

CURRICULUM VITAE

PAUL JOYCE

Professor of Mathematics, Statistics and Bioinformatics
Department of Mathematics, Department of Statistics
University of Idaho, Moscow, Idaho 83844-1103

DATE: October 10, 2019

RESEARCH INTERESTS:

Statistics, probability and stochastic modeling, with particular emphasis on interdisciplinary research involving statistical inference in population genetics, molecular evolution, molecular ecology, systematic biology, molecular biology, and bioinformatics.

EDUCATION:

B.S., Mathematics, 1980, Montana State University
M.S., Mathematics, 1982, Montana State University
Ph.D., Mathematics, 1988, University of Utah (Ph.D. Advisor Simon Tavaré)

EXPERIENCE:

2013-2016	Dean, College of Science, University of Idaho
2012	Interim Dean, College of Science, University of Idaho
2011-2012	Chair, University of Idaho Faculty Senate
2010-2011	Vice-Chair, University of Idaho Faculty Senate
2009-2012	Director, Graduate Program in Bioinformatics and Computational Biology, University of Idaho
2003-2016	Professor of Bioinformatics, University of Idaho
2001-2016	Professor of Mathematics and of Statistics, University of Idaho
1994-2001	Associate Professor of Mathematics and of Statistics, University of Idaho.
1991-1994	Assistant Professor of Mathematics and Statistics, University of Idaho
1989-1991	Visiting Assistant Professor of Mathematics, University of Southern California.
1988-1989	Acting Assistant Professor of Statistics, University of Washington
1988 (July)	Visiting Scholar, Department of Statistical Sciences, University College, London

PUBLICATIONS:

Refereed Publications:

1. Miller CR, Van Leuven JT, Wichman HA, Joyce P. Selecting among three basic fitness landscape models: Additive, multiplicative and stickbreaking. *Theoretical Population Biology*, 122 (2018), pp. 97-109. doi: 10.1016/j.tpb.2017.10.006. 2018.
2. Abdo Z, Joyce P. Determining the distribution of fitness effects using a generalized Beta-Burr distribution. *Theoretical Population Biology*, 122 (2018), pp. 88-96, 2018.

3. Nardin LG, Miller CR, Ridenhour BJ, Krone SM, Joyce P, Baumgaertner BO. Planning horizon affects prophylactic decision-making and epidemic dynamics. *PeerJ*, Nov 8; 4:e2678. doi: 10.7717/peerj.2678. eCollection 2016.
4. Miller CR, Nagel AC, Scott L, Settles M, Joyce P, Wichman HA. Love the one you're with: replicate viral adaptations converge on the same phenotypic change. *PeerJ* July 19; 4:e2227. doi: 10.7717/peerj.2227. eCollection 2016.
5. Baker CW, Miller CR, Tanayott T, Yuan J, Baker MH, Joyce P, Weinreich DM. Genetically determined variation in lysis time variance in the bacteriophage ϕ X174. *G3: Genes, Genomes, Genetics*. 6(4): 939-55. Doi: 10.1534/g3.115.024075, 2016.
6. Wojtowicz AJ, Miller CR, Joyce P. Inference for one-step beneficial mutations using next generation sequencing. *Statistical Applications in Genetics and Molecular Biology* 14 (1): 65-81, 2015.
7. Bull JJ, Joyce P, Gladstone E, Molineaux IJ. Empirical complexities in the genetic foundations of lethal mutagenesis. *Genetics*. 195 (2): 541-552, 2013.
8. Bataillon T, Joyce P, Sniegowski P. As it happens: current directions in experimental evolution. *Biology Letters* 9(1), 20120945, 2013.
9. Tyerman JG, Ponciano JM, Joyce P, Forney LJ, Harmon LJ. The evolution of antibiotic susceptibility and resistance during the formation of *Escherichia coli* biofilms in the absence of antibiotics, *BMC Evolutionary Biology*. Doi: 10 11867/1471-2148-13-22, 2013.
10. Wojtowicz AJ, Miller CR, Joyce P. Estimating the number of one step beneficial mutations. *Statistical Applications in Genetics and Molecular Biology*. 11(4), Article 10, 2012.
11. Joyce P, Genz A, Buzbas EO. Efficient simulation and likelihood methods for non-neutral multi-allele models. *Journal of Computational Biology*. 19(6): 650-661, 2012.
12. Slater GJ, Harmon LJ, Joyce P, Revell LJ, Alfaro ME. Fitting models of continuous trait evolution to incompletely sampled comparative data using Approximate Bayesian Computation. *Evolution*. 66(3):752-762, 2012.
13. Nagel AG, Joyce P, Wichman HA, Miller CR. Stickbreaking: a novel fitness landscape model that harbors epistasis and is consistent with commonly observed patterns of adaptive evolution. *Genetics* 190:669-677, 2012
14. Buzbas EO, Joyce P, Rosenberg NA. Inference on the strength of balancing selection in epistatically interacting loci. *Journal of Theoretical Biology*, 79, Issue 3, 102-113, 2011.
15. Rokyta DR, Joyce P, Caudle SB, Miller CR, Beisel CJ, Wichman HA. Epistasis between beneficial mutations and the phenotype-to-fitness map for a ssDNA Virus. *PLoS Genetics*. Vol. 7, Issue 6. e1002075. Epub 2011.
16. Lee KH, Miller CR, Nagel AC, Wichman HA, Joyce P, Ytreberg FM. First-step mutations for adaptation at elevated temperature increase capsid stability in a virus. *PLoS One*. e25640. Epub 2011.
17. Eastman JM, Harmon LJ, La HJ, Joyce P, Forney LJ. The onion model, a simple neutral model for the evolution of diversity in bacterial biofilms. *J Evol Biol*. 2496-504, 2011.

