

Michael C. Wu

1100 Fairview Avenue North
M3-C102
Seattle, WA 98109-1024
Phone: 206-667-6603
<http://research.fhcrc.org/wu/>

2914 W Mansell St.
Seattle, WA 98199
Cell: 410-917-6621
FAX: 206-667-4408
mcwu@fhcrc.org

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
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.

PROFESSIONAL EXPERIENCE

Division of Public Health Sciences, Fred Hutchinson Cancer Research Center
Seattle, Washington USA

Associate Member

June 2016 – Present

Assistant Member

September 2013 – May 2016

Department of Biostatistics, University of Washington
Seattle, Washington USA

Affiliate Assistant Professor

January 2015 – Present

Fred Hutchinson/University of Washington Cancer Consortium
Seattle, Washington USA

Member

November 2013 – Present

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

Assistant Professor (Adjunct)

November 2014 – Present

Assistant Professor (On Leave)

September 2013 – August 2014

Assistant Professor (Tenure Track)

September 2009 – August 2013

Carolina Center for Genome Sciences, and Center for Environmental Health and Susceptibility, The University of North Carolina at Chapel Hill
Chapel Hill, North Carolina USA

Member

September 2009 – August 2013

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

**HONORS &
AWARDS**

- *American Journal of Epidemiology/Society for Epidemiologic Research* Paper of the Year: 2014
- *American Journal of Epidemiology* “Editor’s Choice” Article: 2014
- Article Selected by *American Journal of Human Genetics* as “Best of” 2011-2012
- UW Biostatistics Retreat, Best Faculty Presentation (as voted by students): 2013
- 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

**PROFESSIONAL
ACTIVITIES**

Grant Review (Extramural)

- Reviewer, NIH, NIDDK Special Emphasis Panel: ZDK1 GRB-1 (J3), 2013.
- Reviewer, NIH, NIEHS Special Emphasis Panel: ZES1 ARL-K (C1), 2015.
- *Ad hoc* Reviewer, NIH: DDK-C Study Section: 2015, 2016.
- External Reviewer, Health Effects Institute, 2012, 2013.
- Biostatistical Reviewer, Susan G. Komen Foundation, 2012, 2014, 2015.

Editorial Roles

- *Stat*, StatBlog Associate Editor: 2013.
- *PLOS Computational Biology*, Guest Editor: 2013.
- *Clinical Cancer Research*, Member, Editorial Board: 2014 – Present.

Paper and Conference Review

- *American Journal of Bioethics*
- *American Journal of Epidemiology*
- *American Journal of Human Genetics*
- *Annals of Applied Statistics*
- *Annals of Human Genetics*
- *Annals of Statistics*
- *Bioinformatics*
- *Biometrical Journal*
- *Biometrics*
- *Biometrika*
- *Biostatistics*
- *BMC Bioinformatics*

- *BMC Genomics*
- *BMC Genetics*
- *BMC Medical Genomics*
- *BMC Medical Research Methodology*
- *Carcinogenesis*
- *Clinical Cancer Research*
- *Environmental Health Perspectives*
- *Epigenetics*
- *Epigenomics*
- *European Journal of Human Genetics*
- *Frontiers in Genetics*
- *Genetic Epidemiology*
- *Genetic Medicine*
- *Genetics*
- *Human Heredity*
- *Intelligent Systems for Molecular Biology*
- *Journal of Applied Statistics*
- *Journal of the American Statistical Association*
- *Microbiome*
- *Molecular Psychiatry*
- *mSystems*
- *The Oncologist*
- *Oncotarget*
- *The Pharmacogenomics Journal*
- *PLOS Computational Biology*
- *PLOS Genetics*
- *PLOS One*
- *Proceedings of the National Academy of Sciences*
- *Statistical Applications in Genetics and Molecular Biology*
- *Statistics in Medicine*
- *Technometrics*

Committee Appointments

- Member, Organizing Committee, BIRS Workshop on *Emerging Statistical Challenges and Methods For Analysis of Massive Genomic Data in Complex Human Disease Studies*, 2012 – 2014.
- Chair, Planning Committee, ENAR Junior Researcher Workshop, 2012 – 2013.
- Member, Planning Committee, ENAR Junior Researcher Workshop, 2011 – 2015.
- JSM Program Chair, ASA Section on Statistical Genetics and Genomics, 2017.

Invited Conference Sessions Organized and Chaired

- Organizer, Session on “Statistical Methods for Addressing Challenges in Microbiome and Metagenomic Analysis,” ENAR 2016, Austin, TX
- Organizer/Chair, Session on “New Statistical Methods for Analysis of High Dimensional Genomic Data,” ICSA and KISS Joint Applied Statistical Symposium, 2014, Portland, OR.
- 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)

GRANTS AND CONTRACTS

Active

- Principal Investigator of the Subcontract and Co-Investigator, “Enhanced Gene Identification in Complex Traits using Kernel Machines,” NIH/NHGRI, R01-HG007508, PI: Michael Epstein (Human Genetics, Emory University), 2013-2017, 15% Effort.
- Principal Investigator, “New Statistical Faculty Translational Medicine Development Award”, The Hope Foundation, 2013-2016. 30% effort.
- Faculty Biostatistician, “SWOG Statistics and Data Management Center (SDMC),” NIH/NCI, U10 CA180819, PI: Michael LeBlanc (FHCRC), 2014-2019. 50% Effort.
- Faculty Biostatistician, “Lung-MAP: S1400 Biomarker-Targeted Second-Line Therapy in Treating Patients With Recurrent Stage IIIB-IV Squamous Cell Lung Cancer”, SWOG-CTI, PI: Michael Leblanc (FHCRC), 2014-2019. 5% Effort

