

Promotion

Ecology & Evolutionary Biology

Dr. Brian O'Meara

Fall 2018

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A. SUMMARY

Summary Sheet

Recommendations for Promotion and/or Tenure

Name of faculty member: Brian O'Meara

Present rank: Associate Professor

Department: Ecology and Evolutionary Biology Highest degree earned: Ph.D.

Original UTK rank: Assistant Professor Subsequent promotions (year, rank): _____

UTK RECORD

Date of original UTK appointment as a full-time probationary faculty member: 1 August 2009

Years of full-time teaching experience at instructor rank or above before UTK probationary period: 0

Years of full-time teaching at UTK, as of the May 31st prior to the review: 5

Total years of teaching: 5 Latest year for tenure review as stipulated in appointment letter: 2014-2015

RECOMMENDATIONS

DEPARTMENTAL FACULTY

Date of departmental discussion: _____

Result of discussion: For: _____ Against: 0 Abstain: 0

Recuse (attach explanation for conflict of interest): N/A

Is there a dissenting report? Yes (please attach) No

Is there a response from the candidate? Yes (please attach) No

INTERDISCIPLINARY COMMITTEE OR DIRECTOR (where appropriate)

For: _____ Against: _____ (Provide letter)

DEPARTMENT HEAD Recommend approval Do not recommend approval

Provide a statement on the professional record and a summary recommendation.

COLLEGE COMMITTEE

For: _____ Against: _____ Abstain: _____

Recuse (attach explanation for conflict of interest): _____

A copy of the report of the departmental and college committees must also be attached. In cases where this report disagrees in any substantial way with the departmental recommendation, this report must go beyond a listing of the vote to indicate as fully as possible the reasons for the differences.

DEAN Approve Disapprove (Provide letter)

CHIEF ACADEMIC OFFICER Approve Disapprove (Provide letter)

CHANCELLOR'S RECOMMENDATION TO THE PRESIDENT

Approve Disapprove (Provide letter)

Educational History and Employment History

Candidate Name: Brian Christopher O'Meara

Educational History

<u>Institution</u>	<u>Program or Degree</u>	<u>Dates in Program</u>	<u>Degree</u>
University of California, Davis	Ph.D.	2002-2008	Ph.D.
Harvard University	B.A. with magna cum laude and highest honors in biology	1997-2001	B.A.

Employment History

<u>Ranks Held</u>	<u>Institution</u>	<u>Department</u>	<u>Effective Date of Rank</u>
Associate Professor	University of Tennessee	Ecology and Evolution	2015-present
Assistant Professor	University of Tennessee	Ecology and Evolution	2009- 2015
Postdoc	NESCent		2008 – 2009

Department of Ecology and Evolutionary Biology

Statement of Responsibilities

Dr. Brian O'Meara

Guidelines for Meeting Expectations at Each Rank in EEB in annual review (approved Sept. 2018).

The department expects that all members of its faculty contribute with respect to research, teaching, and service. A clear record of accomplishment and potential in these areas is necessary for positive tenure and promotion actions. It is recognized that the level of contribution and achievement in each of these areas will differ among individuals, as it will with those faculty with administrative or other special appointments*. Accordingly, lower achievement in one area may be offset by excellence in the others. According to UTK policy, harassment of any kind, to any person, will not be tolerated and will be dealt with promptly by the university administration. See UTK policy for details: <https://titleix.utk.edu/university-policy-procedures/>. Reports or complaints of sex discrimination or prohibited conduct, or questions about the university's policies, procedures, resources, or programs concerning any of those issues, may be directed to the university's Title IX coordinator or one of the university's deputy Title IX coordinators. The following metrics of professional ability and accomplishment, not presented in rank order, will be among the key factors included in deliberations regarding annual retention review of tenure-track Assistant Professors, awarding of tenure and promotion to the rank of Associate Professor, promotion to the rank of Professor, and for annual and accumulative post-tenure reviews. Note that bulleted items are examples of indicators used to assess merit in each category, but they are not an exclusive list, nor must every item be achieved to indicate success in an area. Some faculty may have accomplishments normally associated with, and thus listed at, higher levels than their current ones; these may also be evidence for meeting expectations (for example, assistant faculty typically do not serve on university committees, and so this is not an expectation of them; however, if they do, it can be noted as evidence for service at their current level). For annual retention review, evaluation is based on the three-year reporting period. For appeals of decisions, or at the discretion of the Head or the faculty member being evaluated, additional faculty appointed by the Head can also evaluate the materials and participate in writing an evaluation report.

*(Faculty with appointments that differ from the standard tenure track position (e.g. TENN Herbarium Director, Director of Spatial Analysis Lab, Director of Mathematical Modeling Center, NIMBioS Director, Director of Biology Teaching and Learning), will discuss and create a written document of the expectations of their appointment and how they alter the expectations described in this document).

Assistant Professor:

Teaching:

- Evidence of development and successful teaching of course(s) in EEB and/or BIO
- Strong peer evaluations and positive comments from mentor/mentoring committee
- Evidence of graduate student mentoring as student progress in degree program and productivity, as assessed by the Graduate Affairs committee.
- Undergraduate student mentoring
- Student-generated evidence of quality of teaching (positive or improving SAIS scores or other measures)

Research:

- Evidence of research program development and scholarship through active application for grants. EEB acknowledges the current funding climate; excellent if grant is awarded. [Note: Use mentoring committee and colleagues for feedback on unsuccessful proposals and realize when to move on.]
- Publication of research results of PI, postdocs, and students from the lab in peer-reviewed journals
- Contributed presentation(s) at national and/or international meetings

Service:

- Participation in EEB-related committees as committee member
- Participation in public outreach initiatives
- Other service consistent with directorship duties

Other:

- Meet with mentoring committee each year

Associate Professor

Teaching:

- Positive to strong peer evaluations of teaching
- Possible development of specialty courses or seminars
- Evidence of graduate student mentoring measured as student's timely progress in degree program and their productivity
- Undergraduate student mentoring
- Student-generated evidence of quality of teaching (positive or improving SAIS scores or other measures)

Research:

- Evidence of scholarship through active application and receipt of external funding award(s)
- Sustained publications of research results of PI, postdocs and students in peer-reviewed journals across three-year period
- Regularly contributed presentations at national and/or international meetings
- Invitations to symposia at national and/or international meetings, departmental seminars

Service:

UTK –

- Evidence of successful leadership and outcomes, for example as chair of EEB standing committees, ad hoc, and/or search committees
- Service on College or University Committees

Professional –

- Refereeing or reviewing manuscripts and grant proposals for national and/or international agencies
- Service on federal agency or other grant panels
- Service on editorial board
- Development of public outreach initiatives

Full Professor

Teaching:

- Positive to strong peer evaluations of teaching
- Development of specialty courses or seminars
- Evidence of graduate student mentoring measured as student's timely progress in degree program and their productivity
- Undergraduate student mentoring
- Leadership on teaching initiatives/grant proposals in support of teaching
- Student-generated evidence of quality of teaching (positive or improving SAIS scores or other measures)

Research:

- Maintain external funding for research across three-year period including grants providing graduate student support (e.g. NSF NRT, DOE fellowships)
- Evidence of active application effort of diverse grant proposals (across multiple agencies or programs within a single agency) to support research (or teaching)
- Sustained publications of research results of PI, postdocs and students in peer-reviewed journals across three-year period
- Consistent presence of lab through contributed talks or posters at national and/or international meetings
- Invitations to symposia at national and/or international meetings, departmental seminars, working groups, task forces
- Organizer or co-leader of symposia, working groups, or task forces
- Leadership on initiatives/grant proposals in support of graduate program research and training

Service:

UTK –

- Evidence of successful leadership and outcomes as chair of EEB standing committees and/or search committees
- Service and/or Leadership on College or University Committees

Professional –

- Refereeing manuscripts and grant proposals for national and/or international agencies
- Service on grant panels
- Service on editorial board or service as editor-in-chief of peer-reviewed journals
- Offices and leadership positions held in scientific societies, service of boards of directors, advisory panels, etc.
- Service as scientific and/or educational advisor or evaluator of other universities or departments, local, national or international institutions, NGOs, government agencies, non-profits, etc.
- Public outreach and leadership in these initiatives

APPENDIX to the DEPARTMENTAL BYLAWS

Department of Ecology & Evolutionary Biology University of Tennessee, Knoxville

Criteria for Retention, Tenure, and Promotion

The department expects that all members of its faculty contribute with respect to research, teaching, and service. A clear record of accomplishments and potential in these areas is absolutely necessary for positive tenure and promotion actions. It is recognized that the level of contribution and achievement in each of these areas may not be equal. Accordingly, limited achievement in one area may be offset by excellence in the others. The following metrics of professional ability and accomplishment, not presented in rank order, will be among the key factors included in deliberations regarding annual retention review of tenure-track Assistant Professors, awarding of tenure and promotion to the rank of Associate Professor, promotion to the rank of Professor, and for annual and accumulative post-tenure reviews.

Metrics

Teaching ability and effectiveness

- compilations of student evaluations
- reports from peer teaching review committees
- comments by colleagues (including external reviewers) who have first-hand knowledge of the faculty member's teaching performance and/or communication skills
- written comments of students
- curriculum or pedagogical activities and accomplishments
- national and/or local teaching activities
- level of contribution to the teaching mission of the department

Research and Scholarly Activities

- level of external support (relative to peers in equivalent or similar scientific areas)
- significance of comments by professional peer reviewers
- national/international awards and recognition
- significance and number of publications in refereed journals, as well as contributions to scientific monographs and textbooks
- invited presentations at scientific meetings
- contributed presentations and involvement in contributed presentations
- invitations to organize symposia, prepare monographs, edit volumes, etc.
- local awards

Service

- participation in departmental Faculty Meetings
- participation in departmental, College, and University committee activities
- participation in professional outreach, including involvement with K-12 schools, regional industry, and community organizations
- contributions to national, regional, and local agencies
- membership and participation in professional organizations
- participation in meetings and symposia as organizer or chairperson
- reviewing and editorship efforts

Criteria by Academic Rank

I. Retention

A non-tenured Assistant Professor should:

- A. hold a doctorate in an appropriate field
- B. have an active research program with the goal of establishing a strong record of accomplishment involving the factors listed above by the time of consideration for tenure and promotion
- C. demonstrate a strong commitment to teaching and clear promise of excellence in classroom performance
- D. participate significantly in professional activities in the discipline beyond formal teaching and research

II. Tenure and Promotion to Rank of Associate Professor (and Expectations of an Associate Professor undergoing Annual or Cumulative Review)

An Assistant Professor applying for tenure and promotion to the rank of Associate Professor, or an Associate Professor undergoing annual or cumulative review, should:

- A. hold a doctorate in an appropriate field
- B. normally have served as an Assistant Professor for a minimum of four years
- C. have a strong internationally-recognized record of research and scholarly activity, as measured by the metrics listed above, with clear promise that promotion to Professor is likely at some point in the future
- D. successfully mentored M.S. and/or Ph.D. students
- E. show clear evidence of competent teaching
- F. have a reasonable and balanced record of contributions to meeting the service needs of the University, the discipline, and the community

III. Promotion to Rank of Professor (and Expectations of a Professor undergoing Annual or Cumulative Review)

An Associate Professor applying for promotion to the rank of Professor, or a Professor undergoing annual or cumulative review, should:

- A. hold a doctorate in an appropriate field
- B. normally have served as an Associate Professor for at least four years
- C. have acquired an international record of research and scholarly activity according to the factors listed above that is indicative of continuous and progressive professional development since appointment to the faculty of the University
- D. have successfully mentored Ph.D. students
- E. have achieved a demonstrated record as an conscientious and effective teacher in his/her field
- F. have contributed significantly and substantially in some combination to meeting the service responsibilities of the University, the discipline, and the community

COLLEGE CRITERIA FOR PROMOTION & TENURE

Recommendations for promotion and tenure by the College of Arts and Sciences shall be made in full accordance with established policies and procedures of the University of Tennessee, Knoxville, as outlined in Sections 2.13 and 2.14 of the September 1996 edition of the Faculty Handbook. College criteria for faculty promotion and tenure are varied and complex. They recognize that each faculty position has its own distinctive requirements and that the missions of academic units within the college are highly diverse. Moreover, advancement in academic rank and/or the award of tenure must be based on a faculty member's demonstrated proficiency in fulfilling his/her particular role and in contributing to the performance of the unit mission.

