

Laura Salter Kubatko

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Education

- 1999 Ph.D., Biostatistics, The Ohio State University.
Thesis Title: Simulation-based Estimation of Phylogenetic Trees
Advisor: Professor Dennis Pearl
- 1996 M.S., Statistics, The Ohio State University.
- 1994 B.A., Mathematics, Hiram College.
- 1994 B.A., Biology, Hiram College.

Professional Experience

- 2006-present Associate Professor, Departments of Statistics (80%) and Evolution, Ecology, and Organismal Biology (20%), The Ohio State University.
- 2008-present Affiliate Faculty, Battelle Center for Mathematical Medicine, Nationwide Childrens Hospital, Columbus, OH.
- 2008-present Faculty Affiliate, Initiative in Population Research, The Ohio State University.
- Fall 2005 Long-term Visitor, Mathematical Biosciences Institute, The Ohio State University.
- 2003-present Adjunct Research Scientist, Lovelace Respiratory Research Institute, Albuquerque, NM.
- 1999-2006 Assistant Professor, Department of Mathematics and Statistics, The University of New Mexico.
- 1999 Instructor, Department of Mathematics, Ohio Wesleyan University.
- 1998-1999 Graduate Research Associate, Department of Statistics, The Ohio State University.
- 1997-1998 Graduate Research Associate, Biostatistics Program, The Ohio State University.
- 1994-1997 Graduate Teaching Assistant, Department of Statistics, The Ohio State University.
- 1996-1997 Intern, Research & Development, Kal Kan Foods, Inc., Columbus, OH.

Publications

Peer-reviewed Journal Articles

- **Salter, L.** and D. Pearl. 2001. Stochastic search strategy for estimation of maximum likelihood phylogenetic trees, *Systematic Biology* 50(1): 7-17.
- Turner, T., **L. Salter**, and J. Gold. 2001. Temporal-method estimates of N_e from highly polymorphic loci, *Conservation Genetics* 2: 297-308.
- **Salter, L.** 2001. Complexity of the likelihood surface for a large DNA data set, *Systematic Biology* 50(6): 970-978.

- Frankel, W., J. Tranovich, **L. Salter**, G. Bumgardner, and P. Baker. 2002. The optimal number of biopsies to evaluate for liver transplantation, *Liver Transplantation*, 8(11): 1044-1050.
- Wang, Q., **L. Salter**, and D. Pearl. 2002. Estimation of substitution model parameters with phylogenetic trees, *Journal of Molecular Evolution* 55(6): 684-695.
- Powell, A., D. Jacobson, **L. Salter**, and D. Natvig. 2003. Variation among natural isolates of *Neurospora* on small spatial scales, *Mycologia* 95: 809-819.
- Gilchrist, M., **L. Salter**, and A. Wagner. 2004. A statistical framework for interpreting high-throughput proteomic datasets, *Bioinformatics* 20(5): 689-700.
- Strandberg, A.K.K. and **L. Salter**. 2004. A comparison of methods for estimating the transition:transversion ratio from DNA sequences, *Molecular Phylogenetics and Evolution* 32(2): 495-503.
- Degnan, J. and **L. Salter**. 2005. Gene tree distributions under the coalescent process, *Evolution* 59(1): 24-37.
- **Kubatko**, **L. Salter** and J. Degnan. 2007. Inconsistency of concatenated-data phylogenetic estimates under coalescence, *Systematic Biology*, 56(1): 17-24.
- Wilbur, A., **L. Salter Kubatko**, J. Feurstein, A. Hurtado, K. Hill, and A. Stone. 2007. Vitamin D receptor polymorphisms and susceptibility of *M. tuberculosis* in Native Paraguayans, *Tuberculosis* 87: 329-337.
- Efromovich, S. and **L. Salter Kubatko**. 2008. Coalescent time distributions in trees of arbitrary size, *Statistical Applications in Genetics and Molecular Biology*, Vol. 7 : Iss. 1, Art. 2, Available at: <http://www.bepress.com/sagmb/vol7/iss1/art2>.
- Shoff, M. E., C. E. Joslin, E. Y. Tu, **L. Kubatko**, and P. A. Fuerst. 2008. Efficacy of contact lens systems against recent clinical and tap water *Acanthamoeba* isolates, *Cornea* 27(6): 713-719.
- Meng, C. and **L. S. Kubatko**. 2009. Detecting hybrid speciation in the presence of incomplete lineage sorting using gene tree incongruence: A model, *Theoretical Population Biology* 75: 35-45.
- Brock, G., W. Beavis, and **L. Salter Kubatko**. 2009. Fuzzy logic and related methods as a screening tool for detecting gene regulatory networks, *Information Fusion* 10:250-259 (special issue on Bioinformatics).
- **Kubatko**, **L.**, B. C. Carstens, and L. L. Knowles. 2009. STEM: Species Tree Estimation using Maximum likelihood for gene trees under coalescence, *Bioinformatics* 25(7): 971-973.
- Liu, L., L. Yu, **L. Kubatko**, D. K. Pearl, and S. V. Edwards. 2009. Coalescent methods for estimating multilocus phylogenetic trees, *Molecular Phylogenetics and Evolution*, 53(1): 320-328.
- Melman, S.D., M.L. Steinauer, C. Cunningham, **L.S. Kubatko**, I.N. Mwangi, M.W. Mutuku, D.M.S. Karanja, D. G. Colley, C. Black, W.E. Secor, N. Barker, G.M. Mkoji, and E.S. Loker. 2009. Reduced susceptibility of naturally occurring *Schistosoma mansoni* to praziquantel following repeated exposures: origin, measurement and likelihood of persistence, *PLoS Neglected Tropical Diseases*, 3(8): e504. doi:10.1371/journal.pntd.0000504.
- **Kubatko**, **L. S.** 2009. Identifying hybridization events in the presence of coalescence via model selection, *Systematic Biology*, in press.
- **Kubatko**, **L.** and H. L. Gibbs. 2009. Inferring species-level phylogenies using multi-locus data for a recent radiation of *Sistrurus* rattlesnakes, accepted with revisions for *Systematic Biology*.

