Volodymyr M. Minin

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Education

2007	Ph.D., Biomathematics (Advisor: Marc A. Suchard)	University of California, Los Angeles
2004	M.S., Biomathematics	University of California, Los Angeles
2002	M.S., Mathematics	University of Idaho, Moscow, Idaho
2000	B.S., Mathematics	Odesa National University, Ukraine

Professional Experience

2017–present	Professor of Statistics	University of California, Irvine
2019–present	Associate Director, Infectious Disease Science Initiative	University of California, Irvine
2021–present	Honors Program Director, School of Inf. & Comp. Sciences	University of California, Irvine
2018–2021	Dept. of Statistics Vice Chair of Undergraduate Affairs	University of California, Irvine
2013–2017	Associate Professor of Statistics and Biology	Univ. of Washington, Seattle
2015–2017	Dept. of Statistics Undergraduate Program Coordinator	Univ. of Washington, Seattle
2013–2017	Adjunct Associate Professor of Biostatistics	Univ. of Washington, Seattle
2009–2017	Quantitative Ecology and Resource Management Faculty	Univ. of Washington, Seattle
2007–2017	Core Member of the Statistical Genetics Faculty Group	Univ. of Washington, Seattle
2007–2013	Assistant Professor of Statistics	Univ. of Washington, Seattle
Spring 2007	Visiting Assistant Professor, Department of Biomathematics	UCLA
2003–2006	Research Assistant, Departments of Biomathematics and Human Genetics	UCLA
2000–2002	Teaching Assistant, Department of Mathematics	University of Idaho

Visiting Positions

2013–2014	Sabbatical Visitor, Fred Hutchinson Cancer Research Center, Computation Biology Program (host: Dr. Erick Matsen)
Fall 2011	Visiting Faculty Fellow, Institute for Pure & Applied Mathematics, UCLA invited long-term participant in the program on "Mathematical and Computational Approaches in High-Throughput Genomics"

Preprints

highlighted are students who worked with me, * indicates corresponding author(s)

1. Baker CR, Barilar I, de Araujo LS, Rimoin AW, Parker DM, Boyd R, Tobias JL, Moonan PK, Click ES, Finlay A, Oeltmann JE, **Minin VN**, Modongo C, Zetola NM, Niemann S, Shin SS. High-resolution characterization of recent tuberculosis transmission in Botswana using geospatial and genomic data — the Kopanyo Study, medRxiv 2022.04.13.22273731; doi: https://doi.org/10.1101/2022.04.13.22273731.

2. **Goldstein HI**, Jon Wakefield, **Minin VN**. Incorporating testing volume into estimation of effective reproduction number dynamics, arXiv:2208.04418.

3. Awasthi N, **Minin VN**, Huang J, Chow D, Xu J. Fitting a stochastic model of intensive care occupancy to noisy hospitalization time series, arXiv:2203.00229.

4. **Martinez Lomeli LDJ**, Ngo MN, Wakefield J, Shahbaba B*, **Minin VN***. Statistical implications of relaxing the homogeneous mixing assumption in time series Susceptible-Infectious-Removed models, arXiv:2112.03186.

5. **Bayer D**[†], Fintzi J*,[†], **Goldstein I**[†], Lumbard K, Ricotta E, Warner S, Busch LM, Strich JR, Chertow DS, Parker DM, Boden-Albala B, Dratch A, Chhuon R, Quick N, Zahn M, **Minin VN***,[†]. Semi-parametric modeling of SARS-CoV-2 transmission in Orange County, California using tests, cases, deaths, and seroprevalence data, arXiv:2009.02654. [†] - joint first authors

Book Chapters

highlighted are students who worked with me

1. Wakefield J, Dong TQ, **Minin VN**. Spatio-temporal analysis of surveillance data, *Handbook of Infectious Disease Data Analysis*, edited by Held L, Hens N, O'Neill PD, and Wallinga J, 2019.

2. **Dhar A** and **Minin VN**. Maximum likelihood methods for phylogenetic inference, in *Encyclopedia of Evolutionary Biology*, edited by Kliman P (Phylogenetic Methods section edited by Kubatko L), 2016.

3. **Palacios JA**, Gill MS, Suchard MA, **Minin VN**. Bayesian nonparametric phylodynamics, in *Bayesian Phylogenetics: Methods, Algorithms, and Applications*, edited by Chen MH, Kuo L, and Lewis PO, 2014.

Commentary and Discussions

1. **Faulkner JR**, **Magee AF**, Shapiro B, **Minin VN**. Rejoinder for discussion on "Horseshoe-based Bayesian nonparametric estimation of effective population size trajectories," *Biometrics*, 27, 695–699, 2020.

2. **Minin VN**, **Fintzi J**, **Lomeli LJM**, Wakefield J. Discussion of "Dynamic Bayesian Influenza Forecasting in the United States with Hierarchical Discrepancy", *Bayesian Analysis*, 14, 301–306, 2019.

3. Kypraios T and **Minin VN**. Introduction to the Special Section on Inference for Infectious Disease Dynamics, *Statistical Science*, 33, 1–3, 2018.

Refereed Publications

highlighted are students and postdocs who worked with me; * indicates corresponding author(s)

2023 and in press

1. Parker DM, **Medina C**, Bohl J, Lon C, Chea S, Lay S, Kong D, Nhek S, Man S, Doehl JSP, Leang R, Kry H, Rekol H, Oliveira F, **Minin V**, Manning JE. Determinants of exposure to *Aedes* mosquitoes: a comprehensive geospatial analysis in peri-urban Cambodia, *Acta Tropica*, in press, medRxiv 2022.09.12.22278870; doi: https://doi.org/10.1101/2022.09.12.22278870.

2. **Magee AF**, Karcher MD, Matsen FA*, **Minin VN***. How trustworthy is your tree? Bayesian phylogenetic effective sample size through the lens of Monte Carlo error, *Bayesian Analysis*, in press, arXiv:2109.07629.

3. **Tang M**, Dudas G, Bedford T, **Minin VN***. Fitting stochastic epidemic models to gene genealogies using linear noise approximation, *Annals of Applied Statistics*, in press, arXiv:1902.08877. **With a shorter version of this paper, Mingwei Tang won 2019 ASA Section on Bayesian Statistical Science student paper award.**

2022

4. **Goldstein I**, **Bayer D**, Barilar I, Kizito B, Matsiri O, Modongo C, Zetola NM, **Niemann S***, **Minin VN***, **Shin SS***. Using genetic data to identify transmission risk factors: statistical assessment and application to tuberculosis transmission, *PLoS Computational Biology*, 18: e1010696, 2022.

