

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., University of California, Los Angeles, CA, Biomathematics
1994 B.S., Indiana University, Bloomington, IN, Biology & Mathematics, double major with honors

Employment

2007 – Associate Professor, Statistics and GDCB, Iowa State University
2001 – 2007 Assistant Professor, Statistics and GDCB, Iowa State University

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
1994 Chancellor's Fellowship, UCLA, Los Angeles, CA [declined for NSF Fshp.]

Teaching

Spring 14 BCB/STAT 568 Bioinformatics II
Spring 13 BCB/STAT 568 Bioinformatics II (2/3 responsibility)
Spring 13 BCB 570 Bioinformatics IV (0.10 responsibility)
Spring 13 STAT/GDCB 536 Statistical Genetics
Spring 12 STAT 580 Statistical Computing I
Spring 12 BCB/STAT 568 Bioinformatics II (1/3 responsibility)
Spring 11 STAT 580 Statistical Computing I
Spring 11 BCB/STAT 568 Bioinformatics II (1/3 responsibility)
Summer 10 NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.
Fall 10 STAT 430 Empirical Methods for Computer Science Research
Summer 09 NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.
Spring 09 BCB/STAT 568 Bioinformatics II (1/3 responsibility)
Fall 09 STAT 430 Empirical Methods for Computer Science Research
Spring 09 STAT 341 Introduction to Theory and Probability of Statistics I
Summer 08 NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.
Fall 08 STAT/GDCB 536 Genetic Statistics
Summer 07 NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.
Spring 07 STAT/GDCB 537 Statistics for Molecular Genetics
Fall 07 STAT 430 Empirical Methods for Computer Science Research
Summer 06 NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.
Fall 06 STAT/GDCB 536 Genetic Statistics
Summer 05 NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.

Fall 05	STAT 432 Applied Probability Models
Summer 04	NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.
Fall 04	STAT/GDCB 536 Genetic Statistics
Summer 03	NIH-NSF BBSI Summer Inst. in Bioinformatics and Comput. Biol.
Fall 03	STAT 432 Applied Probability Models
Fall 02	STAT/GDCB 537 Statistics for Molecular Genetics
Fall 01	STAT/GDCB 536 Genetic Statistics

Students

BCB=Bioinformatics & Computational Biology

Ph.D.	Luvenia Hellams (Statistics, 2009 –), Xin Yin (BCB/Statistics, 2010 –), Emily King (Statistics, 2012 –), Derek Blythe (Statistics, 2008 – 2014), Wei-Chen Chen (Statistics, 2007 – 2011), Misha L. Rajaram (BCB, 2005 – 2010), Garrett M. Dancik (BCB, 2003 – 2008), Fang Fang (BCB, 2001 – 2006)
Co-major	Min Wang (Mathematics/Statistics, Ph.D., 2009 –), Zebulun Arendsee (BCB, Ph.D., 2012 –), Walker Pett (BCB, Ph.D., 2010 – 2014), Arun Sethuraman (BCB, Ph.D., 2009 – 2013), Alice Wang (Statistics, M.S., 2011 – 2012), Yong Huang (BCB, Ph.D., 2005 – 2010)
M.S.	Emily King (Statistics, 2012 – 2013), Xiujuan Wang (Statistics, 2009 – 2010), Yong Huang (Statistics, 2008 – 2010), Derek C. Blythe (Statistics, 2007 – 2009), Misha L. Rajaram (Statistics, 2005 – 2009), Zach Fredericksen (Statistics, 2005 – 2006), Xiang Gao (Statistics, 2005 – 2006), Garrett Dancik (Statistics, 2003 – 2006), Man-Yu Yum (Statistics, 2004 – 2005), Can Guo (Statistics, 2003 – 2004), LaRon Hughes (BCB, 2002 – 2004), Hua Zhou (BCB, 2002 – 2003)

Grants

Current:

2013-2015	Georgia Institute of Technology 126140 (PI: P. S. Schnable) AF: Medium: Parallel Algorithms and Software for High-Throughput Sequence Assembly, \$262,856 Subcontract to: NSF 1162472 (PI: S. Aluru) \$1,085,330.
2012-2014	Indiana University 117077 (PI: K. S. Dorman) IPGA: Characterization, Modeling, Prediction, and Visualization of the Plant Transcriptome, \$506,563 Subcontract to: NSF 1221984 (PI: V. Brendel) \$3,620,479.
2011-2014	NSF 1120597 (PI: K. S. Dorman) ATD: Models for (Meta)Genome Identification from Next Generation Sequence Data with Errors, \$660,922.

