Laura Salter Kubatko
Department of Statistics
Department of Evolution, Ecology
and Organismal Biology
The Ohio State University

Education

1996-1999	Ph.D.	Biostatistics	The Ohio State University, Columbus, Ohio
1994-1996	M.S.	Statistics	The Ohio State University, Columbus, Ohio
1990-1994	B.A.	Mathematics	Hiram College, Hiram, Ohio
1990-1994	B.A.	Biology	Hiram College, Hiram, Ohio

Professional Experience

2019-present	Co-Director, Mathematical Biosciences Institute, The Ohio State University.
2013-present	Professor, Departments of Statistics (75%) and Evolution, Ecology, and Organismal Biology (25%), The Ohio State University.
2006-2013	Associate Professor, Departments of Statistics (80%) and Evolution, Ecology, and Organismal Biology (20%), The Ohio State University.
1999-2006	Assistant Professor, Department of Mathematics and Statistics, The University of New Mexico.

Other Professional Appointments

2016-present	Section Editor, Theory and Methods Section, *BMC Evolutionary Biology*
2016-present	Faculty Affiliate, Translational Data Analytics Institute (TDAI), 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
2007-present	Associate Editor, *Systematic Biology*
2013-2015	Associate Director, Mathematical Biosciences Institute, The Ohio State University
2012-2014	Chair, Interdisciplinary PhD Program in Biostatistics, The Ohio State University
2012-2015	NIMBioS Board of Advisors, University of Tennessee
2010-2012	Associate Editor, *Evolution*
Fall 2005	Long-term Visitor, Mathematical Biosciences Institute, The Ohio State University
2003-2010	Adjunct Research Scientist, Lovelace Respiratory Research Institute, Albuquerque, NM

Honors, Awards, and Media Coverage

2017	Big Ten Network LiveBIG Feature: How an Ohio State professor will save East Africa $1.25 billion dollars
2017	TDA Big Data for Good Feature: Fighting the Flies
2011	Ohio State University College of Arts and Sciences Outstanding Teaching Award Finalist
1999	Ransom and Marian Whitney Award for Research, Dept. of Statistics, The Ohio State University
1998	Craig Cooley Memorial Prize, Dept. of Statistics, The Ohio State University
1997	Outstanding Graduate Associate Teaching Award, The Ohio State University
1995	Thomas and Jean Powers Memorial Teaching Award, Dept. of Statistics, The Ohio State University

Students

Postdoctoral advising

2005	James Degnan
2009 - 2011	Julia Chifman, MBI post-doctoral associate
2010 - 2011	Rasmus Hovmoller
2014 - 2017	Jeffrey Gaither, MBI post-doctoral associate
2016 - 2019	Colby Long, MBI post-doctoral associate

Ph.D. advising

2003	Guy Brock, Statistics, University of New Mexico
2005	James Degnan, Statistics, University of New Mexico
2008	Chen Meng, Statistics, University of New Mexico
2010	Lori Hoffman, Statistics, The Ohio State University
2013	David Spade, Statistics, The Ohio State University (co-advised with Dr. Radu Herbei)
2013	Katherine Thompson, Statistics, The Ohio State University
2013	Hang (Helen) Fan, Statistics, The Ohio State University
2016	Yuan Tian, Evolution and Ecology, The Ohio State University
Current	Jing Peng, Biostatistics, The Ohio State University
Current	Yuan Gao, Biostatistics, The Ohio State University
Current	Andrew Richards, Statistics, The Ohio State University
Current	Sungsik (Kevin) Kong, Evolution and Ecology, The Ohio State University

M.S. advising

2003	Kristina Strandberg, Statistics, University of New Mexico
2003	Lin Pan, Statistics, University of New Mexico
2005	Jennifer Bryant, Statistics, University of New Mexico
2010	Hang (Helen) Fan, Evolution and Ecology, The Ohio State University
2014	Lingfei Cui, Evolution and Ecology, The Ohio State University
2018	Joy Zeng, Statistics, The Ohio State University (co-advised with Dr. Matt Pratola)

