Mark A. Jensen, PhD
Curriculum Vitae

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LinkedIn profile: http://www.linkedin.com/in/fortinbras

Current Positions

Scientific Review Officer, SRA International (July 2009—present)
Duties: organizing and facilitating high-quality scientific review of research proposals for SRA clients, a process involving reviewer recruitment, proposal assignment, meeting organization, and post-review documentation.
Other Activity: Developed and taught "Bioinformatics Programming and Analysis with BioPerl", SRA University, Fall Semester (October-December) 2009.
Consulting Scientist, Clinical Laboratories, British Columbia Centre for Excellence in HIV/AIDS (March 2009—present)
Supervisor: Dr Richard Harrigan, Director (prharrigan@cfenet.ubc.ca)
Duties: Development, implementation and maintenance of web-based PSSM predictor for HIV genotype; maintenance of UNIX node on which the predictor is installed; scientific and editorial contribution to publications and presentations based on lab research.
Senior Consultant & Principal, Fortinbras Research (http://fortinbras.us) (June 2008—present)
Emphases: to provide design assistance and application code for local and/or web-based bioinformatics applications, with an emphasis on the molecular epidemiology of infectious organisms
Contracts: Richard Harrigan, PhD, British Columbia Centre for Excellence in HIV/AIDS, "A web-based database application for the PSSM prediction method of HIV genotyping, with predictor improvements", July 2008—March 2009.
Associate Editor, *Journal of Molecular Evolution*, Springer (February 2008—present)
Supervisor: Prof Martin Kreitman, Editor-in-Chief (mkre@uchicago.edu)
Duties: For scientific manuscripts assigned to me by the Editor-in-Chief, I choose expert reviewers, read reviewers' responses to the manuscript, communicate reviews and my recommendations to authors, and make recommendations for acceptance, revision, or rejection of manuscripts based on reviews.

Previous Positions

Assistant Professor, Department of Epidemiology & Biostatistics (51%), and Department of Genetics (49%), University of Georgia (Aug 2006-May 2008)
*Research Interests***:** Genetic and functional differences among veterinary methicillin-resistant *Staphylococcus aureus* isolates, West Nile virus molecular epidemiology and evolution, novel immunoassays for West Nile antibody detection, mathematical epidemiology and phylogenetics of bacterial antibiotic resistance, bioinformatic detection of host-specific signatures in biological sequences of infectious microorganisms, experimental host-pathogen evolution, molecular biological techniques of mutation detection, phylogenetic analysis of pathogen strains within and between infected hosts.
Post-doctoral Fellow, Department of Global Health, Rollins School of Public Health, Emory University (Jan 2006-Aug 2006)
Principal Investigator/Supervisor: Prof. Keith Klugman (keith.klugman@emory.edu)
Research: Epidemiology of antibiotic drug use and antibiotic resistance in invasive *Streptococcus pneumoniae* in the U.S.
Post-doctoral Fellow, Department of Biology, Emory University (2004-Dec 2005)
Principal Investigator/Supervisor: Prof. Bruce R. Levin (blevin@emory.edu)
Research: Mathematical modeling of bacteriophage-mediated control of cholera epidemics.

Other work: Impact of long-term nutrient limitation on bacterial evolution and competitive fitness, differential influence of physiological states on overall bacterial fitness.

Senior Fellow, Department of Microbiology, University of Washington School of Medicine (2000-2004)
Principal Investigator/Supervisor: Prof. James I. Mullins (jmullins@u.washington.edu)
Research Interests: Population genetics of human immunodeficiency virus (HIV) within patients, and the relationship between in-host viral evolution, HIV pathogenesis, and clinical prognosis; detection of natural selection and compartmentalization in within-patient HIV populations; development of rational HIV antigens based on host and viral genetic diversity considerations.