5. **Fintzi J**, Wakefield J*, **Minin VN***. A linear noise approximation for stochastic epidemic models fit to partially observed incidence counts, *Biometrics*, 78, 1530–1541, 2022. **With this paper, Jon Fintzi won 2020 ASA Section on Statistics in Epidemiology Norman Breslow Prize for the best student paper.**

2021

6. Parker DM, Bruckner T, Vieira VM, Medina C, **Minin VN**, Felgner PL, Dratch A, Zahn M, Bartell SM, Boden-Albala B. Epidemiology of the early COVID-19 epidemic in Orange County, California: comparison of predictors of test positivity, mortality, and seropositivity, *Emerging Infectious Diseases*, 27, 2604–2618, 2021.

7. Martinez Lomeli L, Iniguez A, Shahbaba B*, Lowengrub JS*, **Minin VN***. Optimal experimental design for mathematical models of hematopoiesis, *Journal of the Royal Society Interface*, 18, 20200729, 2021.

2020

8. Magee AF, Höhna S, Vasylyeva TI, Leaché AD, **Minin VN***. Locally adaptive Bayesian birth-death model successfully detects slow and rapid rate shifts, *PLoS Computational Biology*,16(10): e1007999, 2020.

9. Karcher MD, Suchard MA, Dudas G, **Minin VN***. Estimating effective population size changes from preferentially sampled genetic sequences, *PLoS Computational Biology*, 16(10): e1007774, 2020.

10. Dhar A, Ralph DK, **Minin VN***, Matsen FA*. A Bayesian phylogenetic hidden Markov model for B cell receptor sequence analysis, *PLoS Computational Biology*, 16: e1008030, 2020.

11. Faulkner JR, Magee AF, Shapiro B, **Minin VN***. Horseshoe-based Bayesian nonparametric estimation of effective population size trajectories, *Biometrics*, 76, 677–690, 2020 (with discussion). ***Biometrics Co-Editors recognized this paper as one the best published in the journal during 2020–2022 and selected it for presentation in the Biometrics Showcase session at the the International Biometric Conference 2022.***

12. Fourment M, Magee A, Whidden C., Bilge A, Matsen FA* **Minin VN***. 19 dubious ways to compute the marginal likelihood of a phylogenetic tree topology, *Systematic Biology*, 69, 209–220, 2020.

2019

13. Xu J, Koelle S, Guttorp G, Wu C, Dunbar CE, Abkowitz JL, **Minin VN***. Statistical inference in partially observed stochastic compartmental models with application to cell lineage tracking of *in vivo* hematopoiesis, *Annals of Applied Statistics*, 13, 2091–2119, 2019.

14. Oaks JR, Cobb KA, **Minin VN**, Leaché AD. Marginal likelihoods in phylogenetics: a review of methods and applications, *Systematic Biology*, 68, 681–697, 2019.

15. Feng J, Shaw DA, **Minin VN***, Simon N*, Matsen FA*. Survival analysis of DNA mutation motifs with penalized proportional hazards, *Annals of Applied Statistics*, 13, 1268–1294, 2019.

2018

16. Chattopadhyay S, Chi PB, **Minin VN**, Berg DE, Sokurenko EV. Recombination-independent rapid convergent evolution of the gastric pathogen *Helicobacter pylori*, *BMC Genomics*, 19, 835, 2018.

17. Dhar A, Davidsen K, Matsen FA*, **Minin VN***. Predicting B cell receptor substitution profiles using public repertoire data, *PLoS Computational Biology*, 14, e1006388, 2018.

18. DeWitt WS, Mesin L, Victora GD, **Minin VN***, Matsen FA*. Using genotype abundance to improve phylogenetic inference, *Molecular Biology and Evolution*, 35, 1253–1265, 2018.

19. Ho LST, Xu J, Crawford FW, **Minin VN**, Suchard, MA. Birth(death)/birth-death processes and their computable transition probabilities with statistical applications, *Journal of Mathematical Biology*, 76, 911–944, 2018.

20. Faulkner JR and **Minin VN***. Locally adaptive smoothing with Markov random fields and shrinkage priors, *Bayesian Analysis*, 13, 225–252, 2018. **With a shorter version of this paper, Jim Faulkner was a runner-up (Distinguished Student Paper Award) in 2015 *WNAR student written paper competition*.**

2017

21. **Fintzi J**, Wakefield J, **Minin VN***. Efficient data augmentation for fitting stochastic epidemic models to prevalence data, *Journal of Computational and Graphical Statistics*, 26, 918–929, 2017. **With a shorter version of this paper, Jon Fintzi won 2016** *WNAR student written paper competition*.

22. Hardin W, Li R, Xu J, Shelton A, **Minin VN**, Paredez AR. Myosin-independent cytokinesis in *Giardia* utilizes flagella to coordinate force generation and direct membrane trafficking, *Proceedings of the National Academy of Sciences, USA*, 114, E5854–E5863, 2017.

23. **Dhar A** and **Minin VN***. Calculating higher-order moments of phylogenetic stochastic mapping summaries in linear time, *Journal of Computational Biology*, 24, 377–399, 2017.

24. **Karcher M**[†], Palacios, JA[†], Lan S, **Minin VN***. phylodyn: an R package for phylodynamic simulation and inference, *Molecular Ecology Resources*, 17, 96–100, 2017. [†] - joint first authors

2016

25. **Karcher M**, Palacios, JA, Bedford T, Suchard MA, **Minin VN***. Quantifying and mitigating the effect of preferential sampling on phylodynamic inference, *PLoS Computational Biology*, 12, e1004789, 2016.

26. **Koepke AA**, Longini, IM, Halloran ME, Wakefield J, **Minin VN***. Predictive modeling of cholera outbreaks in Bangladesh, *Annals of Applied Statistics*, 10, 575–595, 2016. **With a shorter version of this paper, Amanda Koepke won a 2015 Young Investigator Award from ASA Statistics in Epidemiology Section.**

27. **Linkem CW**, **Minin VN**, and Leaché AD. Detecting the anomaly zone in species trees and evidence for a misleading signal in higher-level skink phylogeny (Squamata: Scincidae), *Systematic Biology*, 65, 465–477, 2016.

2015

28. **Xu J**, Guttorp P, Kato-Maede M, **Minin VN***. Likelihood-based inference for discretely observed birth-death-shift processes, with applications to evolution of mobile genetic elements, *Biometrics*, 71, 1009–1021, 2015. **With a shorter version of this paper, Jason Xu won ASA Biometrics section student travel award to attend JSM 2015.**

29. Lan S, Palacios JA, **Karcher M**, **Minin VN**, Shahbaba B. An efficient Bayesian inference framework for coalescent-based nonparametric phylodynamics, *Bioinformatics*, 31, 3282–3289, 2015.

