

---

**Education**

|      |                              |                                       |
|------|------------------------------|---------------------------------------|
| 2007 | <i>Ph.D., Biomathematics</i> | University of California, Los Angeles |
| 2004 | <i>M.S., Biomathematics</i>  | University of California, Los Angeles |
| 2002 | <i>M.S., Mathematics</i>     | University of Idaho, Moscow, Idaho    |
| 2000 | <i>B.S., Mathematics</i>     | Odessa National University, Ukraine   |

---

**Professional Experience**

|              |   |                              |
|--------------|---|------------------------------|
| 2013–present | <i>Associate Professor of Statistics and Biology (with tenure)</i>          | Univ. of Washington, Seattle |
| 2013–present | <i>Adjunct Associate Professor of Biostatistics</i>                         | Univ. of Washington, Seattle |
| 2009–present | <i>Quantitative Ecology and Resource Management Faculty</i>                 | Univ. of Washington, Seattle |
| 2007–present | <i>Core Member of the Statistical Genetics Faculty Group</i>                | Univ. of Washington, Seattle |
| 2007–2013    | <i>Assistant Professor of Statistics</i>                                    | Univ. of Washington, Seattle |
| Spring 2007  | <i>Visiting Assistant Professor, Department of Biomathematics</i>           | UCLA                         |
| 2003–2006    | <i>Research Assistant, Departments of Biomathematics and Human Genetics</i> | UCLA                         |
| 2000–2002    | <i>Teaching Assistant, Department of Mathematics</i>                        | Univ. of Idaho               |

---

**Visiting Positions**

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

---

**Book Chapters (highlighted are students who worked with me)**

1. **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), to appear in 2016.
2. **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.

---

**Papers Under Review (highlighted are students who worked with me)**

1. Chattopadhyay S, Chi PB, **Minin VN**, Berg DE, Sokurenko EV. Recombination-independent rapid convergent evolution of the gastric pathogen *Helicobacter pylori*.
2. Ho LST, **Xu J**, Crawford FW, **Minin VN**, Suchard, MA. Birth(death)/birth-death processes and their computable transition probabilities with statistical applications, arXiv:1603.03819.
3. **Faulkner JR** and **Minin VN**. Bayesian trend filtering: adaptive temporal smoothing with shrinkage priors, arXiv:1512.06505.

## 2016 and in press

1. **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(3): e1004789.
2. **Koepke AA**, Longini IM, Halloran ME, Wakefield J, **Minin VN**. Predictive modeling of cholera outbreaks in Bangladesh, *Annals of Applied Statistics*, in press, arXiv:1402.0536. **With a shorter version of this paper, Amanda Koepke won a 2015 Young Investigator Award from ASA Statistics in Epidemiology Section.**
3. **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*, in press, bioRxiv, doi: <http://dx.doi.org/10.1101/012096>.

## 2015

4. **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.**
5. 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.
6. **Xu J** and **Minin VN**. Efficient transition probability computation for continuous-time branching processes via compressed sensing, *Proceedings of the 31<sup>st</sup> Conference on Uncertainty in Artificial Intelligence*, 952–961, 2015.
7. **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.
8. 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.
9. **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

10. 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.
11. **Irvahn J** and **Minin VN**. Phylogenetic stochastic mapping without matrix exponentiation, *Journal of Computational Biology*, 21: 676–690, 2014.
12. **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.**
13. Leaché AD, Fujita MK, **Minin VN**, Bouckaert RR. Species delimitation using genome-wide SNP data, *Systematic Biology*, 63: 534–542, 2014.
14. Crawford FW, **Minin VN**, Suchard MA. Estimation for general birth-death processes, *Journal of the American Statistical Association*, 109: 730–747, 2014.

## 2013

15. **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.
16. 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.
17. **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.*
18. **Irvahn J**, Chattopadhyay S, Sokurenko EV, **Minin VN**. rbrothers: R package for Bayesian multiple change-point recombination detection, *Evolutionary Bioinformatics*, 9: 235–238, 2013.
19. **Palacios JA** and **Minin VN**. Gaussian process-based Bayesian nonparametric inference of population size trajectories from gene genealogies, *Biometrics*, 69: 8–18, 2013.

