Jonathan Paul Bollback, Ph.D – Curriculum Vitae

Postdoctoral Research Scientist
Institute of Evolutionary Biology
School of Biological Sciences
King's Buildings, West Mains Road
University of Edinburgh
Edinburgh EH10 5HY UK
Phone: +44 131 650 8683
Fax : +44 131 650 5456
Email: j.p.bollback@ed.ac.uk
Web: people.binf.ku.dk/∼bollback/

Academics

Degrees Awarded

Ph.D. (Evolutionary Genetics)	March, 2005 University of Rochester, USA
Masters of Science (Evolutionary Genetics)	December, 2000 University of Rochester, USA
Bachelor of Science (Biology)	August, 1995 University of Maryland, USA

History

2005-Present	Postdoctoral Research Associate	University of Copenhagen	Dr. Nielsen
1998-2004	Doctoral Student	University of Rochester	Dr. Huelsenbeck
1995-1998	Masters Student	University of Maryland - College Park	Dr. Borgia
1993-1995	Undergraduate Studies	University of Maryland - College Park	
1990-1993	Undergraduate Studies	SUNY - College at Purchase	

Scientific Impact

Invited Lectures

1) October, 2007. Title: Experimental evolution: the genetics of adaptation, parallel evolution and interference. — First EES Conference — Munich School Ludwig-Maximilians-University, Munich, Germany
2) April, 2007. Title: Experimental microbial evolution: mutation and selection during adaptation. — Mathematical Genetics of Selection and Adaptation — University of Aarhus
3) October, 2005. Title: Stochastic character mapping of morphological traits in evolutionary studies. — Reunión Anual Sociedad de Biología de Chile, Sociedad de Ecología - Sociedad de Botánica
4) May, 2005. Title: An experimental evolutionary study of the frequency of parallel genetic evolution within and between species. — Evolutionary Biology Center, Uppsala Universitet, Uppsala, Sweden
5) March, 2005. Title: Ancestral character reconstruction: Bayesian ancestral state reconstruction and stochastic character histories. — Symposium: Using Ancestral Sequence Reconstruction to Understand Protein Function, Kristineberg, Sweden
6) November, 2003. Title: Bayesian phylogenetic inference and character mapping. — Journees de la Société Française de Systématique, Muséum National d'Historie Naturelle, Paris, France
7) August, 2002. Title: Model selection and model adequacy. — Bayesian inference of phylogeny and molecular evolution, Ph. D. Student course — Department of Systematic Zoology, Uppsala University, Uppsala, Sweden.
8) December, 2001. Title: Bayesian model adequacy and choice in phylogenetics. — Department of Biologie II, Evolutionary Biology, Ludwig-Maximilians-University, Munich, Germany
9) April, 1997. Title: Development and Application of Microsatellites in Behavioral Ecology. — Department of Zoology, University of Maryland — Course Instructor: Dr. Ulrich Mueller
10) Fall, 1996. Title: Microsatellites in Studies of Molecular Systematics. — Department of Plant Biology, University of Maryland — Course Instructor: Dr. Charles Delwiche

Presented Papers

1) 2008. Reassortment and recombination in influenza. The Third European Influenza Conference. Vilamoura, Portugal.
2) 2005. An experimental evolutionary study of the frequency of parallel genetic evolution within and between species. SSE/SSB Conference, University of Alaska - Fairbanks, Alaska
3) 2000. Inferring the root of a phylogenetic tree. Co-authors: John P. Huelsenbeck and Amy Levine — SSE/SSB Conference, Indiana University Bloomington, Bloomington Indiana
4) 1999. Comparative performance of gamma and site-specific methods for accommodating among site rate variation. Co-authors: John P. Huelsenbeck — SSE/SSB Conference, University of Wisconsin, Madison Wisconsin

Journal Reviewer

I participate as peer reviewer for the following international scientific journals: *Evolution*, *Journal of General Virology*, *Journal of Molecular Evolution*, *Molecular Biology and Evolution*, *Molecular Phylogenetics and Evolution*, and *Systematic Biology*.