30. **Xu J** and **Minin VN***. Efficient transition probability computation for continuous-time branching processes via compressed sensing, *Proceedings of the 31st Conference on Uncertainty in Artificial Intelligence*, 952–961, 2015.

31. **Chi PB**, Chattopadhyay S, Lemey P, Sokurenko EV, **Minin VN***. Synonymous and nonsynonymous distances help untangle convergent evolution and recombination, *Statistical Applications in Genetics and Molecular Biology*, 14, 375–389, 2015.

32. McCoy CO, Bedford T, **Minin VN**, Bradley P, Robins H, Matsen FA. Quantifying evolutionary constraints on B-cell affinity maturation, *Philosophical Transactions of the Royal Society B: Biological Sciences*, 370: 20140244, 2015.

33. **Lange JM**, Hubbard, RA, Inoue, L, **Minin VN***. A joint model for multistate disease processes and random informative observation times, with applications to electronic medical records data, *Biometrics*, 71, 90–101, 2015.

2014

34. Pankey MS, **Minin VN**, **Imholte GC**, Suchard MA, Oakley TH. Predictable transcriptome evolution in the convergent and complex bioluminescent organs of squid, *Proceedings of the National Academy of Sciences, USA*, 111:E4736–E4742, 2014.

35. **Irvahn J** and **Minin VN***. Phylogenetic stochastic mapping without matrix exponentiation, *Journal of Computational Biology*, 21: 676–690, 2014.

36. **Chi PB**, Duncan AE, Kramer PA, **Minin VN**∗. Heritability estimation of osteoarthritis in the pig-tailed macaque (*Macaca nemestrina*) with a look toward future data collection, *PeerJ*, 2: e373, 2014. **With a shorter version of this paper, Peter Chi was a runner-up in 2012 *WNAR student written paper competition.***

37. Leaché AD, Fujita MK, **Minin VN**, Bouckaert RR. Species delimitation using genome-wide SNP data, *Systematic Biology*,63: 534–542, 2014.

38. Crawford FW, **Minin VN**, Suchard MA. Estimation for general birth-death processes, *Journal of the American Statistical Association*, 109: 730–747, 2014.

2013

39. **Doss CR**, Suchard MA, Holmes I, Kato-Maeda M, **Minin VN**∗. Fitting birth-death processes to panel data with applications to bacterial DNA fingerprinting, *Annals of Applied Statistics*, 7: 2315–2335, 2013.

40. Leaché AD, **Palacios JA**, **Minin VN**, Bryson RW. Phylogeography of the Trans-Volcanic bunchgrass lizard (*Sceloporus bicanthalis*) across the highlands of southeastern Mexico, *Biological Journal of the Linnean Society*, 110: 852–865, 2013.

41. **Lange JM** and **Minin VN**∗. Fitting and interpreting continuous-time latent Markov models for panel data, *Statistics in Medicine*, 32: 4581–4595, 2013. With a shorter version of this paper, Jane Lange won 2012 WNAR student written paper competition.

42. **Irvahn J**, Chattopadhyay S, Sokurenko EV, **Minin VN**∗. rbrothers: R package for Bayesian multiple change-point recombination detection, *Evolutionary Bioinformatics*, 9: 235–238, 2013.

43. **Palacios JA** and **Minin VN**∗. Gaussian process-based Bayesian nonparametric inference of population size trajectories from gene genealogies, *Biometrics*, 69: 8–18, 2013.

2012

44. Lemey P, **Minin VN**, Bielejec F, Kosakovsky Pond SL, Suchard MA. A counting renaissance: Combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection, *Bioinformatics*, 28: 3248–3256, 2012.

45. **Ryu S**, Goodlett DR, Noble WS, **Minin VN**∗. A statistical approach to peptide identification from clustered tandem mass spectrometry data, *IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW)*, 648–653, 2012.

46. **Palacios JA** and **Minin VN**∗. Integrated nested Laplace approximation for Bayesian nonparametric phylodynamics, *Proceedings of the 28th Conference on Uncertainty in Artificial Intelligence*, 726–735, 2012.

47. **Sawaya SM**[†], **Lennon D**[†], Buschiazza E, Gemmell N, **Minin VN**∗. Measuring microsatellite conservation in mammalian evolution with a phylogenetic birth-death model, *Genome Biology and Evolution*, 4:636–647, 2012. [†] - joint first authors.

48. Kemal K, Kitchen C, Burger H, Foley B, Klimkait T, Hamy F, Anastos, K, Petrovic K, **Minin V**, Suchard M, Weiser B. Recombination between variants from genital tract and plasma: Evolution of multidrug-resistant HIV-1, *AIDS Research and Human Retroviruses*, 28: 1766–1774, 2012.

2011

49. **Minin VN**, O'Brien JD, and Seregin A. Imputation estimators partially correct for model misspecification, *Statistical Applications in Genetics and Molecular Biology*, 1: Article 17, 2011.

2009

50. Chattopadhyay S, Weissman SJ, **Minin VN**, Russo TA, Dykhuizen DE, Sokurenko EV. High frequency of hot-spot mutations in core genes of *Escherichia coli*, *Proceedings of the National Academy of Sciences, USA*, 106:12412–12417, 2009.

51. O'Brien JD*, **Minin VN***, and Suchard MA. Learning to count: robust estimates for labeled distances between molecular sequences, *Molecular Biology and Evolution*, 26:801–814, 2009.
   * - joint first authors.

2008

52. **Minin VN** and Suchard MA. Fast, accurate and simulation-free stochastic mapping, *Philosophical Transactions of the Royal Society B: Biological Sciences*, 363:3985–3995, 2008.

53. **Minin VN**, Bloomquist E, and Suchard MA. Smooth skyride through a rough skyline: Bayesian coalescent-based inference of population dynamics, *Molecular Biology and Evolution*, 25:1459–1471, 2008.

54. **Minin VN** and Suchard MA. Counting labeled transitions in continuous-time Markov models of evolution, *Journal of Mathematical Biology*, 56:391–412, 2008.

2003–2007

55. Rajaram ML, **Minin VN**, Suchard MA, and Dorman KS. Hot and cold: spatial fluctuation in HIV-1 recombination rates, *Proceedings of the 7th IEEE Internation Conference on Bioinformatics and Bioengineering*, 707–714, 2007.

56. **Minin VN**, Fang F, Dorman KS, and Suchard MA. Phylogenetic mapping of recombination hot-spots in HIV via spatially smoothed change-point processes, *Genetics*, 175:1773–1785, 2007.

