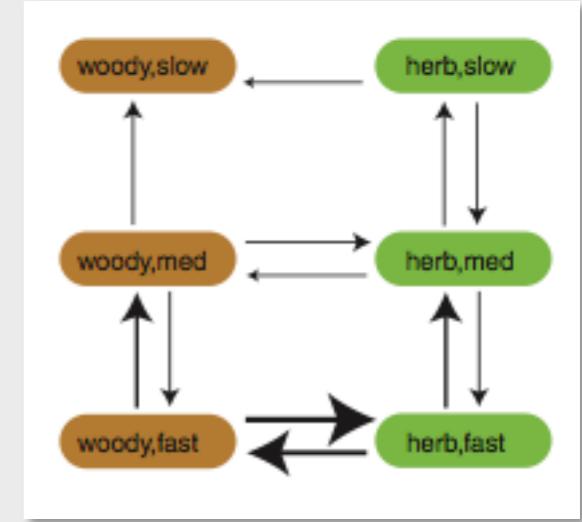
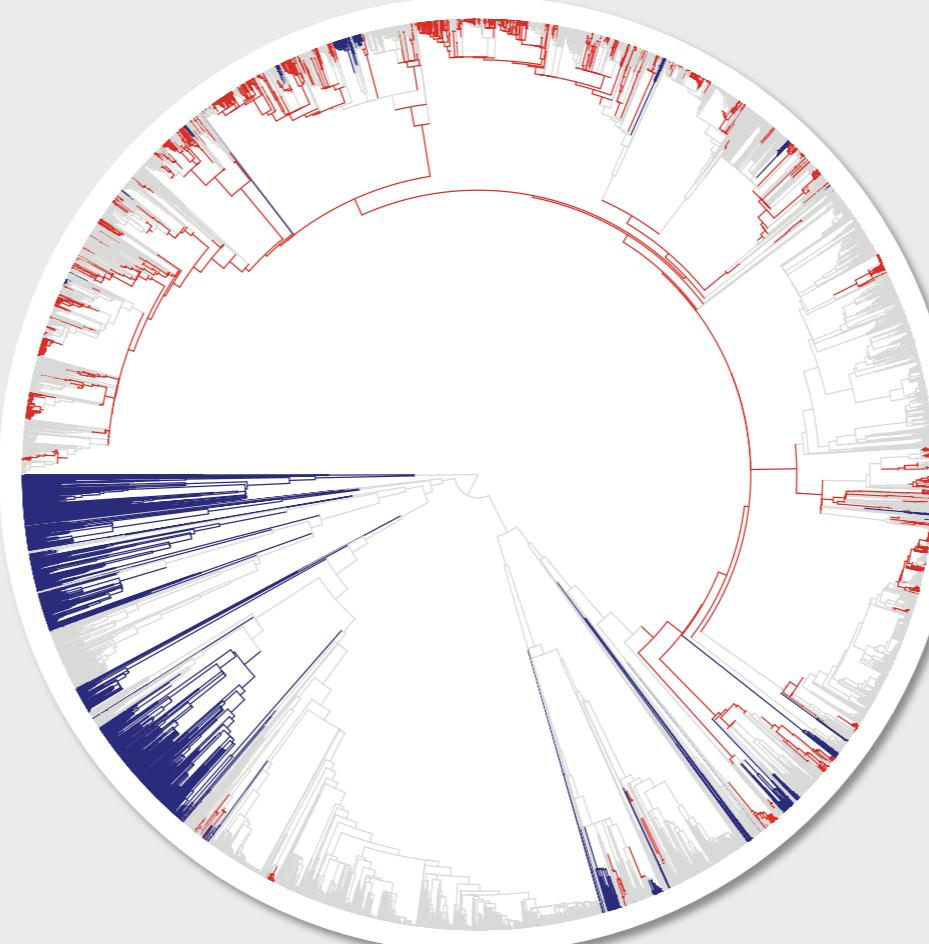
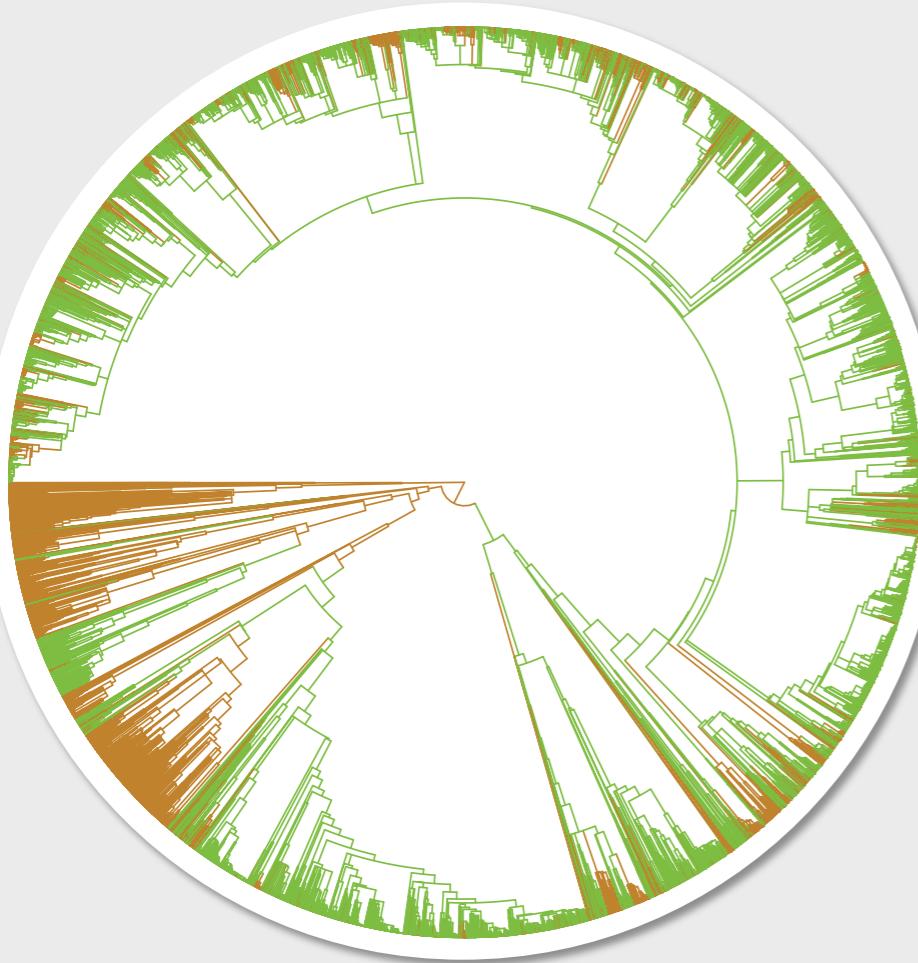
Given a set of sequences from multiple individuals, the general problem is to allocate those individuals into putative species and estimate the species tree. This solution, the species tree with assignment of samples to species, is termed the "delimited species tree." Optimally, a method will assign species and estimate the species tree correctly, in a statistically and computationally efficient manner. An estimate of the delimited species tree may differ from the true delimited species tree in topological error and/or through assignment of individuals to the wrong species. The latter might happen by merging 2 species that should be 1, splitting 1 true species into 2, having an individual of 1 species assigned to a different species, or a complex mixture of these. This is a more difficult problem than is typically addressed in DNA barcoding approaches (Hebert et al. 2003; Tautz et al. 2003), where 1 or more unknown individuals are assigned to existing species (Manel et al. 2005; Matz and Nielsen 2005; Abdo and Golding 2007; Zhang et al. 2008).

