

Karin S. Dorman

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Education

- 2001 Ph.D., 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 – Associate Professor, Departments of Statistics and GDCB, ISU
- 2001 – 2007 Assistant Professor, Departments of Statistics and GDCB, ISU

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 12 STAT 580 Statistical Computing I
- Spring 12 BCB/STAT 568 Bioinformatics II (1/3 responsible)
- Spring 11 STAT 580 Statistical Computing I
- Spring 11 BCB/STAT 568 Bioinformatics II (1/3 responsible)
- 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 responsible)
- 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, current), Xin Yin (BCB, current), Chris Eisley (BCB, current), Derek Blythe (Statistics, current) Wei-Chen Chen (Statistics, 2011), Misha L. Rajaram (BCB, 2010), Garrett M. Dancik (BCB, 2008), Fang Fang (BCB, 2006)

Co-major Alice Wang (Statistics, M.S., current), Arun Sethuraman (BCB, Ph.D., current), Min Wang (Mathematics, Ph.D., current), Walker Pett (BCB, Ph.D., current) Yong Huang (BCB, Ph.D., 2010)

M.S. Xiujuan Wang (Statistics, 2010), Yong Huang (Statistics, 2010), Derek C. Blythe (Statistics, 2009), Misha L. 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)

Grants

Current:

2011-2014 NSF (**PI:** K. S. Dorman) ATD: Models for (Meta)Genome Identification from Next Generation Sequence Data with Errors, \$781,987

2011-2013 NSF (**PI:** V. Brendel) IPGA: Characterization, Modeling, Prediction, and Visualization of the Plant Transcriptome, \$1,499,996

2008-2013 NIH CA128568 (**PI:** S. Carpenter) Strategies of Lentivirus Persistence, \$1,397,652

Pending:

2012-2015 NSF (**PI:** S. Aluru) AF: Medium: Parallel Algorithms and Software for High-Throughput Sequence Assembly, \$1,085,329

Expired:

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

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) , \$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:

- 2012 **Review panel**, NIH, NIAID Systems Approach to Immunity and Inflammation (U19).
- 2011 **Review panel**, NIH, NIMH Integrating Multi-Dimensional Data to Explore Mechanisms Underlying Mental Disorders.
- 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 Carolina 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.
- 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, Jun, Ames, IA.
- 2011 – **Review editor**, Frontiers in Statistical Genetics and Methodology.

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 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:

- 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:

- 2011 – **Associate chair**, Bioinformatics and Computational Biology Graduate Program
2005 **Review panel**, ISU, Center for Integrated Animal Genomics Research Support Program.
2010 **Session chair**, Undergraduate Research Symposium, April, 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**, Enhancing Diversity in Graduate Education – EDGE@ISU Cluster, Mentor.
2011, 3X **Volunteer**, Taking the Road Less Traveled Conference, October, Four 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.
2009 **Volunteer**, Mathematics on the Road Experience, Valley High School visit.
2008 **Volunteer**, AGEF Summer Internship Program, June, Deliver seminar “The Role of Statistics in Research”.

Consulting projects:

- 2010 – K. Sandeep, Modeling of software reliability.
2010 – C. S. Strasburg, Detection of masqueraders from netflow data.
2009 – S. Carpenter, Longitudinal data analysis in EIAV infected horses.
2008 – B. J. Blitvich, Phylogenetic analysis for various virus samples.
2010 X. Wang, Automatic detection of appendix in endoscopy.
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:

- 2009 – **Chair**, Sustainability Committee, Statistics Department
- 2006 – 2007 **Chair**, Diversity committee, Statistics Department
- 2003 **Chair**, Seminar Committee, Statistics Department
- 2011 – **Member**, PhD/MS Exam Committee, Statistics Department
- 2010 – **Member**, Faculty Development Committee, LAS College
- 2010 – **Member**, Honors and Awards Committee, Statistics Department
- 2008 – **Member**, LAS Green Team, LAS College
- 2007 – **Member**, BCBio Supervisory Committee, GDCB Program
- 2010 – 2011 **Member**, Computer Advisory Committee, Statistics Department
- 2006 – 2011 **Member**, Curriculum Committee, Statistics Department
- 2008 – 2009 **Member**, Library 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, Statistis Department
- 2001 **Member**, Search Committee, Statistics Department
- 2006 – **Academic Advisor**, Biology Undergraduate 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)

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 Articles

*graduate; †undergraduate

- [37] Blitvich, B. J., Saiyasombat, R., Dorman, K. S., Garcia-Rejon, J. E., Farfan-Ale, J. A., & Loroño-Pino, M. A. (2011). Sequence and phylogenetic characterization of Cholut virus, a novel orthobunyavirus reassortant between Potosi and Cache Valley viruses from the Yucatan Peninsula of Mexico. *Archives of Virology*, Accepted.
- [36] Blitvich, B. J., Staley, M., Loroño-Pino, M. A., Garcia-Rejon, J. E., Farfan-Ale, J. A., & Dorman, K. S. (2011). Identification of a novel subtype of South River virus (family *Bunyaviridae*). *Archives of Virology*, Accepted.
- [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 and 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). Spatially smoothing change-point processes for phylogenetic mapping of recombination hot-spots. *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

- [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.

Submitted Manuscripts

*graduate; †undergraduate

- [2] Krishnan, S.* , Strasburg, C.* , Lutz, R. R., Goseva-Popstojanova, K., & Dorman, K. S. (2012). Predicting failure-proneness in an evolving software product line. *Information and Software Technology*,
- [1] 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 reveal that they belong to the subtype Tlacotalpan virus. *Archives of Virology*,

Invited Presentations

- [9] Dorman, K. S. (2012). “High resolution mapping of DNA methylation” in *Contemporary Issues and Applications in Statistics*. Kolkata, India.
- [8] Yang, X.* , Aluru, S., & Dorman, K. S. (2011). “Improved error modeling and detection for high-throughput short reads” in *Joint Statistical Meetings*. Miami, FL.
- [7] 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.
- [6] Dorman, K. S. (2011). “A statistical model applied to 544 *in vivo* HIV-1 recombinants reveals that viral genomic features, especially RNA structure, promote recombination” in *Statistics & Mathematics Colloquium*. Baltimore, MD.

- [5] Dorman, K. S. (2011). “A statistical model applied to 544 *in vivo* HIV-1 recombinants reveals that viral genomic features, especially RNA structure, promote recombination” in *Math Bio & Eco Seminar*. Atlanta, GA.
- [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 D.C..
- [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.

Refereed Presentations

- [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 Conference Presentations

- [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.

Software

- 2010 **Phyclust: Phylogenetic Clustering**, CRAN: <http://cran.r-project.org/>, Maximum likelihood inference of population structure from aligned sequenced data.
- 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