57. Fang F, Ding J, **Minin VN**, Suchard MA, and Dorman KS. cBrother: Relaxing parental tree assumptions for Bayesian recombination detection, *Bioinformatics*, 23:507–508, 2007.

58. **Minin VN**, Dorman KS, Fang F, and Suchard MA. Dual multiple change-point model leads to more accurate recombination detection, *Bioinformatics*, 21:3034–3042, 2005.

59. Abdo Z, **Minin VN**, Joyce P, and Sullivan J. Accounting for uncertainty in the tree topology has little effect on the decision theoretic approach to model selection in phylogeny estimation, *Molecular Biology and Evolution*, 22:691–703, 2005.

60. Liu X, **Minin V**, Huang Y, Selingson D, and Horvath S. Statistical methods for analyzing tissue microarray data, *Journal of Biopharmaceutical Statistics*, 14:671–685, 2004.

61. **Minin V**, Abdo Z, Joyce P, and Sullivan J. Performance-based selection of likelihood models for phylogeny estimation, *Systematic Biology*, 52:674–683, 2003.

Unrefereed Publications

1. Fang F, **Minin VN**, Suchard MA, Dorman KS. A Bayesian phylogenetic model for counting recombination events, *2005 Proceedings of the American Statistical Association*, [CD-ROM].

2. **Minin VN**, Dorman KS and Suchard MA. Bayesian recombination identification: new models for incorporating prior information, *2004 Proceedings of the American Statistical Association*, Bayesian Statistical Science Section, [CD-ROM].

Conference Presentations and Posters

1. Fitting stochastic epidemic models to gene genealogies and incidence data using linear noise approximation, contributed talk, *Institute of Mathematical Statistics Annual Meeting*, London, UK, June 2022.

2. Using multiple data streams to estimate and forecast SARS-CoV-2 transmission dynamics, invited talk, *Joint Statistical Meetings*, online, August 2021.

3. Fitting stochastic epidemic models to gene genealogies using linear noise approximation, invited talk, *Bernoulli-IMS 10th World Congress in Probability and Statistics*, online, July 2021.

4. Bayesian modeling and data integration in infectious disease phylodynamics, invited talk, *Casa Matemática Oaxaca Workshop "Mathematics and Statistics of Genomic Epidemiology"*, online, November, 2020.

5. CSI-style enhance button for B cell receptor amino acid profiles, invited talk, *Southern California Systems Biology Conference*, Irvine, CA, 2019.

6. Algorithmic and statistical advances in phylogenetic stochastic mapping, keynote, *Mathematical and Computational Evolutionary Biology Conference*, Saint-Martin-de-Londres, France, 2018.

7. Fitting stochastic epidemic models to incidence time series and gene genealogies, invited talk, *IISA International Conference on Statistics*, Gainesville, Florida, 2018.

8. Fitting stochastic epidemic models to incidence time series and gene genealogies, invited talk, *Oberwolfach Research Institute for Mathematics Workshop "Design and analysis of infectious disease studies"*, Oberwolfach, Germany, February, 2018.

9. Statistical analysis of compartmental models: epidemiology, molecular biology, and everything in between, invited talk, *Banff International Research Station for Mathematical Innovation and Discovery Workshop "Challenges in the Statistical Modeling of Stochastic Processes for the Natural Sciences"*, Banff, Canada, July, 2017.

10. EM algorithms for partially observed continuous-time Markov processes, invited talk, *SIAM Conference on Optimization*, Vancouver, Canada, May, 2017.

11. Advances of Bayesian nonparametrics in population genetics of infectious diseases, contributed talk, *Joint Statistical Meetings*, Chicago, Illinois, August, 2016.

12. Preferential sampling through time when estimating changes in effective population size, contributed talk, *The XXVIIIth International Biometric Conference*, Victoria, BC, July, 2016.

13. Advances of Bayesian nonparametrics in population genetics of infectious diseases, invited talk, *The 4th Institute of Mathematical Statistics Asia Pacific Rim Meeting*, Hong Kong, June 2016.

14. Quantifying and mitigating the effect of preferential sampling on phylodynamic inference, invited talk, *NIH Workshop on Infectious Disease Research: Quantitative Methods and Models in the Era of Big Data*, Bethesda, Maryland, November, 2015.

15. Making the most of data augmentation in phylogenetics, invited talk, *Joint Statistical Meeting*, Seattle, Washington, August, 2015.

16. Balancing statistical and computational trade-offs when extracting selection signal from a large number of DNA sequences, contributed talk, *Joint Statistical Meeting*, Boston, Massachusetts, August, 2014.

17. Phylogenetic stochastic mapping without matrix exponentiation, invited talk, *IPAM High Throughput Genomics Reunion Conference II*, Lake Arrowhead, California, June, 2014.

18. Bayesian inference for Kingman's coalescent process via thinning, invited talk, *36th Conference on Stochastic Processes and Their Applications*, Boulder, Colorado, August 2013.

19. Bayesian nonparametric phylodynamics: a modern perspective, invited talk, *IPAM High Throughput Genomics Reunion Conference I*, Lake Arrowhead, California, June, 2013.

20. Phylogenetic likelihood equations: what do they mean and why should we care? contributed talk, *Joint Statistical Meeting*, San Diego, California, August, 2012.

21. Bayesian nonparametric phylodynamics, invited talk, *WNAR-Graybill Conference*, Fort Collins, Colorado, June 2012.

22. A Bayesian approach to testing the independent origin hypothesis, invited talk,*Workshop on Bayesian Inference in Stochastic Processes*, Getafe, Madrid, September 2011.

23. Imputation estimators and model misspecification in model-based clustering, invited talk, *Model-Based Clustering Working Group*, Glasgow, Scotland, July 2011.

24. Bayesian nonparametric inference of effective population trajectories with Gaussian processes, poster, *MCMSki 3*, Park City, Utah, January 2011.

25. Making phylogenetic inference robust to presence of convergent evolution, contributed talk, *Joint Statistical Meeting*, Vancouver, Canada, August 2010.

26. A Bayesian approach to testing the independent origin hypothesis, poster, *Annual Meeting of the Society for Integrative and Comparative Biology*, Seattle, WA, January 2010.

27. Applications of Markov chain-induced counting processes in evolutionary biology and statistics, contributed talk, *33rd Conference on Stochastic Processes and Their Applications*, Berlin, Germany, July 2009.

28. Bayesian coalescent-based inference of population dynamics, invited talk, *Young Investigators in Populations Genetics Workshop*, University of Arizona, Tucson, AZ, October 2008.