Most methods in systematics work on restrictions of this general problem, such as assuming that assignments to species are known (Nielsen and Wakeley 2001; Carstens and Knowles 2007; Edwards et al. 2007; Liu and Pearl 2007) or assuming that the gene tree matches the species tree (Hebert et al. 2003; Pons et al. 2006). I follow the approach of several recent authors (Pons et al. 2006; Carstens and Knowles 2007; Knowles and Carstens 2007; Mossel and Roch 2007; Kubatko et al. 2009), in restricting the problem using estimated gene trees as input rather than by integrating across a set of possible gene trees. The restricted problem still makes

59

Cited 135 times

Hidden rates



Chapter 16 Hidden Markov Models for Studying the Evolution of Binary Morphological Characters

Jeremy M. Beaulieu and Brian C. O'Meara

Abstract Biologists now have the capability of building large phylogenetic trees consisting of tens of thousands of species, from which important comparative questions can be addressed. However, to the extent that biologists have applied these large trees to comparative data, it is clear that current methods, such as those that deal with the evolution of binary morphological characters, make unrealistic assumptions about how these characters are modeled. As phylogenies increase both in size and scope, it is likely that the liability of a binary character will differ significantly among lineages. In this chapter, we describe how a new generalized model, which we refer to as the “hidden rates model” (HRM), can be used to identify different rates of evolution in a discrete binary character along different branches of a phylogeny. The HRM is part of a class of models that are more broadly known as Hidden Markov models because it presupposes that unobserved “hidden” rate classes underlie each observed state and that each rate class represents potentially different transition rates to and from these observed states. As we discuss, the recognition and accommodation of this heterogeneity can provide a robust picture of binary character evolution.

16.1 Introduction

Underlying many important discoveries in ecology, evolution, and behavior is the use of a phylogenetic tree. Phylogenies allow for the non-independence of taxa to be accounted for while also opening up new ways of examining how traits change

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

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Abstract—The growth of phylogenetic trees in scope and in size is promising from the standpoint of understanding a wide range of evolutionary and ecological questions. Of particular interest to large, older, and more widely distributed clades, it is likely that the liability of a binary character will differ significantly among lineages, which could lead to biases in estimating transition rates and the associated inference of ancestral states. Here we develop and implement a new method for identifying differences in rates of evolution in a discrete binary character along different branches of a phylogeny. We illustrate this approach by exploring the evolution of growth habit in the Campanulidae, a heretofore little-studied clade containing some 35,000 species. The distribution of woody versus herbaceous species calls into question the use of traditional models of binary character evolution. The recognition and accommodation of changes in the rate of growth form evolution in different lineages of the Campanulidae provides a robust picture of growth form evolution across a very large, very old, and very widespread flowering plant clade [Binary character; Campanulidae; comparative methods; flowering plants; growth habit; herbaceous; Hidden rates model; wood; woody].

