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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, School of Inf. & Comp. Sciences	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. **Baniasad A**, **Chao S**, **Nguyen JA**, **Tian E**, Modongo C, **Minin VM***, **Sebastian JN***, Shin SS*. HIV Remains a risk factor for unfavorable tuberculosis treatment outcomes in the era of universal access to antiretroviral therapy in Botswana, medRxiv 2025.11.26.25340699.
2. **Sebastian JN**, **Minin VM***. Gaussian process priors with Markov properties for effective reproduction number inference, arXiv:2511.18797.
3. Geng X, Barilar I, Kesamang M, Tumedi KA, Matsheka M, Modongo C, Minin V, Niemann S, Shin SS. SARS-CoV-2 evolution in an HIV-endemic setting: A genomic epidemiology study from Botswana, medRxiv 2025.11.21.25340589.

4. **Bakis AG**, Vora AA, Araki T, Jia T, Galloway JG, Jennings-Shaffer C, Victora GD, Song YS, DeWitt WS*, Matsen IV FA*, **Minin VM***. Bayesian inference of antibody evolutionary dynamics using multitype branching processes, arXiv:2508.09519.
5. **Goldstein IH**, Parker DM, Jiang S, Pappu AR, **Minin VM***. The signal is not flushed away: Inferring the effective reproduction number from wastewater data in small populations, arXiv:2508.03959.
6. **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.
7. Chi PB and **Minin VM**. Phylogenetic least squares estimation without genetic distances, arXiv:2311.12717.

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)

2026 and in press

1. Yek C, **Sebastian J**, Chea S, Lay S, Oum M, Long L, Chea S, Pacheco AR, Barochia M, Ly P, Ly S, Sath R, Parker DM, **Minin VM**, Chung M, Ghedin E, Oliveira F, Manning JE,7, Lean K, Ny C, Long V, Leang K, Yim V, Kry H, Leang R, Huy R, Chin S, Chau D, Seng H, Ly S, Lon C. Mapping sub-national respiratory virus circulation in Cambodia using metatranscriptomic sequencing: a multi-center hospital-based surveillance study, *Influenza and Other Respiratory Viruses*, in press.
2. **Sebastian JN** and **Minin VM**. Gaussian process priors with Markov properties for effective reproduction number inference, *Journal of the Royal Statistical Society: Series A*, in press, arXiv:2511.18797.
3. Němcová B, Goldstein IH, **Sebastian J**, **Minin VM**, Bracher J. Unjustified Poisson assumptions lead to overconfident estimates of the effective reproductive number, *Epidemiology & Infection*, 154, e79.
4. Tarnas MC, Vasylyeva TI, **Minin VM**, Parker DM. Nighttime lights as a proxy for conflict intensity and infrastructure recovery in Yemen and Ukraine, *Conflict and Health*, 20, 5, 2026.
5. Baker CR, Barilar I, de Araujo LS, Parker DM, Fornace K, Moonan PK, Oeltmann JE, Tobias JL, **Minin VM**, Modongo C, Zetola NM, Niemann S, Shin SS. Using genomic epidemiology and geographic activity spaces to investigate tuberculosis outbreaks in Botswana, *International Journal of Health Geographics*, 25, 30, 2026.

6. Wang Q, Barilar I, **Minin VM**, Modongo C, Moonan PK, Finlay A, Boyd R, Oeltmann JE, Molefi TL, Zetola NM, Brewer TF, Niemann S, Shin SS*. Phylodynamic analysis reveals disparate transmission dynamics of *Mycobacterium tuberculosis*-complex lineages in Botswana, *Scientific Reports*, 16, 1813, 2026.

2025

7. **Medina CM**, Palacios JA, **Minin VM***. Accounting for reporting delays in real-time phylodynamic analyses with preferential sampling, *PLoS Computational Biology*, 21, e1012970, 2025.

