CURRICULUM VITAE

ALAN R. LEMMON

Date of Birth: April 21, 1976 E-mail: alemmon + 'at' + evotutor.org Phone: 850.445.4393 (cell); 850.644.0098 (fax) Mailing Address: Dept. of Scientific Computing, Florida State University, Dirac Science Library, Tallahassee, FL 32306-4120

ACADEMIC HISTORY

Assistant Professor Department of Scientific Computing, Florida State University (12/2008-present)
Postdoctoral Fellow Center for Population Biology, U. of California at Davis (9/2007-12/2008)
Ph.D. Ecology, Evolution, and Behavior, University of Texas – Austin (2001-2007) *Dissertation Title:* Analytical, Computational, and Statistical Approaches to Studying Speciation
Research Associate Laboratory of Evolutionary Genetics, Free University of Brussels (1/2001-7/2001)
B.A. Environmental, Population, and Organismal Biology;
Molecular, Cellular, and Developmental Biology, University of Colorado – Boulder (1995-2000)

AWARDS

First Year Assistant Professor Award, Florida State University: **\$17,000** (5/2009-8/2009) **Publisher's Award** for the Best Student Paper Published in Systematic Biology, 2008: **\$500** (6/2009) NSF **I.G.E.R.T. Fellowship** in Computational Phylogenetics: **\$81,000** (9/2005-8/2007) **Publisher's Award** for the Best Student Paper Published in Systematic Biology, 2004: **\$500** (6/2005) NSF **Graduate Research Fellowship**: **\$100,000** (9/2002-8/2005)

PUBLICATIONS / MANUSCRIPTS (most available at http://www.evotutor.org/pdfs)

- Lemmon, A. R. and E. M. Lemmon. *In Prep*. High resolution analyses of diploid nuclear genomes reveals unexpected levels of genetic diversity. To be submitted to **PNAS**.
- Lemmon, A. R. *In Prep*. Nuclear genome contains thousands of rapidly evolving genes useful for accurate gene tree estimation within-species. To be submitted to **MOLECULAR ECOLOGY**.
- Rokyta, D. R., K. P. Wray, A. R. Lemmon, and E. M. Lemmon. *In Review*. A high-throughput venomgland transcriptome for the Eastern Diamondback Rattlesnake (Crotalus adamanteus) and evidence for pervasive positive selection across toxin classes. **TOXICON**.
- Deiner, K, A. R. Lemmon, A. L. Mack, R. C. Fleischer, and J. P. Dumbacher. *In Review*. A passerine bird's evolution corroborates the geological history of the island of New Guinea. **PLOS ONE**.

- Lemmon, E. M., and A. R. Lemmon. <u>2010</u>. Reinforcement in chorus frogs: lifetime fitness estimates including intrinsic natural selection and sexual selection against hybrids. **EVOLUTION** 64:1748-1761.
- Brown J. M., S. M. Hedtke, A. R. Lemmon, and E. M. Lemmon. <u>2010</u>. When trees grow too long: investigating the causes of highly inaccurate Bayesian branch lengths. **SYSTEMATIC BIOLOGY** 59:145-161.

..... Manuscripts below submitted before arrival at FSU.....

- Lemmon, A. R., J. M. Brown, C. Stanger-Hall, and E. M. Lemmon. <u>2009</u>. The effect of ambiguous data on phylogenetic estimates obtained by obtained by maximum-likelihood and Bayesian inference. SYSTEMATIC BIOLOGY 58:130-145.
- Lemmon, A. R., and E. M. Lemmon. <u>2008</u>. A likelihood framework for estimating phylogeographic history on a continuous landscape. **SYSTEMATIC BIOLOGY** 57:544-561.
- Lemmon, E. M., A. R. Lemmon, J. T. Collins, and D. C. Cannatella. <u>2008</u>. A new North American chorus frog species (Amphibia: Hylidae: *Pseudacris*) from the south-central United States **ZOOTAXA** 1675:1-30.
- Lemmon, E. M., A. R. Lemmon, J. T. Collins, J. A. Lee-Yaw, and D. C. Cannatella. <u>2007</u>. Phylogenybased delimitation of species boundaries in the trilling chorus frogs (*Pseudacris*). **MOLECULAR PHYLOGENETICS AND EVOLUTION** 44:1068-1082.
- Brown, J. M., and A. R. Lemmon. 2007. The importance of data partitioning and the utility of Bayes factors in Bayesian phylogenetics. **SYSTEMATIC BIOLOGY** 56:643-655.
- Lemmon, E. M., A. R. Lemmon, and D. C. Cannatella. <u>2007</u>. Geological and climatic forces driving speciation in the continentally distributed trilling chorus frogs (*Pseudacris*). EVOLUTION 61:2086-2103.
- Lemmon, A. R., and M. Kirkpatrick. <u>2006</u>. Reinforcement and the genetics of hybrid incompatibilities. **GENETICS** 173:1145-1155.
- Lemmon, A. R., C. Smadja, and M. Kirkpatrick. <u>2004</u>. Reproductive character displacement is not the only possible outcome of reinforcement. **JOURNAL OF EVOLUTIONARY BIOLOGY** 17: 177-183.
- Lemmon, A. R., and E. C. Moriarty. <u>2004</u>. The importance of proper model assumption in Bayesian phylogenetics. **SYSTEMATIC BIOLOGY** 53:265-277.
- Lemmon, A. R., and M. C. Milinkovitch. <u>2002</u>. The metapopulation genetic algorithm: an efficient solution for the problem of large phylogeny estimation. **PNAS** 99:10516-10521.