Education

Ph. D., Department of Ecology & Evolution, University of Chicago (1994-2000)
Thesis: Population Genetic Investigations in Drosophila and Saccharomyces.
Research: Survey of nucleotide polymorphism and analysis of natural selection on the non-recombining fourth chromosome of Drosophila; molecular evolution of a prion-like protein in *Saccharomyces cerevisiae*
Supervisors: Profs. Brian Charlesworth (Edinburgh), Martin Kreitman (Chicago), and Susan Lindquist (MIT-Whitehead)
GRE (1993): **800** Verbal / **770** Quantitative / **770** Analytical
Fulbright scholar, Institute of Mathematics, University of Vienna (1990-91)
Research: *Population genetics modeling*
Graduate studies in mathematics, Washington State University (1989-1990)
M. Sc., Mathematics of Non-linear Models, Heriot-Watt University & University of Edinburgh (1988-1989)
Thesis: Investigation of an Implicit Runge-Kutta Method for Numerical Solution of Conservative Hamiltonian Systems
Supervisor: Dr. Dugald B. Duncan (Heriot-Watt University, Edinburgh)
B. S. (*summa cum laude*), Mathematics, Washington State University (1983-1987)

Skills

Computing: Twenty years scientific programming experience. Languages: Perl, R, MySQL, Emacs LISP, C, UNIX shell scripts, XML and XML Schema. Platforms: Windows, Unix, Perl CGI and SOAP web-based applications. Experience developing and coding phylogenetic algorithms, specialized statistical algorithms, sequence motif analysis applications, differential equation models, development of relational databases.

Scientific communication: Nine years as an independent reviewer for multiple scientific journals (see below). Actively publishing since 2001. Actively speaking and presenting research as primary author since 1999. Seven years experience initiating and maintaining productive national and international scientific collaborations.

Mathematics: Sixteen years experience in differential and difference equation modeling and computer simulation of evolutionary and population biological processes. Some experience in maximum likelihood and Bayesian estimation.

Infectious Disease: Nine years experience in the research and teaching of the epidemiology and pathogenesis of infectious diseases, including HIV/AIDS, cholera, *Streptococcus pneumoniae*, West Nile virus, methicillin-resistant *Staphylococcus aureus*, and bacterial antibiotic drug resistance.

Laboratory: Fourteen years total experience and training in molecular biological laboratory techniques, including polymerase chain reaction (PCR), molecular cloning, electrophoresis, DNA sequencing, DNA denaturing high-performace liquid chromatography (dHPLC), bacterial culture, aseptic technique, biosafety. Two years experience in laboratory setup and management. Some hands-on ELISA, tissue culture experience.

Open Source Contributions
(see http://www.ohloh.net/accounts/maj for a summary)

Core Developer, BioPerl (http://www.bioperl.org/wiki/Main_Page), July 2009-present;
Developer, BioPerl, October 2008-July 2009,

　　Modules written (selected):
- Bio::DB::HIV, Bio::DB::Query::HIV (available in BioPerl Release 1.6; see web implementation at http://fortinbras.us/hivq);
  Modules for automated query access to the Los Alamos National Lab's HIV Sequence Database
- Bio::Search::Tiling::TilingI, Bio::Search::Tiling::MapTiling (available in the BioPerl Release 1.6.1; see http://www.bioperl.org/wiki/HOWTO:Tiling).
  Modules for the robust tiling of high-scoring pairs, providing correct global identity/conservation statistics in "pure BioPerl"
- Bio::Tools::Run::Maq, Bio::Assembly::IO::maq (currently in the code trunk; see http://www.bioperl.org/wiki/HOWTO:Short-read_assemblies_with_maq)
  Run wrapper for the maq short-read assembler, plus an output converter to a BioPerl Bio::Assembly::Scaffold object
- Bio::Tools::Run::BWA, Bio::Assembly::IO::sam (currently in the code trunk; http://www.bioperl.org/wiki/HOWTO:Short-read_assemblies_with_BWA)
  Run wrapper for the bwa short-read assembler, plus an output converter to a BioPerl Bio::Assembly::Scaffold object
- Bio::Tools::Run::Samtools (currently in the code trunk)
  Run wrapper for the samtools suite of large-alignment manipulation programs

　　IDE support package:
- Bioperl-mode, an Emacs minor mode for BioPerl documentation viewing and code template insertion (see http://www.bioperl.org/wiki/Emacs_bioperl-mode).