Beyond these specific considerations, the college expects all faculty members to make significant contributions in three general areas of academic life: (a) teaching and corollary activities; (b) research, scholarship, and creative accomplishment; and (c) service to the college, university, public, and profession. It is recognized that individual contributions may not be equal in these three areas. Accordingly, more limited achievement in one area may be offset by unusual excellence in the other two areas. Any such differentiation among the three dimensions of faculty participation must be consistent with the commitment of the University of Tennessee, Knoxville, to a distinctive research mission. Successful faculty members will share that commitment. A clear record of continuing accomplishment and potential in this area is, therefore, absolutely necessary for positive promotion and tenure consideration.

It is the view of the college that the excitement and inspiration of active research and creative accomplishment are essential to sustained enthusiasm for teaching and effectiveness in the classroom. Recognizing the critical importance of the teaching mission in higher education, the college seeks excellence of instruction not only as a goal but also as a demonstrated fact. Systematic documentation of teaching quality and effective results is expected of all faculty under consideration for promotion and/or tenure.

Finally, it is assumed that all members of the faculty will contribute to nonteaching service in their departments, the college and the university, as well as to their professions and the public. They will be expected to provide documentation of such service at the time of promotion and/or tenure consideration.

More specific criteria by academic rank may be summarized as follows:

Professor

1. Should hold the doctorate or other terminal degree in the discipline, or possess outstanding experience and expertise appropriate to the particular appointment;
2. should normally have served as an associate professor for at least five years;

3. should have acquired an established national professional reputation demonstrated through a record of research, scholarship, or creative accomplishment, indicative of continuous and progressive professional development since faculty appointment in the university;
4. should have achieved a demonstrated record as an accomplished teacher in his/her field; and
5. should have contributed significantly and substantially in some combination to meeting the needs of the University, the community, and the profession. Service expectations are greater for full professors than for individuals holding lesser ranks.

Associate Professor

1. Should hold the doctorate or other terminal degree in the discipline, or possess outstanding experience and expertise appropriate to the particular appointment;
2. should normally have served as an assistant professor for at least four years;
3. should have a strong record of research, scholarship, or creative accomplishment with clear promise that promotion to professor is likely at some point in the future. Appropriate evidence would be publication of a book-length manuscript or comparable contributions to the profession; and
4. should show evidence of excellence in teaching, including one or more evaluations by peer visitation of classes prior to consideration of promotion to associate professor.

Assistant Professor

1. Should hold the doctorate or other terminal degree in the discipline, or possess outstanding experience and expertise appropriate to the particular appointment;
2. should have established an active research/creative achievement program with the goal of publishing a book-length manuscript or equivalent research contributions, or making comparable contributions to creative achievement by the time of consideration for promotion and tenure;
3. should demonstrate strong interest in teaching and clear promise of classroom excellence in performance; and
4. should participate significantly in professional activity in the discipline beyond formal teaching and research.

(Revised Fall, 1996)

B. TEACHING ABILITY AND EFFECTIVENESS

Statement of Teaching Philosophy and Description of its Implementation

My overall teaching goal is to create students who have the skills of creative, skeptical scientists, curious about evolutionary processes, while being grounded with deep knowledge of biological patterns and mechanisms. This is accomplished through a mixed upper level undergraduate/introductory graduate student course in macroevolution, a graduate and advanced undergraduate course in phylogenetic methods, and various workshops.

My Macroevolution course (EEB464) explicitly targets four Biology degree-level learning outcomes (“Evolution: Populations of organisms and their cellular components have changed over time through both selective and non-selective evolutionary processes”, “Formulate empirically-testable hypotheses”, “Interpret visual representations (figures and diagrams)”, and “Evaluate data and come to a conclusion (with evidence) (formulate an argument)”). We cover everything from game theory to disease evolution to mass extinctions. My objective is to focus on what students will retain a year or more after taking the course. I will provide details (“Lynn Margulis was a champion for the endosymbiotic theory for origin of mitochondria”) but my main emphasis is on them understanding the process (“a bacterium was ingested by a cell and still hasn’t been digested yet – we call its still undigested descendants mitochondria”) as well as broader questions (“how might the undigested bacterium and the cell that partially ate it have different evolutionary optima?”, “how do scientists fight over hypotheses and decide to support one or the other?”). Classes are a mixture of discussion of students in groups, class-wide discussion, some student presentations, and slides from me to deliver basic facts and inspire discussion. Slides for each class are made freely available online before students arrive, and faculty at other universities have adopted these slides for their classes (last year’s class had 858 slides in total; the number varies by year as presentations are modified). I also include student-choice lectures, where the class brainstorms what topics in macroevolution they are most curious about and I then prepare classes on these. These have included evolutionary medicine, evolution of aggression in humans, dinosaur evolution, and more. Opening the class up this way lets students guide it towards topics they find most compelling while making sure they apply macroevolutionary thinking to these topics. Faculty at other universities have also used my materials for their classes.

My phylogenetic methods class targets graduate students and advanced undergraduates. It was developed as part of an NSF CAREER grant. It is designed to be radically open: all the videos and exercises are available online without registering, I am writing an open textbook that is freely downloadable, even the class chat discussion is open to anyone. The one closed aspect is that only UT students receive grades and course credit, though I plan to work with others at UT to allow online students to also receive credit once the course content is a bit more optimized. A total of 116 people have filled in the online registration form (from the US, UK, Mexico, Brazil, France, and many other countries) and thousands have used materials online without registering. The class is a flipped course where students watch short lectures and do readings outside of class and inside class we work through what was difficult in the background information and exercises. Later in the semester, students start working on projects of developing an approach themselves to answer a question. Sometimes this becomes a part of a student’s dissertation; more frequently, it remains as a class exercise only. In biology, graduate students often just use methods as black boxes without understanding the underlying assumptions; by developing their own methods, they realize the compromises one has to make and encourages more skepticism.

I also train graduate students and postdocs. Two students recently graduated with PhDs in biology as well as Masters degrees in statistics. Two additional are both on track to graduate this academic year. I have also trained nine postdocs in the interval under evaluation. An objective with all my trainees is to help them get into the positions they want, not assume a default, academic track for all. The two recent PhD graduates are working in business, as they wanted to be near family and have more stability than the academic track tends to allow, but the two current students both are actively seeking postdoc positions to continue in academia. I currently have three active postdocs; of the remaining 13 postdocs I have trained in total, eight are in tenure track faculty jobs, two are actively seeking such jobs, and the other three are working in research within private companies, typically health care. Among biologists, my lab's work is fairly rare in that, at least for the postdocs, the work is based on programming and using existing datasets, so there is no need to be in a particular place for access to equipment or specimens. Sometimes strong postdoctoral candidates have constraints limiting their location (such as a spouse who has a tenure track job elsewhere) and it is now possible for them to work remotely. I have reconfigured the lab to make this easier: for example, lab meetings are online for everyone, rather than have some of us in the room and everyone else sharing one screen. We have had online only lab members in France, West Virginia, and Texas and others who have taken shorter stretches of remote work in New York, Colorado, and California.

I also teach through workshops. Every summer in the evaluation period I have taught at the Evolutionary Quantitative Genetics Workshop, organized by Steve Arnold and Joe Felsenstein. There I spend several days teaching approximately two dozen students about macroevolutionary models. Conversations with students there have led to a postdoc application, students pursuing a study on hazards in the field for naturalists, and several publications. I have also taught at workshops focused on my software in Brazil, Louisiana, and Ohio.

Note that while there is substantial evidence of biases in student evaluations of teaching effectiveness based on perceived instructor background (Bosshardt and Watts 2001, Russ et al. 2002, MacNell et al. 2015, Boring 2017), given how I present to students it is likely that these biases artificially inflated my scores rather than harmed them.

References for this section

- Boring, A. 2017. Gender biases in student evaluations of teaching. *Journal of Public Economics* **145**:27-41.
- Bosshardt, W., and M. Watts. 2001. Comparing Student and Instructor Evaluations of Teaching. *The Journal of Economic Education* **32**:3-17.
- MacNell, L., A. Driscoll, and A. N. Hunt. 2015. What's in a name: Exposing gender bias in student ratings of teaching. *Innovative Higher Education* **40**:291-303.
- Russ, T., C. Simonds, and S. Hunt. 2002. Coming out in the classroom... An occupational hazard?: The influence of sexual orientation on teacher credibility and perceived student learning. *Communication education* **51**:311-324.

Summary of Teaching Assignments for Review Period

Semester/ Year	DEPT Course#	Course Title	Credit Hrs.	14-day Enroll.	% Responsibility	Lec(L) and/or Lab(B)	#GTA Assisting	Honors Y/N
Spring 2015	EEB607	HOFF lab meeting	1	8	25%	L	0	N
Fall 2015	EEB464	Macroevolution	3	26	100%	L	0	N
Fall 2015	EEB407	Senior Honors Thesis	1	1	100%	B	0	N
Fall 2015	EEB607	Seminar: Ecology/Evolutionary Biology	4	9	9%	L	0	N
Fall 2015	EEB593	Independent Study	3	1	100%	B	0	N
Fall 2015	EEB600	Doctoral Research/Dissertation	6	1	100%	B	0	N
Spring 2016	BIO150	Organismal/Ecological Biology	3	225	100%	L	1	N
Spring 2016	EEB600	Doctoral Research/Dissertation	6	3	100%	B	0	N
Spring 2016	EEB603	Adv Top: Evolutionary Biology	4	9	9%	B	0	N
Fall 2016	EEB464	Macroevolution	3	28	100%	L	0	N
Fall 2016	EEB595	Independent Study	3	1	100%	B	0	N
Fall 2016	EEB600	Doctoral Research/Dissertation	6	2	100%	B	0	N
Spring 2017	EEB593	Independent Study	3	1	100%	B	0	N
Spring 2017	EEB600	Doctoral Research/Dissertation	6	2	100%	B	0	N
Spring 2017	EEB504/ EEB603	Phylogenetic Methods	3	7	100%	L/B	0	N
Summer 2017	EEB600	Doctoral Research/Dissertation	6	1	100%	B	0	N
Fall 2017	EEB464	Macroevolution	3	26	100%	L	0	N
Fall 2017	EEB600	Doctoral Research/Dissertation	6	2	100%	B	0	N
Spring 2018	EEB504/ EEB603	Phylogenetic Methods	9	3	100%	L/B	0	N
Summer 2018	EEB600	Doctoral Research/Dissertation	6	2	100%	B	0	N

Teaching evaluation summaries

Details					SAIS scores (pre-Fall 2016)										Course Average	# of UG Advisees per Year	
Term	Year	Subject Code	Course #	Section #	# of Students	# of Responses	Response Rate	Q1	Q2	Q3	Q4						
Fall	2015	EEB	464		26	16	61.5%	4.4	4.3	4.4	4.4					4.4	1
Fall	2015	EEB	607		9	3	33.3%	3.7	4.0	4.0	3.3					3.8	1
Spring	2016	Bio	150		225	121	53.8%	2.1	2.5	2.2	1.7					2.1	1
					260	140	53.8%	3.4	3.6	3.5	3.1					3.4	
SAIS Core Evaluation Questions:																	
Q1 - The course as a whole was...																	
Q2 - The course content was...																	
Q3 - The instructor's contribution to the course was...																	
Q4 - The instructor's effectiveness in teaching the subject matter was...																	
Details					TNVoice scores (Fall 2016 - present)										Course Average	# of UG Advisees per Year	
Term	Year	Subject Code	Course #	Section #	# of Students	# of Responses	Response Rate	Q1	Q2	Q3	Q4	Q5	Q6	Q7			Q8
Fall	2016	EEB	464		28	13	46.4%	4.9	4.6	4.0	4.9	4.3	4.8	4.8	4.5	4.6	0
Spring	2017	EEB	603		5	3	60.0%	3.3	4.0	4.0	3.7	2.3	3.7	2.7	3.0	3.3	0
Fall	2018	EEB	464		36	10	27.8%	4.7	5.0	4.6	5.0	4.2	4.9	4.7	4.6	4.7	0
					69	26	37.7%	4.3	4.5	4.2	4.5	3.6	4.4	4.0	4.0	4.2	
TNVoice Core Evaluation Questions:																	
Q1 - The instructor contributed to your understanding of course content.																	
Q2 - The instructor created an atmosphere that invited you to seek additional help.																	
Q3 - The instructor responded to your inquiries about the course (e.g., emails, texts, phone calls) within a reasonable timeframe (i.e., 48-72 hours).																	
Q4 - The instructor created a respectful and positive learning environment.																	
Q5 - The instructor provided useful feedback on course assignments.																	
Q6 - The course challenged you to learn something new.																	
Q7 - The class sessions were well organized.																	
Q8 - The course materials (readings, homework, laboratories, etc.) enhanced your learning in this course.																	

