Tenure Promotion

Ecology & Evolutionary Biology

Dr. Brian O'Meara

Fall 2014

A. SUMMARY

Summary Sheet: Recommendations for Promotion and/or Tenure

Name of faculty member: Brian O'Meara

Present rank: Assistant Professor

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

Original UTK rank: Assist. Prof.   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

Educational History and Employment History

Candidate Name: Brian Christopher O'Meara

Educational History

Institution	Program or Degree	Dates in Program	Degree
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

Ranks Held	Institution	Department	Effective Date of Rank
Assistant Professor	University of Tennessee	Ecology and Evolution	2009- present
Postdoc	NESCent		2008 – 2009

STATEMENT OF RESPONSIBILITIES

Dr. Brian O'Meara

I. Teaching

To receive tenure, a member of the faculty of the Department of Ecology and Evolutionary Biology (EEB) is expected to develop excellence in teaching at either or both of the undergraduate and graduate levels. It is expected that the teaching load of an individual faculty member be reviewed periodically in order to adjust for different levels of research and service activities. There is no set teaching load.

Dr. O'Meara initiated 400-level course in Macroevolution in his first year and has offered it every year since. It has grown from eight students to approximately thirty, including graduate students from the Geology and Ecology & Evolutionary Biology departments as well as undergraduate students majoring in Chemistry, Geology, Ecology & Evolutionary Biology, and Animal Science. This class features a mixture of lecture, clicker questions, discussions, student presentations, and use of statistical software for simulations. He has also taught in EEB511, the team-taught core course in evolution, every fall (and is one of only three faculty in our department to have done so). In Fall 2013 he became the instructor of record for this course. He has also taught Biology 130, Biodiversity, in Spring 2012 (206 students) and in Spring 2014, and has been involved in discussions regarding restructuring this course to meet core learning objectives of Biology. Dr. O'Meara has been an instructor in EEB607 twice, EEB503 twice, EEB504, and EEB511 twice. He has also guest lectured in courses in Sweden, Austria, Louisiana, North Carolina, and Switzerland (in addition to research talks).

II. Research

A junior member of the faculty of EEB is expected to develop a significant, externally funded program of original research in his or her area of expertise. Regular publication is expected, with at least some papers being in high-quality journals.

Dr. O'Meara is conducting research about macroevolutionary processes leading to current diversity. Much of his research involves the development and testing of phylogenetic methods. He has received grants of $132,345, $138,590, and $98,252 (sole recipient) from the iPlant Collaborative (NSF-sponsored), a grant of $141,143 from NSF as Co-PI ($28,228 for his use), a grant of $320,000 from NSF as PI (with additional funds going to Co-PI Bryan Carstens), a grant of $520,000 from NSF as PI (the grant total includes funding for Co-PI Gilchrist), plus various smaller awards, generally to researchers he mentors, from places such as Google Summer of Code and the Encyclopedia of Life. He has published numerous peer-reviewed papers in high impact journals, including invited syntheses of the field in journals such as the *Annual Review of Ecology, Evolution, and Systematics*.

III. Service

A junior member of the faculty of EEB is expected to develop a record of service to the department and the profession.

Locally, Dr. O'Meara serves on the web committee as sole faculty representative as well as the graduate admissions committee and the department head search committee; in the past he has also served on the undergraduate education committee. He served as a member of the Dean's Advisory Council for three years. He organized a multi-department speaker series on women in science using Haines-Morris funds as well as wrote a successful proposal to acquire a cart of laptops for teaching in the EEB department. Dr. O'Meara is faculty advisor for Darwin Day Tennessee.

Internationally, he is an elected member of the Society of Systematic Biologists Council, a member of the Phylotastic Hackathon leadership team, organizer of lightning talks for the Evolution 2013 meeting in Snowbird, Utah (1400 participants from three international societies), co-organizer of the Evolution 2014 meeting in Raleigh, NC (nearly 2000 participants from three international societies), member of the Steering Committee for the iEvoBio meetings, and an associate editor for *Methods in Ecology and Evolution*. He has reviewed for journals and organizations such as NSF, *Science*, *Evolution*, *Systematic Biology*, and many more. Dr. O'Meara is the Society of Systematic Biologists' liaison to three-society initiative for removing barriers to women in science. He has also taught and organized numerous workshops in phylogenetics and computing, locally, nationally, and internationally.

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 teaching a mixture of large introductory lecture courses, graduate seminars and courses, and most centrally, a mixed upper level undergraduate/introductory graduate student course in macroevolution.