18. Eastman JM, Alfaro ME, Joyce P, Hipp AL, Harmon LJ. A novel comparative method for identifying shifts in the rate of character evolution on trees. *Evolution*. 65: 3578-35-89, 2011.
19. Miller CR, Joyce P, Wichman HA. Mutational effects and population dynamics during viral adaptation challenge current models. *Genetics*, 187: 185–202, 2011.
20. Marjoram P, Joyce P. Practical implications of coalescent theory. *Problem Solving Handbook in Computational Biology and Bioinformatics*. Springer Books, 63-85, 2010.
21. Buzbas EO, Joyce P. Maximum likelihood estimates under K-allele models with selection can be numerically unstable. *Annals of Applied Statistics*. 3, 1147-1162, 2009.
22. Ponciano JM, La HJ, Joyce P, Forney LJ. Evolution of diversity in spatially structured *E. coli* populations. *Applied Environmental Microbiology*. 75: 6047-6054, 2009.
23. Buzbas EO, Joyce P, Abdo ZA. Estimation of selection intensity under overdominance by Bayesian methods. *Statistical Applications in Genetics and Molecular Biology*, 8: (1) Article 32, 2009.
24. Joyce P, Rokyta DR, Beisel CJ, Orr HA. A general extreme value theory model for the adaptation of DNA sequences under strong selection and weak mutation. *Genetics*. 180: 1627 - 1643, 2008.
25. Huelsenbeck JP, Joyce P, Lakner C, Ronquist F. Bayesian analysis of amino acid substitution models. *Philosophical Transactions, Series B , Royal Society* 363, (1512): 3941-3953, 2008.
26. Joyce P, Marjoram P. Approximately sufficient statistics and Bayesian computation. *Statistical Applications in Genetics and Molecular Biology*, 7:(1), Article 26, 2008.
27. Rokyta DR, Beisel CJ, Joyce P, Ferris MT, Burch CL, Wichman HA. Beneficial fitness effects are not exponential for two viruses. *J. Mol. Evo.* 67: 368-376, 2008.
28. Miller CR, Waits LP, Joyce P. Ordered vs. unordered samples: Response to Bromaghin. *Molecular Ecology*, 16: 4885-4885, 2007.
29. Beisel CJ, Rokyta DR, Wichman HA, Joyce P. Testing the extreme value domain of attraction for distributions of beneficial fitness effects. *Genetics* 176: 2441–2449, 2007.
30. Ferris MT, Joyce P, Burch CL. High frequency of mutations that expand the host range of an RNA virus. *Genetics* 176: 1013–1022 2007.
31. Ponciano JM, De Gledler L, Top EM, Joyce P. The population biology of bacterial plasmids: a Hidden-Markov model approach. *Genetics* 176: 957–968, 2007.
32. Zhou X, Brown CJ, Abdo ZO, Davis CC, Hansmann A, Joyce P, Foster JA, Forney LJ. Differences in the composition of vaginal microbial communities found in healthy Caucasian and Black women. *International Society for Microbial Ecology Journal* 1: 121-133, 2007.
33. De Gelder L, Ponciano JM, Joyce P, Top EM. Stability of a promiscuous plasmid in

- different hosts: No guarantees for a long-term association. *Microbiology* 153: 452-463, 2007.
34. Wu XL, Forney LJ, Joyce P. Bayesian hierarchical error model for analysis of gene expression data. *Bioinformatics* 22: 2446 - 2451, 2006.
 35. Miller CR, Waits LP, Joyce P. Phylogeography and mitochondrial diversity of extirpated brown bear (*Ursus arctos*) populations in the contiguous United States and Mexico. *Molecular Ecology*, 15, 4477-4485, 2006.
 36. Rokyta DR, Beisel CJ, Joyce P. Properties of uncorrelated landscapes under strong selection and weak mutation. *Journal of Theoretical Biology* 243, (1), 114-120 2006.
 37. Abdo ZO, Schuette U, Bent S, Williams C, Forney LJ, Joyce P. Statistical methods for characterizing diversity in microbial communities by analysis of terminal restriction fragment length polymorphism of 16S rRNA *Environmental Microbiology* 8 (5), 929-938 2006.
 38. Guan G, Fleissner R, Joyce P, Krone SM. Markov Chain Monte Carlo in small worlds. *Statistics and Computing* 16, 193-202, 2006.
 39. Sullivan J, Joyce P. Model selection in phylogenetics. *Annual Reviews of Ecology, Evolution and Systematics* 36, 445-466, 2005.
 40. Miller CR, Joyce P, Waits LP. A new method for estimating the size of small populations from genetic mark-recapture data. *Molecular Ecology* 14, 1991-2005, 2005.
 41. Carstens BC, Bankhead III AR, Joyce P, Sullivan J. The MIGRATE-n test of panmixia. *Genetica* 124, 71-75, 2005.
 42. Ponciano JM, Vandecasteele F, Hess T, Forney LJ, Crawford RL, Joyce P. Use of stochastic models to assess the effect of environmental factors on microbial growth. *Applied Environmental Microbiology* 71 (5), 2355-2364, 2005.
 43. Sullivan J, Abdo ZO, Joyce P, Swofford DL. Evaluating the performance of a successive-approximations approach to parameter optimization in maximum-likelihood phylogeny estimation. *Journal of Molecular Biology and Evolution*. 22, (5), 1386-1392, 2005.
 44. Rokyta DR, Joyce P, Caudle SB, Wichman HA. An empirical test of the mutational landscape model of adaptive evolution using a ssDNA bacteriophage. *Nature Genetics* 37 (4) 441-444, 2005.
 45. Abdo ZO, Minin V, Joyce P, Sullivan J. Accounting for uncertainty in the tree topology has little effect on the decision theoretic approach to model selection in phylogeny estimation. *J. Mol. Bio. Evol.* 22(3):691-703, 2005.
 46. Joyce P, Abdo ZO, Ponciano JM, De Gelder L, Forney L, Top EM. Modeling the impact of periodic bottlenecks, unidirectional mutation and observational error in experimental evolution. *J. Math. Bio.* 50(6) 645-662, 2005.
 47. DeGelder L, Ponciano JM, Abdo ZO, Joyce P, Forney LJ, Top EM. Combining mathematical models and statistical methods to understand and predict the dynamics of