SOFTWARE DEVELOPED

Phylogenetic

PhyloMapper Maximum likelihood estimation of ancestral geographic location Version 1.0 released: September 2008

MrConverge Convergence diagnostics for Bayesian phylogenetics Unreleased

metaPIGA Phylogenetic estimation using a metapopulation genetic algorithm Version 1.0 released August 2002 http://www.ulb.ac.be/sciences/ueg/html_files/MetaPIGA.html

Educational

EvoTutor Java simulations/tutorials of evolutionary processes Version 1.0 Released January 2001 http://www.evotutor.org Reviewed by Nature Reviews Genetics (2001, 2:832)

PROGRAMMING LANGUAGES

Java, C++, R

INVITED PRESENTATIONS

Targeted Phylogenetics

(12/2010) Invited Talk for IBEST Seminar Series University of Idaho, Initiative for Bioinformatics and Evolutionary Studies

Current and Future Genomic Resources for Frogs

(10/2009) Invited Talk for International Meeting on Frog Genomics University of Colorado at Boulder, Department of Biology

MEETING PRESENTATIONS

Will Sequence Capture for Non-Model Organisms Enable High-Throughput Sequencing for Targeted Phylogenetics? (6/2010)

Joint meeting for the Society for the Study of Evolution and the Society of Systematic Biologists Toward a Genomic Approach to Integrating Spatial Ecology and Statistical Phylogeography

(6/2008) Invited Symposium presentation.

Joint meeting for the Society for the Study of Evolution and the Society of Systematic Biologists A Likelihood Framework for Estimating Phylogeographic History Using Geographically

A Likelihood Framework for Estimating Phylogeographic History Using Geographically Continuous Genetic Data (6/2007)

Joint meeting for the Society for the Study of Evolution and the Society of Systematic Biologists Bayes Factors and Partition Choice in Phylogenetic Inference (6/2006)

Joint meeting for the Society for the Study of Evolution and the Society of Systematic Biologists **Reinforcement and the Genetics of Hybrid Incompatibilities** (6/2005)

Joint meeting for the Society for the Study of Evolution and the Society of Systematic Biologists **Convergence in Bayesian Phylogenetics** (6/2004)

Joint meeting for the Society for the Study of Evolution and the Society of Systematic Biologists

OTHER PRESENTATIONS

Targeted Phylogenetics (11/2009)

Florida State University - Department of Scientific Computing

Riding the Wave of New Genome Sequencing Technologies (4/2009) Florida State University – Department of Scientific Computing New Computational Approaches to Studying the Patterns and Processes of Speciation (3/2007) Florida State University - School of Computational Science **Processes Driving Speciation: from Geographic Isolation to Reinforcement** (2/2007) University of California at Davis – Center for Population Biology **Evolution of Reproductive Isolation in Hybrid Zones** (4/2006) University of California at Berkeley - Museum of Vertebrate Zoology **Speciation in Chorus Frogs** (4/2005) Florida Department of Environmental Protection **Reinforcement and the Genetics of Hybrid Incompatibilities** (4/2005) Southeastern Louisiana University **Reinforcement and the Genetics of Hybrid Incompatibilities** (11/2004) University of Texas at Austin Population Biology Seminar Neural Networks (12/2000) University of Colorado at Boulder **EvoTutor: The Web as a Pedagogical Tool** (11/2000) University of Northern Colorado

PROFESSIONAL SERVICE

Editorial Board Member for SYSTEMATIC BIOLOGY

Reviewer for: NATIONAL SCIENCE FOUNDATION PLOS ONE Systematic Biology Evolution Journal of Molecular Evolution Heredity Biochemical Genetics

COURSES DEVELOPED

NEXT-GENERATION SEQUENCING AND ANALYSIS BIOINFORMATICS COLLECTION AND ANALYSIS OF BIOLOGICAL DATA