My Macroevolution course (EEB464) was started in my first year here and has been growing since. The class 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)"). The class is a mixture of lecture, small group discussions, class discussions, and investigations, both computational and empirical. Technology (laptops, clickers, homemade interactive white board, embedded videos) is used as appropriate to engage students and assess progress, but students also get hands on experience looking at fossils or other biological specimens. Lectures are recorded for students to review later if needed. For class discussions, I often will have them break into small groups to talk about an issue and then come together for an entire class discussion, so that students may try out their ideas on one or two peers before voicing them to the entire class. I also encourage class discussions to feature dialog with each other, rather than just response to me. Over the course of a semester the class covers various topics in macroevolution such as differential diversification and the history of life on earth. I emphasize how we know about these things, how to perform experimental tests of these ideas, and current work on the topics, so students see science as an ongoing process of discovery rather than a static set of facts. Students are assessed through clicker questions (some reviewing past topics, some based on a list of key taxa students are assigned to learn, some just to have students commit to hypotheses about data presented in class), essay-based tests, a report on a topic including what work still has to be done on it, and a pair presentation covering a graduate-level research proposal. In addition to positive reviews and growing numbers, one measure that shows the class's impact is the number of graduate students from the EEB and Geology departments who are encouraged by their committees to take it. Committees justifiably want to protect students from taking courses at the cost of their research, but several faculty feel that the content in this course is worth the time it takes for students to take it.

I do extensive teaching at the graduate level. Some of this is for classes that are reading groups, while another is for a shared multiple lab discussion group. This started as simply a joint meeting of four small labs (for example, my lab was originally just me) but is now an active discussion group with students from at least seven lab groups enrolled. It covers a mixture of work in progress as well as recent relevant papers to students' research. My goal in all these classes is to encourage students to focus on the questions being addressed by their work or others: it is easy for students to adopt popular methods without considering whether those are the best way to address their questions. I have also been heavily involved in our Evolution core course, being one of only three faculty to teach in the Evolution or Ecology core each of the past six years. I have been working in that course to have students focus on understanding the questions that can be addressed and why someone might want to rather than focusing on the minutia of current

methods. I try to teach students to see the connections across methods (for example, all the methods that use a discrete state transition matrix, even though some are for inferring trees while others are for investigating biogeographic history). We have also worked to make the core an early way for students to get feedback on their projects before they even set up their committees, which may have some role in EEB's remarkable success at getting NSF graduate research fellowships or honorable mentions (one third of all UT Knoxville students receiving such honors had been through the core course; two additional EEB students won honors before taking the core).

In 2012 I taught the large (206 student) primarily lecture class Bio130, Biodiversity, for the first time. For this class I created 836 new slides, wrote a web app for students to use on smartphones (http://lampyr.org) to help them learn about nearby biodiversity, and graded hundreds of essays. I tried to use readings, clicker questions, MasteringBiology assignments, and parts of lectures to teach basic material, and the remaining parts of lectures to having students learn to think about the material at higher levels of understanding. In addition to anonymous feedback during the class (see below), I embedded observers in the class to see how students were taking notes and engaging with the lectures. However, I think I was only partially successful at achieving my goals in this class. The presentation style I chose to use, with slides with primarily figures, images, and videos accompanying a lecture rather than a more bullet point-heavy presentation was a style many students had trouble with, especially in taking notes (one embedded observer found that the only note a student took from a hybridization lecture was the word "labradoodle"). As the course went on, I modified my slides (which were made available to students as pdfs and as recorded lectures) to include "speaker's notes" describing what was said and the point of each slide. I also assigned more homework, which students described as helping their understanding of the material. My clarity of speech was also difficult for some students and is clearly something to continue to improve. Successes in the class included transmitting enthusiasm for the subject (based on the student evaluations, as well as anecdotes such as students asking to bring a boyfriend or relative to observe the class) as well as creating an environment where students felt comfortable asking and answering questions: i.e., in just one 50 minute lecture, approximately 20 of 200 students volunteered in whole-class discussion. Students rated my enthusiasm high (4.25/5 average). Overall, I think I targeted the class at too high a level of understanding without providing enough basic framework for students. I will be incorporating these lessons when teaching the course again this spring through changes like including more structuring text in slides to make sure students recognize key points. I have also been involved in the ongoing discussion regarding class structure and content organized by Beth Schussler to align with the overall Biology framework.

Due to my expertise in the field I have frequently been asked to teach in short workshops (this is in addition to research talks). I often give these virtually to prevent disruption of regular duties as well as the expense and hassle of travel. I have taught in Sweden, Austria, Louisiana, North Carolina, and Switzerland. I also organized and taught at a workshop at NIMBioS on computational resources for phylogenetics. This course included students from around the world and had a fairly even gender balance.

I have certain approaches I try to extend across all my classes. One is real time assessment of my teaching: I give students a link to an anonymous form (http://www.brianomeara.info/feedback) they can use to give feedback on any part of the class at any time. This allows me to improve the class for the students in it rather than just waiting for SAIS reports at the end. I also try to use all the time students are in the room to promote learning, rather than just the assigned class times. For example, some students may show up half an hour early for some classes, and I typically have an educational video relevant to the day's focal topic running they can learn from while waiting. One consistent theme in student reviews is my enthusiasm for the subject matter. Based on student reactions, my classes are also seen as a safe place to ask questions about confusing material.

