

## Benjamin David Redelings

Department of Biology  
Duke University  
Box 90338  
137 Bio Sciences Building  
130 Science Drive  
Durham, NC 27708-0338

Office: (919) 660-7351  
Mobile: (919) 272-4137  
Fax: (919) 660-7293

<http://ben-redelings.org/>  
[benjamin.redelings@gmail.com](mailto:benjamin.redelings@gmail.com)

### 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

- McTavish EJ, Drew BT, **Redelings BD**, Cranston KA (2017) How and Why to Build a Unified Tree of Life. *BioEssays* [[WWW](#)]
- 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  $\gamma$ -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 2017*, 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