Pending:

2014-2018	Indiana University (PI: K. S. Dorman) Genome-wide functional and evolutionary characterization of plant gene expression control, \$849,028 Subcontract to: NSF (PI: V. Brendel) \$2,849,608.
-----------	--

Expired:

2012-2013	National Pork Board 119035 (PI: S. Carpenter) Identification of genetic mutations that confer escape from innate or adaptive host immune response during PRRSV infection in vivo, \$74,305.
-----------	---

- 2008-2013 NIH CA128568 (**PI:** S. Carpenter) Strategies of Lentivirus Persistence, \$1,397,652.
- 2006-2010 NIH-NSF ECC-0608769 (**PI:** R. Jernigan) BBSI Bioinformatics and Computational Systems Biology Summer Institute at Iowa State University, \$450,000.
- 2004-2007 NIH-NIGMS GM068955 (**PI:** K. S. Dorman) Statistical, Computational and Genetic Analysis of HIV Recombination, \$972,702.
- 2002-2007 NIH-NSF ECC-00234102 (**PI:** V. Brendel) BBSI Summer Institute in Bioinformatics and Computational Biology, \$645,000.
- 2002-2004 NIH CA97936 (**PI:** S. Carpenter) Quasispecies Evolution During Lentivirus Persistence, \$289,700.
- 2010-2011 Clarke University (**PI:** K. S. Dorman) Statistical Analysis of HIV Timecourse Data, \$29,973.

(Local)

- 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:** B. 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) Computing Resource for Teaching, \$17,400.
- 2001-2002 Healthy Livestock Initiative Competitive Grants Program (**PI:** S. Carpenter) Genetic and Computational Analysis of Virus Evolution, \$20,000.

Service

National/International:

- 2013 **Ad hoc reviewer**, NSF, NSF Plant Genome Research Program.
- 2012 **Ad hoc reviewer**, Kentucky Science & Engineering Foundation, Research & Development Excellence Program.
- 2008 **Ad hoc reviewer**, South Carolina EPSCoR/IDeA.
- 2008 **Ad hoc reviewer**, US Civilian Research & Development Foundation.
- 2008 **Ad hoc reviewer**, NIH, AIDS Immunology and Pathogenesis study section.
- 2012 **Co-organizer**, New Statistical Methods for Next-Generation Sequencing Data Analysis, Ames, IA.
- 2011 **Co-organizer**, Statistical, Computational and Visualization Methods in Medical Informatics, Dubuque, IA.
- 2014 **Program cmte.**, SAMSI - Beyond Bioinformatics, Raleigh, NC.

- 2009 **Program cmte.**, Systems Biology: Integrative, Comparative & Multiscale Modeling, Ames, IA.
- 2011, 4X **Review cmte.**, IEEE Symposium Computational Intelligence in Bioinformatics & Computational Biology Conference (average 2.25 reviews)
- 2007 **Review cmte.**, IEEE 7th Symposium on Bioinformatics & Bioengineering, Boston, MA (3 reviews)
- 2012 **Session chair**, Joint Statistical Meetings, Aug, San Diego, CA.
- 2009 **Session chair**, Stat Lab 75th Anniversary, June, 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; 1 in 2010; 2 in 2011; 1 in 2012; 2 in 2013; 1 in 2014 for *Annals of Applied Statistics*, *BMC Bioinformatics*, *BMC Evolutionary Biology*, *Bioinformatics*, *Biosystems*, *Biotechniques*, *Biotechnology Progress*, *Cancer Research*, *Genetics*, *Journal Agricultural, Biological, and Environmental Statistics*, *Mathematical Biosciences*, *Molecular Phylogenetics and Evolution*, *Neuropsychiatric Genetics*, *PLoS ONE*, *PNAS*, *Science*, *Soil Science Society of America Journal*, *Systematic Biology*, *Theoretical Population Biology*.

State:

- 2004 **Session chair**, 4th Biannual All Iowa Virology Symposium, October, Ames, IA.
- 2014, 4X **Volunteer**, Science Center of Iowa - Girls in STEM, February, EDGE@ISU and BCBLab tables.
- 2009 **Volunteer**, Mathematics on the Road Experience, Valley High School visit.

University:

- 2013 – **Chair and DOGE**, Bioinformatics & Computational Biology Program
- 2011 – 2013 **Associate chair**, Bioinformatics & Computational Biology Program
- 2005 – 2007 **Co-organizer**, Mathematical Biology Special Seminar Series, Ames, IA.
- 2005 – 2007 **Co-organizer**, Women in Mathematical Sciences, Distinguished Lecture Series, Ames, IA.
- 2012 **Review cmte.**, Symposium on Undergraduate Research & Creative Expression, (3 reviews)
- 2010 **Session chair**, Undergraduate Research Symposium, April, Ames, IA.
- 2011 – **Volunteer**, Enhancing Diversity in Graduate Education – EDGE@ISU Cluster, Mentor.
- 2012, 4X **Volunteer**, Taking the Road Less Traveled Conference, April, Two presentations to high school and middle school girls.
- 2011, 2X **Volunteer**, VEISHEA, April, LAS Green Team booth.
- 2009 **Volunteer**, Destination Iowa State, August, Collected give-aways from local businesses, set up display, manned a booth.
- 2008 **Volunteer**, AGEP Summer Internship Program, June, Deliver seminar “The Role of Statistics in Research”.

Consulting projects:

- 2014 – **R. Liu**, Electrical and Computer Engineering, Transcript assembly especially to detect alternative splicing.