Undergraduate advising

2009-2010	David Gerard, co-advised with Dr. Lisle Gibbs, NSF UBM Undergraduate Fellow
2010-2011	Tim NeCamp, co-advised with Dr. Andi Wolfe, NSF UBM Undergraduate Fellow
2010-2011	Susan Fassnacht, co-advised with Dr. Andi Wolfe, NSF UBM Undergraduate Fellow
2011-2012	Paul Blischak, co-advised with Dr. Andi Wolfe, NSF UBM Undergraduate Fellow
2011-2012	Theresa Bolaney, co-advised with Dr. Andi Wolfe, NSF UBM Undergraduate Fellow
2011-2013	Erin Harvey, co-advised with Dr. Andi Wolfe, NSF UBM Undergraduate Fellow
2011-2012	Hang Guo, co-advised with Dr. Julia Chifman, NSF UBM Undergraduate Fellow
2011-2012	Josh Walum, co-advised with Dr. Julia Chifman, NSF UBM Undergraduate Fellow
2012-2013	Shannon Kilkenny, co-advised with Dr. Andi Wolfe, NSF UBM Undergraduate Fellow
Summer 2012	Yingle Zhang, co-advised with Dr. Dennis Pearl, MBI REU program
Summer 2013	Divyagash Swargaloganathan, MBI REU program
2014-2015	Ben Stone, co-advised with Dr. Andi Wolfe
Spring 2014	Evan Carfagno, co-advised with Dr. Andi Wolfe
Spring 2015	Niharika Padmalwar, co-advised with Dr. Andi Wolfe
Summer 2015	Tiffany Bailey, SROP student

2016-2018	Coleen Thompson, co-advised with Dr. Andi Wolfe
2016-2018	Emiko Waight, co-advised with Dr. Andi Wolfe
2018-2019	Haoran Wang
2018-2019	Xiaoyu Liang

Grants

2001-2005	QEIB: Statistical issues in combining data for phylogenetic analysis (PI: Laura Salter) NSF DMS 0104290, $125,000
2001-2002	GeneX data analysis and visualization tool development (PI: Laura Salter) Subcontract from the National Center for Genome Resources, $45,837
2003-2005	Genetic regulation of the pulmonary immune response to *Cryptococcus neoformans* (PI: Wilder) American Lung Association, 7% effort, Role: consultant
2004-2006	Methods to compare multivariate arrays (PI: Laura Salter) Subcontract from National Center for Genome Resources, $60,000
2005-2007	Genetic analysis of pulmonary immunity (PI: Wilder) NIAID 1 R21 AI059142-01, 7% effort, Role: consultant
2005-2009	Gene tree-species tree relationships under the coalescent process (PI: Kubatko) NSF DMS 0505265/0702277, $75,000
2008-2009	Coalescent modeling for genetic mapping in population-based samples (PI: Kubatko; Co-PIs: Vieland, Bartlett); Seed grant from the OSU Initiative in Population Research under NIH 1 R21 HD047943-01, $15,000
2008-2013	UBM: BioMathletic training: creating the next generation of BioMath Stars at Ohio State University; (PI: Hamilton; Co-PIs: Kubatko, Best, Lou, Marschall); NSF DBI 0827256, $980,000
2009-2012	Inferring species phylogenies under the coalescent model with hybridization (PI: Kubatko) NSF DEB 0842219, $226,946
2009-2011	Collaborative research: Estimating species trees with population genetic approaches: Working towards a new paradigm for 21^{st} century phylogenetics (PI: Knowles; Co-PI: Kubatko) NSF DEB 0918195, $188,375
2011-2015	Coalescent-based species tree inference using algebraic statistics (PI: Kubatko; Co-PI: Chifman) NSF DMS 1106706, $180,000
2015-2018	REU site: Distributed REU in the Mathematical Biosciences (PI: Golubitsky; Co-PI: Kubatko) NSF DMS 1461163, $149,999
2015-2019	Testing adaptive radiation theory in Penstemon (Plantaginaceae) (PI: Wolfe; Co-PI: Kubatko) NSF DEB 1455399, $758,208
2016-2020	Collaborative research: Estimation of large species/population trees using tree space (PI: RoyChoudhury; Co-PI: Kubatko); NSF DMS 1610305, $76,051

Publications

$^{+}$ denotes graduate student co-author; * denotes undergraduate co-author

Peer-reviewed Journal Articles

1. Salter, L. and D. Pearl. 2001. Stochastic search strategy for estimation of maximum likelihood phylogenetic trees, *Systematic Biology* 50(1): 7-17.

2. Turner, T., L. Salter, and J. Gold. 2001. Temporal-method estimates of N_e from highly polymorphic loci, *Conservation Genetics* 2: 297-308.

3. Salter, L. 2001. Complexity of the likelihood surface for a large DNA data set, *Systematic Biology* 50(6): 970-978.

4. 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.

5. Wang, Q., L. Salter, and D. Pearl. 2002. Estimation of substitution model parameters with phylogenetic trees, *Journal of Molecular Evolution* 55(6): 684-695.

6. Powell, A.$^+$, D. Jacobson, L. Salter, and D. Natvig. 2003. Variation among natural isolates of Neurospora on small spatial scales, *Mycologia* 95: 809-819.

7. Gilchrist, M., L. Salter, and A. Wagner. 2004. A statistical framework for interpreting high-throughput proteomic datasets, *Bioinformatics* 20(5): 689-700.

8. 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.