- Wilbur, A. K., **L. Salter Kubatko**, A. M. Hurtado, K. R. Hill, and A. C. Stone. 2009. Mannose-binding protein diversity and M. tuberculosis susceptibility in two Native South American populations, submitted.
- Stone A.C., **L. S. Kubatko**, G. H. Perry, F. Battistuzzi, and S. Kumar. 2009. Analysis of complete mtDNA sequences in Pan, submitted.
- Boykin, L., **L. Salter Kubatko**, and T. Lowrey. 2009. Phylogenetic relationships of Orcuttieae (Poeaceae: Chloridoideae): Utility of Bayesian rooting methods, submitted.

In Books

- Pearl, D. and **L. Salter**. 2002. The Analysis of DNA Sequences, in Biostatistical Genetics and Genetic Epidemiology, edited by R. Elston, J. Olson, and L. Palmer, pp. 217-227, John Wiley and Sons, New York.
- M. J. Harmon, T. L. VanPool, R. D. Leonard, C. S. VanPool, and **L. Salter**. 2006. Reconstructing the Flow of Information across Time and Space: A Phylogenetic Analysis of Ceramic Traditions from Pre-Hispanic West Mexico, North Mexico, and the U.S. Southwest, in Mapping Our Ancestors: Phylogenetic Methods in Anthropology and Prehistory, edited by Carl P. Lipo, Michael J. O'Brien, Stephen Shennan, and Mark Collard, pp. 209-229.
- **Kubatko, L. Salter**. 2007. Inference of Phylogenetic Trees, pgs. 1-38 in Tutorials in Mathematical Biosciences: Evolution and Ecology (Vol. 4), edited by Avner Friedman, published by Springer-Verlag.
- Brock, G., V. Pihur, and **L. Kubatko**. 2009. Detecting gene regulatory networks from microarray data using fuzzy logic, in Fuzzy Systems in Bioinformatics, Bioengineering, and Computational Biology, edited by Yaochu Jin and Lipo Wang, pages 141-164.
- Nance, T. and **L. Salter Kubatko**. 2009. Constructing an undergraduate biomath curriculum at a large university, part I: Developing first year biomath courses at The Ohio State University, to appear in the MAA volume: Undergraduate Mathematics for the Life Sciences: Processes, Models, Assessment, and Directions, edited by G. Ledder, J. P. Carpenter, and T. Comar.
- **Kubatko, L. Salter**, J. Best, T. Nance, and Y. Luo. 2009. Constructing an undergraduate biomath curriculum at a large university, part II: Implementing first year biomath courses at The Ohio State University, to appear in the MAA volume: Undergraduate Mathematics for the Life Sciences: Processes, Models, Assessment, and Directions, edited by G. Ledder, J. P. Carpenter, and T. Comar.