Peer Review of Teaching

The first section is evaluation by three full professors in EEB of EEB 464 from Fall 2018. The second is an evaluation by a faculty member outside the EEB department in the context of an evaluation for the Chancellor's teaching award in Spring 2017 (which was awarded to a different faculty member that year).

Teaching Evaluation

Dr. Brian O'Meara

Macroevolution EEB 464

Observers: Drs. Sandy Echnacht, Ed Schilling, Jennifer Schweitzer

The observers sat in on two different classes. Both classes began with easy discussions between Dr. O'Meara and the students as everyone arrived (12 of 14 day one and 13 of 14 day two; several arriving late). Dr. O'Meara set the tone for the class by starting a cartoon-style video related to the class topic (Flight) two minutes before the scheduled class time. The first slide on both days was a slide with the day's objectives, followed by engaging video that set the tone for the topic of the day (Disease). The "lecture" was a loose collection of engaging slides, guided "pair and share", situations with voting and discussion, of which the majority of students took part. Students arrived at the class ready to work, having read the material in advance; they also had the slides available to them (either before class or immediately afterwards for review). The topics were presented thoughtfully, with good background and context and the students were

clearly used to working in groups to discuss specific questions and pool their collective knowledge of a topic. Dr. O'Meara skillfully led the discussion with respect for the students answers, thoughts and comments and provided interesting anecdotes to every question that provided great background and helped guide the discussion to the specific topic of that slide. For example, on day two Dr. O'Meara had to work a bit to get the discussion going but, once it got underway, it quickly involved all but one of the students. Dr. O'Meara was very good (and clever) in managing this. If there were no responses to a question he asked, he was silent for quite a while, until finally someone offered an answer. Gradually, more and more students got involved, some to the point of introducing new concepts. Once a student suggested an answer to a question Dr. O'Meara posed, he often followed up by asking the students how the hypothesis suggested by the first student could be tested. That led to further discussion. In one way or another, Dr. O'Meara would always lead the class toward discussing how the behavioral or morphological adaptations for flight evolved, using as a basis for the discussion the phylogenetic position of the taxa under discussion and on the process of natural selection. Overall, the active learning techniques employed throughout the class were excellent, engaging and the students clearly enjoyed the topics and the format of the course.

Evaluation of the syllabus clearly outlines expectations, learning objectives, specific scientific practices that the students are expected to perform and specific topics (and taxon) that are covered for each class period. Assessment of the course is based on a Topic Review, Paired presentation on a topic, in-class work (quizzes, activities and other in class assignments), two take-home Midterms and a Final Exam. The assessments require the students to demonstrate higher order thinking, writing and command of the topic. The expectations for each assignment are clearly spelled out with consequences detailed for when these expectations are not met. Dr. O'Meara requests teaching feedback with a specific anonymous site for students to provide him with feedback (all positive, we imagine). Dr. O'Meara posts all materials on Canvas during the course but also posts all materials on a public site such that students may refer to the slides/topic in other semesters and share with friends and family. Attendance is mandatory but we cannot imagine anyone wanting to miss the class.

When asked (without the instructor present), the students all responded positively to the course. They thought the material was challenging but interesting and they all thought Dr. O'Meara was knowledgeable, thoughtful and cared about their learning. The students found him to be approachable, respectful and flexible. One student said they all felt comfortable talking in class and thought the course was the best one they had taken at UTK; several stating that Dr. O'Meara was their "favorite teacher". When pressed, the only topic they thought could be improved was that he talks too fast (but always

repeats information when requested). This complaint was also raised during previous reviews of Dr. O'Meara's teaching and, while minor, it does detract some from learning and he should take care to pace his speech, especially when excited about a topic.

In summary, Dr. O'Meara uses a wide array of teaching techniques to engage students in meaningful discussion of the daily topics. The in-class work is thoughtful, challenging and allows students to come up with other thoughtful possibilities, and at least a couple of topics involved questions for which there is no accepted "correct" conclusion. This

approach allows students to frame their own hypotheses and compare them to ones proposed by scientists and provides a mechanism to help reinforce the way that scientists put together data to reach hypotheses and to design tests of them. The class covers exciting topics, Dr. O'Meara uses engaging slides and demonstrates skillful classroom management. The assignments and assessments are designed to encourage higher-order learning and to allow the students to develop and enhance their analytical and writing skills. Dr. O'Meara creates a respectful, thoughtful learning community that is engaging and fun.

We rank Dr. O'Meara's teaching as Excellent. He is an exceptional and dedicated teacher!

Following is the evaluation by Dr. Kent of teaching in my graduate level phylogenetic methods class

**Teaching Award Observation
Brian OMeara
PhyloMeth**

**Observation, January 26, 2017
Observer: Michael L. Kent
Public Relations & Advertising, CCI**

Overview of Course and Teaching

I had the pleasure of observing Professor O'Meara as part of his nomination for the 2017 Chancellor's Teaching Award. I found the class to be compelling and well run. I found O'Meara likable, friendly, and approachable. He clearly loves his subject matter and his passion was apparent to the students.

The course (Phylogenetic Methods) teaches about modern techniques for developing useful phylogenetic models, an activity that has gone on for hundreds of years but has become significantly more complicated given the ability to use databases of information, DNA, and modeling software. The graduate students in the class had projects that drew on the software (some in phylogenetics and some not), while the undergraduate students were learning the skills as part of their professional body of knowledge.

O'Meara arrived for class on time (early) and bantered with students for several minutes as he prepared for the class. Brian appeared to know all of the students by name, and had obviously talked with most or all of them before about their interests and extra curricular activities. O'Meara began the class by directing the students to some upcoming issues on the syllabus (projected on the screen) and an overview of upcoming class material.

I observed O'Meara's teaching for most of a three-hour class. I also communicated via e-mail with five of seven of Brian's students, including both undergraduate and graduate students, and was able to obtain detailed feedback about his personality, performance, and compassion (described below).

The course (Phylogenetic Methods) had seven students (five women and two men). The class contained both undergraduate and graduate students. Five of the students were graduate students and two were undergraduate. Some of the graduate students were far down the line and already

working on their theses, but were interested in learning about the course content. The course was also attended by a male professor from another area, who slipped into class late, but attended because he was interested in the subject matter, and another male graduate student who also arrived late. O'Meara handled the distractions and interruptions with aplomb, politely taking time to help both students and visitors get logged into the software packages that were needed to understand the course content.

The heterogeneity of the course is worth commenting on. The fact that undergraduate students, graduate students, and a professor were able to follow, understand, and appreciate the content of the lectures was worth noting. Additionally, I observed no students during the nearly three hours that I was there looking at their cell phones or using their computers to visit social media or other sites. The students all seemed to be engaged in the course content and skill building activities.

The structure of the class revolved around a discussion/lecture format, followed by actual use of several databases, software applications, and provided datasets, used for learning the software. During the class discussions, all of the students at some point participated in class discussion and were capable of explaining the lecture topics and weekly content. O'Meara's approach to lecture and discussion was very mainstream. Brian would ask the students to explain or clarify various concepts from the week's readings and videos, and followed by more questions asking students to go beyond the mere definitions and concepts and be able to explain how they applied in the datasets examined and what the implications were of the various theoretical approaches. O'Meara also used the whiteboard for occasional illustrations and notes.

During the discussion about the readings and videos, I observed O'Meara using some brilliant interaction/discussion techniques—one that I have since started to use—to get the students to be accountable for the material. At one point, O'Meara asked the class to define/explain a central concept. When no one would make eye contact and answer (something every teacher has experienced), Brian told the students to take a minute to talk to each other about it, and then asked them to answer the question. At another point, he directed them to talk among themselves, and then asked them to provide answers while also taking a position and justifying their answers. This technique shifted the burden of learning back to the students. Instead of the teacher being the font of knowledge, the students became accountable for the content themselves. The various discussion techniques also forced the students have to think more about their answers, rather than simply repeating a quote from the text.

During discussion, O'Meara also asked the students pointed questions about their individual research projects and interests in order to help make personalize the content for the students. Brian clearly was familiar with what they were individually working on, and was able to readily answer all student questions raised during the class discussions.

During the classroom software activities, O'Meara moved from student to student helping them with technical and theoretical issues and questions. Brian was genuinely knowledgeable about the software and clearly understood the challenges that the students faced.

In terms of course support, O'Meara has developed an extensive website of information and materials to accompany the course that includes links to scholarly readings, a video database hosted on YouTube, a bibliography linked to articles, a class discussion board, etc. One interesting feature of the site is a prominent link to a place where students can offer “Anonymous

feedback” on the course. I found this to be both pedagogically sound as well a tool likely to make students feel empowered.

Student Feedback

In general there were no negative comments by the students and all agreed that O'Meara deserved a teaching award. The students were asked to respond to seven questions, selected student comments are included below each.

1. How effective is the class structure/organization?

“I like that we focus more on in-class activities here, and we spend enough time in class on video/reading content to make sure it's clear. It's an interesting setup I haven't experienced before, but it's useful! . . . He's very good at driving discussions and handling questions (and answers!). Really knows what he's talking about.”

“Brian is one of the kindest, most encouraging professors I have had. So I think that makes it easier for students to ask questions or participate in discussions. In this class, he talks to students individually as problems arise while they are troubleshooting code or otherwise have questions, which is ideal.”

2. I see Brian is using a flipped approach with videos and texts and then in class activities, how is that approach working?

“I like that we focus more on in-class activities here, and we spend enough time in class on video/reading content to make sure it's clear. It's an interesting setup I haven't experienced before, but it's useful!”

“I like it; the videos are aimed at a basic understanding, which is helpful, as none of us knows everything being presented, and then we use the information in the videos and apply it to class.”

“I'm pretty sure that “flipped classroom” makes every undergrad cringe. Dr. O'Meara's approach is *so* refreshing because he's so attentive to the course structure (providing us with lots of learning materials and lots of exercise material for outside of class...”

3. How does the class work for you as an undergraduate or graduate student (respectively)? Is the class suitably rigorous for the graduate students, and sufficiently understandable for the undergraduates?

“This is a great class for me; I am a graduate student applying to postdoctoral programs right now. The project I have proposed exceeds my current skillset in this type of evolutionary biology, so everything I am learning right now is preparing me for my future research projects. It's scalable for graduates and undergraduates too, as he encourages us to choose projects relevant to us.”

“As a grad student, I joined hoping to gain more knowledge on phylogeny and methods used in this field. So far, it's met expectations—I'm learning about many aspects of it I hadn't even considered, and some of the assignments and readings have been tough, but they've been appropriate in terms of difficulty.”

"I specifically took this class because it pertains directly to the kind of research I am doing. I took Brian's Macroevolution 400-level undergraduate class before this, which sort of paved the way for the material covered in this class, so I don't feel like I am in over my head or anything."

4. *What would you say are his strengths as a teacher?*

"He is extremely good at encouraging students to participate in discussions...He never lets anyone feel bad about asking a question and will repeat material as needed to make sure students really grasp important core topics."

"Brian is incredibly passionate about evolutionary science and educating young students. His passion makes it very easy to listen to him lecture and he doesn't get discouraged when we do not understand what he is asking. He reassesses and asks again."

"His passion, most certainly. I am very familiar with him as an instructor (this is my fourth class with him) and he, more so than many professors, deeply cares about the material and about your level of understanding."

"Dr. O'Meara is great at making his field accessible to people outside of it."

5. *What are his weaknesses?*

"Sometimes he can move a little fast during class and can get caught up in the intricacies of his field, but he's really just so accessible that it doesn't matter. It's easy to get help if we're unclear on anything."

"He, like many professors do, takes on a lot of commitments, so at times it's tough to get him in a room to discuss things and at times, his critiques of your work aren't necessarily clear. However, he is more than willing to explain it to you again to make sure you understand."

"Occasionally talks a little too fast for me, but I can't think of another negative!"

