Michael C. Wu

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PERSONAL INFORMATION

Birthplace: Howard County, Maryland, U.S.A.

Birthdate: July 1982

Citizenship: United States of America

EDUCATION

Ph.D., Biostatistics, June 2009
Minor: Computational Molecular Biology and Genetics
Harvard University, Cambridge, MA.
Committee: Drs. Xihong Lin (Advisor), Tianxi Cai (Co-Advisor), and Jun Liu

A.M., Biostatistics, June 2006
Harvard School of Public Health, Boston, MA.

B.S., Mathematical and Computational Science, Biological Sciences Track, April 2004
Stanford University, Stanford, CA.

RESEARCH EXPERIENCE

Department of Biostatistics, University of North Carolina at Chapel Hill
Chapel Hill, North Carolina USA

Assistant Professor (Tenure Track) **September 2009 – present**

Carolina Center for Genome Sciences, University of North Carolina at Chapel Hill
Chapel Hill, North Carolina USA

Member **September 2009 – present**

Department of Biostatistics, Harvard University
Boston, Massachusetts USA

Graduate Research Assistant **June 2006 – June 2009**

Department of Biostatistics & Computational Biology, Dana Farber Cancer Institute
Boston, Massachusetts USA

Graduate Research Assistant, X.S. Liu Lab **January 2006 – June 2006**
Graduate Research Assistant **June 2005 – August 2005**

National Human Genome Research Institute, NIH
Bethesda, Maryland USA

Summer Intern, Cancer Genetics Branch **Summer 2003**

National Institute of Dental and Craniofacial Research, NIH
Bethesda, Maryland USA

Summer Intern, Craniofacial Developmental **Summer 2000, Summer 2001**
Biology and Regeneration Branch

- Article Selected as one of "Best Papers" in *American Journal of Human Genetics*: 2011-2012
- ASA Statistical Computing & Statistical Graphics Sections Student Paper Award: 2008
- ICSA Applied Statistics Symposium Student Paper Award: 2008
- ENAR Distinguished Student Paper Award: 2008
- Mu Sigma Rho National Statistics Honorary Society: 2007
- Certificate of Distinction in Teaching, Department of Biostatistics: 2006
- NIH Environmental Health Statistics Predoctoral Fellowship: 2008 – 2009
- NIH Interdisciplinary Biostatistics Predoctoral Fellowship: 2005 – 2008
- NIH Cancer Predoctoral Fellowship: 2004 – 2005

Published Papers:

1. Koblinski, J.E., **Wu, M.**, Demeler, B., Kleinman, H.K. (2005). "Matrix cell adhesion activation by non-adhesion proteins". ***Journal of Cell Science***, 118(Pt 13):2965-74.

2. Koblinski, J.E., Kaplan-Singer, B.R., VanOsdol, S.J., **Wu, M.**, Engbring, J.A., Goldsmith, C.M., Piper, J.T., Vostal, J.G., Harms, J.F., Welch, D.R., Kleinman, H.K. (2005). "Endogenous osteonectin/SPARC/BM-40 expression inhibits MDA-MB-231 breast cancer cell metastasis". ***Cancer Research***, 65(16):7370-7.

3. Ji, H., Ramsey, M.R., Hayes, D.N., Fan, C., McNamara, K., Kozlowski, P., Torrice, C., **Wu, M.C.**, Shimamura, T., Perera, S., Liang, M-C., Cai, D., Naumov, G.N., Bao, L., Contreras, C., Li, D., Chen, L., Krishnamurthy, J., Koivunen, J., Chirieac, L.R., Padera, R., Bronson, R.T., Lindeman, N.I., Christiani, D.C., Lin, X., Shapiro, G.I., Janne, P.A., Johnson, B., Meyerson, M., Kwiatkowski, D.J., Castrillon, D.H., Badeesy, N., Sharpless, N.E., Wong, K-K. (2007). "LKB1 modulates lung cancer differentiation and metastasis". ***Nature***, 448(7155):807-10.

4. Harezlak, J.♠, **Wu, M.C.**♠, Wang, M., Schwartzman, A., Christiani D.C., Lin, X. (2008). "Biomarker discovery for arsenic exposure using functional data analysis and feature learning of mass spectrometry proteomic data". ***Journal of Proteome Research***, 7(1):217-224.
   [♠ **Equal Contribution**]

5. Engbring, J.A., Hossain, R., VanOsdol, S.J., Kaplan-Singer, B., **Wu, M.**, Hibino, S., Koblinski, J.E. (2008). "The laminin alpha-1 chain derived peptide, AG73, increases fibronectin levels in breast and melanoma cancer cells". ***Clinical and Experimental Metastasis***, 25(3):241-252.

