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**CONTACT INFORMATION**

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**CITIZENSHIP**

United States of America

**EDUCATION**

2003 Ph.D., Department of Microbiology, University of Washington, Seattle, WA  
Thesis: "Population genetics of human immunodeficiency virus type 1 during within-host chronic infection"

1995 B.S., Department of Microbiology, University of Maryland, College Park, MD  
Graduated summa cum laude

**CONTINUING EDUCATION**

2007: Introduction to Human Population Genetics Theory, August 23–December 4, 2007, University of Alabama at Birmingham, Birmingham, AL

2007: Modeling, Networks and Evolution of Complex Systems, June 18–22, 2007, New England Complex Systems Institute, Cambridge, MA

2007: Statistical Genetics II, January 8–April 26, 2007, University of Alabama at Birmingham, Birmingham, AL

2007: Complex Physical, Biological & Social Systems, January 8–12, 2007, New England Complex Systems Institute, Cambridge, MA

2006: Bayesian Data Analysis, August 22–November 28, 2006, University of Alabama at Birmingham, Birmingham, AL

2006: Statistics, Images, and Perceptions of Truth: Detecting Research Bias and Misconduct, September 14–15, 2006, University of Alabama at Birmingham, Birmingham, AL

2006: Statistical Bioinformatics, June 1–August 1, 2006, University of Alabama at Birmingham, Birmingham, AL

2006: R Fundamentals and Programming Techniques, February 27–28, 2006, University of Alabama at Birmingham, Birmingham, AL

2005: Advanced Gene Mapping/Linkage Course, December 12–16, 2005, Rockefeller University, New York, NY

- Awarded travel stipend

2005: Missing Data, August 4–5, 2005, University of Alabama at Birmingham, Birmingham, AL

2005: 5<sup>th</sup> Annual National Institute of Diabetes & Digestive & Kidney Diseases Short Course on Statistical Genetics, May 16–19, 2005, University of Alabama at Birmingham, Birmingham, AL

## EXPERIENCE

2005–present Postdoctoral Scholar, University of Alabama at Birmingham, Birmingham, AL  
Advisors: Drs. David B. Allison and Nengjun Yi

2004–2005 Postdoctoral Fellow, University of Washington, Seattle, WA  
Advisor: Dr. John E. Mittler

2003–2004 Postdoctoral Fellow, University of Washington, Seattle, WA  
Advisor: Dr. James I. Mullins

1996–2003 Research Assistant, University of Washington, Seattle, WA  
Advisor: Dr. James I. Mullins

1995–1996 Teaching Assistant, University of Washington, Seattle, WA

- MICROM 411: Gene Action
- MICROM 302: General Microbiology Laboratory

1993–1995 Undergraduate Research Assistant, University of Maryland, College Park, MD

Senior thesis: “Recombination in the human immunodeficiency virus: analysis *in vitro* of the influence of specific nucleotide sequences on reverse transcriptase catalyzed recombination”

## PUBLICATIONS

### Articles

- DeStefano, J. J., Roberts, B., and *Shriner, D.* 1997. The mechanism of retroviral recombination: the role of sequences proximal to the point of strand transfer. *Arch. Virol.* 142(9): 1797–1812.

