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Education

Ph.D. Statistics, University of California at Berkeley, 1994
M.A. Statistics, University of California at Berkeley, 1991
B.Math. Mathematics, University of Minnesota, 1989

Academic Appointments

At the University of Wisconsin, Madison, 2002–present

Professor, Departments of Statistics and of Botany, 2013 – present
Associate Professor, Departments of Statistics and of Botany, 2005 – 2013
Assistant Professor, Departments of Statistics and of Botany, 2002 – 2005

At Duquesne University, Pittsburgh, PA, 1994–2002

Associate Professor, Department of Mathematics and Computer Science, 2000 – 2002
Assistant Professor, Department of Mathematics and Computer Science, 1994 – 2000

Professional Positions

Associate Editor, *Annals of Applied Statistics*, 2006 – 2009
Associate Editor, *Journal of Statistics Education*, 2001 – 2003

Awards

Vilas Research Fellowship, \$25,000, 2008–2010

Current External Grants

Principal investigator, *Improved Bayesian phylogenetic inference based on approximate conditional independence*, \$279,808, from NSF (DEB 1354675), August 2014–July 2016.

Co-principal investigator (with PI Nicole Perna, and co-PIs Cécile Ané and Colin Dewey, all from Wisconsin), *ATOL: Assembling a taxonomically balanced genome-scale reconstruction of the evolutionary history of the Enterobacteriaceae*, approximately \$2,998,822 from NSF (DEB 0936214), September 2009–August 2016.

Previous External Grants

Co-principal investigator (with PI Cécile Ané and co-PIs David Baum, David Spooner, and Alain Roy), *Reconciling gene trees: Deciphering the source and extent of genealogical discordance*, approximately \$500,000, from NSF (DEB 0949121), September 2010–May 2014.

Co-principal investigator (with PI Marc Suchard, UCLA, and co-PI John Huelsenbeck, UC Berkeley) *Joint Estimation of Alignment and Phylogeny*, \$1,500,000 (total), from the National Institutes of Health (NIH Grant 1 R01 GM086887), August 2008–July 2014.

Principal Investigator (with David Baum, Mark Derthick, Joseph B. Kadane, and Donald Simon as co-PIs), *Improving Bayesian Phylogeny*, \$1,449,570 (total), from the National Institutes of Health (NIH grant R01 GM068950-01), June 2003 – May 2008.

Co-principal investigator (with PI John Huelsenbeck of University of California, San Diego and co-PI Michael Alfaro, Washington State University), *Model Choice and Model Averaging in Molecular Phylogenetics*, estimated \$300,000 (total, UW portion \$33,333 per year), from the National Science Foundation (NSF grant 0445453), June 2005 – May 2008.

Co-principal investigator (with PI John Huelsenbeck of University of California, San Diego and co-PI Frederik Ronquist, Florida State University), *Extending Bayesian Phylogenetic Analysis*, \$800,000 (total, UW portion \$45,000 per year), from the National Institutes of Health (NIH grant R01 GM069801-01), August 2004 – July 2008.

Principal Investigator (with Don Simon of Duquesne University as co-PI), *Markov Chain Monte Carlo Methodology for Phylogenetic Inference from Genetic Data*, \$185,637, from the National Science Foundation (NSF grant DBI-9723799), September 1997 – August 1999.

Co-Principal Investigator (with John Huelsenbeck of the University of Rochester as PI), *Bayesian estimation of host-parasite cospeciation*, \$250,000 (Duquesne University portion \$35,986), from the National Science Foundation (NSF grant DEB-0075406), September 2000 – August 2003.

Co-principal investigator (with PI Michael Newton, co-PIs Douglas Bates, Sunduz Keles, and Christina Kendziorski, all of UW—Madison), *Statistical Genomics*, equipment and software valued at \$40,000, from the Apple Workgroup Cluster for Bioinformatics Award Program. Awarded 2004.

Refereed Publications

BONTRAGER, M, DA BAUM, C ANÉ, AND **B Larget** (submitted). Statistical evidence of common ancestry: Testing for signal in silent sites. *Systematic Biology*.

Larget, B., CÉCILE ANÉ, MARTIN BONTRAGER, STEVEN J HUNTER, NOAH WM STENZ, AND DAVID A BAUM (submitted). Statistical evidence for common ancestry: New tests of universal ancestry. *Systematic Biology*.

BAUM, DA, C ANÉ, **B Larget**, C SOLIS-LEMUS, L HO, P BOONE, C DRUMMOND, M BONTRAGER, SJ HUNTER, AND B SAUCIER (accepted). Statistical evidence for common ancestry: Application to primates. *Evolution*.

ALGERS, S. J., **B. Larget**, AND L. RITERS (accepted). Novel analyses of male starling songs reveal context-specific differences in structure and a role for the preoptic area. *Animal Behavior*.