## 2012

20. 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.
21. **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.
22. **Palacios JA** and **Minin VN**. Integrated nested Laplace approximation for Bayesian nonparametric phylogenetics, *Proceedings of the 28<sup>th</sup> Conference on Uncertainty in Artificial Intelligence*, 726–735, 2012.
23. **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.
24. 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

25. **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

26. 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.
27. 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

28. **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.
29. **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.
30. **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

31. Rajaram ML, **Minin VN**, Suchard MA, and Dorman KS. Hot and cold: spatial fluctuation in HIV-1 recombination rates, *Proceedings of the 7th IEEE International Conference on Bioinformatics and Bioengineering*, 707–714, 2007.
32. **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.
33. 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.
34. **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.
35. 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.
36. 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.
37. **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. 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.
2. Making the most of data augmentation in phylogenetics, invited talk, *Joint Statistical Meeting*, Seattle, Washington, August, 2015.
3. 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.
4. Phylogenetic stochastic mapping without matrix exponentiation, invited talk, *IPAM High Throughput Genomics Reunion Conference II*, Lake Arrowhead, California, June, 2014.
5. Bayesian inference for Kingman's coalescent process via thinning, invited talk, *36<sup>th</sup> Conference on Stochastic Processes and Their Applications*, Boulder, Colorado, August 2013.
6. Bayesian nonparametric phylodynamics: a modern perspective, invited talk, *IPAM High Throughput Genomics Reunion Conference I*, Lake Arrowhead, California, June, 2013.
7. Phylogenetic likelihood equations: what do they mean and why should we care? contributed talk, *Joint Statistical Meeting*, San Diego, California, August, 2012.
8. Bayesian nonparametric phylodynamics, invited talk, *WNAR-Graybill Conference*, Fort Collins, Colorado, June 2012.
9. A Bayesian approach to testing the independent origin hypothesis, invited talk, *Workshop on Bayesian Inference in Stochastic Processes*, Getafe, Madrid, September 2011.

10. Imputation estimators and model misspecification in model-based clustering, invited talk, *Model-Based Clustering Working Group*, Glasgow, Scotland, July 2011.
11. Bayesian nonparametric inference of effective population trajectories with Gaussian processes, poster, *MCMSki 3*, Park City, Utah, January 2011.
12. Making phylogenetic inference robust to presence of convergent evolution, contributed talk, *Joint Statistical Meeting*, Vancouver, Canada, August 2010.
13. A Bayesian approach to testing the independent origin hypothesis, poster, *Annual Meeting of the Society for Integrative and Comparative Biology*, Seattle, WA, January 2010.
14. Applications of Markov chain-induced counting processes in evolutionary biology and statistics, contributed talk, *33<sup>rd</sup> Conference on Stochastic Processes and Their Applications*, Berlin, Germany, July 2009.
15. Bayesian coalescent-based inference of population dynamics, invited talk, *Young Investigators in Populations Genetics Workshop*, University of Arizona, Tucson, AZ, October 2008.
16. 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, *9<sup>th</sup> World Meeting of the International Society for Bayesian Analysis*, Hamilton Island, Australia, July 2008.
17. Bayesian phylogenetic mapping of recombination hot-spots, contributed talk, *Bayesian Phylogeny Workshop*, Budapest, Hungary, June 2008.
18. 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.
19. Simulation-free algorithms for mapping evolutionary innovations onto phylogenies, invited talk, *Workshop on Computational Aspects of Biological Information*, Microsoft Research, December 2007.
20. Coalescent-based inference of population dynamics with Gaussian Markov random field temporal smoothing, contributed talk, *Joint Statistical Meeting*, August 2007.
21. Zooming into evolution with Markov chain induced counting processes, contributed talk, *Joint Statistical Meetings*, Seattle, WA, August 2006.
22. 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.
23. 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.
24. Mapping HIV Break-Point Hot-Spots with Phylogenetic Recombination Detection and Spatial Smoothing, poster, *Case Studies in Bayesian Statistics Workshop*, Pittsburgh, PA, September, 2005.
25. Mapping Recombination Hot-Spots onto Gaussian Markov Random Fields, poster, *Conference on Intelligent Systems for Molecular Biology*, Detroit, MI, June 2005.
26. Bayesian recombination identification: new models and better ways of incorporating prior information, contributed talk, *Joint Statistical Meeting*, Toronto, Canada, August 2004.
27. 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:
  - *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:
  - 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