- Liu, S.-L., Schacker, T., Musey, L., *Shriner, D.*, McElrath, M. J., Corey, L., and Mullins, J. I. 1997. Divergent patterns of progression to AIDS after infection from the same source: human immunodeficiency virus type 1 evolution and antiviral responses. *J. Virol.* **71**(6): 4284–4295.
- Liu, S.-L., Mittler, J. E., Nickle, D. C., Mulvania, T. M., *Shriner, D.*, Rodrigo, A. G., Kosloff, B., He, X., Corey, L., and Mullins, J. I. 2002. Selection for human immunodeficiency virus type 1 recombinants in a patient with rapid progression to AIDS. *J. Virol.* **76**(21): 10674–10684.
- Nickle, D. C., Jensen, M. A., Gottlieb, G. S., *Shriner, D.*, Learn, G. H., Rodrigo, A. G., and Mullins, J. I. 2003. Consensus and ancestral state HIV vaccines. *Science*. **299**(5612): 1515–1517.
- *Shriner, D.*, Nickle, D. C., Jensen, M. A., and Mullins, J. I. 2003. Potential impact of recombination on sitewise approaches for detecting positive natural selection. *Genet. Res.* **81**(2): 115–121.
- Nickle, D. C., *Shriner, D.*, Mittler, J. E., Frenkel, L. M., and Mullins, J. I. 2003. Importance and detection of virus reservoirs and compartments of HIV infection. *Curr. Opin. Microbiol.* **6**(4): 410–416.
- Nickle, D. C., Jensen, M. A., *Shriner, D.*, Brodie, S. J., Frenkel, L. M., Mittler, J. E., and Mullins, J. I. 2003. Evolutionary indicators of human immunodeficiency virus type 1 reservoirs and compartments. *J. Virol.* **77**(9): 5540–5546.
- Jensen, M. A., Li, F.-S., van 't Wout, A. B., Nickle, D. C., *Shriner, D.*, He, H.-X., McLaughlin, S., Shankarappa, R., Margolick, J. B., and Mullins, J. I. 2003. Improved coreceptor usage prediction and genotypic monitoring of R5-to-X4 transition by motif analysis of human immunodeficiency virus type 1 *env* V3 loop sequences. *J. Virol.* **77**(24): 13376–13388.
- *Shriner, D.*, Shankarappa, R., Jensen, M. A., Nickle, D. C., Mittler, J. E., Margolick, J. B., and Mullins, J. I. 2004. Influence of random genetic drift on HIV-1 *env* evolution during chronic infection. *Genetics* **166**(3): 1155–1164.
- *Shriner, D.*, Rodrigo, A. G., Nickle, D. C., and Mullins, J. I. 2004. Pervasive genomic recombination of HIV-1 *in vivo*. *Genetics* **167**(4): 1573–1583.
- Liu, Y., Nickle, D. C., *Shriner, D.*, Jensen, M. A., Learn, G. H., Jr., Mittler, J. E., and Mullins, J. I. 2004. Molecular clock-like evolution of human immunodeficiency virus type 1. *Virology* **329**(1): 101–108.
- *Shriner, D.*, Liu, Y., Nickle, D. C., and Mullins, J. I. 2006. Evolution of intrahost HIV-1 genetic diversity during chronic infection. *Evolution* **60**(6): 1165–1176.
- Liu, Y., McNevin, J., Cao, J., Zhao, H., Genowati, I., Wong, K., McLaughlin, S., McSweyn, M. D., Diem, K., Stevens, C. E., Maenza, J., He, H., Nickle, D. C., *Shriner, D.*, Holte, S. E., Collier, A. C., Corey, L., McElrath, M. J., and Mullins, J. I. 2006. Selection on the HIV-1 proteome following primary infection. *J. Virol.* **80**(19): 9519–9529.
- Musani, S. K., *Shriner, D.*, Liu, N., Feng, R., Coffey, C. S., Yi, N., Tiwari, H. K., and Allison, D. B. 2007. Detection of gene × gene interactions in genome-wide association studies of human population data. *Hum. Hered.* **63**(2): 67–84.
- Yandell, B. S., Mehta, T., Banerjee, S., *Shriner, D.*, Venkataraman, R., Moon, J. Y., Neely, W. W., Wu, H., von Smith, R., and Yi, N. 2007. R/qtlbim: QTL with Bayesian interval mapping in experimental crosses. *Bioinformatics* **23**(5): 641–643.
- Yi, N., *Shriner, D.*, Banerjee, S., Mehta, T., Pomp, D., and Yandell, B. S. 2007. An efficient Bayesian model selection approach for interacting QTL models with many effects. *Genetics* **176**: 1865–1877.
- *Shriner, D.*, Vaughan, L. K., Padilla, M. A., and Tiwari, H. K. 2007. Problems with Genome-Wide Association Studies. *Science* **316**(5833): 1840–1841.