　　Other significant contributions: key extensions to Bio::Restriction; improvements to module Bio::LocatableSeq (see Bugs #2476, #2682, #2689 at http://bugzilla.bioperl.org for details); improvements the the Bio::Tree namespace (see Bug #2456); BioPerl Scrapbook (http://www.bioperl.org/wiki/Category:Scrapbook).
　　Privileges: Granted commit privileges January 2009; granted wiki sysop privileges March 2009; appointed as Core Developer in July 2009; granted sudo privileges November 2009.

Mentor, Google Summer of Code via NESCent, April 2009-August 2009
　　Project: BioPerl integration of the NeXML exchange standard and Bio::Phylo toolkit
　　Student: Chase Miller, George Washington University, Genomics and Bioinformatics
　　Module Products: Bio::Nexml, Bio::SeqIO::nexml, Bio::AlignIO::nexm, Bio::TreeIO::nexml, see http://www.bioperl.org/wiki/HOWTO:Nexml.

NESCent Hackathon on Evolutionary Database Interoperability, March 2009
(http://evoinfo.nescent.org/Database_Interop_Hackathon):
　　Invited Participant

NeXML (http://nexml-dev.nescent.org/) : evolutionary data exchange standard by Rutger Vos
- Contributed DOM functionality to Bio::Phylo (Perl API to NeXML)

CPAN/PAUSE, Perl open-source module contributions (http://search.cpan.org/~majensen):
- AnyDBM_File::Importer (registered module)
  Imports DBM package symbols when using AnyDBM
- FSSM::SOAPClient
  An interface package to access the Fortinbras Research HIV coreceptor predictor webservice
- PerlIO::via::gzip (registered module)
  PerlIO layer for gzip (de)compression
- PerlIO::via::SeqIO (registered module)

PerlIO layer for biological sequence formats
- SQLite_File
  Tie to SQLite, with DB_File emulation

Editing and Reviewing

Associate Editor, *Journal of Molecular Evolution*, February 2008 – present

Guest Associate Editor, *PLoS Computational Biology*, May 2008 – Oct 2008

Reviewer, McGraw-Hill Inc.
Hartwell et al., *Genetics: From Genes to Genomes, 3rd Ed.*, Chapter 22, "Evolution at the Molecular Level", December 2007
Hartwell et al., *Genetics: From Genes to Genomes, 3rd Ed.*, Appendix A, "A Genetic Portrait of Yeast", June 2008

Reviewer, Elsevier, Schachter, M., *ed. Encyclopedia of Microbiology*, eleven chapters, under associate editor Bruce Levin, June 2008

Reviewer for the following journals:
Antimicrobial Agents and Chemotherapy
Applied Bioinformatics
Evolution
Genetics
Infection and Immunity
Journal of Clinical Microbiology
Journal of Molecular Evolution
Journal of Neurochemistry
Journal of Theoretical Biology
Journal of Virological Methods
Journal of Virology
Molecular Biology and Evolution
Nucleic Acids Research
Nature Biotechnology
PLoS Computational Biology
PLoS Genetics
PLoS ONE
PLoS Pathogens
PNAS
Retrovirology
Virology

Memberships

American Society for Microbiology
International Society for Computational Biology
Open Bioinformatics Foundation

US Patent

#7, 655, 774 : Ancestral and COT viral sequences, proteins and immunogenic compositions, granted 2 Feb 2010

Inventors: Mullins; James I. (Seattle, WA), Rodrigo; Allen G. (Auckland, NZ), Learn; Gerald H. (Kingston, WA), Li; Fusheng (Seattle, WA), Nickle; David C. (Seattle, WA), **Jensen; Mark A.** (Snohomish, WA)
Assignee: University of Washington, Seattle, WA.

Scientific publications

2010. Swenson, L. C, A. Moores, A. J. Low, A. Thielen, W. Dong, C. Woods, **M. A. Jensen**, B. Wynhoven, D. Chan, C. Glascock, and P. R. Harrigan. Improved detection of CXCR4-using HIV by V3 genotyping: application to plasma RNA, proviral DNA, and 'deep' sequencing. *Journal of AIDS*, *in press*.