- SHIM, HEEJUNG AND **B. Larget** (accepted). BayesCAT: Bayesian Co-estimation of Alignment and Tree. *Biometrics*.
- Larget, B.** (2015). Review of *Bayesian Phylogenetics: Methods, Algorithms and Applications*. *International Statistical Review* **83**: 160–161.
- MURFIN, KE, MM LEE, JL KLASSEN, BR McDONALD, **B Larget**, S FORST, SP STOCK, CR CURRIE, AND H GOODRICH-BLAIR (2015). Xenorhabdus bovienii Strain Diversity Impacts Coevolution and Symbiotic Maintenance with Steinernema spp. Nematode Hosts. *mBio* **6**: e00076–15.
- STENZ, NWM, **B. Larget**, DA BAUM, AND C. ANÉ (2015). Exploring Tree-Like and Non-Tree-Like Patterns Using Genome Sequences: An Example Using the Inbreeding Plant Species Arabidopsis thaliana (L.) Heynh. *Systematic Biology* **64**: 809–823.
- WANG, ZHISHI, QIULING HE, **Bret Larget** AND MICHAEL A. NEWTON (2015). A Multi-Functional Analyzer Uses Parameter Constraints To Improve The Efficiency Of Model-Based Gene-Set Analysis. *Annals of Applied Statistics* **9**: 225–246.
- POSAVI, MARIJAN, **Bret Larget**, GREGORY WILLIAM GELEMBIUK, DAVORKA GULISIJA, AND CAROL EUNMI LEE (2014). Testing for beneficial reversal of dominance during salinity shifts in the invasive 4 copepod Eurytemora affinis, and implications for the maintenance of genetic variation. *Evolution* **68** 3166–3183.
- KIM, JOUNGYOUN AND **Bret Larget** (2014). Bayesian estimation of the phylogeography of African gorillas with genome-differentiated population trees. *Biometrics* **70**: 683–694.
- Larget, Bret** (2013). The estimation of tree posterior probabilities using conditional clade probability distributions. *Systematic Biology* **62**: 501–511.
- SOLOMON, C.T., DENISE A. BRUESEWITZ, DAVID C. RICHARDSON, KEVIN C. ROSE, MATTHEW C. VAN DE BOGERT, PAUL HANSON, TIM KRATZ, **Bret Larget**, STEVE CARPENTER, RITA ADRIAN, BRENDA BABIN, CHIH YU CHIU, ELVIRA DE EYTO, CHARLIE DRISCOLL, DAVID HAMILTON, EVELYN GAISER, SUSAN HENDRICKS, VERA ISTVANOVICS, ALO LAAS, MIKE PACE, PETER STAEHR, THOMAS TORGENSEN, MIKE VANNI, KATHLEEN WEATHERS, GUANGWEI ZHU (2013). Ecosystem respiration: drivers of daily variability and background respiration in lakes around the globe. *Limnology and Oceanography* **58**: 849–866.
- KIM, J., N. M. ANTHONY, AND **B. Larget** (2012). A Bayesian Method for Estimating Evolutionary History. *Bayesian Analysis* **7**: 235–292.
- RONQUIST, F. , M. TESLENKO, P. VAN DER MARK, D. L. AYRES, A. DARLING, S. HÖHNA, **B. Larget**, L. LIU, M. A. SUCHARD, AND J. P. HUELSENBECK (2012). MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. *Systematic Biology* **61**: 539–542.
- CORREA, R. J. STANGA, **B. Larget**, A. ROZNOWSKI, G. SHU, B. DILKES, D. A. BAUM (2012). An assessment of transgenomics as a tool for identifying genes involved in the evolutionary differentiation of closely related plant species. *New Phytologist* **193**: 494–503.
- NILSSON, E., C.T. SOLOMON, K.A. WILSON, T.V. WILLIS, **B. Larget**, AND M.J. VANDER ZANDEN (2012). Effects of an invasive crayfish on benthic invertebrate abundance, fish benthivory and trophic position. *Freshwater Biology* **57**: 10–23.

