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

Research Scientist, University of Kansas (with Dr. Mark Holder)
Research Scientist, Duke University (with Dr. Greg Wray)
Postdoctoral Fellow, Duke University (Dr. Marcy Uyenoyama, advisor)
Postdoctoral Fellow, National Evolutionary Synthesis Center (NESCent)
(Competitively awarded).
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

(accepted) Redelings BD, Holder MT. Speeding up iterative applications of the BUILD supertree algorithm. PeerJ [https://www.biorxiv.org/content/10.1101/2023.11.10.566627v1]

- (accepted) Gartner V, **Redelings BD**, Gaither C, Parr JB, Kalonji FP, Brazeau NF, Juliano JJ, Wray GA. Genomic insights into Plasmodium vivax population structure and diversity in central Africa. [https://www.biorxiv.org/content/10.1101/2022.12.16.520826v1]
- (2022) Seo T. K, **Redelings BD**, Thorne JL. Correlations between alignment gaps and nucleotide substitution or amino acid replacement. *PNAS* [doi.org/10.1073/pnas.2204435119]

(2022) 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. Lessons learned from organizing and teaching virtual phylogenetics workshops, *Bulletin of the Society of Systematic Biologists.*

(2021) **Redelings BD**. BAli-Phy version 3: model-based co-estimation of alignment and phylogeny, *Bioinformatics*, 2021 [WWW]

- (2020) 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 The epidemiology of *Plasmodium vivax* among adults in the Democratic Republic of the Congo. *Nat Commun* **12**:4169. [WWW]
- (2017) McTavish EJ, Drew BT, **Redelings BD**, Cranston KA How and Why to Build a Unified Tree of Life. *BioEssays* [WWW]
- (2017) **Redelings BD.** Holder MH A supertree pipeline for summarizing phylogenetic and taxonomic information for millions of species. *PeerJ* doi:10.7717/peerj.3058. [WWW]
- (2015) **Redelings BD**, Kumagai SK, Wang L, Tatarenkov A, Sakai AK, Weller SG, Culley TM, Avise JC, Uyenoyama MK A Bayesian Approach to Inferring Rates of Selfing and Locus-Specific Mutation. *Genetics* **201**:1171-1188 [WWW]
- (2014) **Redelings BD** Erasing Errors Due to Alignment Ambiguity When Estimating Positive Selection. *Mol. Biol. Evol.* **31**(8):1979-1993 [WWW]
- (2012) Sliwa L, Miadlikowska J, Redelings BD, Molnar K, and Lutzoni F. Are widespread morphospecies from the *Lecanora dispersa* group (lichen-forming *Ascomycota*) monophyletic? *The Bryologist*, 115:265-277.
- (2012) Law SHW, **Redelings BD**, Kullman SW 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]
- (2012) Revell LJ, Mahler DL, Peres-Neto PR, and **Redelings BD**. A new method for identifying exceptional phenotypic diversification. *Evolution*, **66**(1):135-146. [WWW]
- (2011) Gaya E, **Redelings BD**, Pere Navarro-Rosinés, Xavier Llimona, Miquel de Cáceres, Lutzoni F. Align, or not to align? Resolving species complexes within the *Caloplaca*

saxicola group as a case study. *Mycologia*, **103**(2):361-378.

- (2009) Liang LJ, Weiss RE, **Redelings BD**, Suchard MA. Improving phylogenetic analyses by incorporating additional information from genetic sequence databases. *Bioinformatics*, **25**(19):2530-2536. [WWW]
- (2009) Lamm K, **Redelings BD** Reconstructing ancestral ranges in historical biogeography: properties and prospects. *Journal of Systematics and Evolution*, **47**(5):369-382. [WWW]
- (2008) Choi SC, Redelings BD, Thorne JL 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]
- (2007) **Redelings BD**, Suchard MA Incorporating Indel Information into Phylogeny Estimation for Rapidly Emerging Pathogens, *BMC Evolutionary Biology*, **7**:40 [WWW]
- (2006) Suchard MA, **Redelings BD** BAli-Phy: simultaneous Bayesian inference of alignment and phylogeny. *Bioinformatics*, 22(16):2047-2048 [WWW]
- (2005) **Redelings BD**, Suchard MA Joint Bayesian Estimation of Alignment and Phylogeny. *Systematic Biology*, **54**(3):401-418 [Winner of Mitchell Prize in 2006][WWW]