- antibiotic sensitive mutants in a population of resistant bacteria during experimental evolution. *Genetics* 168 (3), 1131-1144, 2004.
48. Abdo ZO, Crandall KA, Joyce P. Evaluating the performance of likelihood methods for detecting population structure and migration. *Molecular Ecology* 13, 837-851, 2004.
 49. Genz A, Joyce P. Computation of the normalizing constant for exponentially weighted Dirichlet distribution integrals *Computing Science and Statistics* 35, 181-212, 2003.
 50. Minin V, Abdo ZO, Joyce P, Sullivan J. Performance-based selection of likelihood models for phylogeny estimation. *Systematic Biology* 52 (5), 672-684, 2003.
 51. Joyce P, Krone S, Kurtz T. When can one detect over-dominant selection in the infinite alleles model? *Ann. Appl. Prob.* 13, 181-212, 2003.
 52. Joyce P, Krone S, Kurtz T. Gaussian limits associated with the Poisson-Dirichlet distribution and the Ewens Sampling Formula. *Ann. Appl. Prob.* 12, 101-124, 2002.
 53. Miller C, Joyce P, Waits L. Assessing allelic dropout and genotype reliability using maximum likelihood. *Genetics* 160, 357-366, 2002.
 54. Nordborg M, Donnelly PJ, Joyce P. Likelihood simulation methods and inference for a class of non-neutral population genetics models. *Genetics* 159, 853-867, 2001.
 55. Brown CJ, Garner EC, Dunker KA, Joyce P. The power to detect recombination using the coalescent. *J. Mol. Bio. Evol.* 18, 1421-1424, 2001.
 56. Abdo ZO, Joyce P, Araji AA. "Efficient use of animal wastes on cropland" *Journal of Bioresource Technology* 79: 179-191, 2001.
 57. Joyce P, Fox L, Casavant C, Wichman HA. Linear estimators for the evolution of transposable elements, *Statistics in Molecular Biology and Genetics. Proceedings of the AMS-IMS-SIAM, Joint Summer Research Conference* 33, 207-220, 1999.
 58. Joyce P. No BLUE among phylogenetic estimators. *J. Math. Bio.* 39(5), 421-438, 1999.
 59. Joyce P. Partition structures and sufficient statistics. *J. Appl. Prob.* 35(3), 622-632, 1998.
 60. Joyce P. Robustness of the Ewens sampling formula. *J. Appl. Prob.* 32, 609-622, 1995.
 61. Joyce P, Tavaré S. The distribution of rare alleles. *J. Math. Bio.* 33(6), 602-618, 1995.
 62. Joyce P. Likelihood ratios for the infinite alleles model. *J. Appl. Prob.* 31, 595-605, 1994.
 63. Joyce P, Tavaré S. A convergence theorem for symmetric functionals of random partitions. *Adv. Appl. Prob.* 29, 280-290, 1992.
 64. Donnelly P, Joyce P. Weak convergence of population genealogical processes to a coalescent. *Ann. Prob.* 20, 322-341, 1992.

65. Joyce P. Estimating the frequency of the oldest allele, a Bayesian approach. *Adv. Appl. Prob.*, 23, 456-475, 1991.
66. Donnelly P, Joyce P. Consistent ordered sampling distributions. *Adv. Appl. Prob.*, 23, 229-258, 1991.
67. Joyce P, Tavaré S. Random permutations and neutral evolution models. *Stoch. Proc. Appl.* 36, 245-261, 1990.
68. Tavaré S, Ewens WJ, Joyce P. Is knowing the age-order of alleles in a sample useful in testing for selective neutrality? *Genetics* 122 (3), 705-711, July 1989.
69. Donnelly PJ, Joyce P. Continuity and weak convergence of ranked and size-biased permutations. *Stoch. Proc. Appl.* 31, 9-103, 1989.
70. Joyce P, Tavaré S. Cycles, permutations and the structure of the Yule process with immigration. *Stoch. Proc. Appl.* 25, 89-103, 1987.

Invited and Contributed Discussions:

Contribution to "Statistical modeling and analysis of genetic data." *J. Roy. Stat. Soc. B.* Part 4 (2002).

Contribution to "Inference in molecular population genetics." *J. Roy. Stat. Soc. B.* Part 4 (2000).

Patents:

Categorization of Vaginal Microflora. Patent No. US 7,627,437 B2. Date Awarded: Dec. 1, 2009. Inventors associated with project in alphabetical order of first name: Audra Johnson, Celeste Brown, James A. Foster, Larry J. Forney, Paul Joyce, Xia Zhou and Zaid Abdo.

Software:

EVO-X This program is associated with De Gelder et.al.(2004), wherein a mathematical model is introduced that aims to explain the evolutionary process of the loss of the tetracycline resistance operon from a plasmid contained in *E. coli*. This model is coupled with a statistical framework based on the maximum likelihood to estimate its parameters and to test the associated hypotheses.

<http://www.webpages.uidaho.edu/%7Ejoyce/Lab%20page/Evo-x.html>

DT-ModSel A performance-based method for selecting a likelihood model for phylogenetic estimation.