9. Degnan, J.$^+$ and L. Salter. 2005. Gene tree distributions under the coalescent process, *Evolution* 59(1): 24-37.

10. Kubatko, L. Salter and J. Degnan$^+$. 2007. Inconsistency of concatenated-data phylogenetic estimates under coalescence, *Systematic Biology*, 56(1): 17-24.

11. 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.

12. 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.

13. 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.

14. 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.

15. 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).

16. 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.

17. 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.

18. 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.

19. Kubatko, L. S. 2009. Identifying hybridization events in the presence of coalescence via model selection, *Systematic Biology* 58(5): 478-488.

20. Boykin, L.$^+$, L. Salter Kubatko, and T. Lowrey. 2010. Comparison of methods for rooting phylogenetic trees: A case study using Orcuttieae (Poaceae: Chloridoideae) , *Molecular Phylogenetics and Evolution* 54: 687-700.

21. Huang, H.$^+$, Q. He$^+$, L. S. Kubatko, and L.L. Knowles. 2010. Sources of error for species-tree estimation: Impact of mutational and coalescent effects on accuracy and implications for choosing among different methods, *Systematic Biology* 59(5): 573-583.

22. Stone, A.C., F. Battistuzzi, L. S. Kubatko, G. H. Perry, E. Trudeau, H. Lin and S. Kumar. 2010. More reliable estimates of divergence times in Pan using complete mtDNA sequences and accounting for population structure. *Philosophical Transactions of Royal Society B* 365 (1556): 3277-3288.

23. Hird, S.$^+$, L. S. Kubatko and B. C. Carstens. 2010. Rapid and accurate species tree estimation for phylogeographic investigations using replicated subsampling. *Molecular Phylogenetics and Evolution* 57(2): 888-898.

24. Fan, H.$^+$ and L. S. Kubatko. 2011. Estimating species trees using approximate Bayesian computation, *Molecular Phylogenetics and Evolution* 59:354-363.

25. Roos, C., D. Zinner, L. S. Kubatko, C. Schwarz, M. Yang, D. Meyer, S. D. Nash, J. Xing, M. A. Batzer, M. Brameier, F. H. Leendertz, T. Ziegler, D. Perwitasari-Farajallah, T. Nadler, L. Walter, and M. Osterholz. 2011. Nuclear versus Mitochondrial DNA: Evidence for Hybridization in Colobine Monkeys, *BMC Evolutionary Biology* 11:77.

26. Kubatko, L., H. L. Gibbs and E. Bloomquist. 2011. Inferring species-level phylogenies using multi-locus data for a recent radiation of Sistrurus rattlesnakes, *Systematic Biology,* 60(4): 393-409.

27. Kubatko, L. S. and D. K. Pearl. 2011. Seeing the trees in your terrace, *Science* 333(6041): 411-412.

28. Gerard, D.*, H. L. Gibbs, and L. S. Kubatko. 2011. Estimating hybridization in the presence of coalescence using phylogenetic intraspecific sampling, *BMC Evolutionary Biology* 11: 291.

29. Boykin, L., K. Armstrong, L. Kubatko, and P. DeBarro. 2012. Species delimitation and global biosecurity, *Evolutionary Bioinformatics* 8:1-37.

30. Boykin, L. M., K. Armstrong, L. Kubatko, and P. DeBarro. 2012. DNA barcoding invasive insects: Database roadblocks, *Invertebrate Systematics* 26: 506-514.

31. Hovmoller, R., L. L. Knowles, and L. S. Kubatko. 2013. Effects of missing data on species tree estimation under the coalescent, *Molecular Phylogenetics and Evolution* 69: 1057-1062.

32. Herbei, R. and L. Kubatko. 2013. Monte Carlo estimation of total variation distance of Markov chains on large spaces, with application to phylogenetics, *Statistical Applications in Genetics and Molecular Biology,* 12(1): 39-48.

33. Kubatko, L.S. and H. H. Fan$^+$. 2013. Reply to ”Letter to the Editor on the article entitled ”Estimating species trees using Approximate Bayesian Computation” (Fan and Kubatko, Mol. Phylogenetics Evol. 59, 354 - 363)”, *Molecular Phylogenetics and Evolution* 66(1): 438-439.

34. Thompson, K.L.$^+$ and L. Kubatko. 2013. Using ancestral information to detect and localize quantitative trait loci in genome-wide association studies, *BMC Bioinformatics* 14: 200.

35. Tian, Y.$^{+}$ and L. Kubatko. 2014. Gene tree rooting methods give distributions that mimic the coalescent process, *Molecular Phylogenetics and Evolution* 70: 63-69.

36. Sovic, M.$^{+}$, L. Kubatko, and P. Fuerst. 2014. The effects of locus number, genetic divergence and genotyping error on the utility of dominant markers for hybrid identification, *Ecology and Evolution* doi: 10.1002/ece3.833.