- 2014 – **B. J. Blitvich**, Veterinary Microbiology & Preventative Medicine, Phylogenetic analysis of full-length T'Ho virus.
- 2013 – **K. Sandeep**, Computer Science, Modeling of netflow data.
- 2012 – **A. Bennett**, Animal Science, Detecting selection in PRRSV longitudinal sequence data.
- 2009 – **S. Carpenter**, Animal Science, Longitudinal data analysis in EIAV infected horses and PRRSV infected pigs.
- 2014 **J.-Y. Lee**, GDCB, Fisher's Exact Test for differentially expressed genes enrichment in pathways.
- 2013 **J. Nason**, EEOB, Large-scale SNP genotyping.
- 2012 – 2013 **S. Sharma and A. James**, Government Accountability Office, Washington DC, Review statistical analysis of genetic data from 2001 anthrax attacks.
- 2010 – 2013 **G. Towfic**, Clarke University, Dubuque, IA, Analyzing HIV-1 drug resistance patterns in patient time course data.
- 2013 **A. Severin**, Genome Informatics Facility, Clustering next generation sequencing data.
- 2013 **V. Muthye**, BCB, Multiple correspondence analysis.
- 2013 **R. Liu**, BCB, Simulating variation in next generation sequencing data of gene expression.
- 2010 – 2012 **K. Sandeep**, Computer Science, Modeling of software reliability.
- 2009 – 2012 **F. Fang**, Sloan Kettering Cancer Institute, New York, NY, Modeling of CpG methylation in cancer vs. normal cells.
- 2008 – 2012 **B. J. Blitvich**, Veterinary Microbiology & Preventative Medicine, Phylogenetic analysis for various virus samples.
- 2012 **A. Vincent**, National Animal Disease Center, Ames, IA, Streamlining phylogenetic analysis for next generation sequencing data.
- 2012 **W. Zhang**, Marketing, Regression and relationship between independent variables.
- 2012 **W. Rutter**, PPM, Identification and significance of motifs in nematode receptors.
- 2012 **K. Sridharan**, GDCB, Fast C-based implementation of program to extract structural information from sequence data.
- 2012 **Y. Li**, BCB, Analyzing ChIPseq for change in binding in mutant.
- 2012 **J. Dekkers**, Animal Science, Work with students on phylogenetic analysis of haplotypes linked to PRRSV resistance.
- 2011 **F. Fang**, Sloan Kettering Cancer Institute, New York, NY, Identifying rare SNPs in a GWAS panel.
- 2010 **C. S. Strasburg**, Computer Science, Detection of masqueraders from net-flow data.
- 2010 **L. Beach**, University of Minnesota, Minneapolis, MN, Detecting selection in Trim37.
- 2010 **Y. Chen**, Computer Science, Computing/Understanding the C statistic.

- 2010 **S. Liu**, Plant Pathology and Microbiology, Computing nucleotide diversity, pi.
- 2010 **X. Wang**, Computer Science, Automatic detection of appendix in endoscopy.
- 2005 – 2009 **S. Carpenter**, Washington State University, Pullman, WA, Longitudinal data analysis in EIAV infected horses.
- 2006 – 2008 **K.-J. Yoon and S.-H Cha**, Veterinary Diagnostics & Production Animal Medicine, Detecting and characterizing recombination in PRRS virus.
- 2008 **A. Holguin Fernandez**, Hospital Carlos III, Madrid, Spain, Genotyping HIV-1 sequences isolated from patients.
- 2008 **A. Bogdanove**, EEOB, Phylogenetic analysis of Xanthomonas TAL effectors.
- 2008 **S. Sundararajan**, BCB, Computation of matrix pseudoinverse.
- 2007 **N. Khatibi**, University of California, Irvine, Irvine, CA, Testing for a genetic effect of HTRA and LOC loci on AMD.
- 2006 – 2007 **K. A. Ahmed**, Central Avian Research Institute, Bareilly, India, Characterizing recombination at an avian MHC locus.
- 2007 **C. Petersen**, Veterinary Pathology, Leishmania in canines.
- 2007 **Y. Yin**, GDCB, Probability of 16mer match (reviewer concern).
- 2004 – 2005 **C. Sabeta**, Onderstepoort Veterinary Institute, South Africa, Population genetics of rabies virus.
- 2001 – 2005 **S. Carpenter**, Veterinary Microbiology & Preventative Medicine, Longitudinal data analysis in EIAV infected horses.
- 2004 **G. Marquez**, Entomology, 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**, Entomology, Analyzing selection pressure in baculovirus sequences.
- 2003 **Y. Zhang**, Veterinary Diagnostics & Production Animal Medicine, Transmission of Salmonella in pigs.

Committees:

- 2013 – **Chair**, BCBio Supervisory Committee, Department of GDCB.
- 2012 – 2013 **Chair**, Curriculum Committee, BCB Program.
- 2009 – 2013 **Chair**, Sustainability Committee, Department of Statistics.
- 2006 – 2007 **Chair**, Diversity Committee, Department of Statistics.
- 2003 **Chair**, Seminar Committee, Department of Statistics.
- 2009 – **Academic Advisor**, BCB Graduate Major, BCB Program.
- 2007 – **Academic Advisor**, BCBio Undergraduate Major, GDCB Program (average 3.29 advisees / term).
- 2006 – **Academic Advisor**, Biology Undergraduate Major, Department of Biology (average 1.75 advisees / term).
- 2010 – 2013 **Member**, Faculty Development Committee, LAS College.