With the availability of larger and larger phylogenetic trees comes the promise of evaluating more complicated models of evolution. Considerable attention has been focused on continuously varying characters, and it is now possible to apply comparative, phylogenetic methods for detecting differences on different branches of the tree in the processes associated with phenotypic evolution under Brownian motion (O'Meara 2006; Thomas et al. 2006) or the Ornstein-Uhlenbeck process (Butler and King 2004; Beaulieu et al. 2012a). In contrast, discrete binary characters, such as those that have been the focus of evolutionary studies, have received relatively little attention, and we are continually forced to rely on relatively simple models that apply the same rates of state change to all branches in a tree (but see O'Meara 2007).

Simple models of binary character evolution may make sense in some cases, but they are almost certainly not adequate to explain the evolution of such characters in larger, older, and globally distributed clades. In these instances one might expect the liability of a trait—the propensity to undergo state changes—to differ significantly among clades. In flowering plants,

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AJB CENTENNIAL REVIEW

REPEATED EVOLUTION OF TRICELLULAR (AND BICELLULAR) POLLEN¹

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Premise of study: Male gametophytes of seed plants are sexually immature when they are dispersed as pollen, but approximately 30% of flowering plants have tricellular pollen containing fully formed sperm at anthesis. The classic study of Brewbaker (1969) *American Journal of Botany* 54: 1062–1083 provided a powerful confirmation of the underlying hypothesis that tricellular pollen had more reproductive success than bicellular pollen.

Method: We developed our own and more recent analyses to greatly expand the Brewbaker data set. We modeled trait evolution for 2511 species to a time scale and inferred phylogeny using (1) Binary State Speciation and Extinction (BISSE), which accounts for the effect of species diversification rates on character transition rates and, (2) the hidden rates model (HRM), which incorporates variation in transition rates across a phylogeny.

Key results: Seven percent of species have tricellular pollen. BISSE found a 1.8-fold higher diversification rate than tricellular lineages. HRM found heterogeneity in evolutionary rates, with bidirectional transition rates in three of four rate classes.

Conclusion: The results of this study support the hypothesis that tricellular pollen has greater reproductive success because lower diversification rates of tricellular lineages are counterbalanced by slower state shifts to the bicellular condition. That tricellular lineages diversify slowly and give rise to bicellular lineages slowly reflects a linkage between the evolution of sporophyte lifecycles and the developmental liability of male gametophytes.

Key words: cell cycle; constraint; diversification rate; Dollo's law; evolution; development; panogenesis; heterochrony; pollen; pollen germination; trade-off.

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Empirical papers

Abercrombie et al. *EvoDevo* 2011, **2**:14
http://www.evodevojournal.com/content/2/1/14

 **EvoDevo**

RESEARCH

Open Access

Developmental evolution of flowering plant pollen tube cell walls: callose synthase (*CalS*) gene expression

Jason M Abercrombie*

doi:10.1111/j.1420-9101.2010.01971.x

Abstract

Background: A nucleic acid sequence analysis of the *CalS* gene family revealed that an early step involved in the evolution of flowering plants was the acquisition of distance transport capability in pollen tubes. The *CalS* gene family includes 12 genes, and orthologues are present in all major angiosperm clades.

Results: We investigated the developmental expression of *CalS* in gymnosperms and angiosperms and determined the next step in the evolution of flowering plants was the acquisition of distance transport capability in pollen tubes. The *CalS* gene family includes 12 genes, and orthologues are present in all major angiosperm clades.

Conclusion: The finding of *CalS* expression in pollen tubes supports the hypothesis that the evolution of the pollen tube system was driven by the need to deliver pollen grains to ovules. The finding of *CalS* expression in pollen tubes supports the hypothesis that the evolution of the pollen tube system was driven by the need to deliver pollen grains to ovules.

Background

The pollen tube is a key feature of seed plants. In conifers, it is a long-lived and functionally branched structure that grows in tissues [1-3]. In conifers, it is a long-lived and functionally branched structure that grows in tissues [1-3]. In conifers, it is a long-lived and functionally branched structure that grows in tissues [1-3]. In conifers, it is a long-lived and functionally branched structure that grows in tissues [1-3]. In conifers, it is a long-lived and functionally branched structure that grows in tissues [1-3].