37. Spade, D. A.$^{+}$, R. Herbei, and L. S. Kubatko. 2014. A note on the relaxation time of two Markov chains on rooted phylogenetic tree spaces, *Statistics and Probability Letters* 84: 247-252.

38. Wolfe, A. D., A. McMullen-Sibul, V. J. Tepedino, L. Kubatko, T. NeCamp*, and S. Fassnacht*. 2014. Conservation genetics and breeding system of Penstemon debilis (Plantaginaceae), a rare beardtongue endemic to oil shale talus in western Colorado, USA, *Journal of Systematics and Evolution*, DOI: 10.1111/jse.12100.

39. Chifman, J. and L. Kubatko. 2014. Species tree inference from SNP data under the coalescent model, *Bioinformatics* 30(23): 3317-3324.

40. Chifman, J. and L. Kubatko. 2015. Identifiability of the unrooted species tree topology under the coalescent model with time-reversible substitution processes, site-specific rate variation, and invariable sites, *Journal of Theoretical Biology* 374: 35-47.

41. Spade, D.$^{+}$, R. Herbei, and L. Kubatko. 2015. Geometric ergodicity of a hybrid sampler for Bayesian inference of phylogenetic branch lengths, *Mathematical Biosciences*, 268: 9-21.

42. Kubatko, L. S., P. Shah, R. Herbei, and M. A. Gilchrist. 2016. A codon model of nucleotide substitution that includes the effects of selection related to codon usage and protein production rates, *Molecular Phylogenetics and Evolution* 94: 290-297.

43. Blischak, P.$^{+}$, L. Kubatko, and A. Wolfe. 2016. Accounting for genotype uncertainty in the estimation of allele frequencies in autopolyploids, *Molecular Ecology Resources*, 16(3): 742-754.

44. Tian, Y.$^{+}$ and L. Kubatko. 2016. Distribution of gene tree histories under the coalescent model with gene flow, *Molecular Phylogenetics and Evolution*, 105: 177-192.

45. Wolfe, A. D., T. NeCamp*, S. Fassnacht*, P. Blischak^{+}, and L. Kubatko. 2016. Conservation genetics of Penstemon albomarginatus (Plantaginaceae), a rare Mojave Desert species of deep sand habitats, *Conservation Genetics*, doi:10.1007/s10592-016-0857-y.

46. Gaither, J. and L. Kubatko. 2016. Hypothesis tests for phylogenetic quartets, with applications to coalescent-based species tree inference, *Journal of Theoretical Biology*, 408: 179-186.

47. Thompson, K., C. Linnen, and L. Kubatko. 2016. Tree-based quantitative trait mapping in the presence of external covariates, *Statistical Applications in Genetics and Molecular Biology* 15(6): 473-490.

48. Alicai, T., Ndunguru, J., Sseruwagi, P., Tairo, F., Okao-Okuja, G., Nanvubya, R., Kiiza, L., Kehoe, M., Kubatko, L. and L. Boykin. 2016. Characterization by next generation sequencing reveals the molecular mechanisms driving the faster evolutionary rate of cassava brown streak virus compared with Ugandan cassava brown streak virus, *Scientific Reports*, 6: 36164.

49. Tian, Y.$^{+}$ and L. Kubatko. 2017. Expected pairwise congruence among gene trees under the coalescent model, *Molecular Phylogenetics and Evolution* 106: 144-150.