- 2007 – 2013 **Member**, BCBio Supervisory Committee, Department of GDCB.
- 2013 **Member**, Joint Mathematics/Statistics Search Committee, Department of Statistics.
- 2013 **Member**, Written Exam Question Writer/Grader, Department of Statistics.
- 2011 – 2012 **Member**, Written Exam Committee, Department of Statistics.
- 2010 – 2012 **Member**, Honors and Awards Committee, Department of Statistics.
- 2008 – 2012 **Member**, LAS Green Team, LAS College.
- 2010 – 2011 **Member**, Computer Advisory Committee, Department of Statistics.
- 2006 – 2011 **Member**, Curriculum Committee, Department of Statistics.
- 2010 **Member**, Written Exam Question Writer/Grader, Department of Statistics.
- 2008 – 2009 **Member**, Library Committee, Department of Statistics.
- 2008 – 2009 **Member**, BCB Ad Hoc Curriculum Committee, BCB Program.
- 2009 **Member**, Admissions Committee, IG Program.
- 2007 – 2008 **Member**, Diversity Committee, Department of Statistics.
- 2006 – 2008 **Member**, AGEF Faculty Council.
- 2006 – 2008 **Member**, Computer Advisory Committee, Department of Statistics.
- 2005 – 2008 **Member**, Human Relations & Diversity Committee, Department of GDCB.
- 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, Department of Statistics.
- 2004 **Member**, Admissions Committee, Department of Statistics.
- 2004 **Member**, Search Committee, Department of Statistics.
- 2004 **Member**, Awards and Recognition Committee, Department of GDCB.
- 2001 – 2003 **Member**, Diversity Committee, Department of Zoology & Genetics.
- 2002 **Member**, M.S. Exam Committee, Department of Statistics.
- 2001 **Member**, Search Committee, Department of Statistics.

Book Chapters

- [1] Zhou, H.* & **Dorman, K. S.** (2005). A branching process model of drug resistant HIV. In Wai-Yuan, T. & Wu, H. (Eds.), *Deterministic and Stochastic Models for AIDS Epidemics and HIV Infections with Interventions* (pp. 457–496). London: World Scientific Publishing Co., Inc.

Encyclopedia Entries

- [1] **Dorman, K. S.** (2006). Trees, evolutionary. In *The Wiley Encyclopedia of Biomedical Engineering* (pp. 1–14). Hoboken, NJ: John Wiley & Sons.