Book Chapter and Proceedings

- (2019) **Redelings, BD**, Holder, MT. Taxonomic Supertree Construction with Incertae sedis Taxa. *Bioinformatics and Phylogenetics: Seminal Contributions of Bernard Moret, 29*, 151.
- (2009) **Redelings BD**, Suchard MA "Robust Inferences from Ambiguous Alignments" in "Sequence Alignment: Methods, Concepts, and Strategies", University of California Press, ed. Michael Rosenberg, Chapter 10, pp 209-270
- (2002) Lange K and **Redelings BD**. Disease Gene Dynamics in Population Isolates. *Proceedings of Symposia in Applied Mathematics*, **59**:119-138.

Invited Presentations

- 2023 **Redelings BD**, "Alignments, rate variation, and heterotachy", *SMBE Meeting* 2023, Ferrara, Italy.
- 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", <i>Symposium and Workshop on New Methods for Phylogenomics and Metagenomics</i> , Austin, Texas
2012	Redelings BD , "Robust handling of alignment uncertainty when inferring positive selection from divergent sequences", <i>SMBE Meeting 2012</i> , 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

2023	Redelings, BD, Holder MT. Speeding up taxonomic supertree construction for
	the Open Tree of Life. SSB satellite meeting 2023, Mexico City, Mexico.

- **Redelings, BD**, Gartner, V, Wray G. Apicoplast phylogeny illuminates worldwide dispersal history of Plasmodium vivax, *Evolution 2022*, Cleveland, OH
- **Redelings, BD**, Faster Likelihoods for Sparse Alignments, *SSB satellite meeting 2018*, Columbus, OH
- **Redelings, BD**, Faster Likelihoods for Sparse Alignments, *Evolution 2017*, Portland, OR
- **Redelings, BD**, Kumagai S, Uyenoyama MK, A Bayesian Approach to Inferring Rates of Selfing and Locus-Specific Mutation, *SIAM LS 2016*, Boston, MA
- **Redelings, BD**, Holder MA, New methods for constructing the supertree of life, *Evolution 2016*, Austin, TX
- **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, <i>iEvoBio</i> 2014, Raleigh, NC
2013	Redelings BD , Erasing Errors due to Alignment Ambiguity when inferring (diversifying) positive selection, <i>JSM 2013</i> , Chicago, IL
2011	Redelings BD , Phylogenies Unplugged: Consensus Trees with Wandering Taxa. <i>New Zealand Phylogenetics Meeting 2011</i> , Leigh, Rodney District, North Island, New Zealand
2011	Redelings BD , Phylogenies Unplugged: Consensus Trees with Wandering Taxa. <i>Evolution 2011 Meeting</i> , Norman, OK
2010	Redelings BD , Phylogenies Unplugged: Consensus Trees with Wandering Taxa. <i>SIAM Conference on the Life Sciences</i> , Pittsburgh, PA
2009	Redelings BD , Estimating the Location and Magnitude of Indel Hotspots in Molecular Sequence Alignments, <i>Joint Statistical Meeting</i> , Washington DC
2008	Redelings BD , Modeling Insertion/Deletion Hotspots when Inferring Alignments, <i>Bayesian Phylogenetic Workshop</i> , Budapest, Hungary.
2006	Redelings BD , Joint Estimation of Alignment and Phylogeny, <i>SMBE Meeting</i> 2006, Tempe, Arizona
2004	Redelings BD and Suchard MA, Incorporating Indel Information into Phylogeny Estimation for Rapidly Emerging Diseases, contributed talk at the <i>International Conference on Bioinformatics (INCOB)</i> , Auckland, New Zealand.
2004	Redelings BD and Suchard MA, Joint Bayesian Estimation of Alignment and Phylogeny, poster presented at the <i>Conference on Research in Computational Molecular Biology (RECOMB)</i> , 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, 2023), Hiraklion, Crete

Instructor, *Wellcome Trust Advanced Course on Computational Molecular Evolution* (2013, 2015, 2017, 2019, 2022), Hinxton, Cambridgeshire, UK

Service

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

Contributor to freely distributed software **RevBayes** for phylogenetic inference using graphical models. (CI infrastructure, debugging, programming).

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++11,14,17,23), R, Perl, Python, LaTeX, Haskell, sh, Fortran **Languages Studied:** Japanese, Chinese, Classical Greek