50. Allman, E. S., L. S. Kubatko, and J. A. Rhodes. 2017. Split scores: a tool to quantify phylogenetic signal in genome-scale data, *Systematic Biology* 66 (4): 620-636.
51. Wainaina, J. M.$^{+}$, P. De Barro, L. Kubatko, M. A. Kehoe J. Harvey, D. Karanja, and L. M. Boykin. 2018. Genetic diversity, population structure and species delimitation of Trialeurodes vaporariorum (greenhouse whitefly), *Bulletin of Entomological Research* 108: 5 -13.
52. Blischak, P. D.$^{+}$, L. S. Kubatko, and A. D. Wolfe. 2017. SNP genotyping and parameter estimation in polyploids using low-coverage sequencing data, *Bioinformatics* 34(3): 407-415.
53. Tian, Y.$^{+}$ and L. Kubatko, 2017. Rooting phylogenetic trees under the coalescent model using site pattern probabilities, *BMC Evolutionary Biology* 17: 263.
54. Blischak, P.$^{+}$, J. Chifman, A. D. Wolfe, and L. S. Kubatko. 2018. HyDe: a Python package for genome-scale hybridization detection, *Systematic Biology* 67(5): 821-829 .
55. Long, C. L. and L. S. Kubatko. 2018. The effect of gene flow on coalescent-based species tree inference, *Systematic Biology* 67(5): 770-785.
56. Boykin, L., T. Kinene^{+}, J. Wainaina^{+}, A. Savill, S. Seal, H. Mugerwa, S. Macfadyen, W.T. Tay, P. De Barro, L. Kubatko, T. Alicai, C.A. Omongo, F. Tairo, J. Ndunguru and P. Sseruwagi. 2018. Review and guide to a future naming system of African Bemisia tabaci species, *Systematic Entomology* 43: 427-43.
57. Gory, J.$^{+}$, R. Herbei, and L. Kubatko, 2018. Bayesian inference of selection in the Wright-Fisher diffusion model, *Statistical Methods in Genetics and Molecular Biology* 17(3).
58. Long, C. L. and L. Kubatko. 2019. Identifiability and reconstructibility of species phylogenies under a modified coalescent, submitted, *Bulletin of Mathematical Biology* 81: 408-430.
59. Wainaina, J. M.$^{+}$, L. Kubatko, J. Harvey, E. Ateka, T. Makori, D. Karanja, L. M. Boykin and M. A. Kehoe. 2019. Phylogenomics and evolutionary insights of Bean Common Mosaic Necrosis Virus and Cowpea Aphid Borne Mosaic Virus and impacts on food security in sub Saharan Africa, *PeerJ* 7:e6297.
60. Kubatko, L. and J. Chifman. 2019. An invariants-based method for efficient identification of hybrid speciation from large-scale genomic data, *BMC Evolutionary Biology* 19:112.
61. Wascher, M.$^{+}$ and L. Kubatko. 2019. Consistency of SVDQuartets and maximum likelihood for coalescent-based species tree estimation, submitted, available on arXiv.
62. Peng, J.$^{+}$, D. Swofford, and L. Kubatko. 2019. Estimation of speciation times under the multispecies coalescent, submitted, available on bioRxiv.

Edited Work

1. **Co-authored edited book:** Knowles, L. L. and L. S. Kubatko. 2010. *Estimating Species Trees: Practial and Theoretical Aspects*, Wiley-Blackwell.

   Includes the following co-authored chapters:

   - Knowles, L. L. and L. S. Kubatko. 2010. Estimating species trees: An introduction to concepts and models (Chapter 1, pgs. 1-14).

- L. S. Kubatko and C. Meng^{+}. 2010. Accomodating hybridization in a multilocus phylogenetic framework (Chapter 6, pgs. 99-113).
- L. S. Kubatko and H. L. Gibbs. 2010. Estimating species relationships and taxon distinctiveness in Sistrurus rattlesnakes using multilocus data (Chapter 12, pgs. 193-207).

2. **Section Editor:** "Phylogenetic Methods" Section, Volume 3, page 270 - Volume 4, page 255, In: Kliman, R. (Ed.). 2016. Encyclopedia of Evolutionary Biology.

Chapters in Edited Books

1. 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.
2. 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.
3. 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.
4. 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.
5. Nance, T. and L. Salter Kubatko. 2013. Constructing an undergraduate biomath curriculum at a large univeristy, part I: Developing first year biomath coures at The Ohio State University, for proposed MAA volume: *Undergraduate Mathematics for the Life Sciences: Processes, Models, Assessment, and Directions*, edited by G. Ledder, J. P. Carpenter, and T. Comar, pages 149-154.
6. Kubatko, L. Salter, J. Best, T. Nance, and Y. Luo. 2013. Constructing an undergraduate biomath curriculum at a large univeristy, part II: Implementing first year biomath courses at The Ohio State University, for proposed MAA volume: *Undergraduate Mathematics for the Life Sciences: Processes, Models, Assessment, and Directions*, edited by G. Ledder, J. P. Carpenter, and T. Comar, pages 25-32.
7. Pearl, D. K. and L. Kubatko. 2015. DNA Sequence Evolution, in Wiley StatsRef: Statistics Reference Online (WSR), 1-14.
8. Kubatko, L. 2019. The Multispecies Coalescent, pgs. 219-245 in *Handbook of Statistical Genomics*, 4th edition, volume 1, edited by David Balding, Ida Moltke and John Marioni, John Wiley & Sons Ltd. (Editor and peer-reviewed).

Proceedings and Book Reviews

1. 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).

2. 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.

3. 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.

4. Kubatko, L. S. 2015. Review of *Bayesian Phylogenetics: Methods, Algorithms, and Applications* by Ming-Hui Chen, Lynn Kuo, and Paul O. Lewis, *Journal of the American Statistical Association*, 110(510): 881-882.

Open-source software

Select open-source software written by my group is listed below; see `http://www.stat.osu.edu/~lkubatko/software.html` for complete details.