Mentoring of graduate students and postdocs is also an important part of my teaching. I have had ten postdocs come through my lab: some from internal funds (startup or NSF) and others as co-mentored NIMBioS postdocs. I also advise three graduate students and co-advise a fourth. In addition to my own students, I have served on the committees of eleven other graduate students in three graduate programs at UTK and one at Vanderbilt. With all of them, my goal has been to help the student or postdoc achieve her or his professional goals. This may require more teaching experience for some and more work on programming skills for others. I try to create a supportive environment where people are encouraged to propose new ideas but also know that they will receive constructive, honest feedback.

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SUMMARY OF TEACHING ASSIGNMENTS FOR REVIEW PERIOD

Semester	Dept. Course #	Course Title	Credit Hours	14-day enrlmnt	% Respon	Lec (L)/ Lab (B)	# GTAs assisting	Honors Y/N
Fall 2009	EEB511*	Core	4	7	13	L	0	N
Spring 2010	EEB409	Perspectives	3	13	100	L	0	N
Spring 2010	EEB607	Speciation	1	13	100	L	0	N
Fall 2010	EEB511*	Core	4	8	13	L	0	N
Spring 2011	EEB503	Seminar	1	35	100	L	0	N
Spring 2011	EEB607	Speciation	1	9	100	L	0	N
Fall 2011	EEB464	Macroevolution	3	24	100	L	0	N
Fall 2011	EEB504*	HOFF	1	7	25	L	0	N
Fall 2011	EEB503	Seminar	1	44	100	L	0	N

Fall 2011	EEB511*	Core	4	12	13	L	0	N
Spring 2012	Bio130	Biodiversity	3	206	100	L	1	N
Fall 2012	EEB464	Macroevolution	3	22	100	L	0	N
Fall 2012	EEB511*	Core	4	14	25			
Fall 2012	EEB504*	HOFF	1	5	25	L	0	N
Spring 2013	EEB607*	HOFF	1	8	25	L	0	N
Fall 2013	EEB464	Macroevolution	3	30	100	L	0	Y
Fall 2013	EEB504*	HOFF	1	11	25	L	0	N
Fall 2013	EEB511*	Core	4	19	50	L	0	N

*My responsibility for the Core course varies from 13% to 50%. My involvement for the HOFF course varies from 25% to 33%.

SAIS REPORTS

Sem/Year	Course/Hrs	No. of Students	No. of Responses	Course Overall	Course Content	Instructor's Contribution	Teaching Effectiveness
Spring 2010	EEB409/3	13	11	3.55	3.73	4.09	3.55
Spring 2010	EEB607/1	9	6	3.67	3.83	4.00	3.83
Fall 2011	EEB464/3	24	17	4.24	4.18	4.35	4.24
Fall 2011	EEB503/1	44	18	4.00	3.88	4.25	4.25
Spring 2012	Bio130/3	206	102	3.05	3.14	3.04	2.67
Fall 2012	EEB464/3	22	14	4.36	4.29	4.64	4.36
Fall 2012	EEB607/1	5	5	4.80	4.80	5.00	5.00

Range: 0-5; 5 = excellent, 0 = very poor

PEER REVIEW OF TEACHING

Sandy Echternacht has reviewed my teaching; Randy Small has also attended one of my lectures for Bio130. In Spring 2014 Mike Gilchrist, Ed Schilling, and Sally Horn evaluated my teaching.

GRADUATE SUPERVISION

Summary of Graduate Dissertation (Doctoral) Supervision

Name	Graduation Year	Dissertation Title	Placement
Katie Massana	Started Fall 2012	Statistical biogeography	
Jen Bosco (advisor Riechert; I am co-advisor)	Started Fall 2012	Evolution of spider behavioral traits	
Orlando Schwery	Started Fall 2014	Phylogenetic methods	

Summary of Graduate Dissertation (Masters) Supervision

Name	Graduation Year	Dissertation Title	Placement
Sam Borstein	Started Fall 2013	Cichlid evolution	

GRADUATE COMMITTEES

Name	Dept.	Degree	Project Title	Date Completed
Phillip Hollingsworth	EEB	PhD	Fish evolution	
Ivan Juric	EEB	PhD	Population evolution	
Leonidas Salichos	Vanderbilt	PhD	On the identification of factors influencing phylogenetic accuracy	
Will Atwood	Geology	PhD	Examining Pentremitidae: Species Discrimination, Systematics, and Ontogeny	
Mauricio González Forero	EEB	PhD	Major evolutionary transitions mediated by manipulation	
Sharon Clemmensen	EEB	PhD	Fish evolution	
Will Howell	EEB	PhD	Protein evolution	
Max Rupp	EEB	Masters	Fish evolution and behavior	
Troy Fadiga	Geology	PhD	Echinoderm evolution	
Geetha Saarunya S	GST	PhD	Function and evolution of permafrost bacteria	
Jordan Utley	GST	PhD	Rapid detection of pathogens	