<http://www.webpages.uidaho.edu/%7Ejacks/DTModSel.html>

RelioType A maximum likelihood approach for minimizing genotyping errors for noninvasive genetic sampling of wild populations. The program estimates genotype reliability and strategically directs replication at loci most likely to harbor errors. <http://www.cnrhome.uidaho.edu/default.aspx?pid=69578>

Capwire: This program estimates the size of small populations using noninvasive genetic

samples. The program accounts for possible heterogeneity in capture rates.
<http://www.cnrhome.uidaho.edu/default.aspx?pid=69578>

Testing population structure with Migrate-n: A method for testing for the genetic signal of panmictic population structure with organellar DNA sequence data. While this test is not expected to have the statistical power of tests designed for multi-locus data, it provides an approach suitable for single-locus sequence datasets. As such, it is a useful tool for preliminary exploration of population genetic structure in non-model organisms where the development of microsatellite or SNP libraries can be costly and difficult. The program can be downloaded from Bryan Carstens webpage, by searching for the paper Carstens BC, Bankhead III A, Joyce P, Sullivan J. Testing Population Genetic Structure using Parametric Bootstrapping: The Migrate-n test of Panmixia. *Genetica*, 124, 71-75, 2005.. in his publication list.
<http://www-personal.umich.edu/%7Ebcarssten/Publications.html>

TRFLP-STATS : A statistical analysis of T-RFLP data that include objective methods for

- (a) determining a baseline so that "true" peaks in electropherograms can be identified,
- (b) a means to compare electropherograms and bin fragments of similar size,
- (c) clustering algorithms that can be used to identify communities that are similar to one another, and
- (d) a means to select samples that are representative of a cluster that can be used to construct 16S rRNA gene clone libraries.

<http://www.webpages.uidaho.edu/%7Ejoyce/Lab%20page/TRFLP-STATS.html>

PRESENTATIONS AT SCHOLARLY MEETINGS and SEMINARS:

Invited Presentations:

Stickbreaking: A novel fitness landscape model. Mathematics Department Colloquium, University of Idaho, February 19, 2015.

Theory of adaptive evolution informed by microbial experiments, Isaac Newton Institute for Mathematical Sciences, Cambridge UK, September 4, 2014.

The role of statistics in the theory of adaptive evolution informed by experimental evolution. Statistical methods in bioinformatics. Indian Institute of Science, Indian Statistical Institute and the Statistical and Mathematical Sciences Institute. Bangalore India December 12-14, 2013

Stickbreaking: A novel fitness landscape model that harbors epistasis and is consistent with commonly observed patterns of adaptive evolution. Mathematical tools for evolutionary systems biology, Banff International research station for mathematical innovation and discovery, May 26-31, 2013

Characterizing the distribution of lysis time and burst size in lytic phage. Nordic Conference in Mathematical Statistics, Umeå Sweden, June 10, 2012.

The distribution of burst sizes and burst times for virus evolution. Probability, Population

- Genetics and Evolution, CIRM Marseille-Luminy, France, June 11-15, 2012.
- A simple mutational model that produces diminishing returns epistasis and decelerating fitness trajectories in adaptive walks. Ecology and Evolution of Infectious Diseases PI meeting. University of California Berkeley, Berkeley California, March 26, 2012.
- Efficient simulation methods for a class of nonneutral population genetics models. 30 Years of Computational Biology at USC, Conference in honor of Michael Waterman and Simon Tavaré, University of Southern California, Los Angeles California, March 30-31 2012.
- Mutational effects and population dynamics during viral adaptation challenge current models. Wellcome Trust Centre for Human Genetics Seminar, Oxford University, Oxford UK, April 20, 2011.
- Testing assumptions of models of adaptation using experimental evolution, Li Ka Shing Research Centre Seminar, Cambridge University, Cambridge UK, April 21 2011.
- A predictive model of adaptive evolution, Stochastic Processes and their Applications, invited presentation, Oaxaca Mexico, June 20, 2011.
- Stickbreaking: A simple mutational model that produces diminishing returns epistasis and decelerating fitness trajectories in adaptive walks. Invited presentation, MBI Workshop: New Questions in Probability Theory Arising in Biological Systems. Columbus Ohio, September 14, 2011.
- Statistical methods for testing simple mutational model that produces different patterns of epistasis Mind the Gap Research Conference, Cologne Germany, September 27, 2011.
- Pathways of adaptive evolution in a virus model, Biophysics and Evolution Conference, Aspen Colorado, January 2010.
- Testing the assumptions of models of adaptation using experimental evolution. Institute of Science and Technology, Austria, March 22, 2010.
- Impacts and predictions of adaptive evolution. COBRE Annual Meeting, Bethesda Maryland. June 16, 2010.
- Seeking a predictive theory of adaptation, INBRE presentation, University of Idaho, June 30, 2010.
- Distribution of Fitness effects, Institute of Mathematical Statistics international meeting, Gothenburg Sweden, August 13, 2010.
- Mutational effects and population dynamics during viral adaptation challenges current models, University of Copenhagen, Copenhagen Denmark. August 17, 2010.
- Summer course in human population genetics analysis, University of Copenhagen, Copenhagen Denmark, August 16-20, 2010.

Applications of bioinformatics and computational Biology (BCB), INBRE conference, University of Idaho, June 30, 2010.

Short Course in Stochastic models and inference in science: applications to population genetics, Center for Mathematics and its Applications, Guanajuato Mexico, March 7-21, 2009.

Gumbler's ruin: beneficial fitness effects are not exponential for two viruses, American Mathematical Association Meeting, Ellensburg Washington, April 3, 2009.

An example from population genetics where the parametric bootstrap fails, Probabilistic Models in Evolutionary Biology, Centre International de Recontres Mathematiques, Marseille-Luminy, France, May 25-29, 2009.

Maximum likelihood estimates under K-allele models with selection can be numerically unstable, Institute for Mathematical Statistics Regional Meeting, Portland Oregon, June 16, 2009.

Seeking a predictive theory of adaptation, Mathematics Colloquium, University of Western Ontario, Ontario Canada, July 27, 2009.

A general extreme-value theory model for the adaptation of DNA sequences under strong selection and weak mutation, Workshop on New Mathematical Challenges from Molecular Biology, Banff International Research Station for Mathematical Innovation and Discovery, Banff Canada, September 9-11, 2009.

Mathematical modeling and statistical methods for the theory of adaptation, Statistics Colloquium, University of Washington, Seattle Washington, November 3, 2009.

Adaptive Evolution and Extreme Value Theory, Probability Seminar, University of British Columbia. March 5, 2008.