2009. Kandathil, A. J., R. Kannangai, O. C. Abraham, S. A. Pulimood, **M. A. Jensen**, and G. Sridharan. HIV-1 with predicted CXCR4 genotype identified in clade C from India. *Molecular Diagnosis and Therapy*, **13**:19-24.

2009. Kandathil, A. J., R. Kannangai, O. C. Abraham, S. A. Pulimood, **M. A. Jensen**, and G. Sridharan. A comparison of interpretation by three different HIV-1 genotypic drug resistance algorithms using sequences from non-clade B HIV-1 strains. *AIDS Research and Human Retroviruses*, **25**:315-318.

2008. van 't Wout, A. B. and **M. A. Jensen**. HIV-1 tropism and its detection – impact on infection, transmission and treatment. *European Infectious Disease* **2**:60-64.

2008. **Jensen, M. A.**. Predicting disease outcomes in the clinic. *Nature Biotechnology*, **26**:611-612.

2007. Low, A. J., W. Dong, D. Chan, T. Sing, R. Swanstrom, **M. Jensen**, S. Pillai, B. Good, and P. R. Harrigan. Current V3 genotyping algorithms are inadequate for predicting X4 co-receptor usage in clinical isolates. *AIDS*, **21**:F17-24

2007. Rolland, M., **M. A. Jensen**, D. C. Nickle, J. Yan, G. H. Learn, L. Heath, D. Weiner, J. I. Mullins. Reconstruction and function of Ancestral Center-Of-Tree (COT) HIV-I Proteins. *Journal of Virology* **81**:8507-8514.

2007. Gottlieb, G. S., D. C. Nickle, **M. A. Jensen**, K. G. Wong, R. A. Kaslow, J. C. Shepherd, J. B. Margolick, J. I. Mullins. HIV type 1 superinfection with a dual-tropic virus and rapid progression to AIDS: a case report. *Clinical Infectious Diseases* **45**:501-509.

2007. Nickle, D. C., M. Rolland, **M. A. Jensen**, S. L. Kosokovsy-Pond, W. Deng, M. Seligman, D. Heckerman, J. I. Mullins, N. Jojic. Coping with viral diversity in HIV vaccine design. *PLoS Computational Biology* **3**:e75.

2007. Nickle, D.C., L. Heath, **M. A. Jensen**, P. B. Gilbert, J. I. Mullins, S. L. Kosakovsky-Pond. HIV-Specific Probabilistic Models of Protein Evolution. *PLoS ONE* **2**:e503.

2007. Ross H.A., D. C. Nickle, Y. Liu, L. Heath, **M. A. Jensen**, A. G. Rodrigo, J. I. Mullins. Sources of variation in ancestral sequence reconstruction for HIV-1 envelope genes. *Evolutionary Bioinformatics Online* **2**:53-76.

2006. **Jensen, M. A.,** S. M. Faruque, J. J. Mekalanos, and B. R. Levin. The role of bacteriophage in the control of cholera epidemics. *PNAS* **103**:171-192.

2006. **Jensen, M. A.**, M. Coetzer, A. B. van 't Wout, L. Morris, and J. I. Mullins. A reliable phenotype predictor for HIV-1 subtype C based on envelope V3 sequences. *Journal of Virology* **80**:4698-4704*.*

2006. Mullins, J. I. and **M. A. Jensen**. Evolutionary dynamics of HIV-1 and the control of AIDS. *Current Topics in Microbiology and Immunology* **299**:171-192*.*

2005. Troyer, R.M., K.R. Collins, A. Abraha, E. Fraundorf, D.M. Moore, R.W. Krizan, Z. Toossi, R.L. Colebunders, **M.A. Jensen**, J.I. Mullins, G. Vanham, and E. J. Arts. Changes in human immunodeficiency virus type 1 fitness and genetic diversity during disease progression. *Journal of Virology*, **79**:9006-9018

2004. Gottlieb, G. S., D. C. Nickle, **M. A. Jensen**, K. G. Wong, J. Grobler, F. Li, S.-L. Liu, C. Rademeyer, G. H. Learn, S. S. A. Karim, C. Williamson, L. Corey, J. B. Margolick, and J. I. Mullins. Dual HIV-1 infection associated with rapid disease progression. *The Lancet*, **363**: 619–622