Scientific Software

SIMMAP: Stochastic Mutational Mapping on Phylogenies.
Program Description: A program for stochastically mapping discrete molecular and morphological characters. Program evaluates the posterior history of characters facilitating addressing questions in molecular and phenotypic evolution. SIMMAP uses predictive distributions to test a variety of hypotheses of character evolution.
Current version: 1.0 B2.3
Download Source: http://www.simmap.com

MAPPS: Model Analysis using Posterior Predictive Simulation.
Program Description: A program for determining Bayesian model adequacy and choice in molecular phylogenetics, and for generating the predictive distribution of data to be used in various hypothesis tests.
Current version: 1.1.5
Download Source: people.binf.ku.dk/∼bollback/

Awards, Honors, and Grants

2007-2008	Danish Agency for Science, Technology and Innovation The Danish Natural Science Research Council Forskningsrådet for Natur og Univers, FNU (Ref. No. 272-06-0316)
2006	Danish Agency for Science, Technology and Innovation Danish Medical Research Council Forskningsrådet for Sundhed og Sygdom, FSS (Ref. No. 271-05-0599)
1995-1998	Predoctoral Fellow, Laboratory of Molecular Systematics, Smithsonian Institution
1997	NSF Biology of Small Populations RTG Fellow, University of Maryland - College Park
1996	Sigma Xi Grant
1995	NSF REU Grant, University of Maryland - College Park
1993	Steckler Fellow, SUNY - College at Purchase

Research Experience

1997	Research Assistant, University of Vermont	Dr. Jan Conn
1994	Field Research Assistant, University of Maryland	Dr. Gerald Borgia and Dr. J. Albert Uy
1993	Research Assistant, SUNY Purchase	Dr. Barbara Dexter and Dr. Thomas Nalli
1993	Chemistry Lab Technician, SUNY Purchase	Dr. Taina Chao and Dr. Carlo Paravano

Teaching Experience

2007 Phylogenetics Lectures, University of Copenhagen
2006 Phylogenetics Lectures, University of Copenhagen
1999 Phylogenetics, University of Rochester
1999 Evolution, University of Rochester
1998 Vertebrate Zoology, University of Maryland - College Park
1997 Environmental Biology, University of Maryland - College Park
1996 Genetics, University of Maryland - College Park
1996 Environmental Biology, University of Maryland - College Park
1996 Vertebrate Physiology, University of Maryland - College Park
1995 Vertebrate Zoology, University of Maryland - College Park

Advisors, Collaborators, References

Advisors

Rasmus Nielsen, UC Berkeley — Post-doctoral Advisor 2005–2008 (University of Copenhagen)
John P. Huelsenbeck, UC Berkeley — Doctoral Advisor 1998–2004 (University of Rochester)
Gerald Borgia, University of Maryland — Graduate Advisor 1995–1998

Collaborators

Andrea J. Betancourt (University of Edinburgh)
Andrew J Leigh Brown (University of Edinburgh)
Ross Fitzgerald (University of Edinburgh - Medical School) Paul P. Gardner (Wellcome Trust Sanger Institute)
Travis C. Glenn (University of South Carolina)
Peter Gravlund (University of Copenhagen)
John P. Huelsenbeck (University of California, Berkeley)
Rasmus Nielsen (University of Copenhagen)
Andrew Rambaut (University of Edinburgh)
Jiaye Yu (University of Kansas)

References

Andrew J Leigh Brown, University of Edinburgh — A.Leigh-Brown@ed.ac.uk
Andrew Rambaut, University of Edinburgh — a.rambaut@ed.ac.uk
Rasmus Nielsen, University of Copenhagen — rasmus@binf.ku.dk
John P. Huelsenbeck, UC Berkeley — johnh@berkeley.edu

Publication List

Peer Reviewed Journals/Book Chapters (†)

