

Karin S. Dorman

Department of Statistics

or Department of Genetics, Development & Cell Biology

Iowa State University

Ames, IA 50011

Tel: 515-294-1457 (or 6078)

Fax: 515-294-4040

Email: kdorman@iastate.edu

Education

- 2001 Ph.D., UCLA, Los Angeles, CA, Biomathematics
- 1999 Ph.D. (Qualifying Year), 1999, UCLA, Los Angeles, CA, Biomathematics
- 1994 B.S., Indiana University, Bloomington, IN, Biology with honors
- 1994 B.S., Indiana University, Bloomington, IN, Mathematics with honors

Employment

- 2007–today Associate Professor, Departments of Statistics and Genetics, Development & Cell Biology, Iowa State University
- 2001–2007 Assistant Professor, Departments of Statistics and Genetics, Development & Cell Biology, Iowa State University
- 2001 Instructor, Departments of Statistics and Zoology/Genetics, Iowa State University

Teaching

- 7 classes taught; 1 grant-supported project (times, last)
- (2, Sp11) BCB/STAT 568 Bioinformatics II
- (1, Sp11) STAT 580 Statistical Computing I
- (03 – 10) NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.
- (3, F10) STAT 430 Empirical Methods for Computer Science Research
- (1, Sp09) STAT 341 Introduction to Theory and Probability of Statistics I
- (4, F08) STAT/GDCB 536 Genetic Statistics
- (2, Sp07) STAT/GDCB 537 Statistics for Molecular Genetics
- (2, F05) STAT 432 Applied Probability Models

Students

- 5 Ph.D. (2 current); 3 co-major Ph.D. (2 current); 11 M.S.; 1 postdoc (current); 23 research rotations; 1 Preparing Future Faculty advisee; 16 summer interns; 6 undergraduate researchers; 7 academic advisees
- Ph.D. Derek Blythe (Statistics, current), Wei-Chen Chen (Statistics, current) Misha Rajaram (BCB, 2010), Garrett Dancik (BCB, 2008), Fang Fang (BCB, 2006)
- Co-major Arun Sethuraman (BCB, current), Walker Pett (BCB, current) Alice Wang (Statistics, 2011), Yong Huang (BCB, 2010)
- M.S. Xiujuan Wang (Statistics, 2010), Yong Huang (Statistics, 2010), Derek Blythe (Statistics, 2009), Misha Rajaram (Statistics, 2009), Zach Fredericksen (Statistics, 2006), Xiang Gao (Statistics, 2006), Garrett Dancik (Statistics, 2006),

Man-Yu Yum (Statistics, 2005), Can Guo (Statistics, 2004), LaRon Hughes (BCB, 2004), Hua Zhou (BCB, 2003)

Rotations Ali Berens (BCB, 2011), Priyanka Surana (BCB, 2011), Xin Yin (BCB, 2010), Wei Zhang (IG, 2010), Rasna Walia (BCB, 2009), Chijioke Ummunakwe (BCB, 2009), Susan Vander Plas (BCB, 2009), Arun Sethuraman (BCB, 2008), Chaoliang Yang (BCB, 2008), Anu Jayaraman (BCB, 2006), Nick Larson (Statistics, 2006), Misha Rajaram (BCB, 2005), Rajakuma Sankula (BCB, 2004), Jennifer Quammen (MGET, 2004), Jing Ding (BCB, 2004), Wei Qiao Larson (Statistics, 2003), Garrett Dancik (BCB, 2003), Iris Fung (Statistics, 2003), LaRon Hughes (BCB, 2003), Ying Zheng (BCB, 2003), Fang Fang (BCB, 2002), Tyra Dunn (BCB, 2002), Hua Zhou (BCB, 2002)

Interns Benjamin Mulaosmanovic (BBSI, 2009), John Aidoo (BBSI, 2009), Emily Hartley (BBSI, 2009), Ashley Beck (BBSI, 2009), Chris Morgan (BBSI, 2008), Stephanie Wilkerson (AGEP, 2008), Annie Lee (AGEP, 2007), Ralph Culver (AGEP, 2007), Joshua Wynn (BBSI, 2007), Sarah Spencer (BBSI, 2007), Katherine James (VIGRE, 2004), Lauren Lippincott (BBSI, 2004), Nathan Gotman (BBSI, 2003), Michael Rischmiller (BBSI, 2003), Andrew Halvorsen (VIGRE, 2003), Lam Ho (PWSE, 2002)