1. HyDe: Hybrdization Detection - software to test hypotheses of hybrid speciation in genome-scale datasets (with Paul Blischak).
2. SVDquartets: Singular Value Decomposition Scores for Species Quartets - method to infer species-level phylogenetic trees under the multispecies coalescent model. The method is implemented in the PAUP* software, written by David Swofford.
3. COALGF Calculator - software to compute the probability distribution of gene tree histories and gene tree topolgies for a fixed three-taxon species tree under the coalescent model with gene flow between both pairs of sister populations (with Yuan Tian).
4. STEM-hy: Species Tree Estimation using Maximum likelihood (with hybridization) - a program for inferring maximum likelihood species trees from a collection of estimated gene trees under the coalescent model. It also carries out bootstrap analyses and can evaluate hybridization hypotheses in a model selection framework.
5. HybTree - a perl program for estimating hybridization events and times in the presence of deep coalescence (with David Gerard).
6. COAL - a program for computing gene tree probabilities under the coalescent process (written by James Degnan).
7. SSA - a program to infer maximum likelihood phylogenetic trees using a stochastic search algorithm.

Invited Presentations

2019	Joint Statistical Meetings, Denver, CO
2019	Ecological Integration Symposium, Texas A&M University (plenary talk)
2019	Department of Horticulture and Crop Science, The Ohio State University
2018	G. Evelyn Hutchinson Seminar, Department of Biology, Yale University
2018	Joint Congress on Evolutionary Biology (Evolution Meetings), Montpellier, France
2018	Department of Mathematics, University of Greifswald, Germany
2018	Joint Statistical Meetings, Vancouver
2018	AMS Sectional Meeting, Northeastern University, Special Session, Algebraic Statistics, Boston, MA
2018	Department of Computational Biology, University of Lausanne, Switzerland
2018	AMS Central Section Meeting, Special Session, The Mathematics of Phylogenetics, Columbus, OH

2018	Department of Biology, West Virginia University
2017	Southwest Michigan Chapter of the ASA, Grand Valley State University
2017	iBEST Seminar, University of Idaho
2017	Spotlight Session, Evolution 2017, Portland, OR
2017	Phyloseminar
2017	Department of Evolution and Ecology, University of Connecticut
2016	Department of Biology, Temple University
2016	Center for Genome Research and Biocomputing Fall Conference, Oregon State University
2016	Mathematical and Computational Evolutionary Biology Conference, France
2015	Plant Energy Biology Seminar, University of Western Australia
2015	TDA@OSU Fall Forum
2015	AMS Sectional Meeting, Special Session, The Mathematics of Evolution, Loyola University Chicago
2015	Joint Statistical Meetings, Seattle, WA
2014	Department of Biology, University of Kentucky
2014	Department of Biology, University of Missouri
2014	SAMSI Opening Workshop on "Beyond Bioinformatics"
2014	Joint Statistical Meetings, Boston, MA
2014	NSF-CBMS Conference on Mathematical Phylogenetics, Winthrop University
2012	Computational and Statistical Phylogenetics Conference, Vigo, Spain
2012	Department of Biology, Indiana University
2012	University of Georgia Institute of Bioinformatics Spring 2012 Symposium and Workshop
2011	Evolutionary Genomics Workshop, Institute for Pure and Applied Mathematics at UCLA
2011	Minisymposium on Applications in Mathematical Biology, SIAM Conference on Applied Algebraic Geometry, NC State
2011	Department of Genetics, University of Georgia
2011	Department of Biology, Northern Illinois University
2010	Epidemiology and Biostatistics, University of Cincinnati
2010	OSU-CCF-CWRU Joint Biostatistics Symposium
2010	Department of Mathematics and Statistics, University of Alaska-Fairbanks
2009	Capital University
2009	Ohio Wesleyan University
2009	CAUSEweb Seminar (with Danny Kaplan and Jeff Knisley)
2009	SAMSI Molecular Evolution and Phylogenetics Workshop
2009	Department of Biology, University of Maryland Baltimore County
2009	Estimating Species Trees Symposium, University of Michigan
2008	Epidemiology and Biostatistics, University of Cincinnati
2008	Department of Biology, University of Idaho
2008	SSB Symposium,Species Trees and Gene Tree Heterogeneity: Concepts, Estimation and Empirical Applications, Evolution Meetings, Minneapolis, MN
2008	Center for Computational Biology and Bioinformatics, and Section of Integrative Biology University of Texas at Austin
2008	Department of Bioinformatics and Biostatistics, University of Louisville
2007	MathFest
2007	Department of Ecology and Evolutionary Biology, University of Michigan
2006	Joint Statistical Meetings, Seattle, WA
2005	Department of Ecology, Evolution, and Organismal Biology, The Ohio State University
2005	Department of Statistics, The Ohio State University
2005	Joint Statistical Meetings, Minneapolis, MN
2005	Gordon Research Conference on Quantitative Genetics