Habitat use affects morphological diversification in dragon lizards

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LETTER

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Three keys to the radiation of angiosperms into freezing environments

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Early flowering plants are thought to have been woody species restricted to warm habitats¹⁻³. This lineage has since radiated into almost every climate, with manifold growth forms⁴. As angiosperms spread and climate changed, they evolved mechanisms to cope with episodic freezing. To explore the evolution of traits underpinning the ability to persist in freezing conditions, we assembled a large species-level database of growth habit (woody or herbaceous, 49,064 species), as well as leaf phenology (evergreen or deciduous), diameter of hydraulic conduits (that is, xylem vessels and tracheids) and climate occupancy (exposure to freezing). To model the evolution of species' traits and climate occupancy, we combined these data with an unparalleled detailed molecular phylogeny (32,223 species) for land plants. Here we show that woody clades successfully moved into freezing-prone environments by either possessing transport networks of small safe conduits⁵ and/or shutting down hydraulic function by dropping leaves during freezing. Herbaceous species largely avoided freezing periods by senescing cheaply constructed aboveground tissue. Growth habit has long been considered labile⁶, but we find that growth habit was less labile than climate occupancy. Additionally, freezing environments were largely filled by lineages that had already become herbs or, when remaining woody, already had small conduits (that is, the trait evolved before the climate occupancy). By contrast, most deciduous woody lineages had an evolutionary shift to seasonally shedding their leaves only after exposure to freezing (that is, the climate occupancy evolved before the trait). For angiosperms to inhabit novel cold environments they had to gain new structural and functional trait solutions; our results suggest that many of these solutions were probably acquired before their foray into the cold.

Flowering plants (angiosperms) today grow in a vast range of environmental conditions, with this breadth probably related to their diverse morphology and physiology⁷. However, early angiosperms are generally thought to have been woody and restricted to warm understory habitats¹⁻³. Debate continues about these assertions, in part because of the paucity of fossils and uncertainty in reconstructing habits for these first representatives⁸⁻¹¹. Nevertheless, greater mechanical strength of woody tissue would have made extended lifespans possible at a height necessary to compete for light^{12,13}. A major challenge resulting from increased stature is that hydraulic systems must deliver water at tension

to greater heights: as path lengths increase so too does resistance⁵. Among extant strategies, the most efficient method of water delivery is through large-diameter water-conducting conduits (that is, vessels and tracheids) within xylem¹⁴.

Early in angiosperm evolution they probably evolved larger conduits for water transport, especially compared with their gymnosperm cousins¹⁴. Although efficient in delivering water, these larger cells would have impeded angiosperm colonization of regions characterized by episodic freezing^{14,15}, as the propensity for freezing-induced embolisms (air bubbles produced during freeze/thaw events that block hydraulic pathways)

Figure 1 | Time-calibrated maximum-likelihood estimate of the molecular phylogeny for 31,749 species of seed plants. The four major angiosperm lineages discussed in the text are highlighted: Monocotyledoneae (green), Magnoliidae (blue), Superrosidae (brown) and Superasteridae (yellow). Non-seed plant outgroups (that is, bryophytes, lycophytes and monilophytes) were removed for the purposes of visualization.

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Scaling methods for large trees

BIOINFORMATICS APPLICATIONS NOTE

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Phylogenetics

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treePL: divergence time estimation using penalized likelihood for large phylogenies

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ABSTRACT

Summary: Ever larger phylogenies are being constructed due to the explosion of genetic data and development of high-performance phylogenetic reconstruction algorithms. However, most methods for calculating divergence times are limited to datasets that are orders of magnitude smaller than recently published large phylogenies. Here, we present an algorithm and implementation of a divergence time method using penalized likelihood that can handle datasets of thousands of taxa. We implement a method that combines the standard derivative-based optimization with a stochastic simulated annealing approach to overcome optimization challenges. We compare this approach with existing software including r8s, PATHd8 and BEAST.

Availability: Source code, example files, binaries and documentation for treePL are available at <https://github.com/blackrim/treePL>.

Contact: eebssmith@umich.edu

Supplementary information: Supplementary data are available at Bioinformatics online.

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1 INTRODUCTION

Divergence times make phylogenetic hypotheses easier to interpret in light of other information on geology, biogeography and co-diversification. A number of methods exist for transforming branch lengths to be proportional to time. However, many of these methods do not scale well for phylogenies with thousands of taxa. The number of species included in published phylogenies has exploded (Goloboff *et al.*, 2009; Smith *et al.*, 2009). With the increase in the size of phylogenies, there is the need to develop divergence time methods that are capable of handling larger datasets. Here, we present a method, implemented in the software treePL, for calculating divergence time estimates using penalized likelihood (Sanderson, 2002) on large phylogenies. Penalized likelihood uses a semi-parametric approach that allows for different rates on different branches but has a smoothing parameter, set using cross-validation, that affects how much rate differences over the tree are penalized. Our approach attempts to overcome the problem of local minima, a problem amplified by including more taxa.

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2 METHODS

2.1 Penalized likelihood

The optimality criterion used in this article is the penalized likelihood framework described in Sanderson (2002). Note that though this is framed as a likelihood method, it is possible to interpret this as a maximum *a posteriori* estimate in a Bayesian context given particular priors (Thorne and Kishino, 2005). It is also possible, following Sanderson's modifications to r8s, to use a related penalty that uses the differences of log rates rather than differences of untransformed rates (the additive penalty). This has been implemented in treePL, but analyses below use the original additive penalty.