29. Computationally efficient posterior predictive mapping of evolutionary histories makes estimation of selection forces possible in large scale studies of viral evolution, Savage session invited talk, *9th World Meeting of the International Society for Bayesian Analysis*, Hamilton Island, Australia, July 2008.

30. Bayesian phylogenetic mapping of recombinaton hot-spots, contributed talk, *Bayesian Phylogeny Workshop*, Budapest, Hungary, June 2008.

31. Robust estimation of genetic distances with applications to the convergent evolution problem, invited talk, *Phylogenetics Workshop, held at the Santa Fe Institute prior to the HIV Dynamics and Evolution Meeting*, Santa Fe, NM, April 2008.

32. Simulation-free algorithms for mapping evolutionary innovations onto phylogenies, invited talk, *Workshop on Computational Aspects of Biological Information*, Microsoft Research, December 2007.

33. Coalescent-based inference of population dynamics with Gaussian Markov random field temporal smoothing, contributed talk, *Joint Statistical Meeting*, August 2007.

34. Zooming into evolution with Markov chain induced counting processes, contributed talk, *Joint Statistical Meetings*, Seattle, WA, August 2006.

35. Testing the presence of recombination hot-spots in the HIV genome and their association with local sequence properties, poster, *International Biometrics Conference*, Montreal, Canada, July, 2006.

36. Investigating an evolutionary footprint of recombination hot-spots in the HIV genome, contributed talk, *SMBE Annual Meeting: Genomes, Evolution, and Bioinformatics*, Tempe, AZ, May, 2006.

37. Mapping HIV Break-Point Hot-Spots with Phylogenetic Recombination Detection and Spatial Smoothing, poster, *Case Studies in Bayesian Statistics Workshop*, Pittsburgh, PA, September, 2005.

38. Mapping Recombination Hot-Spots onto Gaussian Markov Random Fields, poster, *Conference on Intelligent Systems for Molecular Biology*, Detroit, MI, June 2005.

39. Bayesian recombination identification: new models and better ways of incorporating prior information, contributed talk, *Joint Statistical Meeting*, Toronto, Canada, August 2004.

40. Dual multiple change-point model leads to more accurate recombination detection, poster, *Conference on Research in Computational Molecular Biology*, San Diego, CA, March 2004.

Invited Seminars

- Outside of the home institution:
    - *Mathematics and Statistical Science*, University of Idaho, March 2022 (Wellner Lecture)
    - *CA COVID Modeling Consortium*, online, June 2021
    - *Biostatistics*, UCLA, February 2021
    - *Statistics*, UC Riverside, October 2020
    - *Statistical Science*, Duke University, September 2020
    - *Statistics and Data Science*, University of Arizona, December 2019
    - *Biosystems Science & Engineering*, Swiss Federal Institute of Technology Zurich, September 2019
    - *Data Sciences and Operations*, University of Southern California, November 2018
    - *Biomathematics*, UCLA, January 2018
    - *Biomedical Data Science*, Stanford University, October 2017

- – *Statistics*, UC Irvine, November 2016
- – *Mathematics*, University of Oregon, October 2016
- – *Biostatistics and Biomathematics*, Fred Hutchinson Cancer Research Center, April 2015
- – *Statistics*, North Carolina State University, October 2013
- – *Statistics*, University of Missouri, Columbia, November 2012
- – *Biostatistics and Biomathematics*, Fred Hutchinson Cancer Research Center, May 2012
- – *Pacific Northwest Research Station*, US Forest Service, February 2012
- – *National Marine Mammal Laboratory*, NOAA, February 2012
- – *Statistics*, UC Irvine, November 2011
- – *Biomathematics*, UCLA, October 2011
- – *Biomathematics*, UCLA, February 2011
- – *Biostatistics*, UCLA, February 2011
- – *Biostatistics and Biomathematics*, Fred Hutchinson Cancer Research Center, January 2009
- – *Mathematics*, University of Idaho, February 2008
- – *Biostatistics*, John Hopkins University, February 2007
- – *Statistics*, University of Washington, Seattle, January 2007
- • Within the home institution:
  - – UCI: COVID-19 Dynamics Symposium (October 2020), Statistics (April 2019), Systems Biology Retreat (March 2018), ML/AI (November 2017)
  - – UW: *Aquatic and Fishery Sciences* (January 2014), *Biology* (April 2013), *Statistics* (April 2012, May 2011), *Computational Molecular Biology Symposium* (May 2010), *Biostatistics* (January 2009, March 2008), *Mathematics Dept. Probability Seminar* (November 2008), *Center for Statistics and the Social Sciences* (October 2007)
  - – UCLA: *Biostatistics* (November 2006), *Computational Biology Seminar* (May 2006)

Software Developed

stemr	R package for fitting stochastic epidemic models to surveillance data (*co-developer*) https://github.com/fintzij/stemr
phylodyn	R package for phylodynamic inference with emphasis on infectious disease appliactions (*co-developer*) https://github.com/vnminin/indorigin
indorigin	R package for testing independent origin hypotheses in evolutionary biology (*principal developer*) https://github.com/vnminin/indorigin
bayessir	R package for fitting SIR-like models to sparse and unevenly spaced incidence data (*co-developer*) https://github.com/vnminin/bayessir
phylomap	R package implementing phylogenetic stochastic mapping algorithms (*co-developer*) https://github.com/vnminin/phylomap
rbrothers	R package for interfacing with `DualBrothers` software for recombination detection (*co-developer*) http://r-forge.r-project.org/projects/evolmod/
cthmm	R package for fitting continuous-time hidden Markov models (*co-developer*) http://r-forge.r-project.org/projects/multistate/
DOBAD	R package for estimation of linear birth-death processes (*co-developer*) http://cran.r-project.org/web/packages/DOBAD/index.html
markovjumps	R package for robust estimation of genetic distances, mapping innovations onto phylogenies, and a few other things (*principal developer*) www.stat.washington.edu/vminin/markovjumps

BEAST	open source package, Bayesian evolutionary analysis by sampling trees. (*contributor*) http://beast.bio.ed.ac.uk/
DT-ModSel	Performance-based method for selecting likelihood models for phylogenetic estimation (*principal developer*) www.webpages.uidaho.edu/ jacks/DTModSel.html
DualBrothers	Phylogenetic recombination detection software based on the dual multiple change-point model. (*principal developer*) www.biomath.ucla.edu/msuchard/DualBrothers/

