

Bret R. Larget

Department of Statistics
University of Wisconsin, Madison
Medical Sciences Center
1300 University Avenue
Madison, WI 53706

1250A MSC
608-262-7979 (phone)
608-262-0032 (FAX)
larget@stat.wisc.edu
<http://www.stat.wisc.edu/~larget/>

Department of Botany
University of Wisconsin, Madison
Birge Hall
430 Lincoln Drive
Madison, WI 53706

241 Birge Hall
608-265-6799 (phone)
608-262-7509 (FAX)

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

Assistant Professor, Departments. of Statistics and of Botany, University of Wisconsin, Madison,
Fall 2002 – present
Associate Professor, Department of Mathematics and Computer Science, Duquesne University,
Fall 2000 – Spring 2002
Assistant Professor, Department of Mathematics and Computer Science, Duquesne University,
Fall 1994 – 2000

Professional Positions

Associate Editor, *Journal of Statistics Education*, 2001 – 2003

Current External Grants

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 2007.

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 \$33,000 per year), from the National Science Foundation, three years beginning in 2005.

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.

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.

Previous External Grants

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.

Refereed Publications

Larget, B., D.L. SIMON, AND J.B. KADANE (accepted). A Bayesian approach to the estimation of ancestral genome arrangements. *Molecular Phylogenetics and Evolution*.

Larget, B., D.L. SIMON, AND S. SOHN (accepted). A Comparison between BADGER and GRAPPA. *Bioinformatics*.

Larget, B., D.L. SIMON, J.B. KADANE, D. SWEET (accepted). A Bayesian analysis of metazoan mitochondrial genome arrangements. *Molecular Biology and Evolution*.

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.

Manuscripts under review

- HOLDER, M.T., P.O. LEWIS, D.L.SWOFFORD, AND **B. Larget**. Hastings ratio of the LOCAL proposal used in Bayesian phylogenetics. Submitted to *Systematic Biology*.
- ANÉ, C., **B. Larget**, R. LUO, AND S. SOHN. Inconsistency of maximum parsimony and maximum likelihood when evolution is heterogeneous. Submitted to *Nature*.

Dissertation

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

Distributed Software

SIMON, D. AND B. LARGET (2004). Bayesian Analysis to Describe Genomic Evolution by Rearrangement (BADGER), 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.)

Technical Reports (not published elsewhere)

LARGET, B. AND D. SIMON (1998). Faster likelihood calculations on trees. Technical Report #98-02, Department of Mathematics and Computer Science, Duquesne University.

MICHAEL NEWTON, BRET LARGET, RICK CHAPPELL, AND RUSSELL JACOBY (1997). Random allocations in comparative experiments of known size: balance without blocking. Technical Report #97-04 at the Department of Mathematics and Computer Science, Duquesne University.

BRET LARGET (1996). Developing intuition for the standard deviation via computer graphics. Technical Report #96-02 at the Department of Mathematics and Computer Science, Duquesne University.

Summer Research Programs

Statistical Inference from Genetic Data on Pedigrees, at Michigan Technological University. Participation supported by the NSF for one week in the summer of 1999.

Biomolecular Function and Evolution in the Context of the Genome Project at the Isaac Newton Institute for Mathematical Sciences, Cambridge University, United Kingdom. Participation supported by the NSF for six weeks in the summer of 1998.

Probability Intern Program at the University of Wisconsin, Madison, Wisconsin. Participation supported by the NSF for eight weeks in the summer of 1997 to study the topic Mathematical Finance and Stochastic Control.

Probability Intern Program, at the University of Wisconsin, Madison, Wisconsin. Participation supported by the NSF for eight weeks in the summer of 1995 to study the topic Markov Chains and Simulation.

Internal Grants

Reconstructing Complicated Evolutionary Histories, 2000 Duquesne University Faculty Development Grant

Integrating Advanced Statistical Software into the Teaching of Introductory Probability and Statistics, 1995 Hunkele Grant for Teaching with Technology

Implications of a New Theorem on Hidden Markov Models, 1995 Duquesne University Faculty Development Grant

Invited Presentations at National and International Meetings

“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

“Bayesian phylogenetics” in April, 2004, 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.

Referee for Academic Journals

The American Statistician, Bioinformatics, Biometrics, Evolution, Genetics, Journal of Molecular Evolution, Journal of Statistics Education, Journal of the American Statistical Association (JASA), Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, Palaeontologia Electronica, Science, and Systematic Biology.

Session Organizer

Invited session on statistical phylogenetics, Joint Statistical Meetings, Minneapolis, MN, August 2005.

Topic contributed session on Bayesian phylogenetics, Joint Statistical Meetings, Minneapolis, MN, August 2005.

Session Chair at National Meetings

Session on longitudinal data, Joint Statistical Meetings, Baltimore, Maryland, August 8–12, 1999.

Session on molecular evolution methods, Evolution 99, Madison, Wisconsin, June 22–26, 1999.

Membership in Professional Organizations

The American Association for the Advancement of Science, The American Statistical Association, The Institute of Mathematical Statistics, The Mathematics Association of America, Project Kaleidoscope Faculty for the 21st Century, Society for Molecular Biology and Evolution, and The Society of Systematic Biologists.

Current Graduate Students

Ruiyan Luo (Statistics) and Soowan Sohn (Statistics)

Courses Taught at the University of Wisconsin (6 total)

Statistics 371, Introductory Applied Statistics for the Life Sciences, in Fall 2002, 2003, 2004.

Statistics 571, Statistical Methods for Bioscience I, in Fall 2004.

Statistics 992, Statistical Phylogenetics, in Spring 2004.

Statistics 333, Applied Regression Analysis, in Spring 2003.

Courses Taught at Duquesne University (45 total)

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 Committees

Commission on Faculty Compensation and Economic Benefits, 2004–2005.

Departmental Committees: Botany

Undergraduate Majors Advisors (co-chair), 2002–2005.

Academic Advisory, 2004–2005.

Honors Program Coordinator, 2004–2005.

Endowment Funds, 2003–2005.

Assessment, 2002–2003.

Departmental Committees: Statistics

Computer Policy Committee (chair), 2004–2005.

Undergraduate Advising, 2003–2004.

Graduate Admissions, 2002–2003.

Graduate Student Committees

Statistics: Hyuna Yang, Liang Sun

Biometry: Andy Birch

Computer Science: Aaron Darling

Other University Service

Undergraduate Advising, Biology Major, 2004–2005.

Undergraduate Advising, College of Letters and Science, 2002–2005.

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;