POSTDOCTORAL MENTEES

Name	Funding
Hugo Alamillo	Startup
Barb Banbury	iPlant
Jeremy Beaulieu	NIMBioS
JJ Chai	NIMBioS
Nathan Jackson	NSF
Tony Jhwueng	NIMBioS
Sandy Kawano	NIMBioS
Michelle Lawing	NIMBioS
Ryan Martin	NIMBioS
Nick Matzke	NIMBioS

C. RESEARCH, SCHOLARSHIP, CREATIVE ACTIVITY

CANDIDATE'S STATEMENT

My research addresses key questions in macroevolution to understand the processes leading to present diversity. I do this through construction and extensive testing of new approaches and the implementation of these in user-friendly software, as well as by examination of particular biological examples. These papers aim to be major works that move the field rather than mere examples of things we already know. One focus in my work has been dealing with heterogeneity of biological processes. The factors affecting oak tree evolution probably differ from those affecting water lily evolution, but nearly all methods apply the same set of parameters to all taxa being investigated. My work on dealing with different evolutionary rates (O'Meara et al. 2006) has been cited 241 times and has been used for things as varied as fish jaw evolution and flower size. This work has continued to deal with heterogeneity of multiple parameters for a single trait on a tree (Beaulieu et al. 2012). Work on discrete characters (O'Meara 2007) has also been extended to deal with hidden rates (Beaulieu et al. 2013). In the lab we have also created a general forward in time simulation model that was featured in an invited Evolution symposium in 2012. I have also coauthored other publications using or testing various phylogenetic methods (Farrell et al. 2001; Driskell et al. 2004; Collar et al. 2009; Smith and O'Meara 2009; Collar et al. 2010; Abercrombie et al. 2011; Hulsey et al. 2013; Soltis et al. 2013; Jhwueng et al. 2014; Williams et al. 2014).

I have also worked on species delimitation (O'Meara 2010). An NSF grant based on using these techniques, with others, on fungal datasets, with PI Karen Hughes and me as one of the CoPIs, was recently funded. I have continued to develop the method, which was presented at a different Evolution symposium in 2013. I was also PI on a preproposal and proposal based on this work which resulted in a grant awarded in the past round, which includes $340,000 for UTK as well as additional funds for my CoPI Bryan Carstens. This is funding another postdoc in my lab; we are currently finishing simulations for a manuscript we will submitting to *PNAS*.

Another aspect of research effort has been on extending phylogenetic models. From collaborations with JJ Chai, a NIMBioS postdoc, and Mike Gilchrist, a faculty member in EEB at UTK, I have helped to create codon and amino acid models which use explicit parameters about optimal amino acids, strength of selection, and amino acid similarities to create transition

matrices for phylogenetic inference with realistic features such as different rates for different optimal amino acids and unequal gain and loss rates for amino acids or codons (it is more likely to evolve towards a codon representing the optimal amino acid than away from it, for example). We have recently been awarded $520K from the NSF to continue this work (me as PI, Dr. Gilchrist as Co-PI) and are readying a publication on the approaches. Our source code for the model is an R package available on github.

Another creative activity has been making sure that other biologists can do analyses. This has resulted in papers on re-usability of trees (Stoltzfus et al. 2012), hackathons to create new tools (Stoltzfus et al. 2013), and cyberinfrastructure for phylogenetics (Goff et al. 2011), for which my lab received a total of $369,187 from three sets of funding. We have also received $50,000 from the Encylopedia of Life as a Rubenstein fellowship to Barb Banbury with summer funding for me as well for an R interface to the Encyclopedia of Life (Banbury and O'Meara 2014). Work has also involved developing fast algorithms for analyses (Smith and O'Meara 2012) and new implementations of my software (Stack et al. 2011) (funded by Google Summer of Code).

I have also been involved in reviews, often invited, of comparative methods or phylogenetics, including a review of methods for the *Annual Review of Ecology, Evolution, and Systematics* (O'Meara 2012) (which was the most downloaded paper in the journal), a chapter on phylogenetic reconstruction in the *Encyclopedia of Theoretical Ecology* (Hastings and Gross 2012), a review of phylogenetic methods in R (O'Meara 2014), and book chapters (Beaulieu and O'Meara 2014; O'Meara and Beaulieu 2014) as well as other invited works in prep.

There is other work in the pipeline that is not listed here. For example, I am lead author on a manuscript on floral evolution that pioneers use of multiple characters simultaneously to look at their joint effect on diversification and transition and show the importance of non-equilibrium processes in structuring life; this was reviewed and rejected for *PNAS* and is being revised for a mid-tier journal. I am revising a manuscript for *Systematic Biology* on extending comparative methods for a network. By the time this tenure packet is due (mid-October, 2014), a manuscript about settlement bias of plants on Hawaii and a manuscript about a new general diversification

model will be in review. A paper questioning the widespread belief that extinction cannot be estimated from neontological phylogenies is currently in review at *Evolution*.

RESEARCH AND SCHOLARLY PUBLICATIONS

My work is highly cited, with 1138 citations overall, 925 since 2009 alone.