---

|              |  |
|--------------|--|
| indorigin    | R package for testing independent origin hypotheses in evolutionary biology (principal developer) <a href="https://github.com/vnminin/indorigin">https://github.com/vnminin/indorigin</a>  |
| bayessir     | R package for fitting SIR-like models to sparse and unevenly spaced incidence data ( <i>co-developer</i> ) <a href="https://github.com/vnminin/bayessir">https://github.com/vnminin/bayessir</a>   |
| phylomap     | R package implementing phylogenetic stochastic mapping algorithms ( <i>co-developer</i> ) <a href="https://github.com/vnminin/phylomap">https://github.com/vnminin/phylomap</a>  |
| rbrothers    | R package for interfacing with <code>DualBrothers</code> software for recombination detection ( <i>co-developer</i> ) <a href="http://r-forge.r-project.org/projects/evolmod/">http://r-forge.r-project.org/projects/evolmod/</a>                            |
| cthmm        | R package for fitting continuous-time hidden Markov models ( <i>co-developer</i> ) <a href="http://r-forge.r-project.org/projects/multistate/">http://r-forge.r-project.org/projects/multistate/</a>   |
| DOBAD        | R package for estimation of linear birth-death processes ( <i>co-developer</i> ) <a href="http://cran.r-project.org/web/packages/DOBAD/index.html">http://cran.r-project.org/web/packages/DOBAD/index.html</a>   |
| markovjumps  | R package for robust estimation of genetic distances, mapping innovations onto phylogenies, and a few other things ( <i>principal developer</i> ) <a href="http://www.stat.washington.edu/vminin/markovjumps">www.stat.washington.edu/vminin/markovjumps</a> |
| BEAST        | open source package, Bayesian evolutionary analysis by sampling trees. ( <i>contributor</i> ) <a href="http://beast.bio.ed.ac.uk/">http://beast.bio.ed.ac.uk/</a>  |
| DT-ModSel    | Performance-based method for selecting likelihood models for phylogenetic estimation ( <i>principal developer</i> ) <a href="http://www.webpages.uidaho.edu/jacks/DTModSel.html">www.webpages.uidaho.edu/jacks/DTModSel.html</a>                             |
| DualBrothers | Phylogenetic recombination detection software based on the dual multiple change-point model. ( <i>principal developer</i> ) <a href="http://www.biomath.ucla.edu/msuchard/DualBrothers/">www.biomath.ucla.edu/msuchard/DualBrothers/</a>                     |

## Awards

---

- |      |   |
|------|---|
| 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 <i>Theory and Methods</i> and <i>Applied Methodology</i> ) |
| 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<br>(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

---

|           |   |
|-----------|---|
| 2016–2020 | <i>NSF</i> (PI: Erick Matsen, FHCRC)<br>Title: “Enabling phylogenetic inference for modern data sets.”<br>Role: Co-Investigator, Amount to VM: \$343K   |
| 2013–2018 | <i>NIH</i> R01<br>Title: “Bayesian Modeling and Data Integration in Infectious Disease Phylodynamics.”<br>Role: PI, Total amount: \$1.7M  |
| 2014–2019 | <i>NIH</i> (PI: Erick Matsen, FHCRC; joint DMS/NIGMS program in mathematical biology)<br>Title: “Leveraging deep sequencing data to understand antibody maturation.”<br>Role: Co-Investigator, Amount to VM: \$110K |
| 2014–2019 | <i>NIH</i> U54 (PI: M Elizabeth Halloran, FHCRC)<br>Title: “Center for Statistics and Quantitative Infectious Diseases.”<br>Role: Co-Investigator, Amount to VM: \$220K   |

### Completed Funded Projects

---

|           |   |
|-----------|---|
| 2009–2014 | <i>NSF</i> (joint DMS/NIGMS program in mathematical biology)<br>Title: “New statistical methods for neutral phylogenetic reconstruction.”<br>Role: PI, Total amount: \$1.2M                               |
| 2010–2013 | <i>NIH</i> (PI: Sokurenko, UW Microbiology)<br>Title: “ <i>E. coli</i> Variome.”<br>Role: Co-Investigator, Amount to VM: \$325K   |
| 2009–2010 | <i>UW Royalty Research Fund</i><br>Title: “New estimation principle for continuous-time Markov chains to remedy the convergent evolution problem in phylogenetics.”<br>Role: Sole PI, Total amount: \$39K |

### Ph.D. Students Supervised

---

|           |   |
|-----------|---|
| 2015–     | Jonathan Fintzi, UW Biostatistics — current Ph.D. student   |
| 2014–     | Jim Faulkner, UW QERM — current Ph.D. student   |
| 2014–     | Jason Xu, UW Statistics — current Ph.D. student   |
| 2013–     | Mike Karcher, UW Statistics — current Ph.D. student   |
| 2010–2015 | Jan Irvahn, UW Statistics — Ph.D. student   |
| 2011–2014 | Amanda Koepke, UW Statistics — Ph.D. student, co-advised with Ira Longini (now postdoc at the National Institute of Standards and Technology) |
| 2010–2014 | Jane Lange, UW Biostatistics — Ph.D. student (now Staff Scientist at the Fred Hutchinson Cancer Research Center)                              |
| 2009–2013 | Peter Chi, UW Biostatistics — Ph.D. student (now Assistant Professor of Statistics at Ursinus College)  |
| 2009–2013 | Julia Palacios, UW Statistics — Ph.D. student (now postdoc at Harvard and Brown)  |