2024

8. **Goldstein HI**, Parker DM, Jiang S, **Minin VM***. Semiparametric inference of effective reproduction number dynamics from wastewater pathogen surveillance data, *Biometrics*, 80, ujae074, 2024.
9. **Bayer D**, **Goldstein I**, Fintzi J, 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 VM***. Semi-parametric modeling of SARS-CoV-2 transmission using tests, cases, deaths, and seroprevalence data, *Annals of Applied Statistics*, 18, 2307–2325, 2024.
10. **Goldstein HI**, Jon Wakefield, **Minin VM***. Incorporating testing volume into estimation of effective reproduction number dynamics, *Journal of the Royal Statistical Society: Series A*, 187, 436–453, 2024.
11. **Magee AF**, Karcher MD, Matsen FA*, **Minin VM***. How trustworthy is your tree? Bayesian phylogenetic effective sample size through the lens of Monte Carlo error, *Bayesian Analysis*, 19, 565—593, 2024.

2023

12. Awasthi N, **Minin VM**, Huang J, Chow D, Xu J. Fitting a stochastic model of intensive care occupancy to noisy hospitalization time series, *Statistics in Medicine*, 42, 5189–5206, 2023.
13. 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. Use of high-resolution geospatial and genomic data to characterize recent tuberculosis transmission, Botswana, *Emerging Infectious Diseases*, 29, 977–987, 2023.
14. **Tang M**, Dudas G, Bedford T, **Minin VN***. Fitting stochastic epidemic models to gene genealogies using linear noise approximation, *Annals of Applied Statistics*,17, 1–22, 2023. **With a shorter version of this paper, Mingwei Tang won 2019 ASA Section on Bayesian Statistical Science student paper award.**
15. 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 VM**, Manning JE. Determinants of exposure to *Aedes* mosquitoes: a comprehensive geospatial analysis in peri-urban Cambodia, *Acta Tropica*, 239, 106829, 2023.

2022

16. **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.
17. **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

18. 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.
19. **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

20. **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.
21. **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.
22. **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.
23. **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.**
24. 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

25. **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.
26. Oaks JR, Cobb KA, **Minin VN**, Leaché AD. Marginal likelihoods in phylogenetics: a review of methods and applications, *Systematic Biology*, 68, 681–697, 2019.
27. 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

28. 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.
29. **Dhar A**, Davidsen K, Matsen FA*, **Minin VN***. Predicting B cell receptor substitution profiles using public repertoire data, *PLoS Computational Biology*, 14, e1006388, 2018.
30. 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.
31. 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.
32. **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

33. **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.***
34. 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.
35. **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.

36. **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

37. **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.
38. **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.**
39. **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

40. **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.**
41. 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.
42. **Xu J** and **Minin VN**∗. Efficient transition probability computation for continuous-time branching processes via compressed sensing, *Proceedings of the* 31^{st} *Conference on Uncertainty in Artificial Intelligence*, 952–961, 2015.
43. **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.
44. 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.
45. **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

46. 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.
47. **Irvahn J** and **Minin VN**∗. Phylogenetic stochastic mapping without matrix exponentiation, *Journal of Computational Biology*, 21: 676–690, 2014.
48. **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*.**
49. Leaché AD, Fujita MK, **Minin VN**, Bouckaert RR. Species delimitation using genome-wide SNP data, *Systematic Biology*,63: 534–542, 2014.
50. Crawford FW, **Minin VN**, Suchard MA. Estimation for general birth-death processes, *Journal of the American Statistical Association*, 109: 730–747, 2014.

2013

51. **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.
52. 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.
53. **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*.
54. **Irvahn J**, Chattopadhyay S, Sokurenko EV, **Minin VN***. rbrothers: R package for Bayesian multiple change-point recombination detection, *Evolutionary Bioinformatics*, 9: 235–238, 2013.
55. **Palacios JA** and **Minin VN***. Gaussian process-based Bayesian nonparametric inference of population size trajectories from gene genealogies, *Biometrics*, 69: 8–18, 2013.