- M. J. CAFARO, M. POULSEN, A. E. F. LITTLE, S. L. PRICE, N. M. GERARDO, B. WONG, A. E. STUART, **B. Larget**, P. ABBOT, AND C. R. CURRIE (2011). Specificity in the symbiotic association between fungus-growing ants and protective *Pseudonocardia* bacteria. *Proceedings of the Royal Society B (Biological Sciences)* **278**: 1814–1822.
- B. R. Larget**, S. K. KOTHA, C. N. DEWEY, AND C. ANÉ (2010). BUCKy: Gene tree/species tree reconciliation with Bayesian concordance analysis *Bioinformatics* **26**: 2910–2911.
- AGUERRE, M., T. HUNT, **B Larget**, M. WATTIAUX (2010). Effect of dietary crude protein on ammonia-N loss measured by herd nitrogen mass balance in a freestall dairy barn under Wisconsin farm-like conditions. *Animal* **4**: 1390–1400.
- ZHENG, LI, ANTHONY R. IVES, THEODORE GARLAND JR., **Bret R. Larget**, YANG YU, AND KUNFANG CAO (2009). New multivariate tests for phylogenetic signal and trait correlations applied to ecophysiological phenotypes of nine *Manglietia* species. *Functional Ecology* **23**: 1059–1069.
- WHITE, M.A., C. ANÉ, C.N. DEWEY, **B. Larget**, AND B.A. PAYSEUR (2009). Fine-Scale Phylogenetic Discordance across the House Mouse Genome. *PLOS Genetics* **5**: e729.
- LUO, R. AND **B. Larget** (2009). Modeling Substitution and Indel Processes for AFLP Marker Evolution and Phylogenetic Inference. *The Annals of Applied Statistics* **3**: 222–248.
- HUELSENBECK, J.P., C. ANÉ, **B. Larget**, AND F. RONQUIST (2008). A Bayesian Perspective on a Non-parsimonious Parsimony Model. *Systematic Biology* **57**:406–419.
- LAKNER, C., P. VAN DER MARK, J.P. HUELSENBECK, **B. Larget**, AND F. RONQUIST (2008). Efficiency of MCMC Tree Proposals in Bayesian Phylogenetics. *Systematic Biology* **57**:86–103.
- LUO, R., A.L. HIPPE, AND **B. Larget** (2007). A Bayesian Model of AFLP Marker Evolution and Phylogenetic Inference. *Statistical Applications in Genetics and Molecular Biology* 6(1): Article 11.
- ANÉ C., **B. Larget**, D.A. BAUM, S.D. SMITH, AND A. ROKAS (2007). Bayesian Estimation of Concordance among Gene Trees *Molecular Biology and Evolution* **24**: 412–426.
- REYNAL, S., **B. Larget**, AND G. BRODERICK (2006). Effectiveness of sample duplication to control error in ruminant digestion studies. *Journal of Dairy Science* **89**: 3501–3504.
- RONQUIST, F., **B. Larget**, J.P. HUELSENBECK, J.B. KADANE, D.L. SIMON, AND P. VAN DER MARK (2006). Phylogenetic MCMC Algorithms are not Misleading. *Science* **312**: 367. Technical comment on Mossel and Vegoda (2005). “Phylogenetic MCMC Algorithms Are Misleading on Mixtures of Trees” in *Science*.
- HOLDER, M.T., P.O. LEWIS, D.L. SWOFFORD, AND **B. Larget** (2005). Hastings ratio of the LOCAL proposal used in Bayesian phylogenetics. *Systematic Biology* **54**: 961–965.
- Larget, B.**, D.L. SIMON, AND J.B. KADANE (2005). A Bayesian approach to the estimation of ancestral genome arrangements. *Molecular Phylogenetics and Evolution* **36**: 214–223.
- Larget, B.**, D.L. SIMON, J.B. KADANE, D. SWEET (2005). A Bayesian analysis of metazoan mitochondrial genome arrangements. *Molecular Biology and Evolution* **22**: 486–495.

- ATALLAH, Z. K., **B. Larget**, X. CHEN, AND D.A. JOHNSON (2004). High genetic diversity, phenotypic uniformity and evidence of outcrossing in *Sclerotinia sclerotiorum* in the Columbia Basin of Washington State. *Phytopathology* **94**: 737–742.
- Larget, B.** (2004). Introduction to Markov Chain Monte Carlo Methods in Molecular Evolution. In *Statistical Methods in Molecular Evolution*, Rasmus Nielsen (editor), Springer-Verlag, New York, New York.
- HUELSENBECK, J.P., **B. Larget**, AND M. ALFARO (2004). Bayesian phylogenetic model selection using reversible jump Markov chain Monte Carlo. *Molecular Biology and Evolution* **21**: 1123–1133.
- SCHLOSS, P.D., **B. Larget**, AND J. HANDELSMAN (2004). Integration of microbial ecology and statistics: a test to compare gene libraries. *Applied and Environmental Microbiology* **70**: 5485–5492.
- HUELSENBECK, J. P., **B. Larget**, R. E. MILLER, AND F. RONQUIST (2002). Potential applications and pitfalls of Bayesian inference of phylogeny . *Systematic Biology* **51**: 673–688.
- HUELSENBECK, J., B. RANNALA, AND **B. Larget** (2002). A statistical perspective for reconstructing the history of host-parasite associations. In Page, R (Ed.), *Tangled Trees: Phylogenies, Cospeciation, and Coevolution*. The University of Chicago Press.
- Larget, B.**, D. L. SIMON, AND J.B. KADANE (2002). On a Bayesian approach to phylogenetic inference from animal mitochondrial genome arrangements (with discussion). *Journal of the Royal Statistical Society B* **64**: 681–693.
- SIMON, D. L. AND **B. Larget** (2001). Phylogenetic inference from mitochondrial genome arrangement data. In Alexandrov, V. N., J. Dongarra, B. Juliano, R. Renner, C. Tan (Ed.), *Computational Science — ICCS 2001*. Springer-Verlag Lecture Notes in Computer Science, **2074**: 1022–1028.
- MIZANUR RAHMAN, G. M., T. L. ISENHOUR, **B. Larget**, AND P. D. GREENLAW (2001). Statistical Analysis of DOE EML QAP Data from 1982 to 1998. *Journal of Chemical Information and Computer Sciences* **41** 1099–1105.
- Discussant of STEPHENS, M. AND P. DONNELLY (2000). Inference in molecular population genetics (with discussion). *Journal of the Royal Statistical Society, Series B* **62**(4):605–655, on pages 646–647.
- HUELSENBECK, J., **B. Larget**, AND D. SWOFFORD (2000). A compound Poisson process for relaxing the molecular clock. *Genetics* **154**:1879–1892.
- HUELSENBECK, J., B. RANNALA, AND **B. Larget** (2000). A Bayesian framework for the analysis of cospeciation. *Evolution* **54**(2):353–364.
- HUO, D., S. KINGSTON, AND **B. Larget** (2000). Application of isotope dilution in elemental speciation: speciated isotope dilution mass spectrometry (SIDMS). In Caruso, J., K.L. Sutton, K.L. Ackley (Ed.), *Elemental Speciation, New Approaches for Trace Element Analysis*. Elsevier Comprehensive Analytical Chemistry, **XXXIII**, 277–313.
- Larget, B.** AND D. SIMON (1999). Markov chain Monte Carlo algorithms for the Bayesian analysis of phylogenetic trees. *Molecular Biology and Evolution* **16**:750–759.