"He has a tendency to talk quite fast and sometimes trip over his words, which can make understanding him a little difficult at times. It seems like his is making a conscious effort to improve this, though."

6. *Does he deserve an award (please briefly explain)?*

"Yes, I've been a student under some 40 different undergraduate teachers at a couple of different schools, and I will say that Brian is a great teacher who makes the classroom a more welcoming place than just about any other teacher I've had."

"Yes, absolutely. This is my second class (first was in Fall 2014) with Brian and he is on my dissertation committee. He has incredibly high expectations but never out of the realm of possible."

"I believe Brian O'Meara deserves an award..."

"Absolutely. He does so much to make learning easy for students. Especially considering his status in the field (he's kind of a big deal in the world of phylogenetics), it's amazing that he's as good of a teacher as he is."

“He does; in every class, from his introductory level courses to his graduate level courses receives his full attention. He has anonymous feedback forms so that you can address issues that come up during the class, and he takes his feedback seriously.”

7. *How is his teaching in relation to the other professors in your area?*

“I’ve had classes with about 6 other professors in EEB, 2 of whom were very good teachers (one being Brian). I think scientists often struggle to communicate material effectively to students, but in my experience Brian is able to communicate topics effectively while engaging students.”

“I do not have experience with other professors from the EEB department (I’m a graduate student in Microbiology), but he is definitely one of the better professors I’ve had so far in my time here at UTK.”

“His sincere dedication to all levels of teaching sets him apart from other professors.”

Minor Critique or Issue

I had no real concerns about the substance of the class or criticism about the lecture or materials. Some minor suggestions included the following:

- Typographically, the syllabus itself is difficult to read and follow. Some efforts to increase readability are in order.
- Brian talks quite quickly (something several of the students noted his speed as a weakness) and could perhaps slow down just a bit. I did not see this as a problem, but with international students a slower pace will make the content easier to follow.

Overall Assessment

I would recommend O'Meara for the teaching award without hesitation. Indeed, the students' responses to question six about whether he deserves a teaching award speak for themselves. Brian is teaching in a difficult area and is adapting to a diverse class of students very effectively. His lecture and course content is interesting and engaging and his supplementary materials are excellent.

Selection of Student Comments

Teaching style

EEB464, Fall 2017: Dr.O'Meara is one of the best professors I have ever had. He is very upbeat and keeps the class involved through creating an open dialogue style of teaching. The class allowed me to expand upon how I see the world by really digging deep into why things evolved the way they have on such an immense timescale.

Bio150, Spring 2016: I struggled greatly in this class. There was too much material to grasp in one unit to truly understand what was needed.

Bio150, Spring 2016: I liked how it was a flipped class, forcing me to do notes before there was a lecture on them

Assignments and exams

EEB464, Fall 2016: Only suggestion is possibly providing a better grading rubric for assignments.

Bio150, Spring 2016: [Q: What suggestions do you have] Grading at a faster pace.

Use of technology

EEB464, Fall 2015: Powerpoints being posted to the webpage was a help and the student involvement discussion wise was a great way to keep the class involved and asking questions.

EEB464, Fall 2016: Use of clickers is inconsistent and doesn't help anything

Student relations

EEB464, Fall 2016: He is very punctual and efficiently engages the audience. His style of teaching leaves room for discussion between students, which is very beneficial.

EEB464, Fall 2015: Dr. O'Meara made this course an awesome experience. He really encouraged students to ask questions and get involved with the material. His lecture style was very refreshing: very few words on slides, a lot of explanations of scientific figures, videos, etc. He kept the course exciting, lectured on recent and relevant topics, even gave lectures on topics selected by students. He also is genuinely interested in and excited about what he lectures about and is not afraid to show it.

Summary of Graduate Dissertation (Doctoral) Supervision

List students who have completed work and whose work is in progress

Student	Grad. Year	Fellowships / Awards	Dissertation Title	Placement
Katie Massana	2017	Outstanding progress by graduate student	Using Phylogenetic Comparative Methods To Understand Diversification and Geographic Range Evolution	IQVIA (Human Data Science)
Jennifer Bosco (note: coadvised with Susan Riechert)	2017		Trait Evolution in Spiders: Perspectives on the Evolution of Behavioral Syndromes and Web Structures	Pratt & Whitney

Sam Borstein	2019 (estimated)	NSF DDIG	In progress	
Orlando Schwery	2019 (estimated)			

Summary of Graduate Dissertation (Masters) Supervision

None

Summary of Undergraduate Research/Thesis Supervision

*Include in this table supervision of "honors by contact" by giving the course number or N/A

Name	Thesis/ Research Project Title	Honors Thesis Option Yes/No	Placement (if applicable)	Year(s) Supervised
Christian Yarber	Evolution of salamander neoteny	Y	Washington State U Graduate program	2015

Note that this student also received the undergraduate outstanding research and undergraduate outstanding poster award from the EEB department for his work in my lab.

Membership on Graduate Committees

Name	Dept.	Degree	Project Title if appropriate; if exam option, so note	Date Completed
Jen Bauer	EPS	PhD	Blastoid evolution	05/2018
Sharon Clemmensen	EEB	PhD	Morphological and Gene Expression Plasticity in Neotropical Cichlid Fishes	12/2017
Aaron Floden	EEB	PhD	Molecular phylogenetic studies of the genera of tribe Polygonateae (Asparagaceae: Nolinoideae): Disporopsis, Heteropolygonatum, and Polygonatum.	05/2017
Nicholas Gladstone	EPS	Masters	In progress	
Alannie-Grace Grant	EEB	PhD	In progress	
Cedric Landerer	EEB	PhD	In progress	
Jasper Lee	Microbio.	PhD	Withdrew	
Bryan Looney	EEB	PhD	Systematics, diversification, and functional diversity of Russulaceae (Russulales)	05/2017
Liam Mueller	EEB	PhD	In progress	
Tyson Paulson	EEB	PhD	In progress	
Todd Pierson	EEB	PhD	In progress	
Ryan Rooney	EPS	PhD	Withdrew	
Sarah Sheffield	EPS	PhD	The Homology and Phylogeny of the Diploporita (Blastozoa: Echinodermata)	05/2017
Rachel Wooliver	EEB	PhD	Ecology and evolution of plant nitrogen limitation	05/2018
John Reese	EEB	PhD	In progress	
Sarah Lipshutz	EEB	PhD	Behavioral mechanisms of reproductive isolation	05/2018
Jessica Welch	EEB	PhD	Conservation Biology of Bats: Invasive Threats, Research Effort, and Extinction Risk	05/2017
Marisol Sanchez-Garcia	EEB	PhD	Systematics, diversity and evolution of the suborder Tricholomatineae (Agaricales)	05/2016
Qidong Jia	GST	PhD	Computational Identification of Terpene Synthase Genes and Their Evolutionary Analysis	05/2016

Whittaker Hoskins	EEB	Masters	Using phylogenetics to understand the evolutionary relationships of <i>Hibiscusseccion Furcaria</i>	05/2016
Jeremy Blaschke	EPP	PhD	Evolution and Phylogeny of the Parasitoid Subfamily Phasiinae (Diptera: Tachinidae)	08/2015

Summary of Post-doctoral Supervision

Name of Individual Supervised	Year(s) Supervised
David Bapst	2017-present
Jeremy Beaulieu	2012-2016
Dominic Evangelista	2018
Nathan Jackson	2013-2016
Sandy Kawano	2014-2016
Megan Rua	2015-2016
Luna Sanchez Reyes	2017-present
Sergey Tarasov	2016-2018
Jodie Wiggins	2016-present

**C. RESEARCH,
SCHOLARSHIP,
CREATIVE ACTIVITY**

Candidate's Statement Non-Technical

Candidate's Non-technical research/scholarship/creative activity summary. This summary (one-page maximum) should be written in non-technical (jargon-free) language describing the candidate's scholarly program and its significance. This summary is intended for non-disciplinary audiences including the College's Deans, its Promotion & Tenure Committee, and the UTK Central Administration.

Horses, bats, alligators, and birds all have four limbs not because four is the best number for locomotion (spiders, starfish, trout, centipedes, and moths do just fine), but because they have inherited this number from their ancestor and evolution has since molded them into forms able to compete and survive. One ancestral species eventually led to a wide variety of vertebrates, each evolved into its current form due to a mixture of processes. Understanding this history lets us investigate the processes that led to what we see today (i.e., selection for running resulted in horses evolving longer legs with fewer toes) as well as understand what leads to speciation (the splitting of one species into two) and extinction. I develop tools to help understand how species are related to each other, what their history has been, why and how they change, what affects how many species survive, and what leads to their extinction. I also develop approaches to understand how individuals move between populations and whether populations are different enough to be different species. I use these approaches to examine key questions in biology, ranging from evolution of flowers to behavioral evolution in primates.

The impact of this work is twofold. One aspect comes from answering questions directly myself and with collaborators. For example, a major question in biology is what has led to the diversity of flowering plants we see today. Grasses, dogwoods, magnolias, tomatoes, and soybeans all are flowering plants. One hypothesis has been that it is the flower itself that led to this diversity, but we found, using new methods, that diversity largely came from a combination of floral traits that took millions of years to finally assemble, and that the effect of these traits is likely still playing out in the world.

The other impact comes from writing methods and software that scientists and the broader public can use. The software I write is all free to use (though its development was funded by millions of dollars in grants to the University of Tennessee, Knoxville) and open so that others can inspect how it works and improve on it. Hundreds of scientists around the world use the tools I create here to help understand biological questions for other organisms. One important set of tools I helped develop and test recently allow biologists to figure out groups of organisms in different areas interact: do they exchange genes, and if rarely or not at all, are they distinct enough to be different species? This can be a key question to address for conservation, and we found that our approach could both lead to new discoveries (unexpected connections between populations, for example) and also led to less "oversplitting" into different species than earlier approaches. Other biologists can now use these tools on their own systems to help evaluate how landscapes connect and whether populations are evolutionary distinct enough to warrant protection as different groups.

Candidate's statement on research/scholarship/creative activity. This statement (no page limit) should describe activity as clearly as possible and is primarily intended for external reviewers and internal disciplinary audiences. Be sure to discuss work in all stages, as follows:

Work completed during review period

Work in-progress (indicate current state of work)

Plans for future work

My research addresses key questions in macroevolution for understanding the processes leading to present diversity and disparity across life. I do this through development of new approaches and the implementation of open access software, and applying these techniques to compelling biological questions. Particular areas of focus include factors affecting diversification rates, including the effect of traits interacting, including unsampled traits. I also work at the phylogeographic scale, where the distinction between populations and species becomes uncertain but important for conservation. A common theme is on methods that allow discovery. An increasingly frequent approach in evolutionary biology is to compare a model that has an effect someone hypothesizes exists (say, that a pre-specified trait increases speciation rate) with a simpler, uninteresting model (i.e., that the speciation rate is constant through all time), find that the more complex model fits better, and conclude that one's hypothesis is justified. Biologists are generally clever and know their study systems well: it is likely that the hypothesis they are testing is correct, and it is just a matter of having power to reject a null model to find a significant result. More problematically, this prevents surprise and actual learning. I have seen some of my earlier work, which has methods that allow estimation of rates of evolution, long term evolutionary optima, and other biologically relevant parameters, often be used in dull hypothesis rejection in this way: are two different groups of organisms (different trophic levels, different life styles, etc.) evolving at *exactly* the same rate, for example. Darwin's great insight was that variation exists all through life: we know that two different groups are not going to be exactly equal for almost anything, so testing for the presence of difference, while framed as hypothesis testing and rejecting of nulls, does not really tell us much about biology. In my post-tenure work, I have pursued projects that push the field into estimating the magnitude of parameters, which can reveal much more about the underlying evolutionary processes, as well as methods that generate new ideas not just lower p-values.

