

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

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

- 2015- Research Scientist, University of Kansas (with Dr. Mark Holder)
- 2016-2022 Research Scientist, Duke University (with Dr. Greg Wray)
- 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

- Seo T. K, **Redelings BD**, Thorne JL (2022) Correlations between alignment gaps and nucleotide substitution or amino acid replacement. *PNAS* [doi.org/10.1073/pnas.2204435119]
- Barido-Sottani J, Justison, JA, Borges R, Brown JM, Dismukes WT, do Rosario Petrucci B, Fabreti LG, Höhna S, Landis MJ, Lewis PO, May MR, Mendes FK, Pett W, **Redelings BD**, Tribble CM, Wright AM, Zenil-Ferguson R, Heath TA (2022) Lessons learned from organizing and teaching virtual phylogenetics workshops, *Bulletin of the Society of Systematic Biologists*. [doi.org/10.32942/osf.io/kp8sz]

- Redelings BD** (2021) BAli-Phy version 3: model-based co-estimation of alignment and phylogeny, *Bioinformatics*, 2021 [\[WWW\]](#)
- Brazeau NF, Mitchell CL, Morgan AP, Deutsch-Feldman M, Watson OJ, Thwai KL, Waltmann A, Emch M, Gartner V, **Redelings BD**, Wray G, Mwandagalirwa MK, Tshefu AK, Likwela JL, Edwards JK, Verity R, Parr JB, Meshnick SR, Juliano JJ (2020) The epidemiology of *Plasmodium vivax* among adults in the Democratic Republic of the Congo. *Nat Commun* **12**:4169. [\[WWW\]](#)
- 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 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**, Holder, MT (2019). Taxonomic Supertree Construction with Incertae sedis Taxa. *Bioinformatics and Phylogenetics: Seminal Contributions of Bernard Moret*, **29**, 151.
- 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

- 2018 **Redelings, BD**, Taxonomic supertree construction with *incertae sedis* taxa, *SSB satellite meeting 2018*, Columbus, OH
- 2018 **Redelings, BD**, Faster Likelihoods for Sparse Alignments, *SSB satellite meeting 2018*, Columbus, OH
- 2017 **Redelings, BD**, Faster Likelihoods for Sparse Alignments, *Evolution 2017*, Portland, OR
- 2016 **Redelings, BD**, Kumagai S, Uyenyoyama 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**, Uyenyoyama 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.

Short Course Instructor

- Software School on New Methods for Phylogenomics and Metagenomics (2014) Raleigh, NC, USA
- Instructor, *EMBO Practical Course on Computational Molecular Evolution* (2012, 2014, 2016,2018), Hiraklion, Crete
- Instructor, *Wellcome Trust Advanced Course on Computational Molecular Evolution* (2013, 2015, 2017,2019), Hinxton, Cambridgeshire, UK

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*.

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++11,14,17), R, Perl, Python, LaTeX, Haskell, sh, Fortran
Languages Studied: Japanese, Chinese, Classical Greek