6. **Wu, M.C.**, Zhang, L., Wang, Z., Christiani, D.C., Lin, X. (2009). "Sparse linear discriminant analysis for simultaneous testing for the significance of a gene set/pathway and gene selection". ***Bioinformatics***, 25(9):1145-1151.
   [⋆⋆ **An earlier version won a 2008 ICSA Applied Statistics Symposium Student Award** ⋆⋆]

7. Huang, Y.T., Heist, R.S., Chirieac, L.R., Lin, X., Skaug, V., Haugen, A., **Wu, M.C.**, Wang, Z., Su, L., Asomaning, K., Christiani, D.C. (2009). "Genome-wide analysis of survival in early-stage non-small cell lung cancer". ***Journal of Clinical Oncology***, 27(16):2660-2667.

8. **Wu, M.C.**, Lin, X. (2009). "Prior biological knowledge based approaches for the analysis of genome-wide expression profiles using gene sets and pathways". ***Statistical Methods in Medical Research***, 18(6): 577-593.

9. **Wu, M.C.**, Kraft, P., Epstein, M.P., Taylor, D.M., Chanock, S.J., Hunter, D.J., Lin, X. (2010). "Powerful SNP-set analysis for case-control genome-wide association studies". ***The American Journal of Human Genetics***, 86(6): 929-942.

10. Liu, C.Y., **Wu, M.C.**, Chen, F., Ter-Minassian, M., Asomaning, K., Zhai, R., Wang, Z., Su, L., Heist, R., Kulke, M.H., Lin, X., Liu, G., Christiani, D.C. (2010). "A large scale genetic association study of esophageal adenocarcinoma risk." ***Carcinogenesis***, 31(7):1259-63.

11. Locke, A.E., Dooley, K.J., Tinker, S.W., Cheong, S.Y., Feingold, E., Allen, E.G., Freeman, S.B., Torfs, C.P., Cua, C., Epstein, M.P., **Wu, M.C.**, Lin, X., Capone, G., Sherman, S.L., Bean, L.J.H. (2010). "Variation in folate pathway genes contributes to risk of congenital heart defects among individuals with Down syndrome". *Genetic Epidemiology*, 34:613-23.

12. Ter-Minassian, M., Wang, Z., Asomaning, K., **Wu, M.C.**, Liu, C.Y., Paulus, J., Liu, G., Bradbury, P., Zhai, R., Su, L., Frauenhoffer, C., Hooshmand, S.M., DeVivo, I., Lin, X., Christiani, D.C., Kulke, M.H. (2011). "A large-scale SNP evaluation of associations with sporadic neuroendocrine tumor risk". *Carcinogenesis*, 32(8):1216-22.

13. **Wu, M.C.**♠, Lee, S.♠, Cai, T., Li, Y., Boehnke, M., Lin, X. (2011). "Rare variant association testing for sequencing data with the sequence kernel association test (SKAT)". *The American Journal of Human Genetics*, 89(1): 82-93. [♠ **Equal Contribution**]
[⋆⋆ **This paper was selected by** *AJHG* **as one the "Best Papers" of 2011-2012** ⋆⋆]

14. Lin, Xinyi, Cai, T., **Wu, M.C.**, Zhou, Q., Liu, G., Christiani, D.C., Lin, X. (2011). "Kernel machine SNP-set analysis for censored survival outcomes in genome-wide association studies". *Genetic Epidemiology*, 35(7):620-31.

15. Glickman, S.W., Shofer, F.S., **Wu, M.C.**, Scholer, M.J., Ndubuizu, A., Cairns, C.B., Glickman, L.T. (2012). "Development and validation of a prioritization rule for obtaining an immediate 12-lead electrocardiogram in the emergency department to identify ST-elevation myocardial infarction ". *The American Heart Journal*, 163(3): 372-382.

16. Theken, K.N., Schuck, R.N., Edin, M.L., Tran, B., Ellis, K., Bass, A., Lih, F.B., Tomer, K.B., Poloyac, S.M., **Wu, M.C.**, Hinderliter, A.L., Zeldin, D.C, Stouffer, G.A., Lee, C.R. (2012) "Evaluation of cytochrome P450-derived eicosanoids in humans with advanced cardiovascular disease". *Atherosclerosis*, 222(2): 530-6.

