

Benjamin David Redelings

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Education

- 2006 Ph. D. Department of Biomathematics, University of California at Los Angeles, Los Angeles, 90095 (Dr. Marc Suchard, advisor)
1999 B.S. Department of Mathematics, University of California at San Diego, La Jolla, CA 92093

Professional Experience

- 2006-Present Postdoctoral Associate, North Carolina State University (Dr. Jeff Thorne, advisor)

Awards and Honors

- 2006 Mitchell Prize for using a Bayesian approach to solve an important applied problem. Sponsored by the American Statistical Association's Section on Bayesian Statistical Science and the International Society for Bayesian Analysis.

Refereed Papers and Proceedings

Choi SC, **Redelings BD**, Thorne JL (2008) Basing population genetic inferences and models of molecular evolution upon desired stationary distributions of DNA or protein sequences. *Philosophical Transactions of the Royal Society B*, (online).

Redelings BD, Suchard MA (2007) Incorporating Indel Information into Phylogeny Estimation for Rapidly Emerging Pathogens, *BMC Evolutionary Biology*, 7:40

Suchard MA, **Redelings BD** (2006) BAli-Phy: simultaneous Bayesian inference of alignment and phylogeny. *Bioinformatics*, 22(16):2047-2048

Redelings BD, Suchard MA (2005) Joint Bayesian Estimation of Alignment and Phylogeny. *Systematic Biology*, 54(3):401-418 [Winner of Mitchell Prize in 2006]

Lange K and **Redelings BD** (2002) Disease Gene Dynamics in Population Isolates. *Proceedings of Symposia in Applied Mathematics*, 59:119-138, 2002

Additional Papers

Redelings, BD (in preparation) “Phylogenies unplugged: Extending Majority Consensus Trees to handle Wandering Taxa”

Redelings, BD, Suchard MA (in press) “Robust Inferences from Ambiguous Alignments” in *Perspectives on Biological Sequence Alignment*, University of California Press, ed. Michael Rosenberg

Invited Seminars

2008 Department of Statistics, Virginia Tech
2008 Phylogenetics Workshop -- HIV Evolution and Dynamics Meeting, Santa Fe, NM

Presentations and Posters

2008 **Redelings BD**, Modeling Insertion/Deletion Hotspots when Inferring Alignments, *Bayesian Phylogenetic Workshop*, Budapest, Hungary.

2007 **Redelings BD**, Phylogenies Unplugged: Consensus Trees with Wandering Taxa. *Society for Molecular Biology and Evolution (SMBE)* Meeting, Tempe, AZ.

2004 **Redelings BD** and Suchard MA, Incorporating Indel Information into Phylogeny Estimation for Rapidly Emerging Diseases, contributed talk at the *International Conference on Bioinformatics (INCOB)*, Auckland, New Zealand.

2004 **Redelings BD** and Suchard MA, Joint Bayesian Estimation of Alignment and Phylogeny, poster presented at the *Conference on Research in Computational Molecular Biology (RECOMB)*, San Diego, CA.

Service

Author of freely distributed software **BAl i - Phy** for co-estimating evolutionary trees and multiple sequence alignments. (See <http://www.biomath.ucla.edu/msuchard/bali-phy/>)

Reviewer for *Evolution*, *Bioinformatics*, *Molecular Biology and Evolution*, and *PLOS Computational Biology*.

Professional Organizations and Affiliations

American Statistical Association (ASA)
Society for Molecular Biology and Evolution (SMBE)