MAU, B., M.A. NEWTON, AND **B. Larget** (1999). Bayesian phylogenetic inference via Markov Chain Monte Carlo methods. *Biometrics* **55**:1–12.

NEWTON, M.A., B. MAU, AND **B. Larget** (1999). Markov chain Monte Carlo for the Bayesian analysis of evolutionary trees from aligned molecular sequences. In F. Seillier-Moseiwitch (Ed.), *Statistics in Molecular Biology and Genetics*. IMS Lecture Notes-Monograph Series, **Vol. 33**, 143–162.

Larget, B. (1998). A Canonical Representation for Hidden Markov Models. *Journal of Applied Probability* **35**:313–324.

ALDOUS, D. AND **B. Larget** (1992). A tree-based scaling exponent for random cluster models. *Journal of Physics A: Mathematical and General* **25** L1065 – L1069.

Dissertation

The Equivalence of Aggregated Markov Processes with Application to Ion Channels, advisor John Rice, University of California, Berkeley.

Distributed Software

Bret Larget (2006/2010). BUCKy, Bayesian Untangling of Concordance Knots (applied to Yeast and other organisms), version 1.1. <http://www.stat.wisc.edu/~ane/bucky/index.html>

SIMON, D. AND B. LARGET (2004). BADGER, Bayesian Analysis to Describe Genomic Evolution by Rearrangement, version 1.01. <http://www.badger.duq.edu/> .

SCHLOSS, P. AND B. LARGET (2004). S-LIBSHUFF, version 1.0.

SIMON, D. AND B. LARGET (2001). Bayesian analysis in molecular biology and evolution (BAMBE), version 2.03 beta. Department of Mathematics and Computer Science, Duquesne University. (Version 1.01 released in 1998.)

Workshops

“BUCKy for Bayesian Concordance Analysis” at the Workshop on New Methods for Phylogenomics and Metagenomics, University of Texas, February 2013.

Invited Presentations at National and International Meetings

“Recent Advances in Bayesian Concordance Analysis” at the AMS Fall Central Section Meeting, Loyola University, Chicago, October 2015.

“A Cluster Version of Bayesian Concordance Analysis Using Conditional Clade Probabilities” at the Joint Statistical Meetings, Boston, August 2014.

“Approximate conditional independence of separated subtrees and phylogenetic inference” at the Joint Statistical Meetings, Montreal, Canada, August 2013.

“The consequences of approximate conditional independence of subtrees on phylogeny estimation” at the Symposium on New Methods for Phylogenomics and Metagenomics, University of Texas, February 2013.

“Bayesian Phylogeographical Analysis of Gorilla Divergence” at the Iowa State University 75th Anniversary Conference, Ames, Iowa, June, 2009.