Refereed Journal Publications

*graduate; †undergraduate

- [40] Towfic, G., Graziano, F., Towfic, F., **Dorman, K. S.**, Cook, D., Kettoola, S. & Neal, L. (2013). HIV dynamics impacting the efficacy of HIV/AIDS treatments. *Journal of Proteomics and Bioinformatics*, **6**, 51–57.
- [39] Krishnan, S. *, Strasburg, C. S. *, Lutz, R. R., Goseva-Popstojanova, K. & **Dorman, K. S.** (2013). Predicting failure-proneness in an evolving software product line. *Information and Software Technology*, **55**, 1479–1495.
- [38] Blitvich, B. J., Loroño-Pino, M. A., Garcia-Rejon, J. E., Farfan-Ale, J. A. & **Dorman, K. S.** (2012). Nucleotide sequencing and serologic analysis of Cache Valley virus isolates from the Yucatan Peninsula of Mexico. *Virus Genes*, **45**, 176–180.
- [37] Blitvich, B. J., Saiyasombat, R., **Dorman, K. S.**, Garcia-Rejon, J. E., Farfan-Ale, J. A. & Loroño-Pino, M. A. (2012). Sequence and phylogenetic data indicate that an Orthobunyavirus recently detected in the Yucatan Peninsula of Mexico is a novel reassortant of Potosi and Cache Valley viruses. *Archives of Virology*, **157**, 1199–1204.
- [36] Blitvich, B. J., Staley, M., Loroño-Pino, M. A., Garcia-Rejon, J. E., Farfan-Ale, J. A. & **Dorman, K. S.** (2012). Identification of a novel subtype of South River virus (family *Bunyaviridae*). *Archives of Virology*, **157**, 1205–1209.
- [35] Wu, W., Blythe, D. C. *, Loyd, H., Mealey, R. H., Tallmadge, R. L., **Dorman, K. S.** & Carpenter, S. (2011). Decreased infectivity of a neutralization-resistant equine infectious anemia virus variant can be overcome by efficient cell-to-cell spread. *Journal of Virology*, **85**, 10421–10424.
- [34] Bogdanove, A. J., Koebnik, R., Lu, H. *, Furutani, A., Angiuoli, S. V., Patil, P. B., Van Sluys, M.-A., Ryan, R. P., Meyer, D. F., Han, S.-W., Aparna, G., Rajaram, M. L. *, Delcher, A. L., Phillippy, A. M., Puiu, D., Schatz, M. C., Shumway, M., Sommer, D. D., Trapnell, C., Benahmed, F., Dimitrov, G., Madupu, R., Radune, D., Sullivan, S., Jha, G., Ishihara, H., Lee, S.-W., Pandey, A., Sharma, V., Sriariyanun, M., Szurek, B., Vera-Cruz, C. M., **Dorman, K. S.**, Ronald, P. C., Verdier, V., Dow, J. M., Sonti, R. V., Tsuge, S., Brendel, V., Rabinowicz, P. D., Leach, J. E., White, F. F. & Salzberg, S. L. (2011). Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic *Xanthomonas spp.*. *Journal of Bacteriology*, **193**, 5450–5464.
- [33] Yang, X. *, Aluru, S. & **Dorman, K. S.** (2011). Repeat-aware modeling and detection of short read errors. *BMC Bioinformatics*, **12**, S52.
- [32] Carpenter, S., Chen, W.-C. * & **Dorman, K. S.** (2011). Rev variation during persistent lentivirus infection. *Viruses*, **3**, 1–11.
- [31] Yang, X. *, **Dorman, K. S.** & Aluru, S. (2010). Reptile: representative tiling for short read error correction. *Bioinformatics*, **26**, 2526–2533.
- [30] Staley, M., **Dorman, K. S.**, Fernández-Salas, I., Farfan-Ale, J. A., Loroño-Pino, M. A., Garcia-Rejon, J. E., Ibarra-Juarez, L. & Blitvich, B. J. (2010). Universal primers for the amplification and sequence analysis of actin-1 from diverse mosquito species. *Journal of the American Mosquito Control Association*, **26**, 214–218.
- [29] Saiyasombat, R., **Dorman, K. S.**, Garcia-Rejon, J. E., Loroño-Pino, M. A., Farfan-Ale, J. A. & Blitvich, B. J. (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] Dancik, G. M.*, Jones, D. E. & **Dorman, K. S.** (2010). Parameter estimation and sensitivity analysis in an agent-based model of *Leishmania major* infection. *Journal of Theoretical Biology*, **262**, 398–412.
- [27] Farfan-Ale, J. A., Loroño-Pino, M. A., Garcia-Rejon, J. E., Soto, V., Lin, M., Staley, M., **Dorman, K. S.**, Bartholomay, L. C., Hovav, E. & Blitvich, B. J. (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] Bloomquist, E. W., **Dorman, K. S.** & Suchard, M. A. (2009). Stepbrothers: inferring partially shared ancestries among recombinant viral sequences. *Biostatistics*, **10**, 106–120.
- [25] Farfan-Ale, J. A., Loroño-Pino, M. A., Garcia-Rejon, J. E., Hovav, E., Powers, A. M., Lin, M., **Dorman, K. S.**, Platt, K. B., Bartholomay, L. C., Soto, V., Beaty, B. J., Lanciotti, R. S. & Blitvich, B. J. (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. *American Journal of Tropical Medicine and Hygiene*, **80**, 85–95.
- [24] Blitvich, B. J., Lin, M., **Dorman, K. S.**, Soto, V., Hovav, E., Tucker, B. J., Staley, M., Platt, K. B. & Bartholomay, L. C. (2009). Genomic sequence and phylogenetic analysis of *Culex flavivirus*, an insect-specific flavivirus, isolated from *Culex pipiens* (Diptera: Culicidae) in Iowa. *Journal of Medical Entomology*, **46**, 934–941.
- [23] Soto, V., **Dorman, K. S.**, Miller, W. A., Farfan-Ale, J. A., Loroño-Pino, M. A., Garcia-Rejon, J. E. & Blitvich, B. J. (2009). Complete nucleotide sequences of the small and medium RNA genome segments of Kairi virus (family Bunyaviridae). *Archives Virology*, **154**, 1555–1558.
- [22] Su, B., Zhou, R. W.*, Jones, D. E. & **Dorman, K. S.** (2008). Mathematical modelling of immune response in tissues. *Computational & Mathematical Methods in Medicine*, **10**, 9–38.
- [21] Dancik, G. M.* & **Dorman, K. S.** (2008). Mlegp: statistical analysis for computer models of biological systems using R. *Bioinformatics*, **24**, 1966–1967.
- [20] Sparks, W. O.*, **Dorman, K. S.**, Liu, S.* & Carpenter, S. (2008). Naturally arising point mutations in non-essential domains of equine infectious anemia virus rev alter rev-dependent nuclear-export activity. *Journal of General Virology*, **89**, 1043–1048.
- [19] Sparks, M. E.*, Brendel, V. & **Dorman, K. S.** (2007). Markov model variants for appraisal of coding potential in plant DNA. *Lecture Notes in Bioinformatics*, **4463**, 394–405.
- [18] Minin, V. N., **Dorman, K. S.**, Fang, F.* & Suchard, M. A. (2007). Phylogenetic mapping of recombination hotspots in Human Immunodeficiency Virus via spatially smoothed change-point processes. *Genetics*, **175**, 1–13.
- [17] Fang, F.*, Ding, J., Minin, V. N., Suchard, M. A. & **Dorman, K. S.** (2007). CBrother: relaxing parental tree assumptions for Bayesian recombination detection. *Bioinformatics*, **23**, 507–508.