17. Lee, S., **Wu, M.C.**, Lin, X. (2012). "Optimal tests for rare variant effects in sequencing association studies". *Biostatistics*, 13(4): 762-75.

18. Wu, H., **Wu, M.C.**, Zhi, D., Santorico, S.A., Cui, X. (2012). "Statistical analysis for next generation sequencing". *Frontiers in Genetics*, 3:128.

19. Joubert, B.R., Haberg, S.E., Nilsen, R.M., Wang, X., Vollset, S.E., Murphey, S.K., Huang, Z., Hoyo, C., Midttun, O., Cupul-Uicab, L.A., Ueland, P.M., **Wu, M.C.**, Nystad, W., Bell, D.A., Peddada, S.D., London, S.J. (2012). "450K Epigenome-Wide Scan Identifies Differential DNA Methylation in Newborns Related to Maternal Smoking During Pregnancy". *Environmental Health Perspectives*, 120:1425-31.

20. Bailey, K.M., **Wu, M.C.**, Ward, W.O., Smeester, L., Rager, J.E., Garcia-Varga, G., Del Razo, L., Drobna, Z., Styblo, M., Fry, R.C. (2013). "Arsenic and the epigenome: interindividual differences in arsenic metabolism related to distinct patterns of DNA methylation". *Journal of Biochemical and Molecular Toxicology*, To Appear.

21. Schuck, R.N., Theken, K.N., Edin, M.L., Caughey, M., Bass, A., Ellis, K., Tran, B., Steele, S., Simmons, B.P., Lih, B.P., Tomer, K.B., **Wu, M.C.**, Hinderliter, A.L., Stouffer, G.A., Zeldin, D.R., Lee, C.R. (2013). "Cytochrome P450 derived eicosanoids and vascular function in coronary artery disease patients". *Atherosclerosis*, To Appear.

22. **Wu, M.C.**, Maity, A., Lee, S., Simmons, E.M., Harmon, Q.E., Lin, Xinyi, Engel, S.M, Molldrem, J.J., Armistead, P.M. (2013). "Kernel machine SNP-set testing under multiple candidate kernels". *Genetic Epidemiology*, To Appear.

Technical Reports:
All Reports Available Upon Request:

1. **Wu, M.C.**, Neuberg, D.S., Manola, J., Vail, S. (2005). "Phase III randomized trial of interferon alfa-2b alone versus interferon alfa-2b plus thalidomide in patients with previously untreated metastatic or unresectable renal cell carcinoma". Technical Report 1128E of the *Eastern Cooperative Oncology Group*.

2. **Wu, M.C.**, Lee, J.S. (2006). "Gaussian mixture modeling of polarimetric synthetic aperture radar images for unsupervised terrain classification". Technical Report.

3. **Wu, M.C.**, Lin, X. (2007). "Adaptively penalized logistic regression for testing the significance of gene pathways". Technical Report.

4. Harezlak, J., Jiang, S., **Wu, M.C.**, Wang, M., Christiani, D.C., Lin, X. (2007). "Joint modeling of functional SELDI-TOF mass spectrometry proteomic data and disease risk". Technical Resport.

5. **Wu, M.C.**, Zhang, L., Lin, X. (2008). "Two group classification using sparse linear discriminant analysis". Technical Resport.
   [⋆⋆ **An earlier version won a 2008 ASA Statistical Computing & Graphics Section Student Paper Award** ⋆⋆]

6. **Wu, M.C.** (2009). "Statistical methods for high-dimensional genomic data". Ph.D. Dissertation, Harvard University.

7. Wang, Z., Peterson, M.S., Zhang, L., **Wu, M.C.**, Su, L., Lin, X., Grandjean, P., Christiani, D.C. (2009). "Plasma SELDI-TOF protein profiling in a methylmercury and polychlorinated biphenyl exposed population". Technical Report.

8. Lee, S., **Wu, M.C.**, Cai, T., Li, Y., Boehnke, M., Lin, X. (2011). "Power and sample size calculations for designing rare variant sequencing association studies". Technical Resport.