2012

56. 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.
57. **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.
58. **Palacios JA** and **Minin VN***. Integrated nested Laplace approximation for Bayesian nonparametric phylodynamics, *Proceedings of the* 28^{th} *Conference on Uncertainty in Artificial Intelligence*, 726–735, 2012.
59. **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.
60. 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

61. **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

62. 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.
63. 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

64. **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.
65. **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.

66. **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

67. 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.
68. **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.
69. 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.
70. **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.
71. 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.
72. 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.
73. **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. Accounting for reporting delays in real-time phylodynamic analyses with preferential sampling, invited talk, *Joint Statistical Meetings*, Boston, Massachusetts, August 2026.
2. Probabilistic forecasting via continuously weighted, proper score-optimal ensembles, contributed talk, *Institute of Mathematical Statistics Annual Meeting*, Salzburg, Austria, July 2026.
3. Accounting for reporting delays in real-time phylodynamic analyses with preferential sampling, poster, *The 44th Conference on Stochastic Processes and their Applications*, Wroclaw, Poland, July 2025.
4. Forecasting healthcare demand and mortality during epidemic surges of pathogen variants capable of immune escape, invited talk, *Biostatistics Symposium of Southern California*, Newport Beach, California, February 2025.
5. Forecasting healthcare demand and mortality during epidemic surges of pathogen variants capable of immune escape, invited talk, *Joint Statistical Meetings*, Portland, Oregon, August 2024.
6. Inference, nowcasting, and forecasting using multiple surveillance data streams, poster, *International Pandemic Sciences Conference*, Oxford, England, July, 2024.
7. Inference, nowcasting, and forecasting using multiple surveillance data streams, invited talk, *Statistical Methods for Infectious Diseases across Scales Workshop*, State College, Pennsylvania, April 2024.
8. Fitting stochastic epidemic models to noisy surveillance data: are we there yet?, keynote, *Bayesian Inference of Epidemics Satellite Event at Bayes Comp*, Levi, Finland, March 2023.

9. 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.
10. Using multiple data streams to estimate and forecast SARS-CoV-2 transmission dynamics, invited talk, *Joint Statistical Meetings*, online, August 2021.
11. 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.
12. Bayesian modeling and data integration in infectious disease phylodynamics, invited talk, *Casa Matemática Oaxaca Workshop "Mathematics and Statistics of Genomic Epidemiology"*, online, November, 2020.
13. CSI-style enhance button for B cell receptor amino acid profiles, invited talk, *Southern California Systems Biology Conference*, Irvine, CA, 2019.
14. Algorithmic and statistical advances in phylogenetic stochastic mapping, keynote, *Mathematical and Computational Evolutionary Biology Conference*, Saint-Martin-de-Londres, France, 2018.
15. Fitting stochastic epidemic models to incidence time series and gene genealogies, invited talk, *IISA International Conference on Statistics*, Gainesville, Florida, 2018.
16. 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.
17. 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.
18. EM algorithms for partially observed continuous-time Markov processes, invited talk, *SIAM Conference on Optimization*, Vancouver, Canada, May, 2017.
19. Advances of Bayesian nonparametrics in population genetics of infectious diseases, contributed talk, *Joint Statistical Meetings*, Chicago, Illinois, August, 2016.
20. Preferential sampling through time when estimating changes in effective population size, contributed talk, *The XXVIIIth International Biometric Conference*, Victoria, BC, July, 2016.
21. 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.
22. 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.
23. Making the most of data augmentation in phylogenetics, invited talk, *Joint Statistical Meeting*, Seattle, Washington, August, 2015.
24. 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.
25. Phylogenetic stochastic mapping without matrix exponentiation, invited talk, *IPAM High Throughput Genomics Reunion Conference II*, Lake Arrowhead, California, June, 2014.
26. Bayesian inference for Kingman's coalescent process via thinning, invited talk, *36th Conference on Stochastic Processes and Their Applications*, Boulder, Colorado, August 2013.
27. Bayesian nonparametric phylodynamics: a modern perspective, invited talk, *IPAM High Throughput Genomics Reunion Conference I*, Lake Arrowhead, California, June, 2013.
28. Phylogenetic likelihood equations: what do they mean and why should we care? contributed talk, *Joint Statistical Meeting*, San Diego, California, August, 2012.
29. Bayesian nonparametric phylodynamics, invited talk, *WNAR-Graybill Conference*, Fort Collins, Colorado, June 2012.