Work completed

In this period, I have been funded from four contemporaneous NSF grants (three awarded before my tenure packet went in, one awarded during the year in which tenure was being evaluated and so eligible for assessment during promotion) as well as a new subaward from a collaborator. One area of research was the PHRAPL project, a collaboration between my lab and that of Bryan Carstens to develop tools to examine phylogeographic hypotheses. This involves the study of how populations (of the same or different species) have evolved geographically through time, ideally including factors such as gene flow between populations, changing population sizes, and varying connections between regions. Popular approaches typically compare or estimate parameters from a handful of pre-specified hypotheses about relationships or make various assumptions (such as no gene flow, constant population size, or no merging of populations back in time). We adopted an approximate likelihood approach to estimate the likelihood (probability of the data given the hypothesis) by simulating many times and assessing the match between

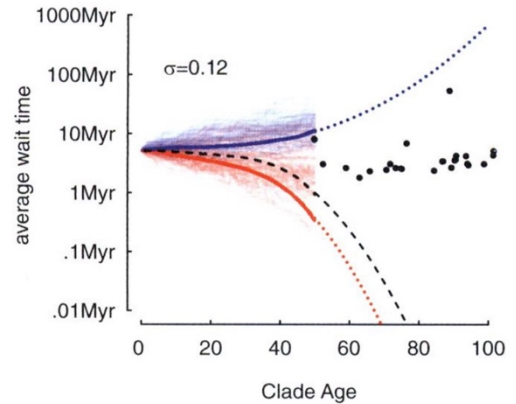
simulated gene topologies and the ones we observed (this is similar to approximate Bayesian computation, often referred to as ABC, but with no prior attached and with the frequency that a topology matches is used as a proxy for the likelihood). Our software generates a wide variety of possible relationships between populations: gene flows of different magnitude, different connections between populations, different histories of populations merging, different population sizes, and so forth. Thus, rather than having to decide between approaches that fit a classic island model (stable populations that exchange migrants) and approaches that fit a classic phylogenetic model (populations do not exchange migrants, but merge further back in the past), our approach allows both of these models, and intermediates between them, to all be compared in the same model selection framework. A key advantage is that it allows for new discoveries: by sampling across more possibilities than a biologist's treasured handful, this model may return an unexpected result (e.g., an unforeseen barrier to reproduction, more recent merging of populations than was expected, a large ancestral population size, etc.). This work was extended for use in species delimitation. The point at which populations are distinct enough (with lack of interbreeding or other factors) to be considered different species is necessarily fuzzy, but there is utility in saying, "population A is evolving independently from population B: individuals will not move between them and successfully interbreed." Our software helps taxonomists assess whether this statement is true, while incorporating relevant factors like potential gene flow or histories of populations splitting.

I have also worked on understanding how traits evolve and affect diversification. O'Meara, Smith et al. (2016) resulted from an eight-year collaboration with a working group originally started at the National Evolutionary Synthesis Center. With the rise of methods like BiSSE or MuSSE for correlating diversification with discrete traits, there has been a burst of analyses examining how single traits affect speciation or extinction. Our work looked at six traits at once by splitting them into subset of focal combinations versus all others. This allows the models to "spend" parameters on fitting which traits have the greatest effect and finding if a particular combination matters more. We found that getting the trait combination of bilateral symmetry, few stamens, and having showy petals (like an orchid) led to high diversification rates. However, I think a more important aspect of our work was our investigation of the process over the long term. We often implicitly assume life is at equilibrium and our models operate under this belief (for example, this is a default, though adjustable, assumption at the root of a tree in many SSE models). In contrast, we examined the time it took to evolve traits and found that it would have taken tens of millions of years for the relevant traits to evolve, and also that flowers are not yet at equilibrium: if current processes continue, the floral world will look very different 10 million years from now.

A related trend in my work has been investigation of diversification models, much of which is in collaboration with my former postdoc (now an assistant professor) Jeremy Beaulieu. It has long been known that extinction rates are difficult to estimate from molecular data alone, but we showed that it is not as hard as people had feared (Beaulieu & O'Meara, 2015). Part of this comes from something I have been trying to emphasize in my work, but which is still surprisingly unusual in my subfield, especially in modeling papers, namely, looking at the biological realism of parameters (Figure 1). It is easy to show models work well by

Figure 1: Trajectory of wait times between speciation events within a lineage under an evolving speciation rate model; black dots represent averages in very diverse plant clades, showing that the simulated range easily includes extreme examples. (Beaulieu & O'Meara, 2015)

limiting to a part of parameter space where this is true, or conversely to show models fail by using extreme parameter values. A key question for a biologist, however, is how a method works in biologically relevant parts of parameter space. The notion that extinction rates cannot be estimated was based on a paper that used a rapidly accelerating rate of speciation, but we showed that when the model was implemented correctly, and limited to extreme but still biologically feasible parameters, extinction rate could be estimated.



A major advance we have made was the use of hidden models in diversification (Beaulieu and O'Meara 2016, O'Meara and Beaulieu 2016), following on earlier work on hidden models for traits only (Beaulieu, O'Meara, and Donoghue, 2013). A common trend in biology has been to compare an interesting model to a null model, find the interesting model fits the data better, and conclude that this model reflects reality. However, one major problem is that reality is complex: when data are presented with a simple model or one with more variation, a more complex model can fit better, even though the process it models does not match the actual source of the heterogeneity. This was most vividly illustrated in a paper by Rabosky and Goldberg (2015), where they showed that on an empirical whale tree (so, likely one with varying speciation and extinction rates), but traits simulated with no effect on diversification, a model for evaluating the effect of a binary trait on diversification (BiSSE) found that a trait-dependent model fit better than a model with no trait dependence. This would be typically seen in the field as Type I error: incorrect rejection of the null. It *is* an error, but a subtler one: BiSSE is forced to choose between a model that assumes an exactly constant speciation and extinction rate for all time (which is certainly not true for whales) or a model that allows up to two different rates for each, but incorrectly links these to a single observed trait. Neither model is true, but the more complex one allows for changes in rate, and so often fits the real data (in this case, the tree plus the trait) better. One of the benefits of our model is that we allow hidden traits: factors that may have affected diversification rate that can generate heterogeneity in rate without requiring the observed trait to be used for this. Thus, if an observed trait is driving diversification, the model can find that, but if there could be other unmeasured factors that drive it, the effect of those could be incorporated as well. The data are thus presented with a variety of models, allowing heterogeneity to be met without forcing an involvement of an observed trait.

These are the main large scale projects that have been completed in this interval. In addition to ongoing work in progress (see below) I have also worked on various smaller projects, whether analyzing traits that lead to play behavior in primates to collaborations with my students on software to help with phylogenetic analyses to continuing my work on dating phylogenies.

Work in progress

I currently have three major projects that are nearing completion (all have usable software and manuscripts actively being developed or already on preprint servers). The most mature is a project to link population genetics with phylogenetics. While there are many complex codon

models available in phylogenetics, most empiricists use simple nucleotide substitution models like General Time Reversible (GTR). In collaboration with faculty member Mike Gilchrist, and later postdocs and students hired on the project, we have developed a model that allows for a nucleotide mutation process and then selection based on distance of the amino acid encoded by the relevant codon to the inferred optimal amino acid. This fits data better than many existing models, but more compellingly it allows inference of population genetic parameters (optimal amino acids, protein expression levels, sensitivity to different amino acid properties) from phylogenetic data. It models the richness of the evolutionary process (does not assume equilibrium, allows different substitution rates towards and away from an optimal amino acid, allowing a different codon substitution table for each optimal amino acid) with relatively few parameters (other than inference of an optimal amino acid at each site). We have an accepted manuscript pending major revisions on this work at *Molecular Biology and Evolution*. There is also a student-led manuscript being written comparing inferences from this model with inferences from mutation accumulation selection experiments. Ongoing work involves extending the model to allow optimal amino acids to evolve on the tree (using a hidden Markov model), testing the effect of this model on accuracy of gene tree branch length estimates, and some more speculative work with REU summer students on the utility of this model for understanding cancer phylogenetics.

Another project is a method for developing custom macroevolutionary models (funded by an NSF CAREER grant). This uses approximate Bayesian computation (related the approximate likelihood approach used in the completed PHRAPL project) to allow biologists to write a model for how a species trait changes in one time unit (ideally, in one generation) and then simulates evolution using this model, varying parameters to find those that generate data most similar to observed data. The current postdoc on the project, paleontologist Dave Bapst, has been working to make the approach accessible for a general audience, adding extensive documentation and examples. The custom models can be as simple as basic shifts from a normal distribution every generation to ones that allow species to be attracted or repelled from the values of others, to have a mixture of processes occur, to have bounds of various types, and more.

The *datelife* project is a collaboration within the umbrella of an NSF ABI grant to a group called phylotastic (primary collaborators are Arlin Stoltzfus, Enrico Pontelli, and Dima Mozzherin). The goal of the project overall is to make the tree of life more accessible to all, especially those without the resources or expertise to build a phylogeny for their group of interest. To that end, we have a web portal where someone can enter species names (or enter a URL or upload a PDF that has names interspersed with other information), have the names resolved to a uniform taxonomy, and extract a phylogeny with species images. There are also R and python packages to use these core tools as well as other services we provide. My subproject, in collaboration with postdoc Luna Sanchez Reyes, is to develop tools to get dates for phylogenies. This builds off a project I started years ago as an open, reproducible, more freely usable alternative to the TimeTree.org project and which was fostered through hackathons at the National Evolutionary Synthesis Center (NESCent), but has blossomed into a series of approaches that allow biologists or other members of the public to go from a tree, a list of species, or even a named clade and get back chronograms of various kinds (a single best estimate using one of three different approaches, a set of empirical chronograms from studies, or more). There is a website to do this

and also an R package. I am currently in the process hiring another postdoc to work on the phylotastic approach more generally, with a focus on education users.

There is smaller scale (in terms of my involvement) projects in the works, as well, including work on comparative methods on phylogenetic networks (a collaboration with past postdoc Tony Jhwieng), a collaborative DOE project on nitrogen fixation in plants, and of course ongoing collaborations with current and recently graduated students on everything from biogeographic models to fish trophic level evolution to the effect of the great faunal interchange on dung beetle diversity.

Plans for future work

I entered biology to understand how evolution works. This remains my passion. I grew up wanting to be a paleontologist, until I first saw the power of molecular-based phylogenetics to address evolutionary questions as a sophomore in college. I threw myself into this field, first doing empirical work, later helping to create methods to better go after questions. There has always been a tension between the questions biologists pose and the limited power of methods to address those questions. This does, of course, cycle a bit. For instance, ancestral state estimation with parsimony was very compelling, then a series of articles showed it could be problematic, then stochastic character mapping made it compelling again, and now many are starting to question again whether we should be estimating ancestral states at all. Fossil data can help tremendously, but there remains a limit on how much we can learn about processes in the past given the species (alive and dead) we have available to us. However, there seems to be a growing bubble of nihilism in the field. There are series of papers saying that we ought not to do certain things (believe overmuch in model comparisons, try to interpret certain parameters, use “complete” trees of all species where most of the species’ placements come from taxonomy alone with random resolution of polytomies and branch lengths are largely invented) while at the same time there are papers, often including the same authors, that do those very things. Basic, deep flaws are found in methods, yet they continue to be used in new high profile, impactful publications, and results from past papers using them are not re-evaluated for soundness. Null models no one believes in (constant rate of trait evolution for all taxa; constant rate of speciation for all time; no extinction, ever) keep being rejected, but with few new discoveries to show. There is even a growing set of nonparametric approaches explicitly designed to reject null models, but which give little information about the alternative model (how *much* faster do herbaceous species speciate? Is this biologically meaningful as well as being significant?). I am not sure about the cause of this malaise: from mentoring over a dozen postdocs and other early career researchers intending to pursue the academic track, there is growing anxiety about what is required to get an academic job and tenure (how many papers are required, in what impact factor journals), and so pressure to craft a compelling story and produce a lot of papers is playing some role, but that does not explain it all.

I aim to continue pushing back on this, which started with HiSSE and the hidden trait diversification models. That is, rather than always confirm a hypothesis, biologists can be (and, based on communications with users of HiSSE, often are) surprised by their results. For instance, perhaps the predicted trait is not solely driving diversification, but requires something else to have a biologically meaningful influence. The approximate Bayesian computation method for

comparative methods that my lab is developing continues the push for biologists to use models that address their questions and have meaningful parameter estimates, with uncertainty, rather than rejecting nulls. Future work will extend this approach to multiple traits with more complex interactions. This will continue in future work: evolutionary biology lags behind other fields in its insistence on p-values and relative indifference to parameter estimates: synthesizing the state of the art in statistics and demonstrating better ways to address questions will help move the field forward.