“BUCKy: Bayesian Untangling of Concordance Knots (applied to yeast and other organisms)” at the Estimating Species Trees Workshop, Ann Arbor, Michigan, January, 2009

- “Markov chain Monte Carlo algorithms for the Bayesian analysis of phylogenetic trees” at the Bayesian Phylogeny Workshop, Rényi Institute, Budapest, Hungary, June, 2008.
- “Bayesian Modeling of Numt Evolution with Application to the Estimation of Gorilla Divergence Times” at the Bayesian Phylogeny Workshop, Rényi Institute, Budapest, Hungary, June, 2008.
- “A New Class of Models in Bayesian Phylogenetics” at the SMBE Meeting, Halifax, Nova Scotia, Canada, June, 2007.
- “Bayesian Phylogenetics” at the European Bioinformatics Institute, Hinxton, UK, September, 2006.
- “A Bayesian Approach to Gene Tree Concordance” at the Joint Statistical Meetings, Seattle, Washington, August, 2006.
- “A Bayesian Approach to Gene Tree Concordance” at the Computational and Statistical Genomics Workshop, Banff, Canada, July, 2006.
- “Bayesian Evolutionary Genomics” at the Gordan Research Conference on Molecular Evolution, Ventura, California, February, 2006.
- “Bayesian MCMC approaches for large gene-order phylogenies”, at the MBI Current Topics Workshop on the problems of phylogenetic analysis of large datasets, The Mathematics and Biology Institute, The Ohio State University, Columbus, Ohio, December 2005.
- “Bayesian phylogenetics” at the Mathematics and Phylogeny Meeting, Institut Henri Poincare, Paris, France, June, 2005.
- “Challenges of estimating the tree of life from molecular data” at the 2004 Annual Beckman Frontiers of Science Symposium, Irvine, California, November, 2004.
- “Phylogeny from genome arrangements: a Bayesian approach” at the 2nd Annual Cape Cod Monte Carlo Workshop, Boston, Massachusetts, August, 2004.
- “A model of AFLP evolution and its use in Bayesian estimation of phylogenetic relationships” at the 2004 Joint Statistical Meetings, Toronto, Canada, August, 2004.
- “A Statistical Approach to the Estimation of Phylogeny from Genome Arrangements” at the IMA/RECOMB satellite meeting on Comparative Genomics, Minneapolis, Minnesota, October, 2003.
- “Bayesian estimation of phylogeny from mitochondrial genome arrangements” at the WNAR/IMS Summer Meeting, Golden, Colorado, June, 2003.
- “Bayesian Phylogenetic Inference from Animal Mitochondrial Genome Arrangements” at the Statistical Society of Canada 2002 Meeting, Hamilton, Ontario, Canada, May, 2002.
- “On a Bayesian approach to phylogenetic inference from animal mitochondrial genome arrangements” at the RSS Extended Ordinary meeting on the Statistical Analysis of Genetic Data, London, England, May, 2002.
- “The combination of sequence data and genome arrangement data to infer evolutionary trees” at the Joint Statistical Meetings, Atlanta, Georgia, August, 2001.
- “A Bayesian analysis of the evolutionary history of the R locus in maize” at the Evolution Meetings, Knoxville, Tennessee, June, 2001.
- “A Bayesian approach to phylogenetic inference from genome arrangement data” at the Deep Green Workshop in College Park, Maryland, June 3, 2000.
- “Phylogenetic inference from genome arrangements”, at the 5th World Congress of the Bernoulli Society and the Year 2000 Institute of Mathematical Statistics Annual Meeting, Guanajuato, Mexico, 15-21 May, 2000.
- “An improved Markov chain Monte Carlo algorithm for phylogenetic inference”, at the 60th annual meeting of the Institute of Mathematical Statistics in Park City, Utah, July, 1997.

Contributed Presentations at International, National, and Regional Meetings

- “Defending Bayesian phylogenetics: a response to the critics” at the 2004 Evolution Meetings, Fort Collins, Colorado, June, 2004.
- “Phylogenetic inference from mitochondrial genome arrangement data”, at the Joint Statistical Meetings, Indianapolis, Indiana, August 16, 2000.
- “Likelihood and Genome Arrangements”, at the Allegheny Mountain Section of the MAA Spring Meeting, Pittsburgh, Pennsylvania, April 7, 2000.
- “A comparison of methods for assessing uncertainty in phylogenetic inference”, at the Evolution Meeting, Madison, Wisconsin, June 22–26, 1999.
- “Bayesian analysis in molecular biology and evolution”, at the Sixth Annual Meeting for the Society for Molecular Biology and Evolution, Vancouver, Canada, June 17–20, 1998 (poster presentation with Don Simon).
- “Minors in statistics”, at the Statistical Education conference at Youngstown State University, Youngstown, Ohio, April, 1997.
- “An excursion approach to phylogenetic inference via Markov chain Monte Carlo”, at the Miami Conference on Statistics, Oxford, Ohio, September 27, 1996.
- “Technology in statistical education” at the Joint Statistical Meetings, Chicago, Illinois, August 7, 1996.
- “Phylogenetic inference via Markov chain Monte Carlo: An excursion approach” at the Gordon Research Conference in Molecular Evolution, Ventura, California, January 28 – February 1, 1996 (poster presentation).
- “Phylogenetic inference using Markov chain Monte Carlo”, at the Third Albany Conference on Computational Biology, Albany, New York, September 28 – October 1, 1995 (poster presentation with Bob Mau).