EXTRAMURAL TALKS & PRESENTATIONS

1. "Flexible Methods for Testing Interactions in Genetic Association Studies", EITC-Bio 2012: Recent Advances in Biomedical Research, Princeton, NJ. (October 2012). {Invited}

2. "Kernel Machine Based Methods for Gene-Environment Interaction Testing In Genetic Association Studies", International Conference on Advances in Interdisciplinary Statistics and Combinatorics, Greensboro, NC. (October 2012). {Invited}

3. "Resampling Based Variable Selection Methods for Next Generation Sequencing Studies", JSM, San Diego, CA. (August 2012). {Topic Contributed}

4. "Estimation and Testing in Genetic Association Studies under the Additive Kernel Machine Model", IMS Asia Pacific Rim, Tsukuba, Japan. (July 2012). {Invited}

5. "Kernel Machine Methods for Assessing Interactions in Genomic Studies", ICSA Applied Statistics Symposium, Boston, MA. (June 2012). {Invited}

6. "Flexible Modeling and Powerful Testing of Interaction in Genome-, Epigenome and Environment-Wide Association Studies in WHI", Annual WHI Investigator Meeting, Washington D.C. (May 2012). {Invited}

7. "Kernel Machine Based Testing of Rare Variant by Environment Interactions", ENAR, Washington D.C. (April 2012). {Invited}

8. "Statistical Issues in Genome Wide Methylation Profiling Studies", Department of Epidemiology and Biostatistics, University of Sourth Carolina, Charleston, SC. (March 2012). {Invited}

9. "Kernel Machine Based Testing of Rare Variant by Environment Interactions", Biostatistics Branch, National Institute of Environmental Health Sciences, Research Triangle Park, NC. (February 2012). {Invited}

10. "Rare Variant Analysis Using the Multi-Kernel Sequence Kernel Association Test", Center for Genomics and Personalized Medicine Research, Wake Forest School of Medicine, Winston-Salem, NC. (February 2012).{Invited}

11. "Rare Variant Analysis Using the Multi-Kernel Sequence Kernel Association Test", Research Triangle Statistical Genetics Conference, Research Triangle Park, NC. (October 2011).{Invited}

12. "Rare Variant Analysis Using the Multi-Kernel Sequence Kernel Association Test", Statistical Analyses for Next Generation Sequencing, University of Alabama at Birmingham, Birmingham, AL. (September 2011).{Abstract Selected for Oral Presentation}

13. "Statistical Issues in the Analysis of Genome Wide Methylation Data", Workshop on Epigenetic Approaches to Studying Prenatal Influences on Childhood Health and Disease, Oslo, Norway. (September 2011). {Invited}

14. "Analysis of High-throughput Sequencing Data via the Sequence Kernel Association Test", Emerging Information and Technology Conferences (EITC-2011), Chicago, IL. (July 2011). {Invited}

15. "Kernel Machine Tests for Rare Genetic Variants in Sequencing Studies", ICSA, New York, NY. (June 2011). {Contributed}

16. "Kernel Machine Based Analysis of High-throughput Sequencing Data", Division of Public Health Sciences, Fred Hutchinson Cancer Research Institute, Seattle, WA. (April 2011). {Invited}

17. "Rare Variant Association Testing Using the Sequence Kernel Association Test (SKAT)", Statistical Genetics Group, GlaxoSmithKline, Research Triangle Park, NC. (December 2010). {Invited}

18. "Rare Variant Association Testing Using the Sequence Kernel Association Test (SKAT)", Department of Statistics, NC State University, Raleigh, NC. (November 2010). {Invited}

19. "Variable Selection in the Kernel Machine Framework via the Garrote Kernel Selector", JSM, Vancouver, BC Canada. (August 2010). {Invited}

20. "Kernel Machine Based Analysis of Genetic Association Studies", First Joint Biostatistics Symposium, Beijing, China. (July 2010). {Invited}

21. "Variable Selection in the Kernel Machine Framework via the Garrote Kernel Selector", Statistical Analysis of Complex Data, Kunming, Yunnan China. (July 2010). {Contributed}

22. "Kernel Machine Methods for the Analysis of Large Scale Genetic Association Studies", ENAR, New Orleans, LA. (March 2010). {Contributed}

23. "Powerful SNP Set Analysis for Case-Control Genome Wide Association Studies", Conference on Human Genetic Variation, Health and Disease: New Knowledge, New Quantitative Challenges. (November 2009). {Poster}

24. "Kernel Machine Approaches for the Analysis of Genome Wide Association Studies", Emerging Information and Technology Conferences (EITC-2009), Cambridge, MA. (August 2009). {Invited}

25. "Kernel Based Variable Selection via the Garrote Kernel Selector", ICSA Applied Statistics Symposium, San Francisco, CA. (June 2009). {Invited}

26. "Variable Selection in the Kernel Machine Framework", ENAR, San Antonio, TX. (March 2009). {Contributed}