Proceedings and Book Reviews

- **Salter, L.** 2000. Algorithms for phylogenetic tree estimation. *Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences, Vol. 2, pgs. 459-465* (refereed conference proceedings).
- **Salter, L.** 2004. Review of The Phylogenetic Handbook: A Practical Approach to DNA and Protein Phylogeny (Edited by Marco Salemi and Anne-Mieke Vandamme. Cambridge, England: Cambridge University Press, 2003.), *American Journal of Human Biology* 16: 354-355 (invited book review).

- **Kubatko, L. S.** 2009. Modeling the past: A resource for the future (review of the book Coalescent Theory: An Introduction by John Wakeley), *Trends in Ecology and Evolution*, 24(3): 125-126.

Research Funding

- Title: *QEIB: Statistical Issues in Combining Data for Phylogenetic Analysis*
PI: Laura Salter
National Science Foundation (DMS Grant 0104290)
July 2001–June 2005
\$125,000.
- Title: *GeneX Data Analysis and Visualization Tool Development*
PI: Laura Salter
Subcontract from the National Center for Genome Resources
September 2001–May 2002
\$45,837.
- Title: *Genetic Regulation of the Pulmonary Immune Response to Cryptococcus neoformans*
PI: Julie Wilder, UNM Department of Pathology and Lovelace Respiratory Research Institute
American Lung Association
May 2003–April 2005
7% effort.
- Title: *Methods to Compare Multivariate Arrays*
PI: Laura Salter
Subcontract from the National Center for Genome Resources
June 2004–May 2006
\$60,000.
- Title: *Genetic Analysis of Pulmonary Immunity*
PI: Julie Wilder, UNM Department of Pathology and Lovelace Respiratory Research Institute
NIAID 1 R21 AI059142-01
March 2005–February 2007
7% effort.
- Title: *Gene Tree-Species Tree Relationships Under the Coalescent Process*
PI: Laura Salter Kubatko
National Science Foundation (DMS 0505265 – now DMS 0702277)
August 2005–July 2009
\$75,000.
- Title: *Coalescent Modeling for Genetic Mapping in Population-based Samples*
PI: Laura Kubatko
Co-PIs: Veronica Vieland, Christopher Bartlett (Nationwide Children's Hospital)
Seed grant from the OSU Initiative in Population Research under NIH 1 R21 HD047943-01
August 2008–July 2009
\$15,000.

- Title: *BioMathletic Training: Creating the Next Generation of BioMath Stars at Ohio State University*
 PI: Ian Hamilton
 Co-PIs: Laura Kubatko, Janet Best, Yuan Lou, Elizabeth Marschall
 National Science Foundation (DBI 0827256)
 August 2008 – July 2013
 \$980,000.
- Title: *Inferring Species Phylogenies Under the Coalescent Model with Hybridization*
 PI: Laura S. Kubatko
 National Science Foundation (DEB 0842219)
 February 2009 – January 2012
 \$226,946.
- Title: *Collaborative Research: Estimating Species Trees with Population Genetic Approaches: Working Towards a New Phylogenetic Paradigm for 21st Century Phylogenetics*
 PI: Laura S. Kubatko (Collaborative with L. Lacey Knowles)
 National Science Foundation (DEB 0918195)
 July 2009 – July 2011
 \$188,375.