Research Benjamin Mulasmanovic (Honors Capstone Project, 2011), Tyler O'Connor (First-Year Honors Mentor Program, 2011), Keely Burke (First-Year Honors Mentor Program, 2010), Benjamin Mulaosmanovic (First-Year Honors Mentor Program, 2009), Michelle Wallace (First-Year Honors Mentor Program, 2009), Denise Mooney (Biol490, 2004)

Advisees Jacqueline Richter (BCBio, current), Shalyn Guthery (BCBio, current), Reka Kelemen (BCBio, current), Nick Booher (BCBio, current), Landon Ludwig (Biology, current), Keely Burke (Biology, current) Juanita Bruce (Biology, 2009)

Grants 2 current grants (\$1,427,625); 2 pending grants (\$4,402,466); 12 expired grants (\$2,507,782); 3 declined grants (\$2,763,446); 5 federal grants (\$3,755,053); 1 state grant (\$29,973); 8 university grants (\$150,381)

Current:

2008-2013 NIH CA128568 (**PI:** S. Carpenter) Strategies of Lentivirus Persistence, \$1,397,652
 2010-2011 Clarke University (**PI:** K. S. Dorman) Statistical Analysis of HIV Timecourse Data, \$29,973

Pending:

2011-2016 NSF (**PI:** V. Brendel) IPGA: Characterization, Modeling, Prediction, and Visualization of the Plant Transcriptome, \$3,620,479
 2011-2014 NSF (**PI:** K. S. Dorman) ATD: Models for (Meta)Genome Identification from Next Generation Sequence Data with Errors, \$781,987

Expired:

- 2007-2010 NIH-NSF ECC-0608769 (**PI:** Jernigan) BBSI Computational and Systems Biology Summer Institute at Iowa State University, \$449,999
- 2004-2007 NIH-NIGMS GM068955 (**PI:** K. S. Dorman) Statistical, Computational and Genetic Analysis of HIV Recombination, \$972,702
- 2003-2007 NIH-NSF ECC-00234102 (**PI:** V. Brendel) BBSI Summer Institute in Bioinformatics and Computational Biology, \$645,000
- 2002-2004 NIH CA97936 (**PI:** S. Carpenter) Multilocus Selection of Lentivirus Variants, \$289,700
- 2008-2009 CIAG Research Support Grant (**PI:** K. S. Dorman and R. Maitra) Phyloclustering – Novel Methods to Identify Genetic Population Structure in Fast-Evolving Pathogens, \$24,451
- 2007-2009 CIAG Research Support Grant (**PI:** K. S. Dorman) Agent Based Model of Treg Function in Leishmania Disease, \$24,530
- 2004-2007 CIAG Research Support Grant (**PI:** K. S. Dorman) Building a Comprehensive Model of Pathogen-Host Interactions During Persistent Infections, \$44,000
- 2006-2006 Provost’s Office (**PI:** Su) Special Interdisciplinary Seminar on Mathematical Biology, \$8,000
- 2005-2006 Women’s Enrichment Fund (**PI:** L. Hogben) Women in Mathematical Sciences Distinguished Lecture Series, \$2,000
- 2002-2003 Healthy Livestock Initiative Competitive Grants Program (**PI:** S. Carpenter) Genetic and Computational Analysis of Virus Evolution, \$10,000
- 2002-2002 Faculty Development Grant (**PI:** K. S. Dorman) , \$17,400
- 2001-2002 Healthy Livestock Initiative Competitive Grants Program (**PI:** S. Carpenter) Genetic and Computational Analysis of Virus Evolution, \$20,000