27. "Regularization and Variable Selection in Classification and Regression Problems using Omics Data", Department of Statistics, Cornell University, Ithaca, NY. (March 2009). {Invited}

28. "Regularization and Variable Selection in Classification and Regression Problems using Omics Data", Division of Public Health Sciences, Fred Hutchinson Cancer Research Institute, Seattle, WA. (February 2009). {Invited}

29. "Inferential Strategies for High-dimensional 'Omics' Data", Department of Biostatistics, University of North Carolina - Chapel Hill, Chapel Hill, NC. (February 2009). {Invited}

30. "Inferential Strategies for High-dimensional 'Omics' Data", Department of Epidemiology and Biostatistics, University of Maryland, College Park, MD. (February 2009). {Invited}

31. "Regularization and Variable Selection in Classification and Regression Problems using Omics Data", Department of Statistics, University of Virginia, Charlottesville, VA. (February 2009). {Invited}

32. "Regularization and Variable Selection in Predictive Modelling using Omics Data", Department of Statistics, North Carolina State University, Raleigh, NC. (February 2009). {Invited}

33. "Regularization and Variable Selection in Predictive Modelling using Omics Data", Department of Biostatistics, Johns Hopkins University, Baltimore, MD. (January 2009). {Invited}

34. "Inferential Strategies for High-dimensional 'Omics' Data", Department of Biostatistics, Yale University, New Haven, CT. (January 2009). {Invited}

35. "Regularization and Variable Selection in Predictive Modelling using Omics Data", Department of Statistics, U.C. Davis, Davis, CA. (January 2009). {Invited}

36. "Genomic Feature Based Analysis of Genome Wide Association Studies via Logistic Kernel Machines", Racebrook Environmental Statistics Symposium, Sheffield, MA. (November 2008).

37. "Identification of Genes and Gene Pathways Associated with Metal Particulate Exposure using Sparse Linear Discriminant Analysis", GENI, Boston, MA. (October 2008). {Contributed Poster}

38. "Methods for Detection of Prostate Cancer Auto-antibody Response from High Density Self-Assembling Protein Microarrays", Harvard Institute of Proteomics, HMS, Cambridge, MA. (September 2008). {Invited}

39. "Sparse Linear Discriminant Analysis for Classification and Testing Gene Pathways", JSM, Denver, CO. (August 2008). {Topic Contributed Session for ASA Stat. Computing/Graphics Student Paper Competition Winners}

40. "Use of Sparse Linear Discriminant Analysis in Testing Gene Pathways", ICSA Applied Statistics Symposium, Piscataway, NJ. (June 2008). {Invited}

41. "A Parametric Permutation Test for Regression Coefficients in LASSO Regularized Regression for High Dimensional Data", ENAR, Arlington, VA. (March 2008). {Contributed}

42. "Use of Variable Selection in Testing the Significance of Gene Sets", ENAR, Atlanta, GA. (March 2007). {Contributed}

43. "Prior Biological Knowledge Based Approach for Analysis of Genome-Wide Expression Profiles", Racebrook Environmental Statistics Symposium, Sheffield, MA. (November 2006). – Joint Presentation with Dr. Zhaoxi (Mike) Wang

INTRAMURAL TALKS & PRESENTATIONS

1. "Statistical Methods for the Analysis of Sequencing Data", NC TRaCS Biostatistics Grand Rounds, UNC, Chapel Hill, NC. (January 2012).

2. "Environmentally Friendly Approaches for the Analysis of Genomic Data", Department of Biostatistics Colloqium, UNC, Chapel Hill, NC. (January 2012).

3. "Analysis of Genome Wide Expression Profile Experiments", NC TRaCS Biostatistics Seminar Series, UNC, Chapel Hill, NC. (September 2010).

4. "A Direct and Powerful Approach for Testing Rare Variants", Mini-Symposium on Next-Generation Sequencing and Analysis, UNC, Chapel Hill, NC. (May 2010).

5. "Prior biological knowledge based approaches for the analysis of genome-wide expression profiles using gene sets and pathways", Lineberger Comprehensive Cancer Center, UNC, Chapel Hill, NC. (March 2010).

6. "HD-TVs: An overview of High Dimensional Testing and Variable Selection", (First) Biostatistics Student Invited Seminar, UNC, Chapel Hill, NC. (January 2010).

7. "Gene Set Analysis using Sparse Linear Discriminant Analysis", NC TRaCS Biostatistics Grand Rounds, UNC, Chapel Hill, NC. (November 2009).

