

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

- 2016- Research Scientist, Duke University (with Dr. Greg Wray)
- 2015- Postdoctoral Fellow, University of Kansas (Dr. Mark Holder, advisor)
- 2012-2015 Postdoctoral Fellow, Duke University (Dr. Marcy Uyenoyama, advisor)
- 2009-2012 Postdoctoral Fellow, National Evolutionary Synthesis Center (NESCent) (Competitively awarded).
- 2006-2009 Postdoctoral Fellow, 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 (SBSS)* and the *International Society for Bayesian Analysis (ISBA)*.

Refereed Papers

- Redelings BD, Holder MH** (2017) A supertree pipeline for summarizing phylogenetic and taxonomic information for millions of species. *PeerJ* doi:10.7717/peerj.3058. [[WWW](#)]
- Redelings BD, Kumagai SK, Wang L, Tatarenkov A, Sakai AK, Weller SG, Culley TM, Avise JC, Uyenoyama MK** (2015) A Bayesian Approach to Inferring Rates of Selfing and Locus-Specific Mutation. *Genetics* **201**:1171-1188 [[WWW](#)]
- Redelings BD** (2014) Erasing Errors Due to Alignment Ambiguity When Estimating Positive Selection. *Mol. Biol. Evol.* **31**(8):1979-1993 [[WWW](#)]

- Sliwa L, Miadlikowska J, **Redelings BD**, Molnar K, and Lutzoni F (2012). Are widespread morphospecies from the *Lecanora dispersa* group (lichen-forming *Ascomycota*) monophyletic? *The Bryologist*, **115**:265-277. [[WWW](#)]
- Law SHW, **Redelings BD**, Kullman SW (2012) Comparative Genomics of Duplicate γ -Glutamyl Transferase Genes in Teleosts: Medaka (*Oryzias latipes*), Stickleback (*Gasterosteus aculeatus*), Green Spotted Pufferfish (*Tetraodon nigroviridis*), Fugu (*Takifugu rubripes*), and Zebrafish (*Danio rerio*). *JEZ part B*, **318B**(1):35-49. [[WWW](#)]
- Revell LJ, Mahler DL, Peres-Neto PR, and **Redelings BD** (2012) A new method for identifying exceptional phenotypic diversification. *Evolution*, **66**(1):135-146. [[WWW](#)]
- Gaya E, **Redelings BD**, Pere Navarro-Rosinés, Xavier Llimona, Miquel de Cáceres, Lutzoni F (2011) Align, or not to align? Resolving species complexes within the *Caloplaca saxicola* group as a case study. *Mycologia*, **103**(2):361-378. [[WWW](#)]
- Liang LJ, Weiss RE, **Redelings BD**, Suchard MA (2009) Improving phylogenetic analyses by incorporating additional information from genetic sequence databases. *Bioinformatics*, **25**(19):2530-2536. [[WWW](#)]
- Lamm K, **Redelings BD** (2009) Reconstructing ancestral ranges in historical biogeography: properties and prospects. *Journal of Systematics and Evolution*, **47**(5):369-382. [[WWW](#)]
- 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*, **363**(1512):3931-3939. [[WWW](#)]
- Redelings BD**, Suchard MA (2007) Incorporating Indel Information into Phylogeny Estimation for Rapidly Emerging Pathogens, *BMC Evolutionary Biology*, **7**:40 [[WWW](#)]
- Suchard MA, **Redelings BD** (2006) BAli-Phy: simultaneous Bayesian inference of alignment and phylogeny. *Bioinformatics*, **22**(16):2047-2048 [[WWW](#)]
- Redelings BD**, Suchard MA (2005) Joint Bayesian Estimation of Alignment and Phylogeny. *Systematic Biology*, **54**(3):401-418 [Winner of Mitchell Prize in 2006][[WWW](#)]

Book Chapter and Proceedings

- Redelings BD**, Suchard MA (2009) “Robust Inferences from Ambiguous Alignments” in “Sequence Alignment: Methods, Concepts, and Strategies”, University of California Press, ed. Michael Rosenberg, Chapter 10, pp 209-270
- Lange K and **Redelings BD** (2002) Disease Gene Dynamics in Population Isolates. *Proceedings of Symposia in Applied Mathematics*, **59**:119-138.