30. A Bayesian approach to testing the independent origin hypothesis, invited talk,*Workshop on Bayesian Inference in Stochastic Processes*, Getafe, Madrid, September 2011.
31. Imputation estimators and model misspecification in model-based clustering, invited talk, *Model-Based Clustering Working Group*, Glasgow, Scotland, July 2011.
32. Bayesian nonparametric inference of effective population trajectories with Gaussian processes, poster, *MCMSki 3*, Park City, Utah, January 2011.
33. Making phylogenetic inference robust to presence of convergent evolution, contributed talk, *Joint Statistical Meeting*, Vancouver, Canada, August 2010.
34. A Bayesian approach to testing the independent origin hypothesis, poster, *Annual Meeting of the Society for Integrative and Comparative Biology*, Seattle, WA, January 2010.
35. 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.
36. Bayesian coalescent-based inference of population dynamics, invited talk, *Young Investigators in Populations Genetics Workshop*, University of Arizona, Tucson, AZ, October 2008.
37. 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.
38. Bayesian phylogenetic mapping of recombinaton hot-spots, contributed talk, *Bayesian Phylogeny Workshop*, Budapest, Hungary, June 2008.
39. 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.
40. Simulation-free algorithms for mapping evolutionary innovations onto phylogenies, invited talk, *Workshop on Computational Aspects of Biological Information*, Microsoft Research, December 2007.
41. Coalescent-based inference of population dynamics with Gaussian Markov random field temporal smoothing, contributed talk, *Joint Statistical Meeting*, August 2007.
42. Zooming into evolution with Markov chain induced counting processes, contributed talk, *Joint Statistical Meetings*, Seattle, WA, August 2006.
43. 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.
44. 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.
45. Mapping HIV Break-Point Hot-Spots with Phylogenetic Recombination Detection and Spatial Smoothing, poster, *Case Studies in Bayesian Statistics Workshop*, Pittsburgh, PA, September, 2005.
46. Mapping Recombination Hot-Spots onto Gaussian Markov Random Fields, poster, *Conference on Intelligent Systems for Molecular Biology*, Detroit, MI, June 2005.
47. Bayesian recombination identification: new models and better ways of incorporating prior information, contributed talk, *Joint Statistical Meeting*, Toronto, Canada, August 2004.
48. 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 home institution:
  - *Center for Communicable Disease Dynamics*, Harvard University, April 2025
  - *Biostatistics*, University of Michigan, September 2024
  - *Statistics*, UC Santa Cruz, April 2024
  - *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 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

`concRt`	R and Julia packages for inference of the effective reproduction number from gene concentrations in wastewater and case counts (*co-developer*) https://github.com/igoldsteinh/concrt and https://github.com/igoldsteinh/concrt.jl
`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/phylodyn
`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

2026	Elected Fellow, American Statistical Association *For pioneering Bayesian and computational statistical methods in phylodynamics and infectious disease modeling; for exemplary mentorship of doctoral students; and for impactful contributions to public health through interdisciplinary collaboration.*
2026	Dean's Award for Service, School of Information & Computer Sciences, UC Irvine
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

2025–2030 *NIH* P01 (MPIs: John Lowengrub, Arthur Lander, Devon Lawson)
Title: "Tipping Points in Cancer"
Role: Co-Investigator, total amount: $10.6M

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

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)

2020–2026 *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

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)

2022-2023 *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)

2021–2022 *UCI-ICS 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

2023– Christian Bernal Zelaya, UCI Statistics

2022– Jessalyn Sebastian, UCI Statistics

2022– Thanasi Bakis, UCI Statistics

2021–2025 Catalina Medina, UCI Statistics, co-advised with Mine Dogucu (Assistant Professor of Data Science, California State University, Channel Islands)