In terms of concrete projects, one focus is bringing back the importance of extinction to macroevolution and focusing empiricists' attention turnover rates. Birth-death processes can be parameterized in multiple ways. The most common in neontology are speciation rates, extinction rates, or net diversification rate (speciation *minus* extinction). However, one could also look at the turnover rate (speciation *plus* extinction rates) and extinction fraction (extinction rate divided by speciation rate). Given wariness about extinction rate estimates, the field largely focuses on net diversification or speciation rate estimates, and popular methods assume a constant extinction rate, so any changes are imputed to be due to changes in speciation. However, perhaps the best supported finding in macroevolution is that extinction rates change: mass extinctions differ from rates at other times, and we see in the present radically different extinction rates. Moreover, turnover rates also vary. In many cases, we expect evolutionary drivers to be factors affecting both speciation and extinction rates simultaneously: sea levels rise, isolating populations, and so many diverge into species at faster rates, but smaller population sizes also lead to an increase in extinction rates. Specialization by plants on particular pollinators leads to faster speciation (due to decreased gene flow between related populations) but also higher extinction rates (again, lower population size per species). These hypotheses are at least as plausible as ideas that some key adaptive innovation leads to more rapid formation of new species (which is largely an allopatric process, at least in groups with little speciation due to polyploidy) with no involvement of extinction. With longtime collaborator Jeremy Beaulieu, I am currently revising an NSF grant proposal on methods to address the questions of how turnover and extinction change.

Another future project is to continue work on phylogenetic networks with Tony Jhweng on comparative methods on networks. Gene flow between different "species" over evolutionary time remains remarkably frequent. This is more than an annoying model violation. It reflects an important biological reality that has the effect of allowing adaptive traits, for traits like coat color in canids to antibiotic resistance in bacteria, to flow between species. Sexual reproduction within a species is important because it allows for two adaptive traits in different lineages to come together in their offspring; in an asexual population, this has to happen by having one adaptive trait evolve again in a lineage with the other, which takes far longer. On a macroevolutionary time scale, we found (O'Meara, Smith et al. 2016) that it took millions of years for diversification-enhancing traits to appear together in the same lineage, but more frequent gene flow between populations would lead to these combinations appearing more quickly, just as for sexual reproduction within a species. We, and a few other research groups, are just scratching the surface of what can be done with these models.

A longer-term interest is applying phylogenetic models to cancer evolution. Cancer is the result of intrahost evolution: some cells divide more than others, and then some of these develop mutations that lead to more division, and some of these evolve ways to move around the body

and have more descendants, and so forth. While the long term inclusive fitness consequences of this are usually dire (with very rare exceptions of cancers that can move between host individuals, like the cancer plaguing Tasmanian devils), during the development it is at its heart an asexual evolutionary process with some cell lineages outcompeting others. Inferring and using phylogenies of tumor cell lineages is becoming more frequently done, and these can be important in identifying treatments and estimating prognoses. Inferring tumor phylogenies is difficult due to the wild variety of mutational processes that survive and lead to successful substitutions in cancer cell lines that are usually filtered out on trees of multiple species, but there is a growing literature on ways to deal with this. However, there has been less attention paid to using existing or modified macroevolutionary models for tumor evolution, but there is great potential there. A trait-based birth death process typically used to test the influence of flower structure on diversification could be adapted to examine the effect of a deletion of a splicing site in an oncogene on lineage proliferation rate, for example. Phylogenetic methods of trait evolution have been used productively for everything from analyzing the process of transcribing books to evolution of human culture, and so they could have great importance in understanding the cancer evolutionary process.

Other work in the lab

One note about work completed: my lab's standard for authorship is high: substantial contribution to papers is necessary. Thus, my research group as a whole has much higher productivity than the work I claim for myself. This work is at least partially fostered by the discussions, environment, and resources I have helped assemble, but it will not show up on my CV. For completeness, here are the papers published by people who were graduate students, directly funded postdocs, or NIMBioS-funded postdoc mentees in my lab in the relevant time for the evaluation of promotion (2015-8). I am only including papers that were published 1) while they were employed here and 2) where I am not an author. Work where I am an author appears in the following section.

Student work (student in bold)

Martinez, C. M., M. D. McGee, **S. R. Borstein**, and P. C. Wainwright. 2018. Feeding ecology underlies the evolution of cichlid jaw mobility. *Evolution* (in press)

Soto-Trejo, F., N. J. Matzke, E. E. Schilling, **K. A. Massana**, K. Oyama, R. Lira, and P. Davila. 2017. Historical biogeography of Florestina (Asteraceae: Bahieae) of dry environments in Mexico: evaluating models and uncertainty in low-diversity clades. *Botanical Journal of the Linnean Society* 185:497-510.

Riechert, S. E., J. Pruitt, and **J. Bosco**. 2017. In the spider nursery: indifference, cooperation or antagonism? *The Journal of Arachnology* 45:283-286.

McGee, M. D., B. C. Faircloth, **S. R. Borstein**, J. Zheng, C. D. Hulsey, P. C. Wainwright, and M. E. Alfaro. 2016. Replicated divergence in cichlid radiations mirrors a major vertebrate innovation. *Proc. R. Soc. B* 283:20151413.

McGee, M. D., **S. R. Borstein**, R. Y. Neches, H. H. Buescher, O. Seehausen, and P. C. Wainwright. 2015. A pharyngeal jaw evolutionary innovation facilitated extinction in Lake Victoria cichlids. *Science* 350:1077-1079.

Bouchenak-Khelladi, Y., Onstein, R. E., Xing, Y., **Schwery, O.** & Linder, H. P. 2015. On the complexity of triggering evolutionary radiations. *New Phytologist*, 207: 313–326

Schwery, O., Onstein, R. E., Bouchenak-Khelladi, Y., Xing, Y., Carter, R. J. & Linder, H. P. 2015. As old as the mountains: the radiations of the Ericaceae. *New Phytologist*, 207: 355–367.

Postdocs funded on my grants

Jackson, N. D., and L. Fahrig. 2016. Habitat amount, not habitat configuration, best predicts population genetic structure in fragmented landscapes. *Landscape ecology* 31:951-968.

Near, T. J., A. Dornburg, R. C. Harrington, C. Oliveira, T. W. Pietsch, C. E. Thacker, T. P. Satoh, E. Katayama, P. C. Wainwright, J. T. Eastman, and **J. M. Beaulieu**. 2015. Identification of the notothenioid sister lineage illuminates the biogeographic history of an Antarctic adaptive radiation. *BMC Evolutionary Biology* 15:14.

Leslie, A. B., **J. M. Beaulieu**, P. R. Crane, P. Knopf, and M. J. Donoghue. 2015. Integration and macroevolutionary patterns in the pollination biology of conifers. *Evolution* 69:1573-1583.

Dornburg, A., J. Moore, **J. M. Beaulieu**, R. I. Eytan, and T. J. Near. 2015. The impact of shifts in marine biodiversity hotspots on patterns of range evolution: Evidence from the Holocentridae (squirrelfishes and soldierfishes). *Evolution* 69:146-161.

NIMBioS postdocs (for whom I was one of their primary mentors, not postdocs under my supervision as associate director only)

Kawano, S. M., D. R. Economy, M. S. Kennedy, D. Dean, and R. W. Blob. 2016. Comparative limb bone loading in the humerus and femur of the tiger salamander: testing the 'mixed-chain' hypothesis for skeletal safety factors. *The Journal of Experimental Biology* 219:341-353.

McInroe, B., H. C. Astley, C. Gong, **S. M. Kawano**, P. E. Schiebel, J. M. Rieser, H. Choset, R. W. Blob, and D. I. Goldman. 2016. Tail use improves performance on soft substrates in models of early vertebrate land locomotors. *Science* 353:154-158.

Chaudhary, V. B., **M. A. Rúa**, A. Antoninka, J. D. Bever, J. Cannon, A. Craig, J. Duchicela, A. Frame, M. Gardes, and C. Gehring. 2016. MycoDB, a global database of plant response to mycorrhizal fungi. *Scientific data* 3:160028.

Breeschoten T, Doorenweerd C, **Tarasov S**, Vogler AP. 2016. Phylogenetics and biogeography of the dung beetle genus *Onthophagus* inferred from mitochondrial genomes. *Molecular Phylogenetics and Evolution*, 105: 86.

Matzke, N. J. 2016. The evolution of antievolution policies after *Kitzmiller v. Dover*. *Science* 351:28-30.

Rúa, M. A., A. Antoninka, P. M. Antunes, V. B. Chaudhary, C. Gehring, L. J. Lamit, B. J. Piculell, J. D. Bever, C. Zabinski, and J. F. Meadow. 2016. Home-field advantage? evidence of local adaptation among plants, soil, and arbuscular mycorrhizal fungi through meta-analysis. *BMC Evolutionary Biology* 16:122.

Rúa, M. A., E. C. Wilson, S. Steele, A. R. Munters, J. D. Hoeksema, and A. C. Frank. 2016. Associations between ectomycorrhizal fungi and bacterial needle endophytes in *Pinus radiata*: implications for biotic selection of microbial communities. *Frontiers in microbiology* 7:399.

Dembo, M., **N. J. Matzke**, A. O. Mooers, and M. Collard. 2015. Bayesian analysis of a morphological supermatrix sheds light on controversial fossil hominin relationships. *Proceedings Of The Royal Society B-Biological Sciences* 282:133-141.

Meyer, E. L., **N. J. Matzke**, and S. J. Williams. 2015. Remote sensing of intertidal habitats predicts West Indian topsnail population expansion but reveals scale-dependent bias. *Journal of Coastal Conservation* 19:107-118.

C2. Research And Scholarly Publications

In the articles listed below, I am only an author if I contributed substantially to a paper. I have advised several grad students and postdocs on work that led to a publication, but even if they are in my lab group, I am not automatically an author. Standards for this vary dramatically in the field; in some groups, the PI is an author on any publication leaving her or his lab, while others have a stricter criterion for authorship; I am on the stringent end of the spectrum. For work by people in my lab where I did not believe I merited authorship but still may have assisted in some way, please see above.

In my field, first author and last author are typically the most prominent positions: first author typically is the person who has done most of the work required for the publication and last author is often the person who develops the context and who may have designed the project. Authorship in the middle generally represents a more minor contribution. Rarely, two authors are given first authorship; in the set of papers below, only O'Meara, Smith, et al. (2016) qualifies: I am listed first, but Stacey Smith contributed equally to the work despite being listed second. In papers with just two authors, it can be that both contribute equally but this is typically not indicated (since citations of two authored papers typically include both names).

C2a. Articles published in refereed journals

Zanne, A. E, D. C. Tank, W. K. Cornwell, J. M. Eastman, S. A. Smith, R. G. FitzJohn, D. J. McGlinn, B. C. **O'Meara**, A. T. Moles, P. B. Reich, D. L. Royer, D. E. Soltis, P. F. Stevens, M. Westoby, I. J. Wright, L. Aarssen, R. I. Bertin, A. Calaminus, R. Govaerts, F. Hemmings, M. R. Leishman, J. Oleksyn, P. S. Soltis, N. G. Swenson, L. Warman and J. M. Beaulieu (2015a). "Zanne et al. reply". In: *Nature* 521.7552, pp. E6-E7. *Contribution: helping to write a response to a criticism of our paper; author order followed that of the original paper being criticized.*

Beaulieu, J. M. and B. C. **O'Meara** (2016). "Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction". In: *Systematic Biology* 65.4, pp. 583-601. *Contribution: Equal contributions to the model development and writing; the first author did more of the software development, though both contributed.*

Jackson, N. D, B. C. Carstens, A. E. Morales and B. C. **O'Meara** (2016). "Species Delimitation with Gene Flow". In: *Systematic Biology*, 66.5:799-812. *Contribution: Senior author, supervising postdoc Nathan Jackson, developing much of the math and initial code behind the model.*

O'Meara, B. C. and J. M. Beaulieu (2016). "Past, future, and present of state-dependent models of diversification". In: *American Journal of Botany* 103.5, pp. 792-795. *Contribution: Received initial inquiry for a review article; equal writing with second author.*

O'Meara, B. C*, S. D. Smith*, W. S. Armbruster, L. D. Harder, C. R. Hardy, L. C. Hileman, L. Hufford, A. Litt, S. Magallón, S. A. Smith, P. F. Stevens, C. B. Fenster and P. K. Diggle (2016). "Non-equilibrium dynamics and floral trait interactions shape extant angiosperm diversity". In: *Proceedings of the Royal Society B: Biological Sciences* 283.1830, p. 20152304. *Contribution: Part of four person team (O'Meara, Smith, Fenster, Diggle) doing much of the analyses and writing based on work started by the full authorship as a working group. I wrote most of the code and ran all the analyses; the four person core team contributed equally to the writing. O'Meara and Smith are equal coauthors, Fenster and Diggle are equal senior authors.*

Schwery, O. and B. C. **O'Meara** (2016). "MonoPhy: a simple R package to find and visualize monophyly issues". In: *PeerJ Computer Science* 2, p. e56. *Contribution: Assist in debugging, program design, use case, and editing; the lead author is my PhD student and did the bulk of the work and writing.*

Morales, A. E, N. D. Jackson, T. A. Dewey, B. C. **O'Meara** and B. C. Carstens (2017). "Speciation with Gene Flow in North American *Myotis* Bats". In: *Systematic Biology*, 66(3):440-45. *Contribution: Assist in designing analyses and writing.*

Bosco, J. M, S. E. Riechert and B. C. **O'Meara** (2017). "The ontogeny of personality traits in the desert funnel-web spider, *Agelenopsis lisa* (Araneae: Agelenidae)". In: *Ethology* 123.9. Ed. by E. Hebets, pp. 648-658. *Contribution: Note here that author order follows conventions of behavioral ecology (so Riechert's contribution was greater than mine): Bosco did the experiments and much of the writing; Riechert helped design the experiments, teach technique, and substantially revised the writing; I helped revise the writing and with statistical analyses and plots. Bosco was a PhD student coadvised by Riechert and me.*

Carstens, B. C, A. E. Morales, N. D. Jackson and B. C. **O'Meara** (2017). "Objective choice of phylogeographic models". In: *Molecular Phylogenetics and Evolution* 116, pp. 136-140.