Refereed Publications

*graduate; †undergraduate

- [33] X. Yang*, S. Aluru, **K. S. Dorman**. (2011) “Repeat-Aware Modeling and Detection of Short Read Errors.” *BMC Bioinformatics*. **12**(suppl 1):S52.
- [32] S. Carpenter, W. Chen*, **K. S. Dorman**. (2011) “Rev variation during persistent lentivirus infection.” *Viruses*. **3**:1-11.
- [31] X. Yang*, **K. S. Dorman**, S. Aluru. (2010) “Reptile: Representative Tiling for Short Read Error Correction.” *Bioinformatics*. **26**:2526-2533.
- [30] M. Staley, **K. S. Dorman**, I. F. Salas, J. A. Farfan-Ale, M. A. Loroño-Pino, J. E. Garcia-Rejon, L. Ibarra-Juarez, B. J. Blitvich. (2010) “Universal primers for the amplification and sequence analysis of actin-1 from diverse mosquito species.” *J. Am. Mosq. Control Assoc.* **26**:214-218.

- [29] R. Saiyasombat, **K. S. Dorman**, J. E. Garcia-Rejon, M. A. Loroño-Pino, J. A. Farfan-Ale, B. J. Blitvich. (2010) “Isolation and sequence analysis of *Culex flavivirus* from *Culex interrogator* and *Culex quinquefasciatus* in the Yucatan Peninsula of Mexico.” *Archives of Virology*. **155**:983-986.
- [28] G. M. Dancik*, D. E. Jones, **K. S. Dorman**. (2010) “Parameter estimation and sensitivity analysis in an agent-based model of *Leishmania major* infection.” *Journal of Theoretical Biology*. **262**:398-412.
- [27] J. A. Farfan-Ale, M. A. Loroño-Pino, J. E. Garcia-Rejon, V. Soto, M. Lin, M. Staley, **K. S. Dorman**, L. C. Bartholomay, E. Hovav, B. J. Blitvich. (2010) “Detection of flaviviruses and orthobunyaviruses in mosquitoes in the Yucatan Peninsula of Mexico in 2008.” *Vector-Borne and Zoonotic Diseases*. **10**:777-783.
- [26] E. W. Bloomquist, **K. S. Dorman**, M. A. Suchard. (2009) “StepBrothers: inferring partially shared ancestries among recombinant viral sequences.” *Biostatistics*. **10**(1):106–120.
- [25] J. A. Farfan-Ale, M. A. Loroño-Pino, J. E. Garcia-Rejon, E. Hovav, A. M. Powers, M. Lin, **K. S. Dorman**, K. B. Platt, L. C. Bartholomay, V. Soto, B. J. Beaty, R. S. Lanciotti, B. J. Blitvich. (2009) “Detection of RNA from a novel West Nile-like virus and high prevalence of an insect-specific flavivirus in mosquitoes in the Yucatan Peninsula of Mexico.” *Am J Trop Med Hyg*. **80**(1):85–95.
- [24] B. J. Blitvich, M. Lin, **K. S. Dorman**, V. Soto, E. Hovav, B. J. Tucker, M. Staley, K. B. Platt, L. C. Bartholomay. (2009) “Genomic sequence and phylogenetic analysis of *Culex flavivirus*, an insect-specific flavivirus, isolated from *Culex pipiens* (Diptera: Culicidae) in Iowa.” *J Med Entomol*. **46**(4):934–941.
- [23] V. Soto, **K. S. Dorman**, W. A. Miller, J. A. Farfan-Ale, M. A. Loroño-Pino, J. E. Garcia-Rejon, B. J. Blitvich. (2009) “Complete nucleotide sequences of the small and medium RNA genome segments of Kairi virus (family Bunyaviridae).” *Arch Virol*. **154**(9):1555–1558.
- [22] B. Su, W. Zhou, D. E. Jones, **K. S. Dorman**. (2008) “Mathematical modelling of immune response in tissues.” *Computational and Mathematical Methods in Medicine*. **10**(1):9-38.
- [21] G. M. Dancik*, **K. S. Dorman**. (2008) “mleqp: statistical analysis for computer models of biological systems using R.” *Bioinformatics*. **24**(17):1966–1967.
- [20] W. O. Sparks*, **K. S. Dorman**, S. Liu*, S. Carpenter. (2008) “Naturally arising point mutations in non-essential domains of equine infectious anemia virus Rev alter Rev-dependent nuclear-export activity.” *J Gen Virol*. **89**(Pt 4):1043–1048.