2020–2024 Isaac Goldstein, UCI Statistics (Postdoctoral researcher, Stanford University)

2020–2023 Damon Bayer, UCI Statistics (Data Scientist, CDC Center for Forecasting and Outbreak Analytics)

2020–2023 Yushang Lai, UCI MCSB, co-advised with John Lowengrub (Data Scientist, Walmart Global Tech)

2016–2021 Andy Magee, UW Biology, co-advised with Erick Matsen (Data Scientist, CDC Center for Forecasting and Outbreak Analytics)

2015–2019 Amrit Dhar, UW Statistics, co-advised with Erick Matsen (Machine Learning Scientist, Amazon)

2014–2019 Jim Faulkner, UW QERM (Mathematical Statistician, National Oceanic and Atmospheric Administration)

2015–2019 Mingwei Tang, UW Statistics (Machine Learning Engineer, Meta)

2015–2018 Jonathan Fintzi, UW Biostatistics, co-advised with Jon Wakefield (Associate Director of Biostatistics, Statistical Methodology and Innovation, Bristol Myers Squibb)

2013–2018 Michael Karcher, UW Statistics (Assistant Professor of Statistics, Muhlenberg College)

2013–2016 Jason Xu, UW Statistics (Associate Professor of Biostatistics, University of California, Los Angeles)

2010–2015 Jan Irvahn, UW Statistics (Staff Scientist, Pacific Northwest National Lab)

2011–2014 Amanda Koepke, UW Statistics, co-advised with Ira Longini (Mathematical Statistician, National Institute of Standards and Technology)

2010–2014 Jane Lange, UW Biostatistics (Staff Scientist, Oregon Health & Science University)

2009–2013 Peter Chi, UW Biostatistics (Associate Professor of Data Science, University of California, San Diego)

2009–2013 Julia Palacios, UW Statistics (Associate 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

2004–present Isabel Zhang, UCI Data Science — undergraduate research assistant

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*, 2022–2026 (undergraduate)
- **Department of Statistics, University of California, Irvine**
- *Stats 211P: Statistical Methods II*, 2022–2023 (graduate, Masters of Data Science core course)
- *Stats 230: Statistical Computing Methods*, 2022–2026 (graduate, PhD core course)
- *Stats 275: Stochastic Processes*, 2020 (graduate, elective course)

  Stats 170A: Project in Data Science, Part I, 2019–2022, 2026 (undergraduate, capstone course)

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

  Stats 5: Seminar in Data Science, 2019–2021, 2026 (undergraduate)

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

  Stats 295: Statistical Methods in Infectious Disease Research, 2018, 2021, 2025 (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)
- **Irvine Sumer Institute for Biostatistics and Undergraduate Data Science, Irvine, CA**
  Multiple 2.5 day modules (*probability, data wrangling and visualization*), 2022–2025
- **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*, 2009–2023
- **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)

Professional Service

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:

- Program Chair and Lead Local Organizer of the ASA Conference on Statistical Learning and Data Science, Newport Beach, California, November 2024
- 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 33rd 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 Board on Undergraduate Scholarships, Honors & Financial Aids (BUSHFA), 2024–present
- Chair, UCI Statistics Faculty Hiring Committee, 2024–2025
- Member of UCI Academic Senate Committee on Rules and Jurisdiction, 2019–2022
- DECADE Faculty Mentor, UCI Statistics PhD Program, 2022–2026
- Director of ICS Honors Program, 2021–present
- Member of the ICS Executive Committee, 2019–2021

- Chair of PhD Admissions Committee, UCI Department of Statistics, 2002–2023
- 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

2024	Gave 2 guest lectures for Orange County high school students during the ReachOut TeachOut at UCI events.
2023	Panelist, Panel on Data Science organized by the Mathematics Association of America Southern California-Nevada Section
2021–present	Member of the Rapid Response Team, UC-CDPH Modeling Consortium
2020–present	UC Health and California Department of Public Health Modeling Consortium
2020–2022	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/`

2020–2022 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.