Awards and Honors

2022   Latino Excellence and Achievement Outstanding Faculty Mentorship Award, UC Irvine

2022   Jon A. Wellner Lecture, Department of Mathematics and Statistical Science, University of Idaho, `https://www.uidaho.edu/sci/mathstat/news/wellner-lecture`

2008   Savage Award in Applied Methodology, International Society for Bayesian Analysis
(The Savage Award, named in honor of Leonard J. "Jimmie" Savage, is bestowed each year to two outstanding doctoral dissertations in Bayesian econometrics and statistics, one each in *Theory and Methods* and *Applied Methodology*)

2007   Laha Travel Award, Institute of Mathematical Statistics
(Provides funds for travel to present a paper at the IMS Annual Meeting)

2006   Dissertation Year Fellowship, Graduate Division, UCLA

2005   Dr. Ursula Mandel Scholarship, Graduate Division, UCLA
(Awarded for scholastic and research achievements to graduate students in scientific fields related, allied, or of value to the medical field)

2002   Award for Excellence in Teaching, Department of Mathematics, University of Idaho

Active Funded Projects

2022–2024   *UCI Office of Research* Investing to Develop Center-Scale Multidisciplinary Convergence Research Programs Seed Funding Award
Title: "New data streams and predictive analytics for pandemic preparedness"
Role: PI, total amount: $150K (direct)

2022–2026   *NIH* R01 (PI: Sanghyuk Shin, UCI Nursing)
Title: "The effect of HIV on SARS-CoV-2 transmission and emergence of variants of concern"
Role: Co-I, amount to VM: $150K (direct)

2022–2027   *NIH* R25 (MPIs: Mine Dogucu, Dan Gillen, Vladimir Minin, Babak Shahbaba, UCI Statistics)
Title: "Irvine Summer Institute in Biostatistics and Data Science"
Role: Contact PI, total amount: $1.2M (direct + indirect)

2022-2023   *UC Health & CDPH Modeling Consortium* Research Award
Title: "Improving accuracy and precision of forecasts and scenarios by fitting mechanistic transmission models to multiple disaggregated surveillance data sources."
Role: Sole PI, total amount: $100K (direct)

2020–2025   *NIH* R01 (PI: Sanghyuk Shin, UCI Nursing)
Title: "Improved understanding of TB transmission by accounting for within-host heterogeneity of M. Tuberculosis: a population-based molecular epidemiology study in a high HIV prevalent setting."
Role: Co-I, amount to VM: $200K (direct)

Completed Funded Projects

2021–2022   *UCI-ISC Exploration Award* (PIs: Veronica Berrocal, Volodymyr Minin, and Padhraric Smyth)
Title: "Digital infectious disease surveillance: Preparing Southern California for future pandemics"
Role: Contact PI, amount: $75K (direct)

2019–2021   *CRDF Global* (PI: Sanghyuk Shin, UCI Nursing)
Title: "Impact of HIV infection on molecular diagnosis of drug-resistant tuberculosis in India"
Role: Co-I, amount to VM: $15K (direct)

2019–2022   *NSF* (PI: Babak Shahbaba, UCI Statistics)
Title: "MODULUS: Data-driven mechanistic modeling of hierarchical tissues."
Role: Co-PI, amount to VM: $75K (direct)

2016–2020   *NSF*
Title: "III: AF: Medium: Collaborative Research: Enabling phylogenetic inference for modern data sets."
Role: PI, amount to VM: $343K (direct + indirect)

2013–2019   *NIH* R01
Title: "Bayesian modeling and data integration in infectious disease phylodynamics."
Role: PI, total amount: $1.7M (direct + indirect)

2018–2019   *UCI CCBS Opportunity Award* (Co-PIs: Lowengrub, Minin, Shahbaba)
Title: "Optimal experimental design for feedback models of hematopoiesis"
Role: Co-PI, amount to VM: $3K

2014–2019   *NIH* (PI: Erick Matsen, FHCRC; joint DMS/NIGMS program in mathematical biology)
Title: "Leveraging deep sequencing data to understand antibody maturation."
Role: Co-Investigator, Amount to VM: $110K

2014–2017   *NIH* U54 (PI: M Elizabeth Halloran, FHCRC)
Title: "Center for Statistics and Quantitative Infectious Diseases."
Role: Co-Investigator, Amount to VM: $130K

2009–2014   *NSF* (joint DMS/NIGMS program in mathematical biology)
Title: "New statistical methods for neutral phylogenetic reconstruction."
Role: PI, total amount: $1.2M

2010–2013   *NIH* (PI: Sokurenko, UW Microbiology)
Title: "*E. coli* Variome."
Role: Co-Investigator, amount to VM: $325K (direct + indirect)

2009–2010   *UW Royalty Research Fund*
Title: "New estimation principle for continuous-time Markov chains to remedy the convergent evolution problem in phylogenetics."
Role: Sole PI, total amount: $39K (direct)

Ph.D. Students Supervised

2022–   Jessalyn Sebastian, UCI Statistics

2022–   Thanasi Bakis, UCI Statistics

2021–   Yushang Lai, UCI MCSB, co-advised with John Lowengrub

2021–   Catalina Medina, UCI Statistics

2020–   Damon Bayer, UCI Statistics

2020–   Isaac Goldstein, UCI Statistics

2016–2021   Andy Magee, UW Biology, co-advised with Erick Matsen (Postdoctoral Associate, UCLA)

2015–2019   Amrit Dhar, UW Statistics, co-advised with Erick Matsen (Statistician, Google)

2014–2019	Jim Faulkner, UW QERM (Mathematical Statistician, National Oceanic and Atmospheric Administration)
2015–2019	Mingwei Tang, UW Statistics (Data Scientist, Facebook)
2015–2018	Jonathan Fintzi, UW Biostatistics, co-advised with Jon Wakefield (Mathematical Statistician, National Institutes of Health)
2013–2018	Michael Karcher, UW Statistics (Assistant Professor of Statistics, Muhlenberg College)
2013–2016	Jason Xu, UW Statistics (Assistant Professor of Statistical Sciences, Duke University)
2010–2015	Jan Irvahn, UW Statistics (Staff Scientist, Pacific Northwest National Lab)
2011–2014	Amanda Koepke, UW Statistics, co-advised with Ira Longini (Staff Scientist, National Institute of Standards and Technology)
2010–2014	Jane Lange, UW Biostatistics (Staff Scientist, Oregon Health & Science University)
2009–2013	Peter Chi, UW Biostatistics (Assistant Professor of Statistics, Villanova University)
2009–2013	Julia Palacios, UW Statistics (Assistant Professor of Statistics and Biomedical Data Sciences, Stanford University)
2008–2011	So Young Ryu, UW Statistics, co-advised with Dave Goodlett (Associate Professor of Biostatistics, University of Nevada, Reno)

Other Student Supervision

Fall 2020	Jessica George, UCI Data Science — undergraduate research assistant
Fall 2020	Thanasi Bakis, UCI Statistics — graduate research assistant
2015–2016	Xiaoxiao Li, UW Statistics — undergraduate research assistant
2009–2010	Charles Doss, UW Statistics — graduate research assistant
2009	Dan Kowalczyk, UW Statistics — undergraduate research assistant, sponsored by VIGRE
2008–2010	Dustin Lennon, UW Statistics — graduate research assistant

Postdocs Supervised

2013–2016	Jamie Oaks, UW Biology, co-advised with Adam Leaché (Assistant Professor of Biological Sciences at Auburn University)
2012–2015	Charles Linkem, UW Biology, co-advised with Adam Leaché (Sr. Computational Biologist at Adaptive Biotechnologies Corp.)