2004	Annual Meeting of the Albuquerque Chapter of the American Statistical Association
2004	Franciscan University of Steubenville
2001	National Center for Genome Resources, Santa Fe, NM
2001	Joint Statistical Meetings, Atlanta, GA
2001	Annual Meeting of the Albuquerque Chapter of the American Statistical Association
2000	International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences, Las Vegas, NV
2000	Department of Mathematics, Arizona State University
1999	The Ohio State University Department of Statistics Silver Anniversary Conference
1999	Department of Statistics, Carnegie Mellon University
1999	Department of Statistics, University of Pittsburgh
1999	Department of Statistics and Probability, Michigan State University

Tutorials and Lectures in Short Courses

2007	"Model-Based Phylogenetics", North American Workshop in Cladistic Methods, The Ohio State University
2008	"Model-Based Phylogenetics", North American Workshop in Cladistic Methods, The Ohio State University
2008	"Model-based Phylogenetics", Department of Entomology, University of Kentucky
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
2008	"STEM: Species Trees Estimation using Maximum likelihood", Estimating Species Trees Symposium, University of Michigan
2010	"STEM and STEM-hy", Species Delimitation Symposium, University of Gothenburg, Sweden
2010	MBI Spring Semester Course, "Statistical Phylogenetics" (with Dr. Dennis Pearl)
2011	"Species Tree Inference", Workshop on Molecular Evolution, Woods Hole
2012	"STEM and STEM-hy", Estimating Species Trees Symposium, The Ohio State University
2012	STEM Software Tutorial, University of Georgia Institute of Bioinformatics Symposium and Workshop
2012	"Tutorial on Coalescent Theory", Algebraic Statistics in the Alleghenies, Penn State University
2012	"Species Tree Inference", Workshop on Molecular Evolution, Woods Hole
2013	MBI Spring Semester Course, "Stochastic Processes in Biology" (with Dr. Radu Herbei)
2013	"Coalescent Theory and Species Tree Estimation", Phylogenomics Workshop, NESCent
2013	"Species Tree Inference", Workshop on Molecular Evolution, Woods Hole
2014	"Gene Family Evolution Workshop", Las Cruces, New Mexico
2014	"Species Tree Inference", Workshop on Molecular Evolution, Woods Hole
2015	"Species Tree Estimation" and "SVDquartets Lab", Workshop on Molecular Evolution, Cesky Krumlov, Czech Republic
2015	"Species Tree Estimation From SNPs to Sequences" (with Dave Swofford), Society of Systematic Biologists Stand-alone Meeting
2015	"Species Tree Inference", Workshop on Molecular Evolution, Woods Hole
2016	"Species Tree Inference", Workshop on Molecular Evolution, Woods Hole
2017	"Species Tree Estimation" and "SVDquartets Lab", Workshop on Molecular Evolution, Cesky Krumlov, Czech Republic
2017	"Species Tree Inference", Workshop on Molecular Evolution, Woods Hole
2018	"SVDQuartets Tutorial" (with Dave Swofford), Species Tree Estimation Workshop, Society of Systematic Biologists Stand-alone Meeting
2018	"Species Tree Inference", Workshop on Molecular Evolution, Woods Hole
2019	"Species Tree Estimation" and "SVDquartets Lab", Workshop on Phylogenomics,

	Cesky Krumlov, Czech Republic
2019	“Species Tree Inference”, Workshop on Molecular Evolution, Woods Hole

Professional Service

Grant Reviews

2002-2019	Ad-hoc grant reviews for the National Science Foundation
2008	National Science Foundation Third Year Review Team Member for UBM Program
2011	National Science Foundation Panel
2012	National Science Foundation Panel
2013	National Science Foundation Panel
2014	National Science Foundation Panel
2016	National Science Foundation Panel
2017	Ad-hoc review for Memo Life (France)
2017	Ad-hoc review for US-Israel Binational Science Foundation (BSF)
2017	Ad-hoc review for Vienna Science and Technology Fund (WWTF)
2017	National Science Foundation Panel
2018	Ad-hoc grant review for the Austrian Science Foundation (FWF)
2018	Ad-hoc review of a Research Allocation Grant for the Ohio Supercomputer Center
2019	National Science Foundation Panel

Promotion and Tenure Reviews for Other Universities

2011	University of South Carolina
2011	University of Kentucky
2013	University of Kentucky
2014	Simon Fraser University
2014	University of Florida
2014	University of Connecticut
2014	Iowa State University
2015	Dalhouise University
2015	Rice University
2015	New Mexico State University
2016	Louisiana State University
2016	University of Colorado, Denver
2016	University of New Mexico
2017	Colorado State University
2018	University of Tennessee
2018	Penn State University
2019	Emory University
2019	University of Florida
2019	Virginia Tech

(10 in Statistics/Mathematics/Computer Science Departments, 9 in Biology Departments)