Presentations at Seminars and Colloquia

- “Recent Advances in Bayesian Phylogenetic Inference” at the Biology Seminar, Duquesne University, Pittsburgh, PA, 2015.
- “Approximate Conditional Independence of Separated Subtrees and Phylogenetic Inference” at the Probability Seminar, University of Wisconsin, January, 2013.
- “An introduction to RevBayes”, at Evolution Seminar, University of Wisconsin, March, 2012.
- “A Phylogeographical Analysis of Gorilla Divergence”, at Dalhousie University, May, 2010.
- “Markov Chain Monte Carlo and Gorilla Evolution”, at the Undergraduate Statistics Club, University of Wisconsin, May, 2010.
- “Gorilla Evolution and Statistics”, at the Undergraduate Genetics Club, University of Wisconsin, April, 2010.
- “Bayesian Modeling of Numt Evolution with Application to the Estimation of Gorilla Divergence Times” at the Undergraduate Mathematics Club, University of Wisconsin, May, 2009.
- “Bayesian Phylogenetics” at the Department of Statistics, University of Wisconsin, February, 2007.
- “Bayesian Concordance Analysis” at the Department of Biology, Northern Illinois University, DeKalb, Illinois, September, 2006.
- “Case Studies in Bayesian Phylogenetics”, on September 26, 2005, in the CIBM seminar series, University of Wisconsin—Madison.

- “Bayesian phylogenetics”, on April , 2005, at the Department of Human Genetics, UCLA University, Los Angeles California.
- “Probability and Evolutionary Trees”, on December 3, 2003, at the Department of Mathematics, Lawrence University, Appleton, Wisconsin.
- “Bayesian Estimation of Phylogenetic Relationships from Mitochondrial Genome Arrangements”, on October 10, 2003, at the Department of Biological Sciences, University of Wisconsin—Parkside, Kenosha, Wisconsin.
- “Probability and Evolutionary Trees”, on May 8, 2003, for the Honors Day at the Department of Mathematics, University of Wisconsin—Madison.
- “A Markov chain Monte Carlo approach to the estimation of evolutionary relationships from genome arrangements”, on February 13, 2003, at the Department of Mathematics, University of Wisconsin—Madison.
- “Phylogenetic inference from mitochondrial genome arrangement data”, on December 7, 2000, at the Department of Chemistry at Duquesne University.
- “Phylogenetic inference from mitochondrial genome arrangement data”, on September 20, 2000, at the Department of Biostatistics at Johns Hopkins University, Baltimore, Maryland.
- “A Bayesian approach to phylogenetic inference”, on March 19, 1999, at the Department of Biology at the University of Rochester, Rochester, New York.
- “Bayesian analysis of evolutionary trees using Markov chain Monte Carlo”, on November 23, 1998, at the Department of Computer Science at Columbia University, New York, New York.
- “Bayesian analysis of evolutionary trees using Markov chain Monte Carlo”, On November 18, 1998, at the Department of Statistics at the University of Wisconsin, Madison, Wisconsin.
- “Phylogenies from Genome Rearrangements: Preliminary Ideas”, on October 21, 1998, at the Department of Mathematics and Computer Science, Duquesne University.
- “Bayesian analysis of evolutionary trees”, on August 24, 1998, at the Department of Applied Statistics at Reading University, Reading, United Kingdom.
- “Statistical methods for inferring evolutionary relationships from molecular sequence data”, on February 27, 1998, at the Department of Biological Sciences at Duquesne University, Pittsburgh, Pennsylvania.
- “MCMC methods for statistical inference of evolutionary trees from genetic data”, on November 12, 1997, at the Department of Statistics at Carnegie Mellon University, Pittsburgh, Pennsylvania.
- “MCMC methods for statistical inference of evolutionary trees from genetic data”, in October, 1997, at the Department of Mathematics and Computer Science, Duquesne University, Pittsburgh, Pennsylvania.
- “An Improved Markov Chain Monte Carlo Algorithm for Phylogenetic Inference”, in July, 1997, as part of the Probability Intern Program at the University of Wisconsin, Madison, Wisconsin.
- “The Equivalence of Aggregated Markov Processes”, in June, 1997, as part of the Probability Intern Program at the University of Wisconsin, Madison, Wisconsin.
- “Phylogenetic inference via Markov chain Monte Carlo: A finite excursion approach”, on August 2, 1996, at the Center for the Mathematical Sciences, University of Wisconsin, Madison, Wisconsin.
- “The Use of S-PLUS in the Teaching of Introductory Probability”, on November 8, 1995, at the Duquesne University Teaching with Technology Fair, Pittsburgh, Pennsylvania.
- “Statistical Inference of Phylogenies Using Markov Chain Monte Carlo”, on October 11, 1995, at the Department of Mathematics and Computer Science, Duquesne University, Pittsburgh,

Pennsylvania.