2.2 The algorithm

Divergence time estimation, and penalized likelihood especially, presents a number of optimization challenges. One challenge is the large number of parameters and the ratio of free parameters to observations. This can be damped by a large penalty function, but still presents a parametric optimization problem. The second challenge is the presence of barriers placed by both the user and the hierarchical nature of phylogenies. We present a first step to overcoming these problems with extremely large phylogenies. Our algorithm includes two main phases: a greedy hill-climbing phase and a stochastic phase. This combination is meant to both speed optimization and avoid local optima.

The greedy phase of the optimization step consists of two gradient-based optimization rounds. The first round of optimization uses gradient values from an exact gradient calculator with math derived from Sanderson (2002). The second round of optimization uses auto-differentiation (Gay, 2005; Griewank *et al.*, 1996). Auto-differentiation, because it has the same complexity as the original function, often continues hill climbing after the exact gradient calculator fails. However, we have found, empirically, that alone it is not as efficient and requires more rounds and restarts than combining exact gradients and auto-differentiation.

We found that a stochastic phase, in this case a partial simulated annealing procedure, is helpful in easing the parameters away from local optima. We consider it partial as the step does not consist of a full simulated annealing run. Instead, the phase consists of thousands of stochastic optimization generations followed by intermittent greedy phases. Although this additional step may lengthen convergence time, the result will often improve.

The performance of optimization methods can vary dramatically by dataset. We have provided a 'priming' step that will run through each optimization option and report those that show the greatest difference in starting and stopping likelihood scores. Although this can help, researchers should replicate analyses and experiment with settings to assure convergence. We have also provided a 'wiggle' option that will report divergence times that are within two log likelihood units of the best likelihood, suggested by Edwards (1992) as a confidence window. This allows for the visualization of nodes that are particularly uncertain, but

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frontiers in
PLANT SCIENCE

REVIEW ARTICLE
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The iPlant collaborative: cyberinfrastructure for plant biology

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The iPlant Collaborative (iPlant) is a United States National Science Foundation (NSF) funded project that aims to create an innovative, comprehensive, and foundational cyberinfrastructure in support of plant biology research (PSCIC, 2006). iPlant is developing cyberinfrastructure that uniquely enables scientists throughout the diverse fields that comprise plant biology to address Grand Challenges in new ways, to stimulate and facilitate cross-disciplinary research, to promote biology and computer science research interactions, and to train the next generation of scientists on the use of cyberinfrastructure in research and education. Meeting humanity's projected demands for agricultural and forest products and the expectation that natural ecosystems be managed sustainably will require synergies from the application of information technologies. The iPlant cyberinfrastructure design is based on an unprecedented period of research community input, and leverages developments in high-performance computing, data storage, and cyberinfrastructure for the physical sciences. iPlant is an open-source project with application programming interfaces that allow the community to extend the infrastructure to meet its needs. iPlant is sponsoring community-driven workshops addressing specific