- [19] M. E. Sparks*, V. Brendel, K. S. Dorman. (2007) “Markov model variants for appraisal of coding potential in plant DNA.” *Lecture Notes in Bioinformatics*. **4463**:394-405.
- [18] V. N. Minin, **K. S. Dorman**, F. Fang*, M. A. Suchard. (2007) “Spatially smoothing change-point processes for phylogenetic mapping of recombination hot-spots.” *Genetics*. **175**:1–13.
- [17] F. Fang*, J. Ding, V. N. Minin, M. A. Suchard, **K. S. Dorman**. (2007) “cBrother: relaxing parental tree assumptions for Bayesian recombination detection.” *Bioinformatics*. **23**(4):507–508.
- [16] K. A. Ahmed, V. K. Saxena, M. Saxena, A. Ara, A. B. Pramod, M. L. Rajaram*, **K. S. Dorman**, S. Majumdar, T. J. Rasool. (2007) “Molecular cloning and sequencing of MHC class II beta 1 domain of turkey reveals high sequence identity with chicken.” *Intl. J. Immunogenet.*.
- [15] **K. S. Dorman**. (2007) “Identifying dramatic selection shifts in phylogenetic trees.” *BMC Evol Biol*. **7 Suppl 1**:S10.
- [14] V. N. Minin, **K. S. Dorman**, F. Fang*, M. A. Suchard. (2005) “Dual Multiple Change-Point Model Leads to More Accurate Recombination Detection.” *Bioinformatics*. **21**(13):3034-3042.
- [13] J. D. Wolt, Y. Y. Shyy, P. J. Christensen, **K. S. Dorman**, M. Misra. (2004) “Quantitative exposure assessment for confinement of maize biogenic systems.” *Environ Biosafety Res*. **3**(4):183–196.
- [12] **K. S. Dorman**, J. S. Sinsheimer, K. Lange. (2004) “In the Garden of Branching Processes.” *SIAM Review*. **46**(2):202-229.
- [11] J. S. Sinsheimer, M. A. Suchard, **K. S. Dorman**, F. Fang*, R. E. Weiss. (2003) “Are You my Mother? Bayesian Phylogenetic Inference of Recombination among Putative Parental Strains.” *Applied Bioinformatics*. **2**(3):131–144.
- [10] M. A. Suchard, R. E. Weiss, J. S. Sinsheimer, **K. S. Dorman**, M. Patel, E. R. B. McCabe. (2003) “Evolutionary Similarity Among Genes.” *J Am Stat Assoc*. **98**(463):653-662.
- [9] M. A. Suchard, R. E. Weiss, **K. S. Dorman**, J. S. Sinsheimer. (2003) “Inferring Spatial Phylogenetic Variation Along Nucleotide Sequences: A Multiple Change-point Model.” *J. Am. Stat. Assoc.*. **98**(462):427-437.
- [8] P. Baccam, R. J. Thompson, Y. Li, W. O. Sparks*, M. Belshan, **K. S. Dorman**, Y. Wannemuehler, J. L. Oaks, J. L. Cornette, S. Carpenter. (2003) “Subpopulations of equine infectious anemia virus Rev coexist in vivo and differ in phenotype.” *J Virol*. **77**(22):12122–12131.