"Extreme Value Theory and the Generalized Pareto Distribution," Center for the Investigation of Mathematics, Guanajuato Mexico. March 10-12, 2008

Seeking a Predictive Theory of Adaptation, NIH-NSF joint Principal Investigators meeting on Ecology and Evolution of Infectious Diseases. December 3-4, 2007.

Seeking a Predictive Theory of Adaptation through Mathematical Modeling and Statistical Analysis of Experimental Evolution, Idaho-INBRE Sixth Annual Research Conference, Aug 6-8, 2007.

The Role of the Generalized Pareto Distribution in Testing the Mutational Landscape Model for Experimental Evolution, Mathematical Genetics of Selection and Adaptation, University of Aarhus, Denmark April 16-17, 2007.

Gumbeler's ruin: Beneficial Fitness effects are not Exponential for Two Viruses, University of California and Davis, March 16, 2007.

Molecular evolution: genetic drift or genetic draft? Part I: The genetic theory of adaptation, A course supported by the Center for Dynamical Processes and

- Structure Formation, Uppsala University, November 6-9, 2006.
- Testing the Theory of Adaptive Evolution, Bioinformatics Colloquium, University of Southern California, October 5, 2006.
- Efficient Simulation Methods for a Class of Nonneutral Population Genetics Models, Bioinformatics Seminar, North Carolina State University, April 7, 2006.
- Statistical Inference for Population Genetics Models., NSF sponsored 2nd Cornell Probability Summer School, Ithaca New York, June 26-July 7 2006.
- Statistical Models in Experimental Evolution, Western NIH INBRE Symposium on Infectious Disease. April 18-20 2006.
- Uniform integrability and its implications for likelihood ratios from population genetics, McMaster University, April 12, 2005.
- Efficient Simulation Methods for a Class of Nonneutral Population Genetics Models, Mathematical Biosciences Institute Workshop, Ohio State University, June 12-17, 2005.
- Experimental evolution and the theory of adaptation, Uppsala University, Sweden, September 10, 2004.
- Microbial diversity and experimental evolution, Annual Idaho NSF-EPSCoR (Experimental Program to Stimulate Competitive Research) Conference, Moscow Idaho, September 20, 2004.
- Testing the theory of adaptive evolution, Banff International Research Station, Mathematical Innovation and Discovery, Stochastic Processes in Evolution and Disease Genetics, Banff Canada, August 7-12, 2004.
- Testing the theory of adaptive evolution, do two wrongs make a Wright?, London Mathematical Society Research Symposium on Mathematical Genetics, Durham, United Kingdom, July 3-13, 2004.
- Adaptive evolution of DNA sequences, Evolution - Washington, Idaho, British Columbia, and Oregon (EVO-WIBO), Fort Worden State Park, Washington, April 2004.
- Gaussian limits and likelihood ratios associated with the infinite alleles model of evolution, Research Network on interacting Stochastic Systems at Technical University, Berlin Germany, April 2003.
- Mathematical and statistical methods in biocomplexity, Annual Idaho NSF-EPSCoR (Experimental Program to Stimulate Competitive Research) Conference, Moscow Idaho, September 22, 2003.
- Likelihood, simulation and evaluation of a class on non-neutral models with selection, International Conference on Mathematics and Biology and Annual Meeting of The Society for Mathematical Biology, Knoxville, Tennessee, July 2002.
- Likelihood ratios for population models with selection, Spring Western Section Meeting

- of the American Mathematical Society, Special Session on Mathematical Biology, June 2002.
- When can one detect overdominant selection in the infinite alleles model, Hawaii International Conference on Statistics and Related Fields, June 5-9, 2002.
- A short course on gene genealogies, Uppsala University, Sweden, March 15-23, 2002.
- Assessing allelic dropout and genotype reliability using maximum likelihood, 11th Annual Meeting on Mathematical and Statistical Aspects of Molecular Biology, Isaac Newton Institute for Mathematical Sciences, Cambridge, United Kingdom, March 20- 21, 2001.
- The role of population size in detecting selection, Workshop on Stochastics in Sequence Alignment and Population Biology, Holzhausenschloesschen Frankfurt Germany, sponsored by the Max Planck Institute, October 12-14, 2000.
- Detecting selection for large populations with high mutation rate, Statistics Colloquium Oxford University, United Kingdom, March 2000.
- Linear estimation theory for coalescent models, Applied Statistics Seminar, University of Reading, United Kingdom, March 13, 2000.
- Comments on inference in molecular population genetics. Royal Statistical Society Meeting, London England, March 2000.
- Linear theory for estimating parameters in population genetics, Department of Mathematics, Probability Seminar, University of Southern California, October 23, 1997.
- Statistical inference for population genetics models, Center for Mathematical Science, University of Wisconsin, Madison Wisconsin, July 1996.
- The theory of inference for the infinite alleles model, Institute of Mathematical Statistics Regional Meeting, Pullman, Washington, June 1996.
- Statistical methods for the evolution of transposable elements, Department of Statistics Colloquium, University of Chicago, November 1995.
- The distribution of rare variants, University of London Mathematical Biology Seminar, Queen Mary College, London, United Kingdom, May 1994.
- Likelihood ratios for infinite alleles model, American Mathematical Society Regional Meeting, Salt Lake City, Utah, April 1993.

GRANTS AND CONTRACTS:

Completed:

- National Science Foundation, NSF-DEB 1450653 A Bayesian Approach to Inferring the Strength of Selection of Coevolution, Co-PI (S. Nuismer PI) April 1, 2015-March 31, 2018.