- [16] Ahmed, K. A., Saxena, V. K., Saxena, M., Ara, A., Pramod, A. B., Rajaram, M. L.*, **Dorman, K. S.**, Majumdar, S. & Rasool, T. J. (2007). Molecular cloning and sequencing of mhc class ii beta 1 domain of turkey reveals high sequence identity with chicken. *International Journal of Immunogenetics*, **34**, 97–105.
- [15] **Dorman, K. S.** (2007). Identifying dramatic selection shifts in phylogenetic trees. *BMC Evolutionary Biology*, **7 Suppl 1**, S10.
- [14] Minin, V. N., **Dorman, K. S.**, Fang, F.* & Suchard, M. A. (2005). Dual multiple change-point model leads to more accurate recombination detection. *Bioinformatics*, **21**, 3034–3042.
- [13] Wolt, J. D., Shyy, Y. Y., Christensen, P. J., **Dorman, K. S.** & Misra, M. (2004). Quantitative exposure assessment for confinement of maize biogenic systems. *Environ Biosafety Res*, **3**, 183–196.
- [12] **Dorman, K. S.**, Sinsheimer, J. S. & Lange, K. (2004). In the garden of branching processes. *SIAM Review*, **46**, 202–229.
- [11] Sinsheimer, J. S., Suchard, M. A., **Dorman, K. S.**, Fang, F.* & Weiss, R. E. (2003). Are you my mother? Bayesian phylogenetic inference of recombination among putative parental strains. *Applied Bioinformatics*, **2**, 131–144.
- [10] Suchard, M. A., Weiss, R. E., Sinsheimer, J. S., **Dorman, K. S.**, Patel, M. & McCabe, E. R. B. (2003). Evolutionary similarity among genes. *J Am Stat Assoc*, **98**, 653–662.
- [9] Suchard, M. A., Weiss, R. E., **Dorman, K. S.** & Sinsheimer, J. S. (2003). Inferring spatial phylogenetic variation along nucleotide sequences: a multiple changepoint model. *J. Am. Stat. Assoc.*, **98**, 427–437.
- [8] Baccam, P., Thompson, R. J., Li, Y., Sparks, W. O.*, Belshan, M., **Dorman, K. S.**, Wannemuehler, Y., Oaks, J. L., Cornette, J. L. & Carpenter, S. (2003). Subpopulations of Equine Infectious Anemia virus Rev coexist in vivo and differ in phenotype. *J Virol*, **77**, 12122–12131.
- [7] Suchard, M. A., Weiss, R. E., **Dorman, K. S.** & Sinsheimer, J. S. (2002). Oh brother, where art thou? a bayes factor test for recombination with uncertain heritage. *Syst. Biol.*, **51**, 715–728.
- [6] **Dorman, K. S.**, Kaplan, A. H. & Sinsheimer, J. S. (2002). Bootstrap confidence levels for HIV-1 recombination. *J Mol Evol*, **54**, 200–209.
- [5] Patel, M., **Dorman, K. S.**, Zhang, Y.-H., Huang, B.-L., Arnold, A. P., Sinsheimer, J. S., Vilain, E. & McCabe, E. R. B. (2001). Primate dax1, sry, and sox9: evolutionary stratification of sex-determination pathway. *Am J Hum Genet*, **68**,
- [4] **Dorman, K. S.**, Kaplan, A. H., Lange, K. & Sinsheimer, J. S. (2000). Mutation takes no vacation: can structured treatment interruptions increase the risk of drug-resistant hiv-1?. *Journal of Acquired Immune Deficiency Syndromes*, **25**, 398–402.
- [3] Perez, C., Vial, P., **Dorman, K. S.**, Wang, G., Abarca, K., Sinsheimer, J. S. & Kaplan, A. H. (1999). [molecular epidemiology of the human immunodeficiency virus type 1 in santiago, chile]. *Rev Med Chil*, **127**, 1294–304.
- [2] Lech, W. J., Wang, G., Yang, Y. L., Chee, Y., **Dorman, K.**, McCrae, D., Lazzeroni, L. C., Erickson, J. W., Sinsheimer, J. S. & Kaplan, A. H. (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**, 2038–43.

- [1] Yang, Y. L., Wang, G., **Dorman, K.** & Kaplan, A. H. (1996). Long polymerase chain reaction amplification of heterogeneous hiv type 1 templates produces recombination at a relatively high frequency. *AIDS Res Hum Retroviruses*, **12**, 303–306.