- [7] M. A. Suchard, R. E. Weiss, **K. S. Dorman**, J. S. Sinsheimer. (2002) “Oh Brother, Where Art Thou? A Bayes Factor Test for Recombination with Uncertain Heritage.” *Syst. Biol.* **51**(5):715-728.
- [6] **K. S. Dorman**, A. H. Kaplan, J. S. Sinsheimer. (2002) “Bootstrap Confidence Levels for HIV-1 Recombination.” *J Mol Evol.* **54**(2):200-209.
- [5] M. Patel, **K. S. Dorman**, Y. Zhang, B. Huang, A. P. Arnold, J. S. Sinsheimer, E. Vilain, E. R. B. McCabe. (2001) “Primate DAX1, SRY, and SOX9: Evolutionary Stratification of Sex-Determination Pathway.” *Am J Hum Genet.* **68**:
- [4] **K. S. Dorman**, A. H. Kaplan, K. Lange, J. S. Sinsheimer. (2000) “Mutation Takes No Vacation: Can Structured Treatment Interruptions Increase the Risk of Drug-Resistant HIV-1?.” *Journal of Acquired Immune Deficiency Syndromes.* **25**(5):398-402.
- [3] C. Perez, P. Vial, **K. S. Dorman**, G. Wang, K. Abarca, J. S. Sinsheimer, A. H. Kaplan. (1999) “[Molecular epidemiology of the human immunodeficiency virus type 1 in Santiago, Chile].” *Rev Med Chil.* **127**(11):1294-304.
- [2] W. J. Lech, G. Wang, Y. L. Yang, Y. Chee, **K. Dorman**, D. McCrae, L. C. Lazzeroni, J. W. Erickson, J. S. Sinsheimer, A. H. Kaplan. (1996) “In vivo sequence diversity of the protease of human immunodeficiency virus type 1: presence of protease inhibitor-resistant variants in untreated subjects.” *J Virol.* **70**(3):2038-43.
- [1] Y. L. Yang, G. Wang, **K. Dorman**, A. H. Kaplan. (1996) “Long polymerase chain reaction amplification of heterogeneous HIV type 1 templates produces recombination at a relatively high frequency.” *AIDS Res Hum Retroviruses.* **12**(4):303–306.

Book Chapters

- [2] **K. S. Dorman**. “Trees, Evolutionary” in *The Wiley Encyclopedia of Biomedical Engineering*. Hoboken, NJ, 2006.
- [1] H. Zhou*, **K. S. Dorman**. “A branching process model of drug resistant HIV” in *Deterministic and Stochastic Models for AIDS Epidemics and HIV Infections with Interventions*. London, 2005.

Proceedings

- [6] G. M. Dancik*, **K. S. Dorman**, D. E. Jones. (2006) “An agent-based model for Leishmania infection” in *Proceedings of the Sixth International Conference on Complex Systems*. Boston, MA.

- [5] F. Fang*, M. A. Suchard, V. N. Minin, **K. S. Dorman**. (2005) “A Bayesian phylogenetic model for testing recombination event” in *Proceedings of the Joint Statistical Meetings*. Minneapolis, MN.
- [4] **K. S. Dorman**, X. Gu. (2005) “Bayesian inference for functional divergence” in *Proceedings of the Joint Statistical Meetings*. Minneapolis, MN.
- [3] V. N. Minin, **K. S. Dorman**, M. A. Suchard. (2004) “Bayesian recombination identification: new models for incorporating prior information” in *Proceedings of the Joint Statistical Meetings*. Toronto, Canada.
- [2] M. A. Suchard, R. E. Weiss, **K. S. Dorman**, M. Patel, E. R. B. McCabe, J. S. Sinsheimer. (2000) “Evolutionary similarity among genes when data are sparse” in *Proceedings of the Joint Statistical Meetings*. Indianapolis, IN.
- [1] **K. S. Dorman**, A. H. Kaplan, J. S. Sinsheimer. (1999) “Estimating confidence in the inference of HIV recombination” in *Proceedings of the Joint Statistical Meetings*. Baltimore, MD.

Invited Presentations

- [6] **K. S. Dorman**. (2011) “TBD” in *Math Bio & Eco Seminar*. Atlanta, GA.
- [5] X. Yang*, S. Aluru, **K. S. Dorman**. (2010) “Improved Error Modeling and Detection for High-Throughput Short Reads” in *Conference on Resampling Methods and High Dimensional Data*. College Station, TX.
- [4] W. Chen*, **K. S. Dorman**, R. Maitra. (2010) “Phyloclustering: New Phylogenetic Methods for Inferring Population Structure” in *International Conference on Statistics, Probability, Operators Research, Computer Science and Allied Areas*. Visakhapatnam, India.
- [3] W. Chen*, **K. S. Dorman**. (2009) “Phyloclustering: new phylogenetic methods for fast-evolving quasispecies” in *Joint Statistical Meetings*. Washington D.C..
- [2] W. Chen*, **K. S. Dorman**, R. Maitra. (2009) “Phyloclustering: model-based inference of population structure from genetic sequence data” in *ISU 75th Statistical Laboratory Conference*. Ames, IA.
- [1] S. Carpenter, C. Casovant, **K. S. Dorman**, V. Minin, M. L. Rajaram*, M. A. Suchard. (2007) “Survey of recombination in the HIV genome to identify hotspots and associations with sequence patterns” in *Joint Statistical Meetings, Computationally Intensive Methods in AIDS Research*. Salt Lake City, UT.