Realistic substitution models

Work with Mike Gilchrist and JJ Chai

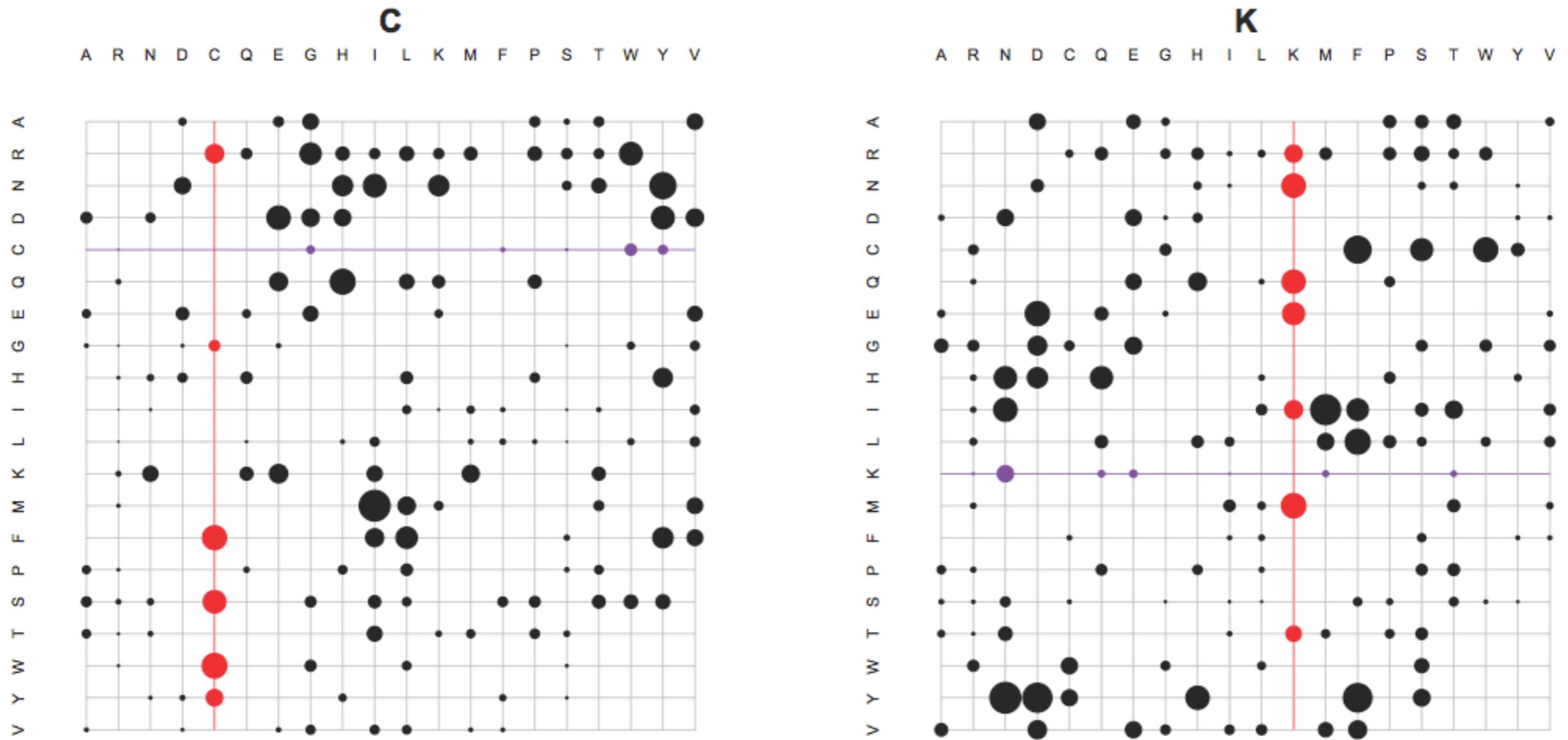


Figure 3: Instantaneous substitution rates from amino acid on row to amino acid in column under our preliminary model. The left panel is when cysteine is the optimal amino acid, the right is when lysine is the optimal amino acid. These are just two of the substitution matrices that are present in a given SAC_{AA} model. Bubble area (not diameter) shows the relative substitution rate from the amino acid listed on the left to the amino acid listed above. Red highlights the substitutions moving towards the optimal amino acid, purple those moving away from the optimal amino acid.

Large scale syntheses of the field

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Evolutionary Inferences from Phylogenies: A Review of Methods

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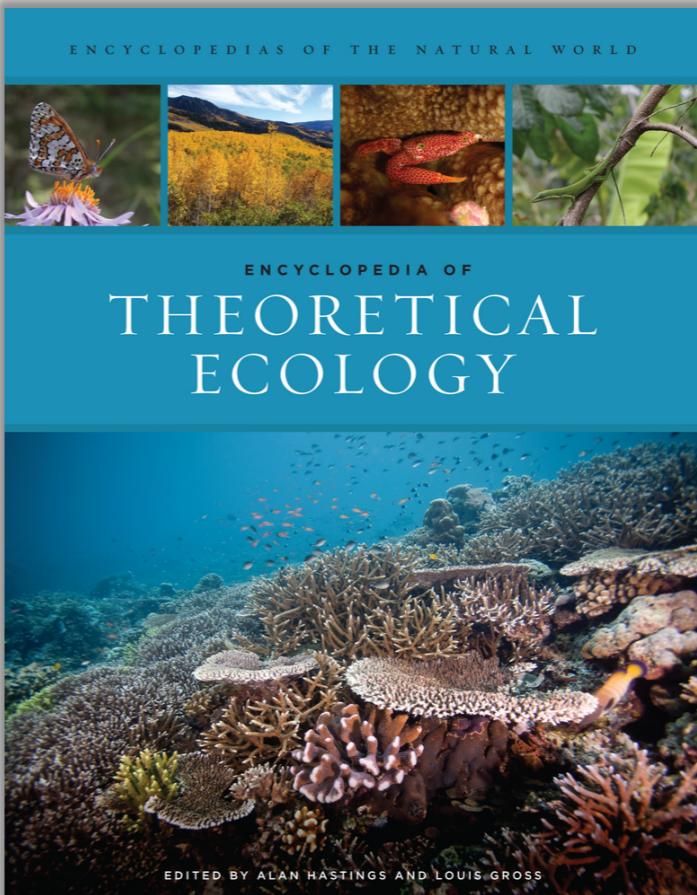
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Keywords

methods, continuous-time Markov Chain, multivariate normal, birth-death, tree stretching

Abstract

There are many methods for making evolutionary inferences from phylogenetic trees. Many of these can be divided into three main classes of models: continuous-time Markov chain models with finite state space (CTMC-FSS), multivariate normal models, and birth-death models. Numerous approaches are just restrictions of more general models to focus on particular questions or kinds of data. Methods can be further modified with the addition of tree-stretching algorithms. The recent realization of the effect of correlated trait evolution with diversification rates represents an important advance that is slowly revolutionizing the field. Increased attention to model adequacy may lead to future methodological improvements.



by adaptation in a fixed (nonplastic) genotype. Under this scenario, individuals having genetic variation for phenotypic plasticity will be favored. Whether the population will adapt by increasing its capacity for phenotypic plasticity ultimately depends on the costs and physiological limits associated with the plastic phenotype. Finally, it is worth noting that already in 1881 (in a letter to Karl Semper) Charles Darwin, clearly before his time, was able to envision the possibility of plastic phenotypes evolving in response to environmental changes: "I speculate whether a species very liable to repeated and great changes of conditions might not assume a fluctuating condition ready to be adapted to either condition."