Contribution: This work arose from a funded project the four of us worked on together, where Carstens and I were each the funded investigators and Morales and Jackson were the student and postdoc, respectively. We all contributed to the writing though Carstens contributed the most.

Jackson, N. D, A. E. Morales, B. C. Carstens and B. C. **O'Meara** (2017). "PHRAPL: Phylogeographic Inference Using Approximate Likelihoods". In: *Systematic Biology* 66.6, pp. 1045-1053. *Contribution: I developed the initial method in consultation with Carstens; Jackson, the postdoc on the project, radically improved it, performed extensive simulations to test it, and did the bulk of the writing.*

Beaulieu, J. M. and B. C. **O'Meara** (2018). "Can we build it? Yes we can, but should we use it? Assessing the quality and value of a very large phylogeny of campanulid angiosperms". In: *American Journal of Botany* 105.3, pp. 417-432. *Contribution: Beaulieu did much of the writing and analyses; I also contributed substantially to the writing and overall paper design.*

Borstein, S.R. and B.C. **O'Meara** (2018). "AnnotationBustR: an R package to extract subsequences from GenBank annotations". In: *PeerJ* 6: e5179. *Contribution: Assist in debugging, program design, use case, and editing; the lead author is my PhD student and did the bulk of the work and writing.*

Caetano, D.S., B.C. **O'Meara**, J.M. Beaulieu (2018). "Hidden state models improve state-dependent diversification approaches, including biogeographical models". In: *Evolution* 10.1111/evo.13602. *Contribution: Assisted with design of simulations, models, coding, and writing. Caetano did the main simulations, and Beaulieu did the empirical analyses.*

C2k. Manuscripts submitted for publication

(include where and when submitted and status of submission)

Borstein, S.R., J. Fordyce, B.C. **O'Meara**, P. Wainwright, M. McGee (2018) "Reef fish functional traits evolve fastest at trophic extremes". **Accepted** In *Nature Ecology & Evolution*. Letter from editor below. *Contribution: Assist with design of study, analyses, and writing; lead author is a PhD student in my lab.*

Subject: Decision on Nature Ecology & Evolution manuscript NATECOLEVOL-18044241B

21st October 2018

Dear Dr Borstein,

We are pleased to inform you that your Article entitled "Reef fish functional traits evolve fastest at trophic extremes", has now been accepted for publication in *Nature Ecology & Evolution*.

Before your manuscript is typeset, we will edit the text to ensure it is intelligible to our wide readership and conforms to house style. We look particularly carefully at the titles of all papers to ensure that they are relatively brief and understandable.

[details of letter removed: information on formatting figures, restrictions on distribution, etc.]

Thank you again for choosing Nature Ecology & Evolution for your manuscript; I look forward to seeing it published soon.

Best regards
Marian

Marian Turner, PhD
Senior Editor, Nature Ecology & Evolution
Level 1, 15-19 Claremont St, South Yarra, Victoria 3141, Australia
T +61 3 9825 1181
email redacted
@marianturner @NatureEcoEvo
orcid.org/0000-0002-3343-1136

Beaulieu, J., B.C. O'Meara, R. Zaretzki, C. Landerer, J. Chai, M.A. Gilchrist. **Revision being reviewed after being accepted pending major revision** at *Molecular Biology and Evolution*. Letter from editor below. Note the preprint is also available at <https://www.biorxiv.org/content/early/2018/10/09/120238>. *Contribution: Help develop the initial model in association with Chai and Gilchrist; assist in coding, designing analyses, and writing.*

Date: Tue, 3 Jul 2018 07:02:07 +0000
From: Molecular Biology and Evolution <onbehalf@manuscriptcentral.com>
Reply-To: *redacted*
To: mikeg@utk.edu
Cc: *redacted*
Subject: Editorial Decision to (major) Revise MBE-18-0448
Resent-From: <mikeg@utk.edu>

03-Jul-2018

MS: MBE-18-0448
Title: Population Genetics Based Phylogenetics Under Stabilizing Selection for an Optimal Amino Acid Sequence: A Nested Modeling Approach

Dear Dr. Gilchrist:

The in-depth review of your manuscript by the editors and the peer reviewers is now complete. Based on their assessment, it is clear that your manuscript requires a substantial revision before it can be considered further for

publication in MBE. Comments from the editors and external reviewers are included below.

We invite you to revise your manuscript within 60 days and submit it for further consideration. A delayed submission will be treated as a new submission. If you need an extension, please contact Marj by e-mail (*email redacted*) before the deadline.

Most importantly, the revised manuscript will be subject to editorial and external reviews, and its eventual acceptance depends on the reviewers' and editors' enthusiasm. Note that manuscripts invited to be revised are accepted at a very high rate. But, manuscripts deemed to require more than one major revision are often rejected. So, it is critical that you revise it to satisfy all editorial and reviewer concerns. A re-review by original and new reviewers may raise additional concerns so anticipate them in advance and revise thoroughly.

You can create a revision by using the URL:

*** PLEASE NOTE: This is a two-step process. After clicking on the link, you will be directed to a webpage to confirm. ***

[link omitted]

Following is a checklist of needed actions and files.

[checklist omitted]

We look forward to receiving a revised version of the manuscript for further consideration.

Sincerely,

Board of Editors
Molecular Biology and Evolution

[List of detailed associate editor and reviewer comments omitted]

C4. Projects, grants, commissions, and contracts

*Note I am only including grants that were awarded after tenure; grants that were awarded before that packet was considered are **not** listed, even if they continued into this funding period (includes two NSF grants where I was a PI, worth \$520K and \$340K respectively). At the time of tenure application, the CAREER and ABI grants were in review but had not been awarded.*

Funded and in progress

2015: NSF, "CAREER: Reducing barriers for comparative methods." \$738,000 total award, O'Meara PI, 100% allocated to me.

2015: NSF, "Collaborative Research: ABI Development: An open infrastructure to disseminate phylogenetic knowledge." \$148,101 total award, O'Meara Co-PI (on overall grant, though 100% control of the UT allocation of \$148K).

2017: NSF, "DISSERTATION RESEARCH: Morphological consequences of trophic evolution." \$19,630. O'Meara PI, PhD student Sam Borstein Co-PI

2018: University of Maryland, subaward for Phylotastic project. \$165,492, 100% control to O'Meara (subaward from a colleague on the ABI grant).

Under review

2018: NSF, "IGE: CLIMB: Case-based Learning: Internships in Mathematical Biology." \$499,996 requested. O'Meara, PI, 50% of credit; Fefferman and Bishop, Co-PIs, 50% each.

2018: NSF NRT (UT internal competition). O'Meara, PI; Armsworth, Blum, Emrich, Heath, Kalisz, Kwit, Papeş, Sims, Stanton, Co-PIs. No budget yet, but this will be a \$3M grant if we are allowed to submit it.

Submitted but not funded

2015: NSF, "NRT-DESE: Pioneering Research Integration in STEM Modeling (PRISM)." \$2,999,978. Jonsson, PI; O'Meara, Von Arnim, Lenhart, Co-PIs.

2016: NSF, "DISSERTATION RESEARCH: How Do Trophic Level Transitions Affect Morphological Disparity?" \$19,631. O'Meara PI, Borstein Co-PI (it was funded the next year)

2017: NSF, "Preliminary Proposal: Phylogenetic measures of contemporary evolution and their application to island systems." No budget (preliminary proposal). O'Meara Co-PI, Beaulieu PI.

2017: NSF, "NRT: Next-Generation Biodiversity Training." \$2,948,586. O'Meara PI, Staton, Moulton, Kwit, Kalisz Co-PIs.

2017: NSF, “Collaborative Research: Novel framework for estimating continuously-varying diversification rates.” \$64,653 to UT, O’Meara Co-PI but with 100% allocation (separate funding would go to PI Beaulieu at U. Arkansas). Note this passed an earlier preproposal round.

C5. Other evidence of research or creative accomplishments

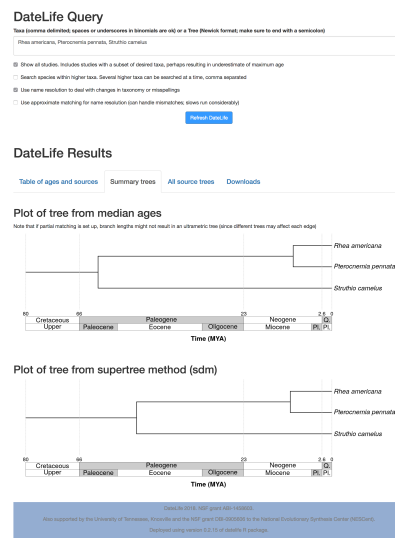
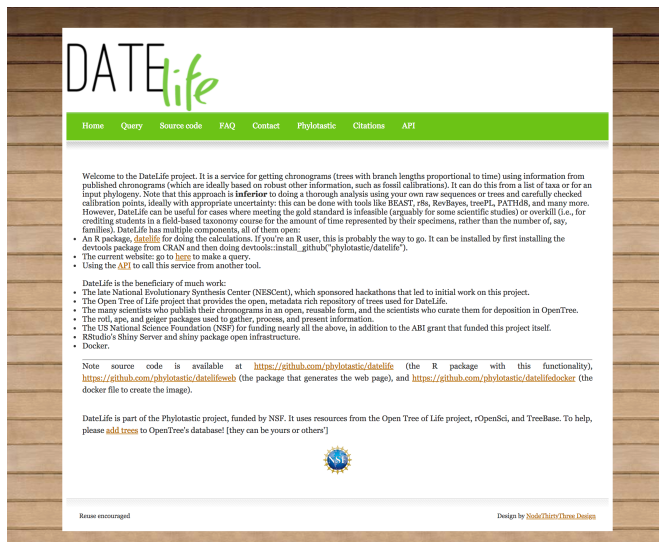
CRAN Task View for Phylogenetics: Curated description and links to dozens of software packages for using the programming language R for phylogenetics: <https://cloud.r-project.org/web/views/Phylogenetics.html>. Last updated June 11, 2018.

phrapl: R software for phylogeographic inference: <https://github.com/bomeara/phrapl>. Last updated March 14, 2018.

selac: R software for understanding amino acid evolution on phylogenies: <http://bomeara.github.io/selac/reference/index.html>. Last updated Sept. 19, 2018.

hisse: R software for analyzing diversification rates: <https://github.com/thej022214/hisse>. Last updated Oct. 20, 2018.

Datelife: R software and interactive website for determining ages of groups on phylogenetic trees. Website: <http://www.datelife.org>. R package: <https://github.com/phylotastic/datelife>. Last updated Oct. 21, 2018.



