

[8] **Wu, X.** and Kimmel, M. (2013). Modeling neutral evolution using infinite-allele Markov branching processes. *International Journal of Stochastic Analysis*, Volume 2013, Article ID 963831.

[9] **Wu, X.** and Kimmel, M. (2010). A note on the path to extinction of critical Markov branching processes. *Statistics and Probability Letters*, 80, 263–269.

[10] **Wu, X.**, Strome, E.D., Meng, Q., Hastings, P.J., Plon, S.E. and Kimmel, M. (2009). A robust estimator of mutation rates. *Mutation Research*, 661, 101–109.

[11] Strome, E.D., **Wu, X.**, Kimmel, M. and Plon, S.E. (2008). Heterozygous screen in *Saccharomyces Cerevisiae* identifies dosage-sensitive genes that affect chromosome stability. *Genetics*, 178, 1193–1207.

Submitted and in Revision

[1] Zhu, H., Casters, P., Morris, J.S., **Wu, X.** and Muller, R. A unified analysis of structured sonar-terrain data using Bayesian functional mixed models. Submitted to *Technometrics*.

[2] Leon-Novelo, L.G., Womack, A., Zhu, H. and **Wu, X.**. A Bayesian analysis of bioassay experiments. In revision. *Statistics in Medicine*.

[3] Jin, X., **Wu, X.**, Du, X., Xiang, X., Sun, W., Bai, Q., Zhou, Y. Co-ordination of land exploitation, exploitable farmland reserves and national planning in China. In revision. *Land Use Policy*.

[4] Sun, M., Sun, Z., **Wu, X.**, Rajaram, V., Keimig, D., Lim, J., Zhu, H. and Xie, H. Mammalian brain development is accompanied by a dramatic increase in cell-subset specific DNA methylation. In revision. *Scientific Reports*.

[5] Tran, H., **Wu, X.**, Tithi, S., Sun, M., Xie, H. and Zhang, L. A Bayesian assignment method for ambiguous bisulfite short reads. In revision. *PLoS ONE*.

Manuscripts

co-first author; † corresponding author

[1] **Wu, X.**, Guan, T.#, Zhu, H., Liu, D. and Leon-Novelo, L.G. Optimal burden test for association between quantitative traits and genotype data with bi-directional correlations: the equivalence of burden and kernel tests.

[2] **Wu, X.** and McPeck, M.S. L-GATOR: Genetic association testing for a longitudinally-measured quantitative trait in samples with related individuals.

[3] **Wu, X.**, Zhu, H. and Leon-Novelo, L.G. Dictionary learning for genetic data in related individuals.

[4] **Wu, X.**, Tang, M., Zhang, L. and Wei, F. A Markov chain based next generation sequencing reads and variants simulator.

[5] Wang, Z., Xu, K., Zhang, X., **Wu, X.** and Wang, Z. Longitudinal SNP-set association analysis of quantitative phenotypes.

[6] Tang, M., Zhu, H., Zhang, L. and **Wu, X.**[†] Unified calling for genetic variants and methylation.

Conference Proceedings

[1] Tran, H., **Wu, X.** and Zhang, L. (2015). A Bayesian method for assigning ambiguous bisulfite short reads. *The 7th International Conference on Bioinformatics and Computational Biology*.

[2] Zhu, H., **Wu, X.**, Xu, X. and Wu, C. (2007). Feature extraction and categorization of patient respiration pattern in radiation therapy. *The 15th International Conference on the Use of Computers in Radiation Therapy*.

[3] **Wu, X.**, Chan, Y., Preissl, H., Eswaran, H., Wilson, J., Murphy, P. and Lowery, C.L. (2004). Time-frequency and coherence analysis of fMEG signals. *The 14th International Conference on Biomagnetism*.

TALKS AND PRESENTATIONS

Contributed Talks

[1] Dictionary learning for genetic data in related individuals, 2013 the annual meeting of the Statistical Section of the Virginia Academy of Sciences, Blacksburg, VA, USA, May 2013.

[2] Bayesian analysis of array CGH data. 2009 the Joint Statistical Meeting, Washington, DC, USA, Aug 2009.

[3] Variability study of a robust estimator of mutation rate in fluctuation analysis. 2007 the Joint Statistical Meeting, Salt Lake City, UT, USA, Jul 2007.

[4] Some estimation problems in fluctuation analysis. The 3rd Erich L. Lehmann Symposium, Houston, TX, May 2007.

Posters

[1] Nonparametric Bayesian clustering to detect bipolar methylated genomic loci. The 4th Workshop on Biostatistics and Bioinformatics, Atlanta, GA, USA, May 2015.

[2] Wavelet-based imaging genomic modeling in Autism Spectrum Disorder study. The 4th Workshop on Biostatistics and Bioinformatics, Atlanta, GA, USA, May 2015.

[3] An optimal quasi-likelihood-based burden test for rare-variant association. The 63th Annual Meeting of the American Society of Human Genetics, Boston, MA, USA, Oct 2013.

[4] Bayesian dictionary learning in genetic studies on related individuals. The 22nd Annual Conference of the International Genetic Epidemiology Society, Chicago, IL, USA, Sep 2013.

[5] Genetic association testing for a longitudinally-measured trait in samples with related individuals. The 60th Annual Meeting of the American Society of Human Genetics, Washington, DC, USA, Nov 2010.

GRANTS AND PROPOSALS

Awarded

[1] VTCAR Seed Award, Source: Virginia Tech Center for Autism Research (VTCAR). Title: Imaging Genomic Modeling in Autism Spectrum Disorder Study. Role: Co-PI. Amount: \$5,000 (My share: 20%). Effective Date: 01/01/2015 - 06/15/2015.

[2] VT New Tenure-track Assistant Professors' Mentoring Project Award, Source: Virginia Tech. Role: PI. Amount: \$1,500. Effective Date: 03/01/2012 - 03/01/2013.

Pending

[1] Testing Genetic Association for Data with Complex Correlation Structures, Source of Support: NSA, Role: PI, Amount: \$39,998 (My share: 100%)

[2] New Statistical Methods for Genetic Data Modeling and Association Analysis, Source of Support: Simons Foundation, Role: PI, Amount: \$35,000 (My share: 100%)

[3] Wavelet-based Analytical Neuroscience Tool Suite—a platform for scalable analysis of ultra-high dimensional neuroscience data, Source of Support: Virginia Tech Institute for Critical Technology and Applied Science (VT ICTAS), Role: PI, Amount: \$120,000 (My share: 75%)

[4] Traffic Prediction Based Radio Access Point Handover Control in Mobile Networks, Source of Support: NSF-China, Role: Co-PI

JOURNAL REVIEW EDITOR

• *Frontiers*, the Editorial Board of Bioinformatics and Computational Biology

JOURNAL REFEREE

- *Genetica*
- *Computational and Mathematical Methods in Medicine*
- *BMC Genetics*
- *Scientific Reports*
- *Journal of Theoretical Biology*

TEACHING EXPERIENCE

- Applied Stochastic Processes: Spring 2015
- Inference Fundamentals with Applications to Categorical Data: Fall 2014, 2015
- Introduction to Statistical Genomics: Spring 2013, 2014
- Probability and Statistics for Electrical Engineers: Fall 2012, 2013