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PHYLOGENETIC RECONSTRUCTION

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A phylogeny is a depiction of the evolutionary history of a set of organisms. Typically, this is a branching diagram showing relationships between species, but phylogenies can be drawn for individual genes, for populations, or for other entities.

WHAT DO PHYLOGENIES MEAN?

A phylogeny represents a history of populations. Take the example of Figure 1. Starting at the bottom (root) of the tree, one population splits into two. The population on the left speciates again, but one of the descendant species eventually goes extinct without leaving any descendants. Various other processes occur: population sizes (width of the tree's branches) vary, speciation happens through a gradual rather than instant reduction of gene flow, populations develop and lose subdivision, one species forms as a hybrid of two other species, a few genes introgress from one species to another, and so forth. The history of genes evolving within these populations may be even more complex, with selective sweeps, ancestral polymorphisms persisting across speciation events, gene copies being duplicated and lost within the genome, and recombination shuffling histories within and between genes. All of this complex history is typically summarized by a figure like that of Figure 1, with most of the complex history abstracted away to leave only a simplified history of populations.

It is important to interpret phylogenies correctly. Chimpanzees (*Pan troglodytes*) and bonobos (*Pan paniscus*)

Much more...

Stoltzfus et al. BMC Research Notes 2012, 5:574
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DATA NOTE

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Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis

Arlin Stoltzfus^{1*}, Brian O'Meara², Jamie Whitacre³, Ross Mounce⁴, Emily L Gillespie⁵, Sudhir Kumar⁶, Dan F Rosauer⁷ and Rutger A Vos⁸

Abstract

Background

phylogenetic trees and associated data from different sources are often published in separate papers.

Findings: We propose a system for sharing and reusing phylogenetic trees and associated data that will facilitate synthesis of phylogenetic trees and associated data from different sources.

Conclusion: Our system will facilitate synthesis of phylogenetic trees and associated data from different sources, and will help to improve the quality of phylogenetic trees and associated data used in synthesis.

Keyword

Findings

Re-use of phylogenetic trees and associated data may take many forms, including reuse of the tree topology, aggregation of multiple trees, and reuse of instances of the same tree topology in different research contexts.

The distinction between science and engineering is important in this context, as the reuse of phylogenetic trees and associated data in engineering contexts is often done without explicit acknowledgement of the original source.

DE GRUYTER

Stat. Appl. Genet. Mol. Biol. 2014; 13(4): 459–475

Dwueng-Chwuan Jhwueng, Snehalata Huzurbazar, Brian C. O'Meara and Liang Liu*

Investigating the performance of AIC in selecting phylogenetic models

Abstract: The popular likelihood-based model selection criterion, Akaike's Information Criterion (AIC), is a breakthrough mathematical result derived from information theory. AIC is an approximation to Kullback-Leibler (KL) divergence with the derivation relying on the assumption that the likelihood function has finite second derivatives. However, for phylogenetic estimation, given that tree space is discrete with respect to tree topology, the assumption of a continuous likelihood function with finite second derivatives is violated. In this paper, we investigate the relationship between the expected log likelihood of a candidate model, and the expected KL divergence in the context of phylogenetic tree estimation. We find that given the tree topology, AIC is an unbiased estimator of the expected KL divergence. However, when the tree topology is unknown, AIC tends to underestimate the expected KL divergence for phylogenetic models. Simulation results suggest that the degree of underestimation varies across phylogenetic models so that even for large sample sizes, the bias of AIC can result in selecting a wrong model. As the choice of phylogenetic models is essential for statistical phylogenetic inference, it is important to improve the accuracy of model selection criteria in the context of phylogenetics.

Keywords: AIC; Kullback-Leibler divergence; model selection; phylogenetics.

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1 Introduction

Probabilistic models are fundamental to statistical phylogenetic inference (Johnson and Omland, 2004; Sullivan and Joyce, 2005; Kelchner, 2009). A phylogenetic model assumes that the evolution of molecular sequences follows a substitution process along the branches of a phylogenetic tree. The random process of nucleotide substitutions over time is described probabilistically by a substitution model; over the years many such substitution models have been developed. The parameters in a phylogenetic model include the branch lengths and topology of the phylogenetic tree, as well as the parameters in the substitution model (Bos and Posada, 2005).

One of the major goals of phylogenetic model selection is to select a good substitution model for estimating phylogenetic trees from sequence data (Shapiro et al., 2006). Since statistical approaches for phylogenetic inference are based on particular models, model choice may significantly affect the resulting estimates of the phylogenetic parameters (Buckley and Cunningham, 2002; Posada and Buckley, 2004). Standard model selection criteria have been introduced for selecting phylogenetic models, but the biggest challenge in

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Ecology and Evolution

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Reol: R interface to the Encyclopedia of Life

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Keywords

Application programming interface, Encyclopedia of Life, programmatic access, reproducible research, taxonomy.

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Availability: *Reol* is a freely-available package with a GPL license. A stable version can be downloaded through the Comprehensive R Archive Network (<http://cran.r-project.org/web/packages/reol/index.html>) and the working repository can be found on R-Forge at <https://r-project.org/projects/reol/>.