- Liu, Y., McNevin, J., Zhao, H., Tebit, D. M., Troyer, R. M., McSweyn, M., Ghosh, A. K., Shriver, D., Arts, E. J., McElrath, M. J., and Mullins, J. I. 2007. Evolution of human immunodeficiency virus type 1 cytotoxic T-lymphocyte epitopes: fitness-balanced escape. *J. Virol.* **81(22)**:12179–12188.
- Yi, N., and Shriver, D. Advances in Bayesian multiple QTL mapping in experimental crosses. *Heredity*, in press.
- Shriver, D., Baye, T. M., Padilla, M. A., Zhang, S., Vaughan, L. K., and Loraine, A. E. Commonality of Functional Annotation: a method for prioritization of candidate genes from genome-wide linkage studies. *Nucleic Acids Res.*, accepted.

### Book Chapters

- Anderson, J. P., Rain, M., Shriver, D., Rodrigo, A. G., Wang, Y., Nickle, D., Learn, G. H., Naugler, W. E., and Mullins, J. I. 2002. “The Genetics of HIV-1” in *The Human Immunodeficiency Virus: Biology, Immunology, and Therapy*, ed. Emini, E. A. (Princeton University Press, Princeton, NJ).
- Shriver, D., Musani, S., and Yi, N. “Statistical methods for multiple QTL mapping in experimental crosses” in *Current Topics in Human Genetics: Studies of Complex Diseases*, eds. Deng, H.-W., Shen, H., Liu, Y., and Hu, H.
- Shriver, D., Coulibaly, I., Ankra-Badu, G., Baye, T. M., and Allison, D. B. “Genetic Contribution to the Development of Obesity” in *Understanding Obesity: Biological, Psychological and Cultural Influences*, eds. Akabas, S. R., Aronne, L. J., Nonas, C. A., Pi-Sunyer, F. X., and Wadden, T. A. (Wadsworth Publishers, Belmont, CA).

### Submitted Manuscripts

- Shriver, D., Moses, M., Allison, D. B., Ruden, D. M., Yi, N., and De Luca, M. Identification of genes affecting obesity-related traits in *Drosophila melanogaster*.
- Shriver, D. Mapping multiple interacting QTL under Bayes error control.
- Shriver, D., and Yi, N. Deviance information criterion (DIC) in Bayesian multiple QTL mapping.
- Shriver, D., and Vaughan, L. K. A Bayesian variable selection approach to genome-wide association testing.
- Ankra-Badu, G. A., Pomp, D., Shriver, D., Allison, D. B., and Yi, N. Genetic influences on growth and body composition in mice: multilocus interactions.

### Manuscripts in Preparation

- Shriver, D., and Yi, N. Deviance information criterion (DIC) in Bayesian multiple QTL mapping for binary and ordinal traits.
- Shriver, D., Padilla, M. A., Vaughan, L. K., and Loraine, A. E. Multiple comparison procedures and the Gene Ontology.
- Ruden, D. M., Chen, L., Shriver, D., Ye, J., Rasouli, P., Lu, X., Yi, N., Garfinkel, M. D., Hirsch, H., Page, G. P. Toxicogenetic genomics of lead in *Drosophila* identifies *trans*-eQTL epistatic switches.

### PROFESSIONAL ACTIVITIES

- 1995–2006, member of American Society for Microbiology
- 1997–present, member of American Association for the Advancement of Science
- 2006–present, member of the NAASO, The Obesity Society
- 2006–present, member of the American Statistical Association
- 2007–present, member of the American Society for Nutrition

- Invited Referee: *Evolution*, *Journal of Leukocyte Biology*, *Journal of Molecular Evolution*, *Journal of Theoretical Biology*, *Molecular Biology and Evolution*, *Physiological Genomics*, 2006 Computational Systems Bioinformatics Conference, *Journal of the American Medical Association*, *Computational Statistics and Data Analysis*, *PLoS Computational Biology*, *American Journal of Human Genetics*, *Molecular Ecology*, *International Journal of Immunogenetics*, *Molecular Phylogenetics and Evolution*, *BMC Genetics*, *Statistical Applications in Genetics and Molecular Biology*, *PLoS Genetics*