Phylotastic: A web portal to allow scientists, teachers, and others to easily get a phylogeny. Website: <http://phylotastic.org>. R package: <https://github.com/phylotastic/rphylostatic>

PHYLO**astic** Feedback Help About Hello, Guest ▾

Public lists

- _Jungle Book
- Are seaweeds plants?
- Birds of Maryland
- Birds, reptiles and mammals
- Evolution of eyes
- Finding Nemo
- Fungi, animals and plants
- Mammals return to the water

Welcome to the Phylotastic web portal!

The portal makes a tree from a list of species names. Choose from the "Make a new list" menu (at right) to

- upload your list (one name per line or DwC-A)
- extract names from a document (PDF, .docx, etc)
- extract names from a web page
- choose a taxon (e.g., Felidae) and sample from that

If you don't have any lists of your own, choose a pre-made example from "Public Lists".

To find out more, go to [Help](#).

New list

- Extract from web
- Extract from doc
- Upload my list
- Choose taxon

Get names

Manage list

Get tree

f t G+ in Instagram P

© 2018 Copyright: Phylotastic Project

C6. Participation in seminars and workshops

I am listing here major seminars and workshops, omitting numerous short (less than two hour) training sessions with EEB students, NIMBioS postdocs, and UTK faculty on anything from making a website and curating social media presence to imposter syndrome to writing research statements to putting together grants.

June 26, 2015: Society of Systematic Biologists-sponsored phylogeography workshop at Evolution meetings in Guarujá, Brazil. Instructor.

August 12-15, 2015: Evolutionary Quantitative Genetics workshop at the National Institute of Mathematical and Biological Synthesis (NIMBioS), Knoxville, TN. Instructor.

September 8, 2015: Invited seminar on evolutionary heterogeneity at Texas A&M. Invited speaker.

- May 20, 2015: Comparative methods in R workshop at the Society of Systematic Biologists satellite meeting in Ann Arbor, Michigan. Organizer/Instructor
- August 10-12, 2016: Evolutionary Quantitative Genetics workshop at the National Institute of Mathematical and Biological Synthesis (NIMBioS), Knoxville, TN. Instructor.
- January 8, 2017: Workshop on use of phrapl (software developed as a research product in my lab and that of a collaborator): Baton Rouge, LA. Organizer/Instructor
- March 10, 2017: Invited seminar on three recent research projects at U. of Idaho, Moscow
- June 7-9, 2017: Evolutionary Quantitative Genetics workshop at Friday Harbor Marine Lab, Washington State. Instructor.
- September 8, 2017: Workshop on the NSF GRFP, National Institute of Mathematical and Biological Synthesis (NIMBioS), Knoxville, TN. Co-organizer
- June 6-8, 2018: Evolutionary Quantitative Genetics workshop at Friday Harbor Marine Lab, Washington State. Instructor.
- September 7, 2018: Workshop on the NSF GRFP, National Institute of Mathematical and Biological Synthesis (NIMBioS), Knoxville, TN. Co-organizer

C7. Papers Presented

- August 2016: Talk on linking leaf spectra to phylogenies at Ecological Society of America 2016 annual meeting. Jose Eduardo Meireles, Brian O'Meara, Anna Schweiger, Aditya Singh, Phil Townsend, Susan Ustin, Michael Schaeppman, Franziska Schrodte, John Gamon and Jeannine Cavender-Bares. Co-author.
- September 2016: Invited symposium talk on Approximate Bayesian computation for trait evolution on phylogenies at Geological Society of America annual meeting. Presenter
- June 2017: Invited symposium talk on phylogenetic networks at Evolution 2017 meeting: co-lead author was Tony Jhwueng; I presented.
- June 2017: Poster on inference of amino acid functionality from DNA sequences using a novel phylogenetic approach at the Society for Molecular Biology and Evolution meeting in Austin, TX. Cedric Landerer, Jeremy Beaulieu, Brian O'Meara, Mike Gilchrist. Co-author on poster.

June 2018: Talk on DateLife project for getting chronograms for the tree of life. Presented at the Society of Systematic Biologists meeting in Columbus, OH. Luna Sanchez Reyes (presenter) & Brian O'Meara.

**D. INSTITUTIONAL,
DISCIPLINARY, AND/OR
PROFESSIONAL SERVICE**

D1. Candidate's Statement

I contribute to service within the department, throughout the University, and in the broader academic community. I am entering my third year as associate head for the Ecology and Evolutionary Biology department. There, my main role is to focus on the graduate students: helping graduate affairs and graduate admissions to work well, helping to make sure students progress adequately, fostering discussions about policy. My goals have been to remove barriers

(i.e., we finally stopped requiring the GRE, given the limited utility it was providing to our department, cost and expense for students, and data showing its lack of utility in general (Moneta-Koehler et al. 2017)) and help make sure students stay on track. For the latter goal, I have created a system

where students enter annual data in a form and then software checks for any issues. Overall evaluation of progress comes from a faculty committee

engaging with each student's materials rather than from an algorithm, but this can flag issues that are easy to overlook. For example, one issue that aggregating information across students revealed is the long time it took for many students to take qualifying exams. In response, the department has made a stronger requirement for this as well as more clearly delineated what is included in the exam. I also assist with various other administrative duties in the department as needed (evaluating forms, proposing bylaw revisions, helping to draft the diversity plan, meet with external evaluators of another biology department, and similar) and work with graduate student training (discussions on grant budgeting and imposter syndrome organized by our graduate student organization, co-organizing training sessions on the NSF Graduate Research Fellowship program, and so forth). I have also written several training grants to raise funds and improve training for our students (see grants section).

Within the university, I served as associate director for postdocs at the National Institute for Mathematical and Biological Synthesis (NIMBioS) for two years (the position has recently been eliminated as a result of NIMBioS' current federal grant winding down, though I remain involved with the postdocs). The position involved helping to orient postdocs once they arrive and helping with their exit as well as mentoring and helping to foster vocational training while they are here (making sure there are workshops on skills like writing teaching and research statements, though the postdocs do an admirable job of largely organizing these themselves). As

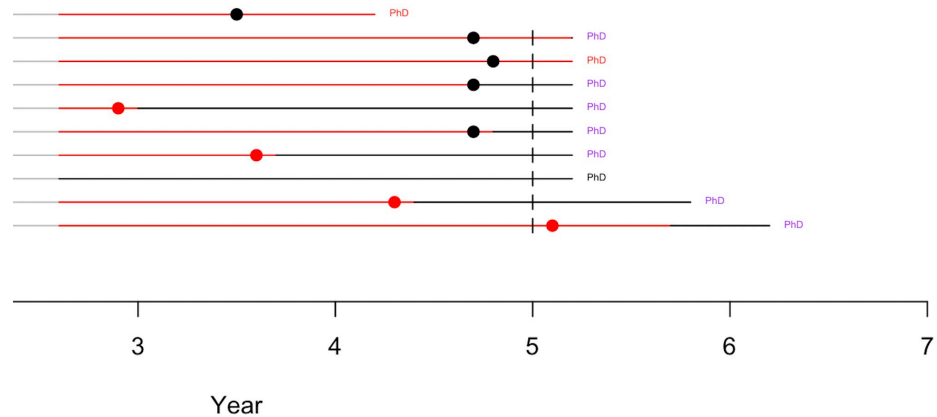


Figure 2: Detail of figure used for graduate progress reporting (with student names removed), generated using a form and software I developed. Student-entered data is processed and individual reports constructed flagging any potential issues; there is also an overview plot showing students who have not taken their qualifying exams on schedule (red lines) and dots showing when their most recent committee meeting was (black dots if within the last year, red otherwise).

a member of the NIMBioS leadership team I also helped with discussions of NIMBioS strategy under two directors and helped with the search for a director once Director Colleen Jonsson announced her intention to move on. I have also done work at the college level by, for example, serving on graduate education strategic planning committee and an alternate careers task force, and by speaking at the Office of Research & Engagement's training sessions for faculty seeking CAREER or other NSF grants.

Internationally, I was elected as the first communications director for the Society of Systematic Biologists, an executive level position. This society publishes *Systematic Biology*, the third highest rated (by the flawed but readily available metric of impact factor) journal in evolutionary biology (where I am also an editorial board member). Despite the journal's importance, there were a series of substantial problems when the publisher switched to new software: associate editors were incorrectly converted to authors (both on the journal's website and downloadable citations but also in places like Google Scholar), articles appeared in the wrong journal online, DOIs would go to the wrong article, open access articles were put behind paywalls, equations stopped rendering, and similar issues. I documented and curated discussions between authors and readers with the publisher and other journal leadership and worked to help remedy problems (for example, making sure open access were available to all while the system was being repaired). I also then led a team gathering bids from other publishers and the journal's current one to allow the society to get a better deal.

I have also become more involved in conduct issues through that society. There were public reports of harassment issues at its joint annual conference in 2017 as well as an internal discussion that suggested that a code of ethics (which guides conduct of members in general), as well as a better procedure for enforcing the existing code of conduct at its meetings, would be important. I put together a quick survey to get suggestions of how the society should respond, advocated for creation of a code of ethics (which is now moving forward), and joined a task force working on implementation details for a code of conduct. This task force has five scientists from the three major US-based evolution societies (Society of Systematic Biologists, Society for the Study of Evolution, American Society of Naturalists) and has worked together for months, in consultation with experts in these issues, to create and have approved a [detailed code of conduct implementation procedure](#) that respects confidentiality and due process and has substantial consequences for violations. We have also constructed, got approval from UT Knoxville's institutional review board, and distributed a survey on harassment in evolutionary biology to thousands of attendees and members of the societies and their meetings and are currently analyzing the hundreds of survey responses for a peer-reviewed paper. Though there have been other publications showing widespread harassment in sciences (examples are Clancy et al. 2014, Clancy et al. 2017, National Academies of Sciences and Medicine 2018) it is our hope that by demonstrating its incidence in our field, as well as in what situations it is most prevalent, to build widespread support for further approaches to make the field more welcoming to all.

Other work at the national/international level has included work to try to find ways to restore funding for the NSF's Doctoral Dissertation Improvement Grant program in biology, an important program that funded student projects that was recently cut (one of my current students has this award; I also benefited from this award as a student). This included a proposal to have scientific societies administer the program for NSF (discussed in the *Chronicle of Higher*

Education (Basken 2017)). I also, working with Kimberly Eck and UT's Office of Research & Engagement, put together a white paper to NSF offering to have UT administer it. NSF discussed it internally among program officers but ultimately declined. I have also worked on breaking down barriers in other ways, such as by allowing for more remote work in academia (see news article in *The Scientist* (Yeager 2018)). I also continue to review for scientific journals and the National Science Foundation and work on other prosocial activities (organizing symposia organizing meetings, and more).

References for this section

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<https://www.the-scientist.com/careers/scientists-are-opting-for-remote-postdoc-positions-64289>

D2. Summary of service record

D2a. Institutional Service

pre-2015-present: Darwin Day advisor: ensure stable student leadership, offer advice.

Aug. 2015-July 2016: Head of graduate admissions committee.

Sept. 2015-Jan. 2017: Support to EEB's Women in Science group: listening at meetings and handling mundane details like arranging polls to find meeting times, taking group notes, and so forth.

Sept. 2016-Jan. 2017: College Strategic Planning committee, graduate education subcommittee (led by Todd Moore).

Aug. 2016-present: Associate head for department of Ecology & Evolutionary Biology.

Aug. 2016-July 2018: Associate director for postdocs for National Institute of Mathematical and Biological Synthesis

Oct. 2017-April 2018: College Career Planning Task Force, graduate students (led by Todd Moore).

2017-present: Serving on mentoring committees for three junior faculty.

Disciplinary Service

May 2015: Co-organizer of iEvoBio meeting (small meeting that meets aligned with the much larger Evolution meetings)

June 2015: Co-organizer of SSB symposium on Breaking Barriers: Empirical, Theoretical, and Gender Issues in Phylogenetics for Evolution meetings in Brazil

Jan. 2016-Dec. 2017: Society of Systematic Biologists: communications director

June 2016: Co-organizer of iEvoBio meeting

June 2017-present: Joint Code of Conduct committee for Society for the Study of Evolution, Society of Systematic Biologists, and American Society of Naturalists

Also see notes about workshops above.

Evaluation of peer research

I have been a reviewer for *Proceedings of the National Academy of Sciences*, NSF, *Systematic Biology*, among others