8. "Sparse Linear Discriminant Analysis for Simultaneous Testing for the Significance of a Gene Set/Pathway and Gene Selection", Correlated and High-Dimensional Data Seminar Series, HSPH, Boston, MA. (October 2008).

9. "Sparse Linear Discriminant Analysis for Testing Differential Gene Pathway Activity Induced by Metal Particulate Exposure", Environmental Statistics Seminar Series, HSPH, Boston, MA. (May 2008).

10. "An Overview of Variable Selection Procedures for High Dimensional Data", Correlated and High-Dimensional Data Seminar Series, HSPH, Boston, MA. (October 2006). – Joint Presentation with Dr. Tianxi Cai

SELECTED BIOMEDICAL ABSTRACTS & POSTERS

1. Vincent, B., Singh, D., **Wu, M.C.**, Hunsucker, S.A., Alatrash, G., Ruisaard, K., Sukhu-malchandra, P., Clise-Dwyer, K., Serody, J., Prins, J., Molldrem, J.J., Armistead, P.M. "RNA-Seq expression profiling of AML leukemia stem cells reveals differential expression of lineage differentiation markers and novel splice variants". *American Society of Hematology*, Atlanta, GA. (December 2012).

2. Harmon, Q.E., Engel, S.M., **Wu, M.C.**, Stuebe, A., Avery, C.L. "Applying Inverse Probability Weighting to Estimate Risk Ratios when Genotyping Data are Available in a Subset". *Society for Epidemiologic Research*, Minneapolis, MN. (June 2012).

3. Harmon, Q.E., Engel, S.M., **Wu, M.C.**, Stuebe, A., Avery, C.L., Moran, T., Luo, J., Olshan, A.F. "Polymorphisms in genes associated with natural killer cells are associated with preterm birth". *Society for Epidemiologic Research*, Minneapolis, MN. (June 2012).

4. Joubert, B.R., Haberg, S.E., Nilsen, R.M., Wang, X., Bell, D.A., Cupul-Uicab, L., **Wu, M.C.**, Vollset, S.E., Ueland, P.M., Peddada, S.D., Nystad, W., London, S.J. "Maternal tobacco smoke exposure relates to epigenetic changes in fetal cord blood: A genome-wide methylation study". *American Thoracic Society International Conference*, San Francisco, CA. (May 2012), and *Epigenomics of Common Disease*, Baltimore, MD. (September 2012).

5. Carroll, I.M., Ringel-Kulka, T., Bueno, L., **Wu, M.C.**, Siddle, J., Ringel, Y. "Fecal Serine Protease Activity in Patients With IBS is Associated With Specific Alterations in the Intestinal Microbiota". *Digestive Disease Week*, San Diego, CA. (May 2012).

6. Glickman, S.W., Shofer, F.S., **Wu, M.C.**, Scholer, M.J., Ndubuizu, A., Cairns, C.B., Glickman, L.T. "A triage rule to identify patients in need of an immediate 12-lead electrocardiogram in the emergency department to diagnose ST-Elevation Myocardial Infarction". *Society For Academic Emergency Medicine Annual Meeting*, Boston, MA. (June 2011).

7. Ter-Minassian, M., Wang, Z., Asomaning, K., **Wu, M.C.**, Liu, C.Y., Paulus, J., Liu, G., Bradbury, P.A., Zhai, R., Su, L., Frauenhoffer, C., Hooshmand, S.M., DeVivo, I., Lin, X., Christiani, D.C., Kulke, M.H. "A large-scale SNP evaluation of associations with sporadic neuroendocrine tumor risk". *Neuroendocrine Tumor Symposium*, Santa Fe, NM. (October 2010).

8. Ter-Minassian, M., Wang, Z.M., Asomaning, K., **Wu, M.C.**, Liu, C.Y., Su, L., Frauenhoffer, C.S., Hooshmand, S.M., Silver, J., Lin, X., Christiani, D.C., Kulke, M. "Association of a TSC2 SNP with sporadic neuroendocrine tumor risk," Presented at: *AACR Annual Meeting*, Denver, CO. (April 2009), *HSPH Poster Day*⋆, Boston, MA (May 2009), and *Annual Meeting of the North American NeuroEndocrine Tumor Society*, Charlotte, NC. (October 2009). [⋆ **Honorable Mention Best Poster Award**]

9. Ter-Minassian, M., Wang, Z.M., Asomaning, K., **Wu, M.C.**, Liu, C.Y., Su, L., Lin, X., Liu, G., Christiani, D.C. "Genetic susceptibility to esophageal adenocarcinoma," *AACR Annual Meeting*, Denver, CO. (April 2009).