Refereed Conference Proceedings

- [4] Yin, X.* , Song, Z., **Dorman, K. S.** & Ramamoorthy, A. (2013). PREMIER turbo: PProbabilistic Error-correction using Markov Inference in Errored Reads using the turbo principle (invited paper). In *IEEE Global Conference on Signal and Information Processing*. Austin, TX: IEEE Computer Society.
- [3] Yin, X.* , Song, Z., **Dorman, K. S.** & Ramamoorthy, A. (2013). PREMIER - PProbabilistic Error-correction using Markov Inference in Errored Reads. In *IEEE International Symposium on Information Theory (ISIT 2013)*. Istanbul, Turkey: IEEE Computer Society.
- [2] Strasburg, C. S.* , Krishnan, S.* , **Dorman, K. S.**, Basu, S. & Wong, J. (2010). Masquerade detection in network environments. In *10th IEEE/IPSJ International Symposium on Applications and the Internet* (pp. 38-44). Washington, DC: IEEE Computer Society.
- [1] Rajaram, M. L.* & **Dorman, K. S.** (2009). Rapid genotyping for HIV using supervised learning tools. In *Proceedings of the 2009 International Conference on Bioinformatics and Computational Biology* (pp. 334-339). Las Vegas, Nevada.

Non-Refereed Conference Proceedings

- [7] Rajaram, M. L.* , Minin, V. N., Suchard, M. A. & **Dorman, K. S.** (2007). Hot and cold: spatial fluctuation in HIV-1 recombination rates. In *Proceedings of the 7th IEEE International Conference on Bioinformatics and Bioengineering* (pp. 707 -714). San Diego, CA.
- [6] Dancik, G. M.* , **Dorman, K. S.** & Jones, D. E. (2006). An agent-based model for leishmania infection. In Minai, A., Braha, D. & Bar-Yam, Y. (Eds.), *Unifying Themes in Complex Systems: Vol. 6. Proceedings of the Sixth International Conference on Complex Systems* (pp. 243-250). Cambridge, MA: Springer.
- [5] Fang, F.* , Suchard, M. A., Minin, V. N. & **Dorman, K. S.** (2005). A Bayesian phylogenetic model for testing recombination event. In *Proceedings of the Joint Statistical Meetings*. Alexandria, VA: American Statistical Association.
- [4] **Dorman, K. S.** & Gu, X. (2005). Bayesian inference for functional divergence. In *Proceedings of the Joint Statistical Meetings*. Alexandria, VA: American Statistical Association.
- [3] Minin, V. N., **Dorman, K. S.** & Suchard, M. A. (2004). Bayesian recombination identification: new models for incorporating prior information. In *Proceedings of the Joint Statistical Meetings*. Alexandria, VA: American Statistical Association.
- [2] Suchard, M. A., Weiss, R. E., **Dorman, K. S.**, Patel, M., McCabe, E. R. B. & Sinsheimer, J. S. (2000). Evolutionary similarity among genes when data are sparse. In *Proceedings of the Joint Statistical Meetings* (pp. 92-97). Alexandria, VA: American Statistical Association.

- [1] **Dorman, K. S.**, Kaplan, A. H. & Sinsheimer, J. S. (1999). Estimating confidence in the inference of HIV recombination. In *Proceedings of the Joint Statistical Meetings*. Alexandria, VA: American Statistical Association.

Refereed Abstracts

- [14] Rajaram, M. L.*, Minin, V. N., Suchard, M. A. & **Dorman, K. S.** (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.
- [13] Rajaram, M. L.*, Minin, V. N., Suchard, M. A. & **Dorman, K. S.** (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.
- [12] **Dorman, K. S.**, Rajaram, M. L.*, Minin, V. N., Carpenter, S. & Suchard, M. A. (2007). “A computational model discovers multiple recombination hotspots in natural HIV-1 sequences” in *Retrovirus Meeting*. Cold Spring Harbor, NY.
- [11] **Dorman, K. S.**, Fang, F.* & Minin, V. N. (2006). “Statistical methods for detecting repeat events and hotspots in virus recombination: applications to hepatitis B virus” in *Virus Evolution Workshop*. Ardmore, OK.
- [10] Fang, F.*, Minin, V. N., Suchard, M. A. & **Dorman, K. S.** (2006). “Deciphering a web of historical recombination events” in *HIV Dynamics and Evolution 13th International Workshop*. Woods Hole, MA.
- [9] **Dorman, K. S.** (2006). “Identifying divergence points indicative of functional adaptation in phylogenies” in *International Conference in Phylogenomics*. Sainte Adèle, Canada.
- [8] **Dorman, K. S.**, Sinsheimer, J. S. & Lange, K. (2005). “Numerical methods for branching process models” in *The European Conference on Mathematical and Theoretical Biology*. Dresden, Germany.
- [7] Sparks, W. O.*, **Dorman, K. S.** & Carpenter, S. (2005). “Selection on Rev during persistent EIAV infection of horses” in *HIV Dynamics and Evolution 12th International Workshop*. Cleveland, OH.
- [6] **Dorman, K. S.** (2004). “Numerical methods for branching processes with applications to HIV drug resistance” in *Society for Mathematical Biology*. Ann Arbor, MI.
- [5] **Dorman, K. S.** (2004). “Population genetics of EIAV” in *4th Biannual All Iowa Virology Symposium*. Ames, IA.
- [4] Macêdo, M., Carpenter, S., Richt, J. A., Oaks, J. L., Mealey, R. H., McGuire, T. C. & **Dorman, K. S.** (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] Fang, F.*, Rischmiller, M., Suchard, M. A. & **Dorman, K. S.** (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] **Dorman, K. S.** (2003). “Predicting HIV drug resistance with a branching process model” in *HIV Dynamics and Evolution 10th International Workshop*. Lake Arrowhead, CA.
- [1] **Dorman, K. S.** (2002). “Modeling pathways to drug resistance in HIV-1” in *2nd Biannual All Iowa Virology Symposium*. Iowa City, IA.