- National Institute of Health, NIH-R01 GM076040 Patterns of adaptive evolution, PI (H.A. Wichman, C.R. Miller co-PI's) \$1,084,167 Funding period: April 1, 2011-March 31, 2016.
- National Science Foundation, NSF-DMS 1039485 Collaborative Research: UBM - Institutional: UI-WSU Program in Undergraduate Mathematics and Biology, Co-PI, (B. Robison PI, and E. Top, E. Rosenblum, S. Krone other Co-PI's). \$500,000.00 October 1, 2010-September 30, 2015.
- National Science Foundation, DUE -Bridge to Graduate Study in Interdisciplinary Sciences, Co-PI, (M. Dakins PI), \$597,330. June 1, 2008-June 1-2012.
- National Institute of Health, NIH-P20 RR016448-07S1 Interdisciplinary Study of Viral Host Switching, co-PI, (M. Ytreberg PI, H.A. Wichman co-PI), \$911,000. Funding period: August 13, 2009-May 31, 2011.
- National Institutes of Health, NCRR- 1 P20 RR024930-01, Center for Research on Processes in Evolution, Research Oversight Committee Member, (L. Forney, PI), \$9,000,000 Funding period: February 23, 2008- January 31, 2012.
- National Science Foundation, DEB-0717416, Research experience for Undergraduates (REU) Supplement for QEIB-Statistical Modeling and Simulation for Non-Neutral Population Models, PI, \$6000. May 1, 2007-April 31, 2008.
- National Institutes of Health, NIH-R01 GM076040-01. Patterns of adaptive evolution, PI (H. Wichman co-PI) \$1,369,805. February 1, 2006-January 31, 2011.
- National Science Foundation, DEB- 0515738. QEIB-Statistical Modeling and Simulation for Non-Neutral Population Models, PI (A. Genz co-PI) \$276,600. Funding period: September 15, 2005-September 30, 2009.
- National Science Foundation, CSEMS, Undergraduate scholarships for computer science and mathematics, Co-PI (J. Foster PI). February 2004-2007.
- National Institutes of Health, NCRR-1P20RR016448-01, Center for Research on Processes in Evolution, Co-I for computational and mathematical analysis of biomedical data, Co-I (L. Forney, PI), \$10,340,113. Funding period: February 23, 2002- January 31, 2007.
- National Science Foundation, Idaho EPSCoR, EPS-0132626. Research Infrastructure Improvement Grant, Co-I (J. Shreeve, PI), \$9,000,000. Funding period: February 1, 2002-January 31, 2005.
- National Science Foundation, DEB-0089756. An integrative statistical framework for assessing and minimizing errors in ancient, non-invasive forensic genetic studies. Co-PI, (L. Waits PI), \$166,000. Funding period: February 1, 2001-January 31, 2005.
- National Science Foundation DMS 00-72198, Stochastic models in population genetics and ecology. PI, (S. Krone, Co-PI), funded by the Program of Probability, Division of Mathematical Sciences, \$165,608. Funding period: August 1, 2000-July 31, 2004.

National Science Foundation. EPSCoR 00-80935, Multidisciplinary studies in bioinformatics and evolution. Co-investigator, (J. Foster, PI), \$499,994. Funding period: July 15, 2000-July 14, 2004.

National Science Foundation. DMS 96-26764, Stochastic models in population genetics and ecology. Co-PI (S. Krone, PI). Funded by the Program of Probability, Division of Mathematical Sciences, \$32,000. Funding period: August 1, 1996- January 31, 2000.

University of Idaho Seed Grant. KDY509, Mathematical genetics models for hypervariable loci used in DNA forensics. PI. Funded 1994-95, \$5,999.

National Science Foundation. DMS 92-07410, Stochastic models in population genetics and DNA sequencing. PI Funded by the Program of Probability, Division of Mathematical Sciences, \$45,000. Funding period: August 1, 1992-January 31 1996.

National Science Foundation. DMS 90-05833, Group project in probability, statistics, and computational molecular biology. Co-I (M.S. Waterman, S. Tavaré, L. Gordon, R. Arratia, L. Goldstein, W. Navidi. PI's). Funded 1990-91.

National Science Foundation. REU Site, DMS 87-12516, Participant (H. Rossi, R.M. Brooks and S. Tavaré, PI's). Funded, summer 1987. University of Utah, Department of Mathematics.

PROFESSIONAL SERVICE:

Refereeing and Reviewing:

Referee for *Journal of Applied Probability*, *Advances in Applied Probability*, *Annals of Applied Probability*, *Statistics and Probability Letters*, *IMS proceedings on Mathematical and Statistical Methods in Evolutionary Biology*, *Biometrics*, *Environmetrics*, *Molecular Biology and Evolution*, *Evolution*, *Bernoulli*, *Probability Theory and Related Fields*, *Journal of Mathematical Biology*, *Genetics*, *New Zealand Journal of Botany*, *Nonparametric Statistics*, *Theoretical Population Biology*, *Bioinformatics*, *Proceedings of the National Academy of Sciences*, *Conservation Biology*, *Molecular Ecology*, *Systematic Biology*, *Theoretical Population Biology*.

Textbook reviewer for Duxbury Press. Reviewed *Basic Engineering Data Collection and Analysis*, by Stephen Vardeman and Marcus Jobe.

Textbook reviewer for W.H. Freeman, *Introduction to Probability and Mathematical Statistics* by Michael Evans and Jeffrey Rosenthal

Textbook review for Prentice Hall, *Probability and Statistical Inference* by Robert E. Hogg and Elliot A. Tanis, *An Introduction to Mathematical Statistics*, by Ramachandran, Rao, and Tsokos.

Textbook review for Cambridge Press, *A Course and Exercises in Applied Probability*, by Mario Lefbvre.

Grant reviewer for National Science Foundation (NSF).

Grant reviewer for Natural Environment Research Council, (NERC) United Kingdom

Grant reviewer for National Sciences and Engineering Research Council, (NSERC), Canada

Evaluator for the Canadian Research Chair

External Examiner for a Ph.D. candidate, Monash University, Melbourne Australia, 1997

Other Service to the Profession:

Review panel for NSF Division of Mathematics and Statistics (DMS) Mathematical Biology Panel. February 25-27, 2015.