2004. Shriner, D., R. Shankarappa, **M. A. Jensen**, D. C. Nickle, J. E. Mittler, J. B. Margolick, and J. I. Mullins. Influence of random genetic drift on HIV-1 *env* evolution during chronic infection. *Genetics*, **166**: 1155-1164*.*

2004. Liu, Y., D. C. Nickle, D. Shriner, **M. A. Jensen**, G. H. Learn, Jr., J. E. Mittler, and J. I. Mullins. Molecular clock-like evolution of human immunodeficiency virus type 1. *Virology* **329**: 101-108.

2003. **Jensen, M. A.**, F.-S. Li, A. B. van 't Wout, D. C. Nickle, D. Shriner, H.-X. He, S. McLaughlin, R. Shankarappa, J. B. Margolick, and J. I. Mullins. Improved coreceptor usage prediction and genotypic

monitoring of R5-to-X4 transition by motif analysis of HIV-1 env V3 loop sequences. *Journal of Virology*, **77**: 13376-13388.

2003. **Jensen, M. A.** and A. B. van 't Wout. Predicting HIV-1 coreceptor usage using sequence analysis. *AIDS Reviews* **5**:104-112.

2003. Nickle, D. C., **M. A. Jensen**, G. S. Gottlieb, D. Shriner, G. H. Learn, A. G. Rodrigo and J. I. Mullins. Consensus and ancestral state HIV vaccines. *Science* **299**:1515-1517*.*

2003. Z. L. Brumme, W. W. Y. Dong, B. Yip, B. Wynhoven, N. G. Hoffman, R. Swanstrom, **M. A. Jensen**, J. I. Mullins, R. S. Hogg, J. S. G. Montaner and P. R. Harrigan. Clinical and immunological impact of HIV envelope V3 sequence variation after starting initial triple antiretroviral therapy. *AIDS*, **18**:F1-F9.

2003. Shriner, D., D. C. Nickle, **M. A. Jensen**, and J. I. Mullins. The potential impact of recombination on sitewise approaches for detecting positive natural selection. *Genetical Research* **81**:115-121.

2003. Nickle, D. C., **M. A. Jensen**, D. Shriner, S. J. Brodie, L. M. Frenkel, J. E. Mittler, and J. I. Mullins. Evolutionary indicators of HIV-1 reservoirs and compartments. *Journal of Virology* **77**:5540-5546.

2003. Dybul, M., M. Daucher, **M. A. Jensen**, C. W. Hallahan, T.-W. Chun, M. Belson, B. Hidalgo, D. C. Nickle, C. Yoder, J. A. Metcalf, R. T. Davey, L. Ehler, D. Kress-Rock, E. Nies-Kraske, S. Liu, J. I. Mullins and A. S. Fauci. Genetic characterization of rebounding plasma HIV-1 during multiple interruptions of highly active antiretroviral therapy. *Journal of Virology* **77:** 3229-3237.

2002. **Jensen, M. A**., B. Charlesworth, and M. Kreitman. Patterns of genetic variation at a chromosome 4 locus of *Drosophila melanogaster* and *D. simulans. Genetics* **160**:493-507.

2001. **Jensen, M. A.**, H. L. True-Krob, Y. O. Chernoff and S. Lindquist. Molecular population genetics and evolution of a prion-like protein in *Saccharomyces cerevisiae*. *Genetics* **159**:527-535.

Other publications and presentations

Publications and Posters

2008. "Phylogenetic Evidence for Possible Reverse Zoonosis and Species-Specific Strains of Methicillin-Resistant *Staphylococcus aureus* in Domestic Animals." Poster Y-024, American Society of Microbiology General Meeting, Boston, MA 3 June 2008.

2004. "Genotypic potential for syncytium induction characterizes early V3 loop evolution in singly and dually-infected individuals with rapid HIV disease progression." Poster 415 at 11th Conference on Retroviruses and Opportunistic Infections, San Francisco, CA 8-11 February 2004.