10. Huang, Y.T., Wang, Z., Chirieac, L.R., **Wu, M.C.**, Lin, X., Haugen, A., Zhou, W., Kulke, M., Heist, R.S., Su, L., Asomaning, K., Christiani, D.C. "Genome-wide survival analysis in early stage non-small cell lung cancer using GeneChip 250K Nsp array: discovery and validation," Presented at: *AACR Annual Meeting*, San Diego, CA. (April 2008) and *HSPH Poster Day*⋆, Boston, MA (May 2008). [⋆ **Won Best Poster Award**]

11. Huang, Y.T., Wang, Z., Chirieac, L.R., **Wu, M.C.**, Lin, X., Zhou, W., Kulke, M., Heist, R.S., Su, L., Asomaning, K., Christiani, D.C. "Genome-wide survival analysis in early stage non-small cell lung cancer using GeneChip 250K Nsp array," Presented at: *AACR Annual Meeting*, Los Angeles, CA (April 2007) and *HSPH Poster Day*⋆, Boston, MA (May 2007). [⋆ **Honorable Mention Best Poster Award**]

Current Grants Served as Co-Investigator

- Mucus and Hypoxia in Heterogeneous and Progressive CF Lung Disease
  NIH/NHLBI, P.I. Marianne Muhlebach
  R01-HL116228, 2012-2016, $1,646,850 (direct)

- Influence of Genetic Markers on Exposure Assessment Models
  CDC/NIOSH, P.I. Leena Nylander-French
  R21-OH010203, 2012-2014, $269,670 (direct)

- Design and Analysis of Sequencing-based Studies for Complex Human Traits
  NIH/NHGRI, P.I. Yun Li
  R01-HG006292, 2011–2016, $1,250,000 (direct)

- Prenatal Smoking, Maternal and Fetal Genetic Variation and Risk of Preeclampsia
  NIH/NICHD, P.I. Stephanie Engel
  R01-HD058008, 2011-2013, $799,732 (direct)

- Elucidating Risks: From Exposure and Mechanism to Outcome - Core D
  NIH/NIEHS, P.I. James Swenberg
  P42-ES005948, 2011–2016, $12,068,587 (direct)

Paper and Conference Review

American Journal of Epidemiology, American Journal of Human Genetics, Annals of Applied Statistics, Annals of Human Genetics, Annals of Statistics, Bioinformatics, Biometrics, Biostatistics, BMC Bioinformatics, BMC Genetics, BMC Medical Genomics, Genetic Epidemiology, Genetic Medicine, Genetics, Human Heredity, Intelligent Systems for Molecular Biology (ISMB), Journal of Applied Statistics, Journal of the American Statistical Association (JASA), The Pharmacogenomics Journal, PLOS Genetics, PLOS One, Proceedings of the National Academy of Sciences (PNAS), Statistical Applications in Genetics and Molecular Biology, Statistics in Medicine, Technometrics.

Editorial Roles

- StatBlog, Associate Editor: 2013 – Present.

Grant Review

- Biostatistical Reviewer, Susan G. Komen Foundation, 2012.
- External Reviewer, Health Effects Institute, 2012.

National Committee Appointments

- Chair, Planning Committee, ENAR Junior Researcher Workshop, 2012 – 2013.
- Member, Planning Committee, ENAR Junior Researcher Workshop, 2011 – Present

Invited Conference Sessions Organized and Chaired

- Organizer, Session on "Statistical Methods for High Dimensional Genomic Data," IMS Asia Pacific Rim Meeting, 2012, Tsukuba, Japan
- Organizer, Session on "Statistical Methods and Applications in Rare Variant Sequencing Studies," ENAR, 2012, Washington D.C.
- Chair, First Joint Biostatistics Symposium, 2010, Beijing, China
- Chair, ENAR, 2009, San Antonio, TX
- Chair, ICSA Applied Statistics Symposium, 2008, Piscataway, NJ

Professional Organization Memberships:

- American Statistical Association (2003 – Present)
- Institute of Mathematical Statistics (2003 – Present)
- International Society for Computational Biology (2003 – Present)

- Eastern North American Region, International Biometric Society (2007 – Present)
- International Chinese Statistical Association (2008 – Present)
- American Society of Human Genetics (2009 – Present)
- International Genetic Epidemiology Society (2009 – Present)