Abercrombie, J. M., B. C. O'Meara, A. R. Moffatt, and J. H. Williams. 2011. Developmental evolution of flowering plant pollen tube cell walls: callose synthase (CalS) gene expression patterns. EvoDevo 2:14.

Banbury, B. L. and B. C. O'Meara. 2014. Reol: R interface to the Encyclopedia of Life. Ecology and Evolution.

Beaulieu, J. M., D.-C. Jhwueng, C. Boettiger, and B. C. O'Meara. 2012. Modeling Stabilizing Selection: Expanding the Ornstein-Uhlenbeck Model of Adaptive Evolution. Evolution 66:2369-2383.

Beaulieu, J. M. and B. C. O'Meara. 2014. Hidden Markov Models for Studying the Evolution of Binary Morphological Characters. Pp. 395-408 in L. Z. Garamszegi, ed. Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology. Springer-Verlag, Berlin.

Beaulieu, J. M., B. C. O'Meara, and M. J. Donoghue. 2013. Identifying hidden rate changes in the evolution of a binary morphological character: the evolution of plant habit in campanulid angiosperms. Systematic biology.

Collar, D. C., B. C. O'Meara, P. C. Wainwright, and T. J. Near. 2009. Piscivory Limits Diversification of Feeding Morphology in Centrarchid Fishes. Evolution 63:1557-1573.

Collar, D. C., J. A. Schulte, B. C. O'Meara, and J. B. Losos. 2010. Habitat use affects morphological diversification in dragon lizards. Journal of Evolutionary Biology 23:1033-1049.

Driskell, A. C., C. Ane, J. G. Burleigh, M. M. McMahon, B. C. O'Meara, and M. J. Sanderson. 2004. Prospects for building the tree of life from large sequence databases. Science 306:1172-1174.

Farrell, B. D., A. S. Sequeira, B. C. O'Meara, B. B. Normark, J. H. Chung, and B. H. Jordal. 2001. The evolution of agriculture in beetles (Curculionidae : Scolytinae and Platypodinae). Evolution 55:2011-2027.

Goff, S. A., M. Vaughn, S. McKay, E. Lyons, A. E. Stapleton, D. Gessler, N. Matasci, L. Wang, M. Hanlon, A. Lenards, A. Muir, N. Merchant, S. Lowry, S. Mock, M. Helmke, A. Kubach, M. Narro, N. Hopkins, D. Micklos, U. Hilgert, M. Gonzales, C. Jordan, E. Skidmore, R. Dooley, J. Cazes, R. McLay, Z. Lu, S. Pasternak, L. Koesterke, W. H. Piel, R. Grene, C. Noutsos, K. Gendler, X. Feng, C. Tang, M. Lent, S.-J. Kim, K. Kvilekval, B. S. Manjunath, V. Tannen, A. Stamatakis, M. Sanderson, S. M. Welch, K. A. Cranston, P. Soltis, D. Soltis, B. O'Meara, C. Ane, T. Brutnell, D. J. Kleibenstein, J. W. White, J. Leebens-Mack, M. J. Donoghue, E. P. Spalding, T. J. Vision, C. R. Myers, D. Lowenthal, B. J. Enquist, B. Boyle, A. Akoglu, G. Andrews, S. Ram, D. Ware, L. Stein, and D. Stanzione. 2011. The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in plant science 2:34-34.

Hastings, A. and L. J. Gross. 2012. Encyclopedia of theoretical ecology. University of California Pr.

Hulsey, D. C., B. P. Keck, H. Alamillo, and B. C. O'Meara. 2013. Mitochondrial genome primers for Lake Malawi cichlids. Molecular ecology resources 13:347-353.

Jhwueng, D.-C., S. Huzurbazar, B. C. O'Meara, and L. Liu. 2014. Investigating the performance of AIC in selecting phylogenetic models. Statistical applications in genetics and molecular biology.

O'Meara, B. C. 2007. Estimating Different Rates of Gene Loss on a Tree. Genetics 177:1415-1416.

O'Meara, B. C. 2010. New Heuristic Methods for Joint Species Delimitation and Species Tree Inference. Systematic Biology 59:59-73.

O'Meara, B. C. 2012. Evolutionary Inferences from Phylogenies: A Review of Methods. Annual Review of Ecology, Evolution, and Systematics 43.

O'Meara, B. C. 2014. CRAN Task View: Phylogenetics. Version 2014-07-17, URL http://cran.r-project.org/web/views/Phylogenetics.html.

O'Meara, B. C., C. Ane, M. J. Sanderson, and P. C. Wainwright. 2006. Testing for different rates of continuous trait evolution using likelihood. Evolution 60:922-933.

O'Meara, B. C. and J. M. Beaulieu. 2014. Modelling Stabilizing Selection: The Attraction of Ornstein–Uhlenbeck Models. Pp. 381-393 in L. Z. Garamszegi, ed. Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology. Springer-Verlag, Berlin.