Invited Presentations

- 2013 **Redelings BD**, Uyenoyama MK, “Bayesian Co-estimation of Selfing Rate and Locus-Specific Mutation Rates for a Partially Selfing Population”, *SMBE Meeting 2013*, Chicago, IL
- 2013 **Redelings BD**, “Robust handling of alignment uncertainty when inferring positive selection from divergent sequences”, *Symposium and Workshop on New Methods for Phylogenomics and Metagenomics*, Austin, Texas
- 2012 **Redelings BD**, “Robust handling of alignment uncertainty when inferring positive selection from divergent sequences”, *SMBE Meeting 2012*, Dublin, Ireland
- 2011 Bioinformatics Research Center, *North Carolina State University*
- 2010 Institute for Bioinformatics and Evolutionary Studies, *University of Idaho*
- 2009 Department of Statistics, *North Carolina State University*
- 2009 Department of Computer Science, *Cornell University*
- 2008 Department of Statistics, *Virginia Tech*
- 2008 Phylogenetics Workshop -- *HIV Evolution and Dynamics Meeting*, Santa Fe, NM

Contributed Presentations and Posters

- 2017 **Redelings, BD**, Faster Likelihoods for Sparse Alignments, *Evolution 2016*, Portland, OR
- 2016 **Redelings, BD**, Kumagai S, Uyenoyama MK, A Bayesian Approach to Inferring Rates of Selfing and Locus-Specific Mutation, *SIAM LS 2016*, Boston, MA
- 2016 **Redelings, BD**, Holder MA, New methods for constructing the supertree of life, *Evolution 2016*, Austin, TX
- 2014 **Redelings, BD**, Uyenoyama MK, Bayesian Co-estimation of Selfing Rate and Locus-Specific Mutation Rates for a Partially Selfing Population, *Evolution 2014*, Raleigh, NC
- 2014 **Redelings BD**, Probabilistic Programming for Evolutionary Biology, *iEvoBio 2014*, Raleigh, NC
- 2013 **Redelings BD**, Erasing Errors due to Alignment Ambiguity when inferring (diversifying) positive selection, *JSM 2013*, Chicago, IL

- 2011 **Redelings BD**, Phylogenies Unplugged: Consensus Trees with Wandering Taxa. *New Zealand Phylogenetics Meeting 2011*, Leigh, Rodney District, North Island, New Zealand
- 2011 **Redelings BD**, Phylogenies Unplugged: Consensus Trees with Wandering Taxa. *Evolution 2011 Meeting*, Norman, OK
- 2010 **Redelings BD**, Phylogenies Unplugged: Consensus Trees with Wandering Taxa. *SIAM Conference on the Life Sciences*, Pittsburgh, PA
- 2009 **Redelings BD**, Estimating the Location and Magnitude of Indel Hotspots in Molecular Sequence Alignments, *Joint Statistical Meeting*, Washington DC
- 2008 **Redelings BD**, Modeling Insertion/Deletion Hotspots when Inferring Alignments, *Bayesian Phylogenetic Workshop*, Budapest, Hungary.
- 2006 **Redelings BD**, Joint Estimation of Alignment and Phylogeny, *SMBE Meeting 2006*, Tempe, Arizona
- 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.

Teaching Experience

Teaching preceptorship, Biomathematics Department, UCLA

Guest Lectures for Dr. Jeff Thorne (1) and Dr. Eric Stone (1) at North Carolina State University

Guest Lectures (2) “Phylogenetics searches without a prior alignment” in Bio237L **Systematic Biology**, with instructors Francois Lutzoni and David Swofford, Duke University.

Service

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

Reviewer for *Evolution*, *Bioinformatics*, *Molecular Biology and Evolution (MBE)*, *Systematic Biology*, *BMC Evolutionary Biology*, and *PLOS Computational Biology*.

Short Courses

Software School on New Methods for Phylogenomics and Metagenomics (2014) Raleigh, NC, USA

Instructor, *EMBO Practical Course on Computational Molecular Evolution* (2012, 2014, 2016), Hiraklion, Crete

Instructor, *Wellcome Trust Advanced Course on Computational Molecular Evolution* (2013, 2015, 2017), Hinxton, Cambridgeshire, UK

Professional Organizations and Affiliations

American Statistical Association (ASA)

Society for Molecular Biology and Evolution (SMBE)

Society of Systematic Biologists (SSB)

Other Skills

Programming: C++ (C++11,14), R, Perl, Python, LaTeX, Haskell, sh, Fortran

Languages Studied: Japanese, Chinese, Classical Greek