Review panel for NIH Genetic Variation and Evolution (GVE). June 20, 2014

Review panel for the DFG-Priority Programme SPP Probabilistic structures in evolution. April 19, 20 2012.

Associate Editor for Biology Letters 2011-present

Joint organizer with Shui Feng a special workshop on Random Measures and Measure-Valued Processes, in Banff 2013.

Joint Editor with Thomas Bataillon, and Paul Sniegowski. Special Issue of Biology Letters. Topic: Experimental Evolution to appear 2012

Member of the Division of Mathematical Sciences, Statistics, NSF panel January 2011.

Taught a short course entitled "Molecular evolution: genetic drift or genetic draft? Part I: The genetic theory of adaptation", supported by the Center for Dynamical Processes and Structure Formation, Uppsala University, Uppsala Sweden. November 6-9, 2006

Taught a short course on "Gene genealogies: inference in molecular population genetics," (September 6-10, 2004) Uppsala University, Sweden.

Taught a short course on "Gene genealogies: inference in molecular population genetics," (March 18-22, 2002) Uppsala University, Sweden.

National Science Foundation, Division of Mathematical Sciences, Probability Panel, 2001

Organized (with Dr. Krishna Jandhyala, WSU) Pacific Northwest Statistics meeting at Washington State University, Pullman, Washington, April 1999

President of the Snake River Chapter of the American Statistical Society 1996-97

Organized the annual meeting of the Snake River Chapter of ASA, May 1997

Local Arrangements Chair (with Dr. M. Evans, WSU) for IMS regional meeting in Pullman, Washington, June 1996.

Invited speaker and mentor, summer workshop for new Ph.D.'s in probability and stochastic processes, Center for Mathematical Science, University of Wisconsin, Madison, Wisconsin, July 1996

Major Committee Assignments:

Departments of Mathematics and Statistics University of Idaho:

Advisor to Graduate Students without Major Professor, 2007-2016
 Freshman Advisor for S-STEM Scholarship Students, 2008-2012
 Math 310-411-420-471-472-480-482 Committee 2011
 Graduate Committee 2011
 Department of Statistics Search Committee 2007-2008.
 Curriculum Committee, (chair) 2007-2009
 Travel Committee. Chair, 2002-2007, 2010
 Graduate Committee, Mathematics, 1998-present, Chair 1999-2000
 M.A.T. (Masters of Arts in Teaching) Committee, 1999-2016
 Graduate Committee, Statistics, Chair, 1999-2000
 Statistics Bylaws Committee, 1997, 1999
 Colloquium Committee Mathematics, Chair, 1996-2003
 Minor Advisor, Mathematics, 1995-98
 Colloquium Committee Statistics, Chair, 1995-2000
 Curriculum Committee, Mathematics, 1992-94, Spring 2010
 Math 451-452 committee 1991-2016
 Mathematics Statistics Supervisory Committee (Chair), appointed 1991-93

University of Idaho:

Faculty Senate (December 2009- July 2012)
 Chair Faculty Senate (August 2011- July 2012)
 Director Bioinformatics and Computational Biology Graduate Program (August 2009-2012)
 Faculty Search Committee member for Math/Bio/Stat position (January 2011-March 2011)
 Staff Search Committee member for Program Manager position IBEST(November 2011-December 2011).
 Vice Chair of Faculty Senate August 2010-July 2011.
 Chair of Committee on Committees, 2010-2011
 Director of Extended Education Search Committee (Chair) January 2010-May 2010
 Dean of the College of Graduate Studies Search Committee (September 2010-2016)
 Faculty Search Committee member for Math/Bio/Stat position (January 2010-2016)
 Member of the University Wide Programs Committee (August 2009-2016)
 College of Science Curriculum Committee, 2007-2009
 Research Oversight Team member to advise the PI for NIH Center Grant (2008-2016)
 Facilitator, Research and Graduate Creative Activities Retreat, May 2008.
 College of Science Promotion Committee, 2007-2009
 Team 2 Strategic Planning Committee for Research and Creative Activities, 2006-2009.
 Research Excellence Award Nominating Committee 2006
 Blue Ribbon Committee to fund President's Initiative Proposals 2005-2006
 University Travel Grant Committee (Chair) 2004-2005
 Research Council to assist the Vice Provost for Research, 2004-2007
 Bioinformatics and Computational Biology (BCB) Governing Board, 2003- 2005.
 University of Idaho: Sabbatical Leave Committee, 2003-2005. (Chair 2004-2005)
 Dean of the College of Science Search Committee, 2002
 Technology Learning Center Faculty Advisory Committee, 2001- 2003
 Goldwater Scholarship Committee, 1998-2001

College of Letters and Sciences Promotion and Tenure Committee, 1995-98
 University Promotions Committee, 1998, 2005, 2006

Membership in Professional and Scholarly Organizations:

Institute of Mathematical Statistics
 American Statistical Association Chapter President (1996-97)
 Society of Mathematical Biology

Honors and Awards:

University Distinguished Professor Award, 2016.
Theoretical Population Biology, Paul Joyce Special Issue. Volume 122: pp 1-158. July 2018.
Alumni Award for Excellence, University of Idaho, faculty mentor for Zaid Abdo, 2004.
Alumni Award for Excellence, University of Idaho, faculty mentor for José Miguel Ponciano, 2005.
College of Science, Distinguished Faculty Award, University of Idaho, 2007.
Alumni Award for Excellence, University of Idaho, faculty mentor for Erkan Buzbas, 2008.
Donald Crawford Graduate Faculty Mentoring Award, University of Idaho, 2009.

Post Doctorate Fellows:

Craig Miller (2004-2005) (2007-2011)
 Darin Rokyta (2006-2008)
 Roland Fleissner (2003-2005)

Graduate Students:

Ph.D. Students.