Smith, S. A. and B. C. O'Meara. 2009. Morphogenera, monophyly, and macroevolution. Proceedings of the National Academy of Sciences of the United States of America 106:E97-E98.

Smith, S. A. and B. C. O'Meara. 2012. treePL: Divergence time estimation using penalized likelihood for large phylogenies. Bioinformatics.

Soltis, D. E., M. E. Mort, M. Latvis, E. V. Mavrodiev, B. C. O'Meara, P. S. Soltis, J. G. Burleigh, and R. Rubio de Casas. 2013. Phylogenetic Relationships and Character Evolution Analysis of Saxifragales Using a Supermatrix Approach. American Journal of Botany 100:916-929.

Stack, J. C., L. J. Harmon, and B. O'Meara. 2011. RBrownie: an R package for testing hypotheses about rates of evolutionary change. Methods in Ecology and Evolution 2:660-662.

Stoltzfus, A., H. Lapp, N. Matasci, H. Deus, B. Sidlauskas, C. M. Zmasek, G. Vaidya, E. Pontelli, K. Cranston, R. Vos, C. O. Webb, L. J. Harmon, M. Pirrung, B. O'Meara, M. W. Pennell, S. Mirarab, M. S. Rosenberg, J. P. Balhoff, H. M. Bik, T. A. Heath, P. E. Midford, J. W. Brown, E. J. McTavish, J. Sukumaran, M. Westneat, M. E. Alfaro, A. Steele, and G. Jordan. 2013. Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. Bmc Bioinformatics 14.

Stoltzfus, A., B. O'Meara, J. Whitacre, R. Mounce, E. L. Gillespie, S. Kumar, D. F. Rosauer, and R. A. Vos. 2012. Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. BMC research notes 5:574-574.

Williams, J. H., M. L. Taylor, and B. C. O'Meara. 2014. Repeated evolution of tricellular (and bicellular) pollen. American Journal of Botany 101:559-571.

PROJECTS, GRANTS, COMMISSIONS, AND CONTRACTS

Since starting at UTK approximately four years ago, I have turned in 23 grants through TeraPams; this includes 16 I have submitted through NSF Fastlane (this includes 12 full proposals and 4 preproposals). Of the 21 that are no longer pending, 8 were awarded (this includes three preproposals). I have been awarded $880,330 in external funds, $689,187 of this as PI. Funds for working groups and large group proposals in which I am not at least a Co-PI are not included in that total or below.

External Funding

Completed

2013: Encyclopedia or Life: "Reol, an R interface to Encyclopedia of Life data." PI Barb Banbury, Subcontractor Brian O'Meara. **$50,000.**

2010-2012: NSF/iPlant: "iPlant-iPToL" PI Mike Sanderson, Co-PIs Michael Donoghue, Pam Soltis, Doug Soltis, Val Tannen, Alexis Stamatakis, Todd Vision. I ran the trait evolution working group, which included two months of summer salary for me and funding for a postdoc for this year and next year. Note that I was not part of the initial proposal (thus not an official PI/co-PI), but was invited to become part of it once it was funded and I function as a co-PI. Funds from NSF via iPlant via University of Arizona. $132,345 to UTK in year 1, $138,590 in year 2 for **$270,935** in total.

2012-2013: NSF/iPlant: "rPlant" funding for a postdoc and summer salary based on a white paper I submitted. **$98,252**

2012: Google: "Optimizing R code for approximate Bayesian computing" Google Summer of Code 2012. **$5000** by Google to pay for U of Nebraska graduate student Daniel Gates to work on speeding up code I wrote. Note that my postdoc, Barb Banbury, and a colleague at U. of Arizona, Derrick Zwickl, handled the mentoring. Funds went directly to the student, not through UTK.

2010: Google: "Ancestral State Reconstruction in R" Google Summer of Code 2010. **$5000** by Google to pay for Penn State graduate student Conrad Stack to work on putting my program Brownie into the R programming language. I was primary mentor, Luke Harmon was co-mentor. Funds went directly to the student, not through UTK.

Funded and In Progress

2014: NSF: "Population Genetics-based Codon Models." PI Brian O'Meara, Co-PI Mike Gilchrist. Amount for UTK: **$520,000**. Funding years 2014-2016.

2013: NSF: "Phylogeographic inference using approximated likelihoods." PI Brian O'Meara, Co-PI Bryan Carstens. Amount for UTK: **$340,000**. Funding years 2013-2015.

2012: NSF: "Historical naming traditions and cryptic speciation bias biodiversity estimates in transatlantic agaric fungi." PI: Ronald Petersen. Co-PIs Brian O'Meara and Karen Hughes. Amount requested for UTK: **$141,143** [though note that the bulk of this goes to Petersen and Hughes, with just summer salary going to me]. Funding years 2012-2014

Under review

(Note that this section still needs to be updated)

Successful Pre-proposals
Some NSF programs now require a preproposal to be approved before a full proposal is invited;
invitation rates are approximately 25%.
2013: NSF: "Preproposal: Population Genetics-based Codon Models". PI Brian O'Meara, Co-PI
Mike Gilchrist, Co-PI Russell Zaretzki.