1) **Jonathan P. Bollback** and John P. Huelsenbeck. (2009) Parallel Genetic Evolution Within and Among Bacteriophage Species of Varying Degrees of Divergence. *Genetics*. 180. *In Press*
2) **Jonathan P. Bollback**, Tom York, and Rasmus Nielsen. (2008) Estimation of $2N_e s$ From Temporal Allele Frequency Data. *Genetics*. 179: 497–502.
3) Petersen, L., **J. P. Bollback**, M. Dimmic, M. Hubisz, R. Nielsen. (2007) Genes under positive selection in *Escherichia coli*. *Genome Research*. 17: 1336–1343.
4) **Jonathan P. Bollback** and John P. Huelsenbeck. (2007) Clonal interference is alleviated by high mutation rates in large populations. *Molecular Biology and Evolution*. 24(6):1397–1406.
5) Jonas Binladen, M. T. P. Gilbert, **Jonathan P. Bollback**, F. Panitz, C. Bendixen, R. Nielsen, E. Willerslev. (2007) The use of coded PCR primers enables high-throughput sequencing of multiple homolog amplification products by 454 parallel sequencing. *PLoS ONE*. 2(2): e197.
6) Eva Freyhult, **Jonathan P. Bollback**, and Paul P. Gardner. (2007) Exploring genomic dark matter: homology search for non-coding RNA. *Genome Research*. 17:117–125.
7) Sheila M. Reynolds, Katie Dryer, **Jonathan P. Bollback**, J. Albert C. Uy, Gail L. Patricelli, Timothy Robson, Gerald Borgia, and Michael J. Braun (2007) Behavioral paternity predicts genetic paternity in satin bowerbirds, a species with a non-resource-based mating system. *The Auk*. 124(3):857–867.
8) **Jonathan P. Bollback**†, Paul P. Gardner, and Rasmus Nielsen. (2007) Estimating the history of mutations on a phylogeny. *In* "Ancestral Sequence Reconstruction" (Liberles, D. Ed.) Oxford University Press, UK.
9) **Jonathan P. Bollback** (2006) SIMMAP: Stochastic character mapping of discrete traits on phylogenies. *BMC Bioinformatics*. 7:88.
10) Jan E. Conn, Joseph H. Vineis, **Jonathan P. Bollback**, David Y. Onyabe, Richard C. Wilkerson and Marinete M. Póvoa. (2006) Population structure of the malaria vector *Anopheles darlingi* in a malaria-endemic region of eastern Amazonian Brazil. *Am. J. Trop. Med. Hyg.* 74(5): 798–806.
11) Andrea J. Betancourt and **Jonathan P. Bollback**. (2006) The mutational landscape model in experimental evolution. *Current Opinions in Genetics and Development*. 16:618–623.
12) **Jonathan P. Bollback**†. (2005) Posterior mapping and predictive distributions. *In* "Statistical methods in Molecular Evolution" (Nielsen, R. Ed.) Springer Verlag New York, Inc. New York, USA.
13) John Harshman, Christopher J. Huddleston, **Jonathan P. Bollback**, Thomas J. Parsons, and Michael J. Braun. (2003) True and false gavials: A nuclear gene phylogeny of Crocodylia. *Systematic Biology* 52(3): 386-402.
14) John P. Huelsenbeck, Rasmus Nielsen, **Jonathan P. Bollback**. (2003) Stochastic mapping of morphological characters. *Systematic Biology* 52(2):131-158.
15) **Jonathan P. Bollback** (2002) Bayesian model adequacy and choice in phylogenetics. *Molecular Biology and Evolution*. 19 (7): 1171-1180.
16) John P. Huelsenbeck, **Jonathan P. Bollback**, and Amy Levine. (2002) Inferring the root of a phylogenetic tree. *Systematic Biology*. 51 (1): 32-43.
17) John P. Huelsenbeck, Frederick Ronquist, Rasmus Nielsen and **Jonathan P. Bollback**. (2001) Bayesian inference of phylogeny and its impact on evolutionary biology. *Science*. 294: 2310-2314.
18) Jan E. Conn, **Jonathan P. Bollback**, Davide Y. Onyabe, Tessa N. Robinson, Richard C. Wilkerson, and Marinete M. Povoa. (2001) Isolation of polymorphic microsatellite markers from the malaria vector *Anopheles darlingi*. *Molecular Ecology Notes*. 1 (4): 223-225.
19) John P. Huelsenbeck and **Jonathan P. Bollback**. (2001) Empirical and hierarchical Bayesian estimation of ancestral states. *Systematic Biology*. 50 (3): 351-366.
20) John P. Huelsenbeck and **Jonathan P. Bollback**†. (2001) Application of the likelihood function in phylogenetic analysis. *In* "Handbook of Statistical Genetics" (Balding. D.J., Bishop, M., and Cannings, C., Eds.) Chapter 15, pp. 415-439. John Wiley and Sons, Inc. New York, USA.
21) **Jonathan P. Bollback** and John P. Huelsenbeck. (2001) Phylogeny, genome evolution, and host specificity of single-stranded RNA bacteriophage (Family Leviviridae). *Journal of Molecular Evolution*. 52: 117-128.

***Manuscripts in Preparation or Review* as of Jan 2009**

1) **Jonathan P. Bollback**, Jiaye Yu, and Rasmus Nielsen. Reassortment and intragenic recombination in Avian A influenza H5N1 and H9N2 serotypes.
2) **Jonathan P. Bollback**, Melissa J Ward, Samantha J. Lycett, and Andrew J. Leigh Brown. A lineage specific Bayesian method for estimating positive selection.
3) Dorita Avila, **Jonathan P. Bollback**, and Andrew J. Leigh Brown. Patterns of synonymous and non-synonymous evolution in pathogenic avian influenza varies by serotypic combinations.
4) Peter Gravlund, Kim Aaris-Sørensen, Michael Hofreiter, Matthias Meyer, **Jonathan P. Bollback** and Nanna Noe-Nygaard. An analysis of ancient DNA extracted from Danish aurochs (*Bos primigenius*): genetic diversity, genealogical history and sample preservation.