Advancement Committees (non-chair role)

2020–	Robert Macdonald, UCI Economics
2020–	Preston Putzel, UCI Computer Science
2019–	Peeyush Gupta, UCI Computer Science
2019–	Disi Ji, UCI Computer Science

Doctoral Committees (non-chair roles)

2017–2021	Luis Lomeli, UCI MCSB
2019	Nicola Muller, ETH Zurich Biosystems Science and Engineering (external examiner)
2015–2019	Arianna Danielle Miles-Jay, UW Epidemiology (GSR)
2015–2016	Chad Young, UW Statistics (reading committee)
2015–2016	Jean Morrison, UW Biostatistics (GSR)
2013–2016	Mauricio J. Del Razo Sarmina, UW Applied Mathematics (GSR)
2014–2015	You Ren, UW Statistics (reading committee)
2013–2015	Kit Curtius, UW Applied Mathematics (GSR)
2013–2015	Stefan Sharkansky, UW Statistics (reading committee)
2014	Chieh-Hsi Wu, University of Auckland, New Zealand, CS and Statistics (external examiner)
2008–2014	Ryan Miller, UW Biology (reading committee)
2013–2014	Ryan Kappedal, UW Statistics (reading committee)
2013–2014	Serge Sverdlov, Statistics
2012–2014	Chris Glazner, Statistics (reading committee)
2011–2013	Charles Doss, UW Statistics (reading committee)
2012–2013	Yufan Huang, UW Economics (GSR)
2011–2013	Amy Laird, UW Biostatistics (reading committee)
2011–2013	Charles Cheung, UW Biostatistics (reading committee)
2011–2012	Sergey Feldman, UW Electrical Engineering (GSR)
2011–2012	Dominique Perrault-Joncas, UW Statistics (reading committee)
2011–2012	Aditya Khanna, UW QERM (reading committee)
2010–2012	Cici Chen, UW Statistics (reading committee)
2010–2011	Ranran Wang, UW Statistics (reading committee)
2010	Shameek Biswas, UW Genome Sciences (GSR)
2009–2010	Eric Garcia, UW Electrical Engineering (reading committee)
2009–2011	Hil Lyons, UW Statistics (reading committee)
2008–2011	David Trossman, UW Oceanography
2008	Krista Gile, UW Statistics (reading committee)

Master's Thesis Committees

2010–2013	Miranda Fix, UW QERM
2010	Richard Chmielecki, UW Statistics
2009	Sergey Feldman, UW Electrical Engineering

Teaching Experience

- **School of Information & Computer Sciences, University of California, Irvine**
- *ICS 197H: Honors Seminar*, 2022 (undergraduate)
- **Department of Statistics, University of California, Irvine**
- *Stats 211P: Statistical Methods II*, 2022 (graduate, Masters of Data Science core course)
- *Stats 230: Statistical Computing Methods*, 2022 (graduate, PhD core course)
- *Stats 275: Stochastic Processes*, 2020 (graduate, elective course)

  Stats 170A: Project in Data Science, Part I, 2019–2022 (undergraduate, capstone course)

  Stats 170B: Project in Data Science, Part II, 2019–2022 (undergraduate, capstone course)

  Stats 5: Seminar in Data Science, 2019–2021 (undergraduate)

  Stats 67: Introduction to Probability and Statistics for Computer Science, 2018 (undergraduate)

  Stats 295: Statistical Methods in Infectious Disease Research, 2018, 2021 (graduate, special topic course)

- **Department of Statistics, University of Washington, Seattle**

  Stat 516: Stochastic Modeling in Scientific Applications I, 2007–2010 (graduate)

  Stat 517: Stochastic Modeling in Scientific Applications II, 2009–2010, 2012–2013 (graduate)

  Stat 518: Stochastic Modeling Project, 2009–2012 (graduate)

  Stat 572: Research Prelim Project, 2016–2017 (graduate)

  Stat 550: Statistical Genetics I, 2009–2011 (graduate)

  Stat 403: Introduction to Resampling Inference, 2008, 2012–2015 (undergraduate)

  Stat 390: Probability and Statistics in Engineering and Science, 2012 (undergraduate)

- **Department of Biology, University of Washington, Seattle**

  Biol/Genome 414: Molecular Evolution, 2015–2016 (undergraduate)

- **Department of Mathematics, University of Washington, Seattle**

  Math 498: Undergraduate Mathematical Sciences Seminar, one guest lecture, 2015 (undergraduate)

- **Department of Genome Sciences, University of Washington, Seattle**

  Genome 562: Population Genetics, one guest lecture, 2011 (graduate)

  Genome 541: Computational Biology, taught one week module on phylogenetics, 2011 (graduate)

- **Virus Evolution and Molecular Epidemiology Workshop, Berlin, Germany**

  Two invited lectures on *Phylogenetics and Phylodynamics*, August 2018

- **Taming the BEAST Workshop, Oberägeri, Switzerland**

  Invited lecture on *Bayesian Inference in Phylodynamics*, June 2018

- **Summer Institute in Statistics and Modeling in Infectious Diseases, Seattle WA**

  Module (2.5 days) on *MCMC Methods for Infectious Disease Studies*, 2009–2022

- **Department of Biomathematics, UCLA**

  Biomathematics 203: Stochastic Models in Biology, 2007 (graduate)

- **Department of Mathematics, University of Idaho**

  Mathematics 170: Calculus I, Fall 2001, Spring 2002 (undergraduate)

  Mathematics 160: Survey of Calculus, Spring 2001 (undergraduate)

  Mathematics 143: Pre-calculus Algebra, Fall 2000 (undergraduate)

Editorial Duties:

2016–2021   Associate Editor, *Bayesian Analysis*

2018–2020   Associate Editor, *Statistical Science*

2015–2017   Guest Co-Editor, *Statistical Science* special issue on "Stochastic Models for Infectious Diseases"

Conference Organization:

• Organized Contributed Session "Statistical inference for continuous-time stochastic processes" at IMS Annual Meeting 2022

• Served as IMS Program Chair for ENAR 2019, coordinating organization of 7 sessions

• Organized IMS-sponsored Invited Session "Statistical modeling in cell biology" at ENAR 2019

• Co-organized (with 6 other people) BIRS Workshop "Challenges in the Statistical Modeling of Stochastic Processes for the Natural Sciences," 2017

• Organized IMS-sponsored Invited Session "Statistical Advances in Evolutionary Dynamics of Infectious Diseases" at the ENAR Spring Meeting, 2016

• Organized Section on Statistics in Epidemiology-sponsored Contributed Session "Counting Processes for Disease Modeling" at the Joint Statistical Meeting, 2014

• Organized WNAR-sponsored Invited Session "Inferring Selection Mechanisms from Genomic Data" at the Joint Statistical Meeting, 2010

• Organized Contributed Session "Statistical Applications of Stochastic Processes in Evolutionary Biology and Ecology" at the 33$^{\text{rd}}$ Conference on Stochastic Processes and Their Applications, 2009

• Organized IMS-sponsored Contributed Session "Statistical Challenges in Evolutionary Biology" at the Joint Statistical Meeting, 2007

Judging:

• Student Paper Competition, WNAR 2011

Reviewer:

Journals and Conferences:

AISTATS 2014, 2015
Annals of Applied Statistics
Bayesian Analysis
Bioinformatics
Biometrics
Biostatistics
Computer Methods and Programs in Biomedicine
Ecology
Evolution
Evolutionary Bioinformatics
Genetics
Human Molecular Genetics
IEEE/ACM Transactions on Comp. Biol. and Bioinformatics
Journal of Molecular Evolution
Journal of Computational and Graphical Statistics
Journal of the Royal Statistical Society, Series A
Journal of the Royal Statistical Society, Series B
Journal of the Royal Statistical Society, Series C
Journal of Mathematical Biology

Journal of the Royal Society Interface
Mathematical Medicine & Biology
Mathematical Biosciences
Molecular Biology and Evolution
Molecular and Cellular Proteomics
Molecular Ecology Resources
Nature
Nature Communications
Open Forum Infectious Diseases
Philosophical Transactions of the Royal Society B
PLoS Computational Biology
PLoS One
PNAS
Science
Statistical Appl. in Genetics and Molecular Biol.
Statistics in Medicine
Statistical Science
Systematic Biology
Virology Journal

Funding Agencies:
UC Lab Fees Research Program (reviewer)
NIH (ad hoc panelist)
NSF (ad hoc reviewer and panelist)
Swiss National Science Foundation (ad hoc reviewer)
U.S. Civilian Research & Development Foundation (ad hoc reviewer)
Institute of Translational Health Sciences (ad hoc reviewer)
Royalty Research Fund, U. of Washington (ad hoc reviewer; panelist — see University Service)

University/School/Departmental Service

- Member of UCI Academic Senate Committee on Rules and Jurisdiction, 2019–2022
- Director of ICS Honors Program, 2021–present
- Member of the ICS Executive Committee, 2019–2021
- Member of PhD Admissions Committee, UCI Department of Statistics, 2020–2022
- Member of ICS Undergraduate Policy Committee, 2018–2021
- Vice Chair of Undergraduate Affairs, UCI Department of Statistics, 2018–2021
- Co-Director, UCI Infectious Disease Science Initiative, 2019–present
- Undergraduate Admissions Augmented Review Committee, 2018–2019
- Organizer of UCI Department of Statistics Seminars, Spring 2019, Fall 2021
- Member of the Committee tasked to create a new degree, Master of Data Science, 2018–2019
- Chair of the Hiring Committee, UCI Department of Statistics, 2018–2019
- Merit Review Committee, UCI Department of Statistics, 2018–2019
- Mid-career Review Committee, UCI Department of Statistics, 2018–2019
- Promotion Review Committee, UCI Department of Statistics, 2017–2018
- MS Admissions Committee, UCI Department of Statistics, 2017–2019
- UCI Graduate Dean's Advisory Council on Diversity, 2017–2018

- UW Statistics Undergraduate Advisor/Program Coordinator, 2015–2017
- Member of the UW Royalty Research Fund Review Panel, 2009–2010, 2014–2015
- Member of the Hiring Committee, Department of Statistics, UW, 2010–2011
- Acting Director, Graduate Certificate Program in Statistical Genetics, UW, 2010–2011
- Chair of the Curriculum Committee, Interdisciplinary Graduate Program in Quantitative Ecology and Resource Management, 2009–2010
- Developer and maintainer of the Statistical Genetics website, UW
  URL: www.stat.washington.edu/statgen, 2007–2017
- Member of UW Statistics Ph.D. preliminary examination committees:
  - Stochastic Modeling, 2007, 2008 (chair), 2009, 2011–2013, 2015 (chair)
  - Statistical Methodology, 2010
  - Consolidated research prelim, 2016 (chair), 2017 (chair)
- Member of UW QERM Ph.D. preliminary examination committee, 2011–2017
- Graduate Admission Committee Member, Department of Statistics, UW, 2008–2009, 2011–2013
- (Co-)organizer of Statistics Department Seminars, UW, 2007–2008, 2009–2010, Autumn 2014

Community Service and Outreach

2020–present	Co-creator and maintainer of COVID-19 Trends by UC Irvine website: `https://www.stat.uci.edu/covid19/`
2020–2021	UCI and Orange County Health Care Agency COVID response working group, includes production of weekly Orange County, CA COVID-19 Situation Reports: `https://www.stat.uci.edu/oc_covid_model/`
2020–present	UC Health and California Department of Public Health Modeling Consortium
2020–2022	Participation in various town hall meetings, panels, and advisory board meetings in Orange County to provide expert opinion on COVID-19 pandemic
2014–2017	Served as a judge at the Annual Math Hour Olympiad for students in grades 6–10, University of Washington.
2016	Gave lectures during 2 UW Stat Days, one day events for high school students, organized by the UW Department of Statistics.
2009	Gave a lecture and co-organized a tour of Genome Sciences data generating facilities together with Josh Akey during the UW Stat Day, a one day event for high school students, organized by the UW Department of Statistics.
2009	Gave a lecture at the UW Math Day, a one day event for high school students, organized by the UW Department of Mathematics and UW Educational Outreach.