2003. "AIDS vaccine must be top priority." Guest editorial in the *Seattle Post-Intelligencer* (circ. 500,000), 2 October 2003.

2003. "A Bioinformatic Predictor of Coreceptor Usage Correlates with Markers of Disease Progression and Supports the Gradual Evolution of X4 Virus via R5X4 Intermediates." Poster 498 at 10th Conference on Retroviruses and Opportunistic Infections, Boston, MA 10-14 February 2003.

2002. "Pattern-Recognition Analysis of V3 Loop Sequence in Known SI and NSI Virus Suggests Single Amino-acid Changes Affect Coreceptor Usage Only in a Complex Genetic Context." Poster at 9th Conference on Retroviruses and Opportunistic Infections, Seattle, WA 24-28 February 2002.

1998. "All about Adam." Feature in *New Scientist* (London), 11 July 1998

1998. "A Beginner's Guide to Finding and Choosing Post-Doc Positions: Part II--The All-Important Funding." Feature in *Science NextWave* (AAAS careers webzine), 20 March 1998.

1998. "A Beginner's Guide to Finding and Choosing Post-Doc Positions." Feature in *Science NextWave*, 13 February 1998

Oral Presentations

2009. "HIV phenotype prediction: coreceptors and computation." Invited talk, Merck Research Laboratories, Molecular Profiling division, West Point, PA. 29 July 2009.

2009. "Coreceptor prediction with integrated data management." Invited talk, Clinical Laboratories, BC Centre for Excellence in HIV/AIDS, Vancouver, BC. 3 March 2009.

2008. "Catching the greased pig: HIV genetic diversity and vaccine antigen design." Invited talk, National Center for Evolutionary Synthesis, Durham, NC. 2 September 2008

2008. "Catching the greased pig: HIV genetic diversity and vaccine antigen design." Invited talk, University of South Carolina at Aiken Spring Seminar Series. 7 March 2008.

2007. "Stalking the killers: molecular tracking of infectious disease." Invited talk, University of Georgia Honors Program Student Committee Seminar. 15 October 2007.

2007. "How to publish a proof in the Journal of Virology and other tales from the interface." Invited talk, Georgia Institute of Technology Mathematics Department, Mathematics in Biology and Ecology Seminar. 24 October 2007.

2007. "An illuminated definition of molecular epidemiology." Invited talk, University of Georgia College of Veterinary Medicine Infectious Disease Seminar, 24 September 2007.

2005. "Bacteriophage control of epidemic cholera." Invited talk, Population Biology, Ecology and Evolution Seminar, Emory University Department of Biology, 21 October 2005.

2004. "Getting started in HIV sequence studies." Workshop at 12th Principles of STD/HIV Research Summer Course, University of Washington Center for AIDS Research, 19-29 July 2004.

2003. "Disease Progression and V3 Genotype in Single and Dual HIV-1 Infection." Invited talk at the British Columbia Centre for Excellence in HIV Research, Vancouver, BC, 17 October 2003.

2003. "Listening to HIV: Biological Sequence Analysis and the Pathogenesis of AIDS." Invited talk at Microsoft Research, Redmond, WA, 12 August 2003.

2003. "A Coalescent Model to Study Reservoir Virus Evolution." Oral presentation at 10th International Discussion Meeting on HIV Dynamics and Evolution, Lake Arrowhead, CA 13-16 April 2003.

2002. Invited speaker, 9th International Discussion Meeting on HIV Dynamics and Evolution, Lake Arrowhead, CA 17-20 March 2002.

1999. "Molecular Evolution of a Yeast Prion." Oral presentation at SSE/ASN/SSB annual meeting "Evolution '99", Madison, WI 22-27 June1999.

1999. "Background Selection Predominates on the Fourth Chromosome of *Drosophila melanogaster*." Natural History Seminar, Department of Ecology & Evolution, University of Chicago.

Grants

(These include only those grants for which I was the principal investigator/applicant. A description of other grants to which I made significant contributions can be provided on request.)

University of Georgia Research Foundation Faculty Development Grant, "Strain-specific serum antibody detection of West Nile virus infection", $5,399, 2008.