Non-Refereed Abstracts

- [7] **Dorman, K. S.** (2011). “Improved detection and correction of next generation sequencing errors” in *XXXI Annual Convention of Indian Society for Probability and Statistics & International Conference on Statistics, Probability and Related Areas*. Cochin, India.
- [6] Yang, X.*, Aluru, S. & **Dorman, K. S.** (2011). “Improved error modeling and detection for high-throughput short reads” in *Joint Statistical Meetings*. Miami, FL.
- [5] Chen, W.-C.*, **Dorman, K. S.** & Maitra, R. (2010). “Evolutionary clustering of snp haplotypes for genome-wide association studies” in *Joint Statistical Meetings*. Vancouver, Canada.
- [4] Chen, W.-C.*, **Dorman, K. S.** & Maitra, R. (2009). “Phyloclustering: model-based inference of population structure from genetic sequence data” in *ISU 75th Statistical Laboratory Conference*. Ames, IA.
- [3] Chen, W.-C.* & **Dorman, K. S.** (2008). “Disentangling the selection pressures acting on overlapping reading frames” in *Fall Conference on Statistics in Biology*. Ames, IA.
- [2] Carpenter, S., Casovant, C., **Dorman, K. S.**, Minin, V. N., Rajaram, M. L.* & Suchard, M. A. (2007). “Survey of recombination in the HIV genome to identify hotspots and associations with sequence patterns” in *Joint Statistical Meetings*. Salt Lake City, UT.
- [1] **Dorman, K. S.** & Gu, X. (2005). “Bayesian inference for functional divergence” in *Joint Statistical Meetings*. Minneapolis, MN.

Invited Presentations

- [9] **Dorman, K. S.** (2013). “Correcting errored sequence reads and connections to viral metagenomes” in *WNAR/IMS Conference*. Los Angeles, CA.
- [8] **Dorman, K. S.** (2012). “High resolution mapping of DNA methylation” in *Contemporary Issues and Applications in Statistics*. Kolkata, India.
- [7] **Dorman, K. S.** (2012). “Penalized mixtures of variable order Markov chains for biological sequence data” in *Joint Statistical Meetings*. San Diego, CA.
- [6] Yang, X.*, Aluru, S. & **Dorman, K. S.** (2011). “Improved error modeling and detection for high-throughput short reads” in *Joint Statistical Meetings*. Miami, FL.

- [5] **Dorman, K. S.** (2011). “Improved detection and correction of next generation sequencing errors” in *ISPS International Conference on Statistics, Probability and Related Areas*. Cochin, India.
- [4] Yang, X.*, Aluru, S. & **Dorman, K. S.** (2010). “Improved error modeling and detection for high-throughput short reads” in *Conference on Resampling Methods and High Dimensional Data*. College Station, TX.
- [3] Chen, W.-C.*, **Dorman, K. S.** & Maitra, R. (2010). “Phyloclustering: new phylogenetic methods for inferring population structure” in *International Conference on Statistics, Probability, Operators Research, Computer Science and Allied Areas*. Visakhapatnam, India.
- [2] Chen, W.-C.* & **Dorman, K. S.** (2009). “Phyloclustering: new phylogenetic methods for fast-evolving quasispecies” in *Joint Statistical Meetings*. Washington DC.
- [1] Carpenter, S., Casovant, C., **Dorman, K. S.**, Minin, V. N., Rajaram, M. L.* & Suchard, M. A. (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.

Software

- 2014 **PREMIER - P**Robabilistic **E**rror-correction using **M**arkov **I**nference in **E**rrored **R**eads, soon to be released, Maximum likelihood inference of errors in next generation sequencing data.
- 2014 **Multiclust**, soon to be released, Rapid maximum likelihood estimation of multinomial clusters for inference of genetic population structure
- 2010 **Phyclust: Phylogenetic Clustering**, CRAN: <http://cran.r-project.org/>, Maximum likelihood inference of population structure from aligned sequenced data.
- 2008 **MleGP**, CRAN: <http://cran.r-project.org/>, Maximum likelihood inference for Gaussian Processes
- 2007 **cBrother - Diverge**, <http://www.biomath.org/>, Inference of dramatic shifts in selection in phylogenetic trees
- 2006 **cBrother - Recombination**, <http://www.biomath.org/>, Inference of recombination