2011: NSF: "Preproposal: Phylogeny and diversification of Lake Malawi Cichlid Flock". PI Darrin
Hulsey, Co-PI Brian O'Meara.

2011: NSF: "Preproprosal: Phylogeographic inference using approximated likelihoods". PI Brian
O'Meara, Co-PI Bryan Carstens.

Unsuccessful grant proposals
2013: Templeton Foundation: Evolution of Play. PI Gordon Burghardt, Co-PI Brian O'Meara.
Declined. Budget: $199,912.

2012: NSF: "Phylogeny and Diversification of Lake Malawi Cichlid Flock". PI Darrin Hulsey, Co-PI
Brian O'Meara. Declined. Budget: $626,470.

2012: Templeton Foundation: Evolution of Play. PI Gordon Burghardt, Co-PI Brian O'Meara.
Declined. Budget: $263,763.

2011: NSF: "Collaborative Research: Phylogeographic Inference using approximated likelihoods" PI
Brian O'Meara, Co-PI Bryan Carstens. Declined. Amount requested for UTK: $329,790

2012: NSF: "Collaborative Research: Assembly the Tree of Life: Interactive Heuristics in Tree
Search (inHits)". PI Michael Sanderson, Co-PI Michelle McMahon, Co-PI Derrick Zwickl, Co-PI
Brian O'Meara, Co-PI Oliver Eulenstein, Co-PI David Fernandez-Baca, Co-PI Stephen Smith.
Declined. Amount requested for UTK: $220,115 (approx. $2M in funding for entire grant)

2011: NSF: "Making comparative methods as easy as ABC" PI: Brian O'Meara. Declined. Amount
requested for UTK: $301,016

2011: NSF: "Preproposal: Participation in AVAToL ideas lab" PI Brian O'Meara. Declined.

2011: NSF: "Dimensions: Collaborative Research: How do Plant-Insect Interactions Generate
Biodiversity? -A Case Study of Euphorb Vines (Euphorbiaceae: Plukenetieae) and Their Insect
Associates" proposal to NSF Dimensions of Biodiversity. Modification and resubmission of above
grant. PI Scott Armbruster, Co-PI Bruce Baldwin. Senior collaborators: André Freitas, Niklas
Wahlberg, Silvana Buzato, Narcísio Costa Bigio, Ricardo Secco, Lynn Gillespie, Christophe
Pélabon, Thomas Hansen, Hans Stenoien , Terry Griswold, Bryan Danforth, Brian O'Meara.
Declined. Amount requested for UTK: $298,826

2010: NSF "SI2-SSE: Phylogenetic needs discovery environment". PI: Brian O'Meara. Declined.
Amount requested for UTK: $454,353

2010: NSF: "Phylogeny and Diversification of Lake Malawi Cichlid Flock" PI Darrin Hulsey, Co-PI Brian O'Meara. Declined. Amount requested for UTK: $527,895

2010: NSF: "Making comparative methods as easy as ABC" PI: Brian O'Meara. Declined. Amount requested: $275,288

2010: NSF: "Dimensions: Collaborative Research: How do Plant-Insect Interactions Generate Biodiversity? -A Case Study of Euphorb Vines (Euphorbiaceae: Plukenetieae) and Their Insect Associates" proposal to NSF Dimensions of Biodiversity. PI Scott Armbruster, Co-PI Bruce Baldwin. Senior collaborators: André Freitas, Niklas Wahlberg, Silvana Buzato, Narcísio Costa Bigio, Ricardo Secco, Lynn Gillespie, Christophe Pélabon, Thomas Hansen, Hans Stenoien , Terry Griswold, Bryan Danforth, Brian O'Meara. Declined. Amount requested for UTK: $205,836

OTHER EVIDENCE OF RESEARCH OR SCHOLARSHIP

I am the maintainer for the CRAN Phylogenetics Task View. This is an overview of the implementations of phylogenetic methods in the popular programming language R. According to statistics compiled by Bob Muenchen, R is used in over 14,000 scientific papers per year and its help list has over 13,000 subscribers. I am one of only 31 maintainers of task views for all these users.