Introduction

The Encyclopedia of Life (housed at www.eol.org) was created to preserve information developed in 2007 to host biodiversity data; however, it has expanded to include resources such as museum collections, scientists, and taxonomic rankings. It brings together scientists, educators, students,

and the general public. Page content comes in several media, common names, and is built from multiple sources. Partnerships that have agreed to contribute content (org/content_partners) and use hierarchical classification

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Abstract

The Encyclopedia of Life is a website that hosts information about life on Earth. Its mission is to increase awareness and understanding of living nature through a freely accessible digital source. Information is publicly available through graphical webpages (browser interface) or through an application programming interface (API). We developed *Reol*, an open-source package for the R environment, which downloads data from the EOL API, searches for and extracts specific information, and builds tables with quantitative data and/or hierarchical classifications. We provide a detailed description how *Reol* can be used as a bridge between the R environment and the EOL API to extract quantitative or hierarchical content. It will be particularly useful for researchers who want information about taxonomic groups of interest (for example, how much

value of a superset of those measurements is to be expected (as is briefly mentioned in the methods section of ref. 1).

To demonstrate this, we correlated the median values of \ln body mass from random sets of 3, 7, and 15 mammal species and 0–30 additional species for 45 simulated genera, using data from ref. 2 (Fig. 1A). Even when the median of 3 species is correlated with those 3 plus 15 additional species, the correlation is significant. Moreover, slightly better than random assignment of species to genera increases the expected correlation. To show this, we compare the results of figure 3A from ref. 1 with simulations where 45 genera of 3 species each were created from species chosen randomly from (i) the same family (Fig. 1B) and (ii) the same order (Fig. 1C) (data from refs. 2 and 3). Correlations between morphogenus median and the smallest clade containing the morphogenus species were significant ($P < 0.0001$). Thus, the observed correlations presented in ref. 1 are not surprising.

Second, ref. 1 also appears agnostic as to whether the morphogenera should be used together with a phylogeny when

Morphogenera, monophly, and macroevolution

Jablonski and Finarelli (1) suggest that morphogenera, even when they are nonmonophyletic, serve as good representatives for large-scale evolutionary studies. We feel there are two issues that warrant further discussion. First, the test used to evaluate the effect of using nonmonophyletic groups for macroevolutionary studies was not conservative and thus does not provide strong evidence about the impact of nonmonophyly on evolutionary studies. Their test examined whether the median trait value for the species in a nonmonophyletic genus correlated with the median trait value for those same species plus the additional species needed to make the set monophyletic. Correlation of the median value of a set of measurements with the median

Detailed description of Figure 1: Panel A is a scatter plot showing the p-value for correlation (Y-axis, 0.0 to 0.8) versus the number of random species added (X-axis, 0 to 30). The data points show a slight upward trend, indicating that the correlation becomes more significant as more species are added. Panel B is a scatter plot of Total Body Mass (Y-axis, 0 to 12) vs. Genus Body Mass (X-axis, 0 to 12) for 45 simulated genera. The data points form a strong positive linear trend. Panel C is a similar scatter plot for 45 simulated genera, showing a strong positive linear correlation. Panel D is a scatter plot of ln gestation (Y-axis, 0 to 12) vs. ln Body Mass (X-axis, 0 to 15) for all genera. It includes various regression lines: a dark solid line for $P = 0.05$, a thick black line for the smallest clade, a medium grey line for all mammals/species, and light grey lines for 95% confidence intervals. Grey dots represent species-level data, and black crosses represent generic-level data.

Fig. 1. Correlation analyses of morphogenera and comparative analysis of body mass and gestation. (A) Significance (Spearman correlation, as in ref. 1) of correlation of mean of \ln body mass of a set of X species with a set of $X + Y$ species (solid circles), 7 (triangles), or 15 (open circles) species, where the size of Z and Z' are the same, but the species differ. The dark solid line represents $P = 0.05$. For each point, 2,000 replicates, each with 45 randomly generated sets, were used. The masses came from ref. 2, pruned down to this set of species also in the tree of ref. 1. (B and C) Plots of \ln body mass 45 simulated morphogenera, as in figure 3A of ref. 1, where genera consist of 3 species chosen at random from within mammal families (B) or orders (C) (species chosen without replacement within genera but with replacement between genera, and genera simulated until 45 nonmonophyletic ones were recovered). The x-axis shows the median value for the morphogenus, the y-axis shows the median for the smallest clade containing all of the species (based on the tree of ref. 3). No distinction between polyphyletic or paraphyletic genera was attempted (open triangle used for both). Otherwise, plot and analysis as in figure 3A of ref. 1. (D) Generalized least-squares analyses of \ln gestation period against \ln body mass for all mammal species and genera. The thick black line shows the fit of these variables for all genera. The medium grey line shows the fit for all mammal species, and the light grey lines show the 95% confidence interval. The thick dashed line shows the fit for the genera without correcting for the phylogeny. Grey dots represent data using species-level values and black crosses represent generic-level data.

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