Invited Presentations

- “Distributions Arising on Gene Trees Under the Coalescent Model”, Statistical and Applied Mathematical Sciences Institute (SAMSI) Molecular Evolution and Phylogenetics Workshop, April 2009.
- “Inferring Evolutionary Relationships from Multi-locus Data”, Department of Biology, University of Maryland Baltimore County, March 2009.
- “Detecting Hybridization in the Presence of Incomplete Lineage Sorting Using Multilocus Data”, Estimating Species Trees Symposium, University of Michigan, January 2009.
- “Inferring Evolutionary Relationships Using Genetic Data From Multiple Loci”, Epidemiology and Biostatistics, University of Cincinnati, November 2008.
- “Inferring Evolutionary Relationships Using Multi-locus Data, with Application to a Recent Radiation of North American Rattlesnakes”, Department of Biology, University of Idaho, September 2008.
- “A Model for Coalescence with Hybridization”, Society of Systematic Biology Symposium on “Species Trees and Gene Tree Heterogeneity: Concepts, Estimation and Empirical Applications”, Evolution Meetings, June 2008.
- “Inferring Evolutionary Relationships from Multi-locus Data”, Center for Computational Biology and Bioinformatics, and Section of Integrative Biology, University of Texas at Austin, April 2008.
- “Inferring Evolutionary Relationships from Multi-gene Data”, Department of Bioinformatics and Biostatistics, University of Louisville, February 2008.

- “Phylogenetics meets genomics: Estimating evolutionary relatedness using whole-genome data”, MathFest, August 2007.
- “Estimating Species-level Phylogenies from Multi-gene Data Under Coalescence”, Department of Ecology and Evolutionary Biology, University of Michigan, February 2007.
- “Inferring Maximum Likelihood Species Phylogenies Under Coalescence”, Joint Statistical Meetings, August 2006.
- “Relationships Between Gene Trees and Species Trees Under Coalescence”, Department of Ecology, Evolution, and Organismal Biology, The Ohio State University, October, 2005.
- “Relationships Between Gene Trees and Species Trees Under Coalescence”, Department of Statistics, The Ohio State University, October, 2005.
- Discussant, Workshop on Phylogenetics and Phylogeography, Mathematical Biosciences Institute at The Ohio State University, September, 2005.
- “Prospects and Pitfalls of Whole Genome Phylogeny Based on DNA Sequences”, Joint Statistical Meetings, August, 2005.
- “Prospects and Pitfalls of Whole Genome Phylogeny Based on DNA Sequences”, Gordon Research Conference on Quantitative Genetics, February, 2005.
- “Prospects and Pitfalls of Whole Genome Phylogeny”, Annual Meeting of the Albuquerque Chapter of the American Statistical Association, September, 2004.
- “An Overview of Current Problems in Statistical Genetics, Biostatistics, and Bioinformatics”, Franciscan University of Steubenville, April, 2004.
- “Estimation of Evolutionary Parameters From Phylogenetic Trees”, National Center for Genome Resources, Santa Fe, NM, August 2001.
- “Statistical Issues in Combining Data for Phylogenetic Analysis”, Joint Statistical Meetings, Atlanta, GA, August 2001.
- “Phylogenetic Inference in the Era of the Human Genome Project”, Annual Meeting of the Albuquerque Chapter of the American Statistical Association, April 2001.
- “Algorithms for Phylogenetic Tree Estimation”, International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences, Las Vegas, NV, June, 2000.
- “A Stochastic Search Strategy for Estimation of Maximum Likelihood Phylogenetic Trees”, Department of Mathematics, Arizona State University, April, 2000.
- “Maximum Likelihood Estimation of Phylogenetic Trees and Associated Substitution Model Parameters”, The Ohio State University Department of Statistics Silver Anniversary Conference, October, 1999.
- “A Stochastic Search Strategy for Estimation of Maximum Likelihood Phylogenetic Trees”, Carnegie Mellon University, March, 1999.
- “A Stochastic Search Strategy for Estimation of Maximum Likelihood Phylogenetic Trees”, University of Pittsburgh, February, 1999.

- “A Stochastic Search Strategy for Estimation of Maximum Likelihood Phylogenetic Trees”, Michigan State University, January, 1999.

Short Courses

- “Model-Based Phylogenetics”, North American Workshop in Cladistic Methods, The Ohio State University, July 2007, July 2008.
- “Model-based Phylogenetics”, Department of Entomology, University of Kentucky, March 2008.
- “Gene Tree-Species Tree Inference Under the Coalescent”, Center for Computational Biology and Bioinformatics and Section of Integrative Biology, University of Texas at Austin, April 2008.
- “STEM: Species Trees Estimation using Maximum likelihood”, Estimating Species Trees Symposium, University of Michigan, January 2009.