While many people who develop new techniques merely publish them, one focus of my research is making well-tested software implementations available. This software is all open source, allowing others to improve upon it. Some of this software includes:

Lampyr: A web app for teaching about biodiversity. http://lampyr.org
corHMM: R package for dealing with discrete trait evolution. http://cran.r-project.org/web/packages/corHMM/index.html
OUwie: R package for dealing with continuous trait evolution. http://cran.r-project.org/web/packages/OUwie/
Brownie: C++ software for species delimitation and trait evolution. http://brianomeara.info/brownie
DateLife: Web service and underlying software for estimating divergence dates for taxa. http://datelife.org/
Reol: R package for extracting information from the Encyclopedia of Life. http://reolblog.wordpress.com/
rPlant: R package to interact with NSF-sponsored high performance computing. http://cran.r-project.org/web/packages/rPlant/index.html
phrapl: R software for testing phylogeographic hypotheses. https://r-forge.r-project.org/projects/phrapl/

PUBLIC TALKS

Note that this section still needs to be updated (Sept 2014)

June 22, 2013: Invited symposium talk at Evolution on "Simulated likelihood for species delimitation and phylogeography"

Aug 17, 2012: Invited talk on "Making comparative methods as easy as ABC" to the U. of Georgia Institute of Bioinformatics

July 9, 2012: Talk at iEvoBio on "DateLife: When lineages meet"

July 7, 2012: Invited symposium talk at Evolution on "Approximate Bayesian computation for continuous characters"

April 17, 2012: Invited talk on "Making comparative methods as easy as ABC" at the Smithsonian.

April 16, 2012: Invited talk on "Making comparative methods as easy as ABC" as one of three speakers for U. of Maryland's "Organismal Biology Day"

Oct. 3, 2011: Invited departmental talk on "Making comparative methods as easy as ABC" at U. of Florida

Sept. 15, 2011: Invited departmental talk on "Making comparative methods as easy as ABC" at U. of Alabama

May 1, 2011: Invited talk on "Phylogenetics" to Rationalists of East Tennessee

March 30, 2011: Invited talk on "Making comparative methods as easy as ABC" at phyloseminar.org (meeting hosted online)

Nov. 8, 2010: Invited talk on "Phylogenetics" at iPlant site visit by NSF

May 24, 2010: Invited talk on "Phylogenetics" at iPlant community outreach meeting in Las Vegas.

April 26, 2010: "Species delimitation": Invited departmental talk at Louisiana State University.

November 3, 2009: Invited talk on "Species delimitation" at National Institute for Biological and Mathematical Synthesis

Oct. 14, 2009: Invited talk on my history in Science at National Institute for Biological and Mathematical Synthesis

D. INSTITUTIONAL, DISCIPLINARY, AND/OR PROFESSIONAL SERVICE

CANDIDATE'S STATEMENT

I contribute to service within the department, throughout the University, and in the broader academic community. Within the department I serve as the head of the web committee, and for years maintained the department website personally, including 76 blog posts with department news. I was the point contact for the recent move of the department web site to new templates by the UT Communications group, and I continue to oversee our website, including our extension into social media. While doing this service, I have also served on the undergraduate curriculum committee and, currently, on the graduate admissions committee. I am also an active participant in departmental questions such as the search for the next head or ways to improve our core course.

In the College and University, I contribute through serving on the Dean of Arts and Sciences' Advisory Committee, both by giving feedback on various questions the Dean poses as well as, when appropriate, communicating ideas from the Dean to our department's faculty. I also am the faculty advisor for Darwin Day Tennessee, a long-running student-organized event that successfully educates students and members of the local community about evolution and related topics. Last year we invited Nobel Prize winner Camille Parmesan to campus to talk about evolution and climate change, while also educating local teachers through a workshop. I organized a cross-department discussion and speaker series about women in science issues, funded via an internal Haines-Morris grant.

I contribute extensively to service in the broader scientific community. I am an elected member of the Council for the Society of Systematic Biologists, publisher of one of the most highly cited journals in evolutionary biology. I am a member of the Phylotastic hackathon leadership team, a group that arranges funding for developers to meet to work together on coding solutions to problems in evolutionary biology. I have been in two invited symposia at our field's major international meetings, the Evolution meetings. I initiated and organized the lightning talks at the most recent Evolution meeting and have been asked to do it at the next Evolution meeting. I have recently been asked to join the leadership team of the iEvoBio meeting, a meeting that overlaps with the Evolution meeting and which focuses on bioinformatics research for evolutionary biology. I review for NSF, *Science*, and many other journals. I also have a strong online media presence as a scientist, with 52 YouTube videos of my talks and lectures (watched a total of 3,282 minutes by the public, and available at https://www.youtube.com/user/bcomeara), 459 followers on Twitter (including faculty from around the world, and available at https://twitter.com/omearabrian), and prominent placement of my personal website in search results (for example, for a widely used statistical approach, the Akaike Information Criterion (AIC), my personal website is the second listing on Google and third listing on Bing; my website overall received 3,200 hits last month alone).

INSTITUTIONAL SERVICE

Record of committee work at department, college, and university levels

Served on strategic planning committee

Served on seminar planning committee

Served on website committee: created department blog, updated website.

Served on undergraduate curriculum committee

Served on graduate admissions committee

Wrote and received grant for laptop teaching cart for EEB

Dean's Advisory Committee

DISCIPLINARY SERVICE

Record of membership and active participation in professional societies
Society of Systematic Biologists, elected member of Council

Evaluation of peer research-
I have been a reviewer for *Science,* NSF*, Systematic Biology, Bioinformatics, Evolution, Nucleic Acids Research, Ecology,* and iEvoBio, among others.