“An Unpolished Presentation of an Application of MCMC to the Estimation of Phylogeny”, on August 3, 1995, as part of the Probability Intern Program at the University of Wisconsin, Madison, Wisconsin.

“The Equivalence of Hidden Markov Models: An Overview of Results and Open Problems”, on June 27, 1995, as part of the Probability Intern Program at the University of Wisconsin, Madison, Wisconsin.

“Continuous Equivalence of Hidden Markov Models”, on February 22, 1995, Department of Mathematics and Computer Science at Duquesne University, Pittsburgh, Pennsylvania.

“Incorporating the Use of SPARCStations into the Teaching of Math 301”, on November 9, 1994, Department of Mathematics and Computer Science at Duquesne University, Pittsburgh, Pennsylvania.

Outside Examiner

Outside Examiner for Ph.D. Examination in Statistics, Dalhousie University, May, 2010.

Graduated Students

Ruiyan Luo (Statistics PhD, 2007), Soowan Sohn (Statistics PhD, 2007), Joungyoung Kim (Statistics PhD, 2008), Erika Mudrak (Biometry MS, 2009), Heejung Shim (Statistics PhD, 2010), Sarah Jane Alger (Biometry MS, 2010), Jeeyeon Kim (Statistics MS, 2012), Daijiang Li (Biometry MS, 2015), Lancine Konate (Statistics PhD, 2015).

Current Graduate Students

Shana Ederer (Biometry).

Undergraduate Student Research Mentor

Alex Kreibich (2009–2010), Emily Lundt (summer 2009), Tram Ta (summer, 2010), Ami Hays (2012), Wanzhen Lu (2013–2014), and Yin Tang (2013–2014).

Courses Taught at the University of Wisconsin

Botany 563, Phylogenetic Analysis of Molecular Data, in Spring 2016;

Botany/Genetics 629, Evolutionary Genetics (1/3 of course), in Fall 2007, 2009, 2011, 2013, 2015;

Botany 940, Systematics seminar (1/3 of course), in Spring 2011, 2014;

Statistics 302, Accelerated Introduction to Statistical Methods, in Spring 2014;

Statistics 309, Probability and Mathematical Statistics I, in Fall 2008, 2010;

Statistics 310, Probability and Mathematical Statistics II, in Spring 2009;

Statistics 333, Applied Regression Analysis, in Spring 2003;

Statistics 371, Introductory Applied Statistics for the Life Sciences, in Fall 2002–2005;

Statistics 571, Statistical Methods for Bioscience I, in Fall 2004, 2005, 2010, 2011;

Statistics 572, Statistical Methods for Bioscience II, in Spring 2007–2008;

Statistics 679, Multilevel Models, in Spring 2016;

Statistics 877, Statistical Methods in Molecular Biology (three lectures), in Spring 2008, 2010, 2012, 2014;

Statistics 992, Statistical Phylogenetics, in Spring 2004;

Statistics 992, Bayesian Computation, in Spring 2007; and

Statistics 998, Statistical Consulting, in Fall 2012, 2013, 2015.

Courses Taught at Duquesne University

Applied Statistics with Regression, one section, in Fall 1999; **Calculus I**, one section, in Fall 1997; **Experimental Design**, two sections, most recently in Spring 2001; **Fundamentals of Statistics**, ten sections, most recently in Fall 2001; **Introduction to Biostatistics**, seven sections, most recently in Spring 2001; **Introduction to Biostatistics computer lab**, seven sections, most recently in Fall 2000; **Introductory Probability and Statistics I**, five sections, most recently in Fall 1998; **Introductory Probability and Statistics II**, four sections, most recently in Spring 1998; **Linear Algebra and Differential Equations**, one section, in Spring 2000; **Probability and Markov Chains** (graduate), two sections, most recently in Fall 2001; **Problem Solving with Creative Mathematics**, one section, in Fall 2001; **Problem Solving Seminar**, one section, in Fall 2001; **Statistical Computing**, one section, in Spring 1997; **Statistical Inference** (graduate), two sections, most recently in Fall 2001;

University Service at the University of Wisconsin

University and Divisional Committees

Biology Major Executive Committee, 2008–2013.
Biology Major Program Committee, 2013–2014.
Biological Sciences Strategic Planning Committee, 2008–2010.
Committee on Committees, 2009–2010.
Commission on Faculty Compensation and Economic Benefits, 2004–2007.
Committee on Women, 2015–2016.
General Education Committee, 2015–2016.
Letters and Science Academic Advising Council, 2010.
Vice Provost/CIO Search Committee, 2006–2007.

College Committees

L&S Curriculum Committee, 2011–2014.