Summary of Other Presentations

- Topic Contributed presentations at JSM/IBC: 3
- Oral presentations by students and collaborators: 14

Special note: Ph.D. student James Degnan won the WNAR student paper award for his presentation at the joint SSC/WNAR/IMS meeting in 2004.

- Poster Presentations by students and collaborators: 5

Professional Service

- Associate Editor for *Systematic Biology*, 2007–present.
- Journal reviews for: *Bioinformatics*, *Journal of the American Statistical Association*, *Molecular Phylogenetics and Evolution*, *Systematic Biology*, *Journal of Biomedical Informatics*, *Evolution*, *BMC Bioinformatics*, *CUR Quarterly*, *Statistical Applications in Genetics and Molecular Biology*, *BMC Evolutionary Biology*, *Science*.
- Chapter review for the edited volume Evolutionary Genetics: Concepts and Case Studies edited by Charles Fox and Jason Wolf, Oxford University Press (2004).
- Ad-hoc grant reviews for the National Science Foundation (2002, 2004, 2005, 2006, 2007, 2009).
- National Science Foundation Panel on Phylobiogeography, 2008.
- National Science Foundation Third Year Review Team Member for UBM Program, 2008.
- Elected to the Council of the Society of Systematic Biology, 2008-2010.
- Co-organizer of 2-day symposium titled “Estimating Species Trees”, held January 10-11, 2009 at the University of Michigan. Sponsored by the University of Michigan Museum of Zoology and the National Science Foundation.
- Organizer and Chair for Invited Session on Phylogenetics, WNAR/IMS Meeting, 2004.

- Program Committee Member for the 2001 International Conference on Computational Science, held in San Francisco in May, 2001. Duties included organizing and chairing a mini-symposium on “Phylogenetic Inference Using Genome Rearrangement Data”.
- Program Committee Member for the Joint Meeting of the Statistics Society of Canada, the Institute of Mathematical Statistics, and the Western North American Region (WNAR) of the International Biometrics Society, held in Vancouver in June, 2001. I served as the chair of all WNAR events, and my duties included organizing WNAR’s invited program, organizing the WNAR Young Researchers Luncheon, and organizing the WNAR Student Paper Competition.
- Albuquerque Chapter Representative to the American Statistical Association, 2001-2003.

Student Advisement

Doctoral Advisement

- Guy Brock, Ph.D. in Statistics, 2003 (University of New Mexico)
Inferring Regulatory Networks From Microarray Data
Guy is currently an Assistant Professor in the Department of Bioinformatics and Biostatistics at the University of Louisville.
- James Degnan, Ph.D. in Statistics, 2005 (University of New Mexico)
Estimating Species Trees from Genes Trees Under Coalescence
James is currently a faculty member in the Department of Mathematics and Statistics at the University of Canterbury.
- Chen Meng, Ph.D. in Statistics, Fall 2008 (University of New Mexico)
Testing Hybridization Hypotheses Using Gene Tree Distributions
Chen is currently a Statistician at Monsanto.
- Lori Hoffman, Ph.D. in Statistics (current)
Lori is studying the coalescent-with-recombination model.

Masters Advisement

- Kristina Strandberg, M.S. in Statistics, 2003 (University of New Mexico)
Estimation of the Transition/Transversion Ratio From DNA Sequence Data
- Lin Pan, M.S. in Statistics, 2003 (University of New Mexico)
Detecting QTL for Pulmonary Immune Response of Mice
- Jennifer Bryant, M.S. in Statistics, 2005 (University of New Mexico)
*Analysis of Protein Interaction Data for DNA Sensitivity Genes in *Saccharomyces cerevisiae**
- Helen Fan, M.S. in EEOB (current)
Helen is examining methods of species tree estimation.

Graduate Committee Memberships (does not include students I’ve advised):

- Doctoral committees in Statistics at OSU: 2
- Doctoral committees in EEOB at OSU: 3

- Masters committees in EEOB at OSU: 3
- Doctoral committees in Statistics at UNM: 5
- Masters committees in Statistics at UNM: 3
- Doctoral committees outside Statistics at UNM: 10
- Masters committees outside Statistics at UNM: 3