Conference Presentations

- [18] W. -C. Chen*, **K. S. Dorman**, R. Maitra. (2010) “Evolutionary clustering of SNP haplotypes for Genome-Wide Association Studies” in *Joint Statistical Meetings*. Vancouver, Canada.
- [17] W. Chen*, **K. S. Dorman**. (2008) “Disentangling the selection pressures acting on overlapping reading frames” in *Fall Conference on Statistics in Biology*. Ames, IA.
- [16] M. L. Rajaram*, V. N. Minin, M. A. Suchard, **K. S. Dorman**. (2007) “Hot and Cold: Spatial Fluctuation in HIV-1 Recombination Rates” in *IEEE 7th Conference on Bioinformatics and Bioengineering, Special Session on Evolutionary Systems Biology*. Boston, MA.
- [15] M. L. Rajaram*, V. N. Minin, M. A. Suchard, **K. S. Dorman**. (2007) “Late Breaking Talk: Spatial Fluctuation of Recombination Rates in the HIV Genome: A Computational Model Identifies Hotspots” in *RECOMB Comparative Genomics Satellite Workshop*. San Diego, CA.
- [14] S. Carpenter, C. Casovant, **K. S. Dorman**, V. N. Minin, M. L. Rajaram*, M. A. Suchard. (2007) “Survey of Recombination in the HIV Genome to Identify Hotspots and Associations with Sequence Patterns” in *Joint Statistical Meetings*. Salt Lake City, UT.
- [13] **K. S. Dorman**, M. L. Rajaram*, V. N. Minin, S. Carpenter, M. A. Suchard. (2007) “A computational model discovers multiple recombination hotspots in natural HIV-1 sequences” in *Retrovirus Meeting*. Cold Spring Harbor, NY.
- [12] **K. S. Dorman**, F. Fang*, V. N. Minin. (2006) “Statistical methods for detecting repeat events and hotspots in virus recombination: Applications to hepatitis B virus” in *Virus Evolution Workshop*. Ardmore, OK.
- [11] F. Fang*, V. N. Minin, M. A. Suchard, **K. S. Dorman**. (2006) “Deciphering a web of historical recombination events” in *HIV Dynamics and Evolution 13th International Workshop*. Woods Hole, MA.
- [10] **K. S. Dorman**. (2006) “Identifying divergence points indicative of functional adaptation in phylogenies” in *International Conference in Phylogenomics*. Sainte Adèle, Canada.
- [9] **K. S. Dorman**, J. S. Sinsheimer, K. Lange. (2005) “Numerical methods for branching process models” in *The European Conference on Mathematical and Theoretical Biology*. Dresden, Germany.
- [8] **K. S. Dorman**, X. Gu. (2005) “Bayesian inference for functional divergence” in *Joint Statistical Meetings*. Minneapolis, MN.

- [7] W. O. Sparks*, **K. S. Dorman**, S. Carpenter. (2005) “Selection on Rev during persistent EIAV infection of horses” in *HIV Dynamics and Evolution 12th International Workshop*. Cleveland, OH.
- [6] **K. S. Dorman**. (2004) “Numerical methods for branching processes with applications to HIV drug resistance” in *Society for Mathematical Biology*. Ann Arbor, MI.
- [5] **K. S. Dorman**. (2004) “Population genetics of EIAV” in *4th Biannual All Iowa Virology Symposium*. Ames, IA.
- [4] M. Macêdo, S. Carpenter, J. A. Richt, J. L. Oaks, R. H. Mealey, T. C. McGuire, **K. S. Dorman**. (2004) “Local dynamics of virus-host interactions as a marker of disease progression: analysis of clinical data in EIAV infected horses” in *VII International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases*. Valencia, Spain.
- [3] F. Fang*, M. Rischmiller, M. A. Suchard, **K. S. Dorman**. (2004) “Recombination in Hepatitis B Virus: a survey with evidence for the presence of hotspots” in *VII International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases*. Valencia, Spain.
- [2] **K. S. Dorman**. (2003) “Predicting HIV drug resistance with a Branching Process Model” in *HIV Dynamics and Evolution 10th International Workshop*. Lake Arrowhead, CA.
- [1] **K. S. Dorman**. (2002) “Modeling pathways to drug resistance in HIV-1” in *2nd Biannual All Iowa Virology Symposium*. Iowa City, IA.