2008–2011 Soyoung Ryu, UW Statistics — Ph.D. student, co-advised with Dave Goodlett (now Assistant Professor of Biostatistics at the University of Nevada, Reno)

---

### Other Student Supervision

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  
2012–2015 Charles Linkem, UW Biology, co-advised with Adam Leaché (now Computational Biologist at Adaptive Technologies)

---

### Doctoral Committees (non-chair roles)

2015– Chad Young, UW Statistics (reading committee)  
2015– Jean Morrison, UW Biostatistics (GSR)  
2015– Arianna Danielle Miles-Jay, UW Epidemiology (GSR)  
2015– Leigh Fisher, UW Biostatistics  
2015– Aaron Zimmerman, UW Statistics  
2015– Jessica Williams-Nguyen, UW Epidemiology  
2014– Gregory Imholte, UW Statistics  
2013– Mauricio J. Del Razo Sarmina, UW Applied Mathematics (GSR)  
2014–2015 You Ren, UW Statistics  
2013–2015 Kit Curtius, UW Applied Mathematics (GSR)  
2013–2015 Stefan Sharkansky, UW Statistics (reading committee)  
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

---

2012– Ian Fraser, UW QERM  
2010–2013 Miranda Fix, UW QERM  
2010 Richard Chmielecki, UW Statistics  
2009 Sergey Feldman, UW Electrical Engineering

## Teaching Experience

---

- **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 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)
- **Summer Institute in Statistics and Modeling in Infectious Diseases, Seattle WA**
  - Module on *MCMC Methods for Infectious Disease Studies*, 2009–2015
- **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

---

### Editor:

- 2015–2016 Guest Co-Editor, *Statistical Science* special issue on “Stochastic Models for Infectious Diseases”
- 2016– Associate Editor, *Bayesian Analysis*

### Organizer:

- “Statistical Advances in Evolutionary Dynamics of Infectious Diseases”, Invited Session, ENAR Spring Meeting, 2016
- “Counting Processes for Disease Modeling”, Section on Statistics in Epidemiology-sponsored Contributed Session, Joint Statistical Meeting, 2014
- “Inferring Selection Mechanisms from Genomic Data”, WNAR-sponsored Invited Session, Joint Statistical Meeting, 2010
- “Statistical Applications of Stochastic Processes in Evolutionary Biology and Ecology,” Contributed Session, 33<sup>rd</sup> Conference on Stochastic Processes and Their Applications, 2009
- “Statistical Challenges in Evolutionary Biology,” IMS-sponsored Contributed Session, Joint Statistical Meeting, 2007

### Judge:

- Student Paper Competition, WNAR 2011

### Reviewer:

#### Journals and Conferences:

|   |   |
|---|---|
| AISTATS 2014, 2015                                      | Journal of Mathematical Biology                   |
| Annals of Applied Statistics                            | Journal of the Royal Society Interface            |
| Bayesian Analysis                                       | Mathematical Medicine & Biology                   |
| Bioinformatics  | Molecular Biology and Evolution                   |
| Biometrics  | Molecular and Cellular Proteomics                 |
| Ecology   | Molecular Ecology Resources                       |
| Evolution   | Philosophical Transactions of the Royal Society B |
| Evolutionary Bioinformatics                             | PLOS Computational Biology                        |
| Genetics  | PNAS  |
| Human Molecular Genetics                                | Statistical Appl. in Genetics and Molecular Biol. |
| IEEE/ACM Transactions on Comp. Biol. and Bioinformatics | Systematic Biology                                |
| Journal of Molecular Evolution                          | Virology Journal                                  |
| Journal of the Royal Statistical Society, Series B      |   |

#### Funding Agencies:

NSF(ad hoc reviewer and panelist)

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 Service

---

- UW Statistics Undergraduate Advisor/Program Coordinator, 2015–
- 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](http://www.stat.washington.edu/statgen), 2007–present
- Member UW Statistics Ph.D. preliminary examination committees:
  - Stochastic Modeling, 2007, 2008 (chair), 2009, 2011–2013, 2015 (chair)
  - Statistical Methodology, 2010
- Member of UW QERM Ph.D. preliminary examination committee, 2011–2015
- 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

## Outreach

---

- |           |  |
|-----------|--|
| 2014–2015 | 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.  |