Hua Feng, Ph.D., Bioinformatics, appointed 2009-2016
 Andrzej Jan Wojtowicz, Ph.D., Bioinformatics, appointed 2007-completed 2012
 Erkan Buzbas, Ph.D., Bioinformatics, appointed 2004-completed 2009
 José Miguel Ponciano, Ph.D., Bioinformatics, appointed 2002-completed 2006
 Zaid Abdo, Ph.D., Bioinformatics, appointed 2002-completed 2005
 Kathrine Johnson, Ph.D., Mathematics, appointed 1992-completed 1998

MS. Students

Michael Shively, MS Mathematics, appointed 2009-completed 2011
 Matthew Peterson, MS Mathematics, appointed 2009-completed 2011
 Amanda Larson, Ms Mathematics, appointed 2009-completed 2011
 Charles William Ormond Von Tagen, MS Mathematics, appointed 2007-completed 2009
 Douglas Torrance, MS Mathematics, appointed 2006-completed 2008
 Igor J Khaykin, MS, Mathematics, appointed 2007-completed 2008
 Jennifer Bennett, MAT, appointed 2007-2008
 Michelle Elaine Jeitler, MAT, Appointed 2005-completed 2007
 Craig Beisel, MS., Bioinformatics, appointed 2004-completed 2007
 Hua Feng, MS. , Bioinformatics, appointed 2004-completed 2006
 Blerina Reza, MS., Mathematics, appointed 2005- completed 2006.
 Roman Fedorovich Makordey, MS, Mathematics, appointed 2001-completed 2003
 Inna Vladimirovna Politayko, MS Mathematics, appointed 2001-completed 2003

Hua Feng, M.S., Statistics, appointed 2000- completed 2003
 Laura Pittard, M.A.T.,, appointed 2000-completed 2002
 Rebecca Wright, M.A.T., appointed 2002-completed 2002
 Yaomin Xu, M.S. Statistics, appointed 2000-completed 2002
 Sarrita Cupp, M.A.T., Mathematics Education, appointed 1999-completed 2001
 Celeste Brown, M.S. Statistics, appointed 1997-completed 2000
 Zaid Abdo, M.S. Statistics, appointed 1997-completed 2000
 Bryan Farren, M.S. Mathematics, appointed 1999-completed 2000
 Li Zeng, M.S. Statistics, appointed 1996-completed 1998
 Linette Fox, M.S. Statistics, appointed 1995-completed 1997
 Anna Griffel, M.S. Statistics, appointed 1992-completed 1995
 Kathleen Wharton, M.S. Statistics, appointed 1992-completed 1994

Committee member for the following students:

Jennifer Stenglein, MS, Environmental Science, appointed 2008
 Thomas Poorten, PhD, Bioinformatics, appointed 2010
 Matthew Pennell, PhD, Bioinformatics, appointed 2011
 Tyler Heather, PhD, Bioinformatics, appointed 2011
 Kevin White, MS, Statistics, appointed 2011
 Lei Yang, PhD, Bioinformatics, appointed 2011
 Zev Kronenberg, MS Biology, appointed 2008-completed 2010
 Xiaojun Hu, Ph.D., Bioinformatics, appointed 2006-completed 2009
 Jacob D. Pierson, MS, Bioinformatics, appointed 2005-completed 2009
 Jennifer Ripplinger, Bioinformatics, appointed 2005-completed 2009
 Benjamin Paul Oswald, Bioinformatics, appointed 2005
 Xue Zhong, Ph.D., Bioinformatics, appointed 2005-completed 2009
 Jason Evans, Ph.D., Bioinformatics, appointed 2003-completed 2009
 Marta De Barba, Ph.D., Fish and Wildlife, appointed 2003-completed 2009
 Luke Sheneman, Ph.D., Bioinformatics, appointed 2003-completed 2008
 Wei Wei, Ph.D., Bioinformatics, appointed 2003-completed 2007
 Yongtao Guan, Ph.D., Bioinformatics, appointed 2002-completed 2006
 Kim Pepin, Ph.D., Biology, appointed 2002-completed 2006
 Darin Rokyta, Ph.D., Bioinformatics, appointed 2001-completed 2006
 Jennifer Adams, Ph.D. Fish and Wildlife, appointed 2002-completed 2006
 Smitha Surakanti, MS, Bioinformatics, appointed 2003-completed 2005
 José Miguel Ponciano, MS, Statistics, appointed, 2002-completed 2004
 Jason Hicks, MS, Fish and Wildlife, appointed 2002-completed 2004
 Jian Shen, MS, Computer Science, appointed 2003-completed 2004
 Rob Keefe, MS., Forestry, appointed 2003-completed 2004
 Koffi Sampson, Ph.D. Mathematics, appointed 1999-completed 2004
 Remko Duursma, Ph.D. Forestry, appointed 2002-completed 2004
 Zhaofei Fan, MS, Statistics, appointed 2002-completed 2003
 Fei Tian, MS, Statistics, appointed 2003-completed 2003
 Richard Remington, MS, Statistics, appointed 2002-completed 2003
 Robert Froese, Ph.D., Forestry, appointed 2001-completed 2003
 Craig Miller, Ph.D. Fish and Wildlife, appointed 2000-completed 2003
 Jennifer Adams, MS. Fish and Wildlife, appointed 2000-completed 2002
 Jeffrey Good, M.S. Biology, appointed 1999-completed 2002
 Michael Morrison, M.S. Mechanical Engineering, appointed 1998-completed 2002
 Song Chen, M.S., Statistics, appointed 2001-completed 2001
 Judy Terrio, M.S. Mathematics, appointed 1996-completed 1998
 Norm Varin, M.S. Statistics, appointed 1997-completed 1998

Hongpei Zhang, M.S. Statistics, appointed 1993-completed 1996
Undupitiya Wijesiri, Ph.D. Mathematics, appointed 1992-completed 1994
Michelle Tichida, M.S. Statistics, appointed 1993-completed 1994
Lifen Zhou, M.S. Statistics, appointed 1992-completed 1993
James Osborne, M.S. Mathematics, appointed 1992-completed 1992