Honors & Awards

2007	LAS Award for Early Achievement in Research, ISU, Ames, IA
2000	Dissertation Year Fellowship, UCLA, Los Angeles, CA
1994	NSF Graduate Fellowship, UCLA, Los Angeles, CA

Service

	National/International: 4 grant review panels; 3 ad hoc grant reviews; 4 conference review cmtes.; 2 program cmtes.; 22 journal reviews.
2010	Review panel , NIH, NIAID Protection of Human Health by Immunology and Vaccines (U01, U19).
2009	Review panel , NSF, Faculty Early Career Development.
2006	Review panel , NSF/NIH, Joint DMS/NIGMS Initiative to Support Research in the Area of Mathematical Biology.
2008	Ad hoc reviewer , South Caroline EPSCoR/IDeA.
2008	Ad hoc reviewer , US Civilian Research & Development Foundation.
2008	Ad hoc reviewer , NIH, AIDS Immunology and Pathogenesis study section.

- 2011 **Program cmte.**, Statistical, Computational and Visualization Methods in Medical Informatics, Dubuque, IA.
- 2009 **Program cmte.**, Systems Biology: Integrative, Comparative & Multiscale Modeling, Ames, IA.
- 2009 **Review cmte.**, IEEE Symposium Computational Intelligence, Bioinformatics, & Computational Biology Conference, Nashville, TN (3 reviews)
- 2007 **Review cmte.**, IEEE Bioinformatics & Bioengineering Conference, Boston, MA (3 reviews)
- 2007 **Review cmte.**, IEEE Symposium Computational Intelligence, Bioinformatics, & Computational Biology Conference, Honolulu, HI (2 reviews)
- 2006 **Review cmte.**, IEEE Symposium Computational Intelligence, Bioinformatics, & Computational Biology Conference, Toronto, Ontario, Canada (2 reviews)
- 2011 **Session chair**, Joint Statistical Meetings, Miami, FL.
- 2009 **Session chair**, Stat Lab 75th Anniversary, Ames, IA.
- Ad hoc journal reviewer**, 2 in 2002; 1 in 2003; 3 in 2004; 1 in 2005; 4 in 2006; 2 in 2007; 4 in 2008; 5 in 2009 for *Biotechniques*, *BMC Bioinformatics*, *BMC Bioinformatics*, *Cancer Research*, *Science*, *Bioinformatics*, *BMC Bioinformatics*, *BMC Bioinformatics*, *BMC Evolutionary Biology*, *Mathematical Biosciences*, *Systematic Biology*, *Biotechnology Progress*, *Mathematical Biosciences*, *Mathematical Biosciences*, *Theoretical Population Biology*, *Genetics*, *Biosystems*, *Mathematical Biosciences*, *Molecular Phylogenetics and Evolution*, *Soil Science Society of America Journal*, *Journal Agricultural, Biological, and Environmental Statistics*, *PNAS*.
- State:** chaired 1 conference session
- 2009 **Review panel**, UI/ISU, Alliance for Graduate Education & the Professoriate REU Mini-Grant Competition.
- 2004 **Session chair**, 4th Biannual All Iowa Virology Symposium, Ames, IA.
- University:** chaired 1 conference session; organized 2 seminar series; volunteered for 6 events
- 2010 **Session chair**, Undergraduate Research Symposium, Ames, IA.
- 2005 – 2007 **Seminar series**, Mathematical Biology Special Seminar Series, Ames, IA.
- 2005 – 2007 **Seminar series**, Women in Mathematical Sciences, Distinguished Lecture Series, Ames, IA.
- 2011 **Volunteer**, Taking the Road Less Traveled Conference, Two presentations to middle school girls.
- 2011 **Volunteer**, VEISHA, LAS Green Team booth.
- 2010 **Volunteer**, Taking the Road Less Traveled Conference, Two presentations to middle school girls.
- 2010 **Volunteer**, VEISHA, LAS Green Team booth.