Departmental Committees: Botany

Academic Advisory, 2004–2007.
Awards (chair), 2008–2010.
Assessment, 2002–2003.
Budget, 2005–2008.
Curriculum, 2015–2016.
Endowment Funds, 2003–2007.
Faculty Senate, 2005–2014, 2015–2016.
Honors Program Coordinator, 2004–2014.
IT, 2006–2009.
Maher Supervisor, 2005–2009.
Merit, 2006–2008, 2012–2014.
Social, 2015 (chair).
Technology, 2009–2014, 2015–2016.
Undergraduate Majors Advisors (co-chair), 2002–2007.

Departmental Committees: Statistics

Computer Policy Committee, 2004–2005 (chair), 2005–2006, 2006–2009 (chair).

Curriculum Committee, 2008–2012.

Secretary of the Executive Committee, 2006–2007.

Undergraduate Advising, 2003–2004, 2010–2014, 2015–2016.

Undergraduate Major, 2012–2014, 2015–2016.

Graduate Admissions, 2002–2003, 2005–2006, 2007–2008, 2012–2013.

Graduate Student Exams (My students bold.) *Bacteriology*: Ainslie Little (2005,2006); *Biometry*: Andy Birch (2004), **Erika Mudrak** (2009), **Sarah Jane Alger** (2010), **Daijiang Li** (2015); *Botany*: Ivalú Cacho (2005,2009), Eunsoo Kim (2006), Shelley Crausbay (2007,2011), Shana Ederer (2008), Leith Nye (2008), Jane Bradbury (2008,2013), Andrew Gardner (2008,2013), Rachel Jabaily (2009), Christopher Cardona-Correa (2010), Daniel Spalink (2012,2015), Kevin Barrett (2013,2016), Kristen Michels (2013), Daijiang Li (2013), Giovanni Giraldo (2013), Jeremy Ash (2014), Jeffrey Rose (2014), Michael Piotrowski (2015), Daijiang Li (2015); *Comparative Biomedical Science*: Michael Gilson (2009,2010); *Computational Biology*: Aaron Darling (2005,2006), Bing Ma (2009,2011); *Dairy Science*: Matias Aguerre (2011); *Educational Psychology*: Tim Grant (2010,2011,2013); *Food Animal Production*; *Medicine*: Ermias Armene (2012,2014,2015); *Food Science*: Anupama Dattatreya (2005,2006), Kim Wiegand (2008,2009), Akhila Vasan (2012,2014); *Genetics*: Mike White (2008), Ryan Haasl (2010,2013); *Philosophy*: Joel Velasco (2008); *Statistics*: Hyuna Yang (2004,2005), Liang Sun (2004,2005), Ping Yan (2005), **Ruiyan Luo** (2005,2007), Deepayan Sarkar (2005,2006), Zhengxiao Wu (2006,2007), Haodu Fu (2006,2007), Xiaoli Li (2006,2006), Sang-hoon Cho (2006), **Soowan Sohn** (2006,2007), Yongho Jeon (2006), **Joungyoun Kim** (2007,2008), Stephen Stanhope (2008), Lane Burgette (2008,2009), Whipple Neely (2008,2009), **Heejung Shim** (2008,2010), Junhee Han (2008), **Lancine Konate** (2008,2015), Hui Wang (2007,2008), Cindy Yang (2007, 2009, Carnegie Mellon University), Zuofeng Shang (2010,2011), Yang Zhao (2010,2012), Yujin Chung (2011,2012), Xu He (2012), Lam Ho (2012,2014), Nick Henderson (2013,2015), Claudia Solis Lemus (2014,2015), Qi Jiang (2015), Junho Lee (2015), Xiaoping Feng (2015); *Zoology*: Matthew Helmus (2005,2009), T. Robert Gilman (2006,2010), Marijan Posavi (2010,2015).

Other University Service

Undergraduate Advising, Biology Major, 2004–2014.

Undergraduate Advising, College of Letters and Science, 2002–2007.

Faculty Appeals Committee, College of Letters and Science, 2005–2014,2016.

University Service at Duquesne University*University Committees*

Research Advisory Committee, 1998–2002; Task Force on Science, Technology, and Society, 1998-99.

College Committees

College Honors Committee, 1996–2002

Department Committees and Positions

Adviser, Duquesne Undergraduate Mathematics Association, 1995–2002; Adviser, Duquesne University Chapter of Pi Mu Epsilon, a national mathematics honorary society, 1999–2002; Course coordinator for Introductory Biostatistics, three semesters, most recently in Fall 1997;

Course coordinator for Fundamentals of Statistics, five semesters, most recently in Fall 2000; Director of Research, Fall 2000–2002; Graduate Program Committee, 1997–2002; Equipment Committee, 1994–2002; Library Committee, 1995–2002; Multimedia Committee, 1999; Placement Test Information Coordinator, 1995–2002; Search Committee, 1998, 2000, 2001; Seminar Organizer, 1998–2002; Technical Report Committee (chair), 1995–2002;