University of Washington Center for AIDS Research STD/AIDS Training Grant, post-doctoral salary support, 2002-2003. *(competitive)*

Travel grant, 11th Conference on Retroviruses and Opportunistic Infections, San Francisco, CA. 2003. *(competitive)*

NIH Genomics Training Grant, post-doctoral salary support, 2000-2002. *(competitive)*

NIH Genetics and Regulation Training Grant, graduate support, 1994-1997

NSF Doctoral Dissertation Improvement Grant, #DEB-9701114, "Dissertation research: Using Patterns of Nucleotide Diversity to Distinguish Between Modes of Selection in Very Low Recombining Regions of the Drosophila Genome," $11,965, 1997-1999

Hinds Fund, University of Chicago, $1000, 1996 *(competitive)*

Sigma Xi, Grant in Aid of Research, $700, 1996 *(competitive)*

Teaching

Courses:

2009. Course: Bioinformatics Programming and Analysis with BioPerl. SRA University (continuing education division of SRA International). October - December 2009.

2007 – 2008. Course: Molecular Epidemiology (EPID 8200). Department of Epidemiology & Biostatistics, College of Public Health, University of Georgia.

2007. Course: Introduction to Genetics (GENE 3200). Department of Genetics, Franklin College of Arts and Sciences, University of Georgia.

Seminar course:
2007. Course: Senior Seminar, Department of Genetics, Franklin College of Arts and Sciences, University of Georgia. Topic: Topics in Antimicrobial Resistance

Guest lectures and workshops:
2008. Guest lecturer, College of Public Health, University of Georgia. Special Topics: Cancer Epidemiology (EPID 8900). Topic: Genetic Epidemiology of Cancer. Instructor: Claire Robb.
2008. Guest lecturer, College of Public Health, University of Georgia. Introduction to Public Health (PBHL 3100). Topic: Epidemiology. Instructor: Heather Edelblute.
2007. Guest lecturer, College of Public Health, University of Georgia. Introduction to Public Health (PBHL 3100). Topic: Epidemiology. Instructor: Ashley Wells.
2006. Guest lecturer, Rollins School of Public Health. Global Issues in Antimicrobial Resistance. Topic: Population biology of antibiotic resistance. Instructor: Keith Klugman.
2005. Guest lecturer, Emory University. Undergraduate Introductory Genetics. Topic: Genomics. Instructor: Bruce Levin.
2004. Guest lecturer, Emory University. Graduate Evolution. Topic: Quasispecies. Instructor: Bruce Levin.
2004. "Getting started in HIV sequence studies." Workshop at 12th Principles of STD/HIV Research Summer Course, University of Washington Center for AIDS Research, 19-29 July 2004. Contact: Jeanne Marrazzo.

Teaching assistantships:
1998. Teaching Assistant, University of Chicago. Graduate Introductory Genetics. *Responsibilities*: led discussion, wrote and graded homework and exams, gave occasional lectures. Instructor: Daphne Preuss
1997. Teaching Assistant, University of Chicago. Graduate Population Genetics. *Responsibilities*: led discussion, graded homework and exams, gave occasional lectures. Instructor: Brian Charlesworth Teaching assistant, Seminar in Evolution of Sex and Recombination. *Responsibilities*: led discussions, performed clerical duties. Instructor: Brian Charlesworth
1996. Teaching Assistant, University of Chicago. Introductory Evolution. *Responsibilities*: taught lab section, graded labs and exams. Instructor: Brian Charlesworth

Other Work Experience

Technical Writer & Programmer, Energy Conversions, Inc, Tacoma, WA, (1991-1994)
  Accomplishments: Published technical and trade articles; wrote and managed production of newsletters, advertising, and technical documents; wrote successful US Department of Energy grant for $100K through NIST Energy-related Inventions Program; developed automatic data logging device for natural-gas-conversion-equipped diesel locomotive; contributed programming to control software of diesel-natural gas conversion equipment.
Scientific Programming Consultant, Transgenomic, Inc., San Jose, CA (1998-1999)
  Accomplishments: Coded DNA fragment melting prediction algorithm based on recursion equations in scientific literature; improved existing recursion equations and coded faster melting algorithm based on these improvements.