- 2009 **Volunteer**, Mathematics on the Road Experience, Valley High School visit.
 2008 **Volunteer**, AGEP Summer Internship Program, Deliver seminar “The Role of Statistics in Research”.

Consulting projects: 15 consulting projects

- 2009 – S. Carpenter, Longitudinal data analysis in EIAV infected horses.
 2010 K. Sandeep, Modeling of software reliability.
 2010 C. Strasburg, Detection of masqueraders from netflow data.
 2010 X. Wang, Automatic detection of appendix in endoscopy.
 2009 – 2010 X. Yang, Identification and correction of errors in next generation sequencing experiments.
 2008 – 2010 B. Blitvich, Phylogenetic analysis for various virus samples.
 2005 – 2009 S. Carpenter, Pullman, WA, Pullman, WA, Longitudinal data analysis in EIAV infected horses.
 2006 – 2008 K.-J. Yoon and S.-H Cha, Detecting and characterizing recombination in PRRS virus.
 2006 – 2007 K. A. Ahmed, Bareilly, India, Bareilly, India, Characterizing recombination at an avian MHC locus.
 2004 – 2005 C. Sabeta, South Africa, South Africa, Population genetics of rabies virus.
 2001 – 2005 S. Carpenter, Longitudinal data analysis in EIAV infected horses.
 2004 G. Marquez, SSCP vs. DNA sequence for assessing genetic diversity in *Musca domestica*.
 2004 J. Wolt, BIGMAP, Developing a model for the risk of spread of foreign genetic material from maize transgenic crops.
 2003 B. Bonning, Analyzing selection pressure in baculovirus sequences.
 2003 Y. Zhang, Transmission of Salmonella in pigs.

Committees: 9 current committees (1 chair; 2 college); 29 total committees (3 chair; 2 college; 1 university)

- 2009 – **Chair**, Sustainability Committee, Statistics Department
 2006 – 2007 **Chair**, Diversity committee, Statistics Department
 2003 **Chair**, Seminar Committee, Statistics Department
 2010 – **Member**, Faculty Development Committee, LAS College
 2010 – **Member**, Computer Advisory Committee, Statistics Department
 2010 – **Member**, Honors and Awards Committee, Statistics Department
 2008 – **Member**, LAS Green Team, LAS College
 2007 – **Member**, BCBio Supervisory Committee, BCB Program
 2006 – **Member**, Curriculum Committee, Statistics Department
 2008 – 2009 **Member**, BCB Ad Hoc Curriculum Committee, BCB Program
 2009 **Member**, Admissions Committee, IG Program
 2009 **Member**, Exam Committee, Statistics Department

2007 – 2008 **Member**, Diversity committee, Statistics Department
2006 – 2008 **Member**, AGEF Faculty Council, University
2006 – 2008 **Member**, Computer Advisory Committee, Statistics Department
2005 – 2008 **Member**, Human Relations & Diversity Committee, GDCB Department
2003 – 2008 **Member**, BCB Curriculum Committee, BCB Program
2006 – 2007 **Member**, BCB Undergraduate Degree Planning Committee, BCB Program
2004 – 2005 **Member**, Admissions Committee, BCB Program
2005 **Member**, Diversity Committee, Statistics Department
2004 **Member**, Admissions Committee, Statistics Department
2004 **Member**, Search Committee, Statistics Department
2004 **Member**, Awards and Recognition Committee, GDCB Department
2001 – 2003 **Member**, Diversity Committee, Zoology & Genetics Department
2002 **Member**, M.S. Exam Committee, Statistics Department
2001 **Member**, Search Committee, Statistics Department
2006 – **Academic Advisor**, Biology Major (average 3 advisees)
2006 – **Academic Advisor**, Bioinformatics and Computational Biology Undergraduate Major (average 3 advisees)
2006 **Academic Advisor**, Bioinformatics and Computational Biology Graduate Major (3 advisees)