Other:
- Judge, ENAR Regional Advisory Board Poster Competition 2012

Doctoral Dissertations Directed
1. Jennifer Clark, 2009 – Present.
2. Eugene Urrutia, 2010 – Present.
   His dissertation received the *2011 American Society of Human Genetics Trainee Research Semifinalist Award.*
3. Thomas Stewart, 2011 – Present. (Co-advisor: Donglin Zeng)
4. Ni Zhao, 2012 – Present.
5. Sebastian Teran Hidalgo, 2012 – Present. (Co-advisor: Michael Kosorok)

Undergraduate Research Mentor
1. Elizabeth Simmons, 2009 – 2011.

Biostatistics Doctoral Committee Membership
1. Qianchuan Chad He, 2011 – 2012. (Advisor: Danyu Lin)
2. Andrea Byrnes, 2011 – Present. (Advisor: Yun Li)
3. Alison Wise, 2011 – Present. (Advisor: Clarice Weinberg)
4. Kuan-Chieh Huang, 2012 – Present. (Advisor: Yun Li)
5. Xiaoxi Liu, 2012 – Present. (Advisor: Donglin Zeng)

Non-Biostatistics Doctoral Committee Membership
1. Christopher Cabanski, 2010 – 2012. (Statistics; Advisor: Steve Marron)
2. Quaker Harmon, 2011 – 2012. (Epidemiology; Avisor: Stephanie Engel)
3. Jeremy Sabourin, 2011 – Present. (Statistics; Advisor: Will Valdar & Andrew Nobel)
4. Zachary Robbins, 2011 – Present. (Environmental Science and Engineering; Advisor: Leena Nylander-French)
5. Brionna Hair, 2012 – Present. (Epidemiology; Advisor: Melissa Troester)
6. Leila Family, 2012 – Present. (Epidemiology; Advisor: Andy Olshan & Melissa Troester)

Academic/Course Advisor
- 2010: Jung In Kim, Maria Reynolds
- 2012: Brian Barkley

Lineberger Comprehensive Cancer Center, The University of North Carolina at Chapel Hill:
- Lineberger Data Warehouse and Biorepository (LDBR) Data Sharing Committee: 2012 – Present.

Department of Biostatistics, The University of North Carolina at Chapel Hill:
- Awards Committee: 2009 – 2012.
- Masters Examinations Committee: 2010 – Present.
- Information Technology Committee: 2012 – Present.

Department of Biostatistics, Harvard University:
- Student Admissions Committee: 2004 – 2005
- Departmental Representative, Graduate Student Council: 2006 – 2009

Community:
- Volunteer martial arts and self-defense instructor

Department of Biostatistics, The University of North Carolina at Chapel Hill
Chapel Hill, North Carolina USA
Instructor

Biostat 660: Probability and Statistical Inference I
Fall 2010, Fall 2012: Core course for MS, DrPH, and beginning Ph.D. students.

Biostat 735: Statistical Computing
Fall 2011: Ph.D. level elective course.

Guest Instructor

2011-2012: BIOS 740, BCB 725
2012-2013: PHYI 703

Department of Biostatistics, Harvard University
Boston, Massachusetts USA
Derek Bok Center Departmental Teaching Fellow

Co-Head Teaching Fellow, Biostatistics Department
2008-2009: Developed, organized, and led training programs for graduate TAs.

Instructor

Summer Course in Probability
Summer 2008 & 2007: Required course for incoming biostatistics Ph.D. students.

Teaching Assistant

Biostat 277: Computational Biology (Advanced)
Fall 2008: Advanced elective course for biostatistics Ph.D. students.

Biostat 251: Statistical Inference II
Fall 2007: Advanced core course for biostatistics Ph.D. students.

Biostat 230: Probability Theory and Applications I
Fall 2006: Core course for first year biostatistics Ph.D. students.

Biostat 205: Biostatistics for Health Policy
Fall 2005: Introductory biostatistics course for social science MPH students.

Biostat 200: Introduction to Biostatistics
Fall 2004: Introductory biostatistics course for biomedical MPH students.

Technical Skills
- Programming Languages: C, C++(STL), JAVA, PYTHON, PASCAL, BASIC, knowledge of LISP and PERL.
- Software: R/S-PLUS, MATLAB, PV-WAVE/IDL, SAS, STATA.
- Operating Systems: Unix and Windows.
- Languages: Mandarin Chinese, knowledge of Spanish.