## CONFERENCES

### Posters

- 7<sup>th</sup> Annual HIV Dynamics and Evolution Conference, Seattle, WA, April 2000: “Inferring phylogenies for large, serially sampled data sets” and “Phylogenetic evidence for recombination within an HIV-1 singly infected individual”
- Joint Statistical Meetings, Seattle, WA, July 2006: “Inferring Quantitative Trait Loci Using a Bayesian Variable Selection Model and Markov Chain Monte Carlo Convergence Diagnostics”
- Annual Scientific Meeting of NAASO, The Obesity Society, New Orleans, LA, October 2007: “Commonality of Functional Annotation: A Method for Prioritization of Candidate Genes from Genome-Wide Linkage Studies”

### Oral Presentations

- Annual Scientific Meeting of NAASO, The Obesity Society, Boston, MA, October 2006: “Bayesian Mapping of Obesity-related Quantitative Trait Loci in *Drosophila melanogaster*”
- 6<sup>th</sup> Annual Meeting of the Complex Traits Consortium, Braunschweig, Germany, May 26–29, 2007: “Bayes Error Control for Multiple QTL Mapping”

## INVITED SEMINARS

- Section on Statistical Genetics Lecture Series, Department of Biostatistics, University of Alabama at Birmingham, December 6, 2006: “Bayes Error Control for Multiple QTL Mapping”
- University of Maryland Bioscience Day, November 13, 2007: “Developing a Comprehensive Research Toolkit”

## HONORS AND AWARDS

- 1994–1995, Howard Hughes Medical Institute Undergraduate Research Fellow
- 1995–present, The Phi Beta Kappa Society
- 1995, P. Arne Hanson Award for the Outstanding Departmental Honors Student, Department of Microbiology, University of Maryland at College Park
- 1995, Honorable Mention, National Science Foundation Graduate Research Fellowship Program
- 1996, Honorable Mention, National Science Foundation Graduate Research Fellowship Program
- 1996–2001, Howard Hughes Medical Institute Predoctoral Fellow in Biological Sciences
- 2006, Finalist for the Ethan Sims Young Investigator Award, The Obesity Society
- Spring 2007, Career Enhancement Award, Office of Postdoctoral Education, University of Alabama at Birmingham

## COMPUTER SKILLS

- Proficiency working under Mac, UNIX, and Windows operating systems
- Experience with C and Python programming languages
- Working knowledge of sequence analysis tools, such as CLUSTALW, DnaSP, LAMARC, MacClade, MEGA, PAML, PAUP\*, Sequencher, TreeEdit, and TreeView
- Working knowledge of sequence simulation software, such as ms, Seq-Gen, and Treevolve
- Working knowledge of statistical analysis tools, such as JMP, Excel, Resampling Stats, R, and WinBUGS

## REFERENCES

- David B. Allison, PhD, Department of Biostatistics, Section on Statistical Genetics, and Clinical Nutrition Research Center, Department of Nutrition Sciences, University of Alabama at Birmingham, Birmingham, AL 35294, Tel: +1 (205)975-9167, E-mail: [dallison@uab.edu](mailto:dallison@uab.edu)
- Hemant K. Tiwari, PhD, Department of Biostatistics, Section on Statistical Genetics, University of Alabama at Birmingham, Birmingham, AL 35294, Tel: +1 (205)934-4907, E-mail: [htiwari@uab.edu](mailto:htiwari@uab.edu)
- Nengjun Yi, PhD, Department of Biostatistics, Section on Statistical Genetics, University of Alabama at Birmingham, Birmingham, AL 35294, Tel: +1 (205)934-4924, E-mail: [nyj@ms.soph.uab.edu](mailto:nyj@ms.soph.uab.edu)