External Examiner of Ph.D. Theses

2013	University of Canterbury
2017	University of Sydney
2018	Australian National University

Service to Professional Societies

2001-2003	Albuquerque Chapter Representative to the American Statistical Association
2008-2010	Elected Member, Council of the Society of Systematic Biologists
2009	Student Grant Judge, Society of Systematic Biologists
2010	Student Grant Judge, Society of Systematic Biologists
2010	Nominations Committee, Society of Systematic Biologists
2011	Chair, Nominations Committee, Society of Systematic Biologists
2013	Student Grant Judge, Society of Systematic Biologists
2016	Student Grant Judge, Society of Systematic Biologists
2016	Fitch Award Committee, Society of Molecular Biology and Evolution
2017	Student Grant Judge, Society of Systematic Biologists
2018	Student Grant Judge, Society of Systematic Biologists
2018	Judge, Mayr Award, Society of Systematic Biologists
2020	President-Elect, Society of Systematic Biologists

Conference/Workshop Organization

2001	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.
2001	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".
2004	Organizer and Chair for Invited Session on Phylogenetics, WNAR/IMS Meeting
2009	Co-organizer of two-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.
2012	Co-organizer of two-day symposium titled "Estimating Species Trees", held January 13-14, 2012 at the MBI at OSU; sponsored by the MBI, EEOB Department, and the National Science Foundation.
2013	Program Committee Member for iEvoBio Meeting, Snowbird, UT.
2018	Co-organizer, Society of Systematic Biologists Stand-alone Meeting, Columbus, OH.
2018	Co-organizer (with Lacey Knowles) of one-day symposium titled "Species Tree Estimation Workshop" , held in conjunction with the Society of Systematic Biology Stand-alone Meeting, June 4, 2018.
2018	Co-organizer (with Laura Boykin) of a session at Evolution 2018 titled "Systematics Research in Africa: Impact for Millions", Montpellier, France, August 2018 (see `https://www.asc.ohio-state.edu/kubatko.2//SystematicsAfrica2018/`).
2019	Co-organzier, MBI Workshop on "Evolutionary Dynamics in Cancer", to be held in November 2019.

Journal Referee

Journal reviews for: Bioinformatics, Biometrics, Journal of the American Statistical Association, eLife, Molecular Phylogenetics and Evolution, Systematic Biology, Journal of Biomedical Informatics, Evolution, BMC Bioinformatics, CUR Quarterly, Statistical Applications in Genetics and Molecular Biology, Nature Communications, BMC Evolutionary Biology, Molecular Biology and Evolution, Journal of Computational and Graphical Statistics, The American Statistician, Bulletin of Mathematical Biology, Science, Trends in Evolutionary Biology, Heredity, PLoSOne, Journal of Theoretical Biology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Molecular Ecology, Proceedings of the National Academy of Sciences, Theoretical Population Biology, Journal of Mathematical Biology, Science

Teaching

At the University of New Mexico

Stat 345	Intro to Mathematical Statistics	2000 (3), 2001, 2002, 2003
Stat 472/572	Sampling Theory	Fall 1999, Fall 2001, Spring 2006
Stat 531	Statistical Genetics I	Fall 2000, Fall 2002, Fall 2004
Stat 532	Statistical Genetics II	Spring 2003, Spring 2005
Stat 574	Survival Analysis	Spring 2005
Stat 434/534	Contingency Tables	Spring 2001
Stat 590	Statistical Computing	Fall 2001

At The Ohio State University

Stat 2480	Statistics for the Life Sciences	2007, 2008, 2009, 2010, 2011, 2012, 2017, 2018 2019
Stat 3202	Intro to Statistical Inference for Data Analytics	2015, 2016, 2017
Stat 3460	Principles of Statistics for Engineers	2016
Stat 4201	Intro to Mathematical Statistics II	2007, 2008, 2009, 2010, 2011, 2012
Stat 6201	Mathematical Statistics	2017, 2018
Stat 6605	Survival Analysis	2013
Stat 6910	Applied Statistics I	2015
Stat 7605	Advanced Regression Modeling of Time-to-Event Data	2017
Stat 832	Applied Probability Models	2008, 2009
Stat 8605	Advanced Survival Analysis	2013
Stat 882	Intro to Stochastic Differential Equations (with Radu Herbei)	2009
EEOB 6330	Phylogenetic Methods (with John Freudenstein)	2019
EEOB 881	Seminar in Evolution (with Lisle Gibbs and Paul Fuerst)	2008 (2), 2009
EEOB 881	Seminar in Evolution (with Andi Wolfe and Paul Fuerst)	2010, 2011
EEOB 8896.15	Current Topics in Mathematical Population Genetics (with Paul Fuerst)	2014, 2015, 2016 (2) 2018, 2019