Submitted (Pending Review, Council or Revision)

- Co-Investigator, “Statistical Methods to Study Immune Microenvironment in Tumors,” NIH, R01, PI: Wei Sun (PHS, FHCRC), 2016-2019.
- Co-Investigator, “Modeling Relationships Between Gut Microbiota and Metabolic Health in the MEC,” NIH, R21, PIs: Tim Randolph, Meredith Hullar, Mario Kratz (PHS, FHCRC), 2016-2018.
- Principal Investigator of the Subcontract and Co-Investigator, “Development of a Clinical Tool to Detect Basal Bladder Cancers,” NIH/NCI, UH2/UH3, PIs: David McConkey (SWOG, MDACC) and Seth Lerner (SWOG, Baylor College of Medicine), 2016-2020.
- Principal Investigator (Multi) , “New Statistical Methods for Microbiome Sequencing Data,” NIH, R01. Multi-PIs: Michael Wu (Contact) and Jun Chen (Mayo Clinic). 2016 - 2021.
- Principal Investigator of the Subcontract and Co-Investigator, “The Vaginal Microbiome and Racial Disparity in Preterm Delivery,” NIH/NICHHD, R01, PI: Stephanie Engel (Epidemiology, UNC), 2016-2020.
- Co-Investigator, “Genetic Fine Mapping with Kernel Machine Methods,” NIH, R21, PI: Q. Chad He (PHS, FHCRC), 2016-2018.
- Co-Investigator, “SCLC Team for Advancing Research (START),” NIH, U24, PI: Ravi Salgia (City of Hope), Subcontract PI: Mary Redman (CRD, FHCRC). 2016 – 2021.

Completed

- Co-Investigator, “Mucus and Hypoxia in Heterogeneous and Progressive CF Lung Disease,” NIH/NHLBI, R01-HL116228, PI: Marianne Muhlebach (Pediatrics, UNC), 2012-2013, 5% Effort.
- Co-Investigator, “Influence of Genetic Markers on Exposure Assessment Models,” CDC/NIOSH, R21-OH010203, PI: Leena Nylander-French (Environmental Sciences and Engineering, UNC), 2012 – 2013, 10% Effort.
- Co-Investigator, “Design and Analysis of Sequencing-based Studies for Complex Human Traits,” NIH/NHGRI, R01-HG006292, PI: Yun Li (Genetics, UNC), 2011–2013, 25% Effort, \$1,250,000 (direct)
- Co-Investigator, “Prenatal Smoking, Maternal and Fetal Genetic Variation and Risk of Preeclampsia,” NIH/NICHHD, R01-HD058008, PI: Stephanie Engel (Epidemiology, UNC), 2011-2013, 20% Effort.
- Co-Investigator, “Elucidating Risks: From Exposure and Mechanism to Outcome - Core D,” NIH/NIEHS, P42-ES005948, PI: James Swenberg (Environmental Sciences and Engineering, UNC), 2011–2013, 5% Effort.

- Biostatistician, “UNC Clinical Translation Science Award - Biostatistics Core,” NIH/NCRR, UL1 TR000083-05, PI: Marschall Runge (Medicine, UNC), 2009 – 2013, 20% Effort.
- Biostatistician, “UNC-CH Center for Environmental Health & Susceptibility - Facility Core 2: Biostatistics & Bioinformatics,” NIH/NIEHS, P30 ES010126-09S1, PI: James Swenberg (Environmental Sciences and Engineering, UNC), 2009 – 2012.

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. PMID: 15976454
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. PMID: 16103089
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., Badesy, N., Sharpless, N.E., Wong, K-K. (2007). “LKB1 modulates lung cancer differentiation and metastasis”. *Nature*, 448(7155):807-10. PMID: 17676035
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. PMID: 18173220
[# 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. PMID: 18185912
- *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. PMC2732305
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. PMC2690391
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. PMC2827341
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. PMC3032061
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. PMC2893800

*AN EARLIER VERSION WON A 2008 ICSA APPLIED STATISTICS SYMPOSIUM STUDENT AWARD AND A 2008 ASA STATISTICAL COMPUTING & GRAPHICS SECTION STUDENT PAPER AWARD

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. PMC3378053
12. Ter-Minassian, M., Wang, Z., Asomaning, K., **Wu, M.C.**, Liu, C.Y., Paulus, J., Liu, G., Bradbury, P., Zhai, R., Su, L., Fraumeni, C., Hooshmand, S.M., DeVivo, I., Lin, X., Christiani, D.C., Kulke, M.H. (2011). "Genetic associations with sporadic neuroendocrine tumor risk". *Carcinogenesis*, 32(8):1216-22. PMC3149206
- [†]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. PMC3135811 [# Equal Contribution]
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. PMC3373190
15. Glickman, S.W., Shofer, F.S., **Wu, M.C.**, Scholer, M.J., Ndubizu, 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. PMID: 22424007
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 stable atherosclerotic cardiovascular disease". *Atherosclerosis*, 222(2): 530-6. PMC3361525
17. Lee, S., **Wu, M.C.**, Lin, X. (2012). "Optimal tests for rare variant effects in sequencing association studies". *Biostatistics*, 13(4): 762-75. PMC3440237
18. Wu, H., **Wu, M.C.**, Zhi, D., Santorico, S.A., Cui, X. (2012). "Statistical analysis for next generation sequencing – meeting report". *Frontiers in Genetics*, 3:128. PMC3395795
- [‡]19. Joubert, B.R., Håberg, S.E., Nilsen, R.M., Wang, X., Vollset, S.E., Murphey, S.K., Huang, Z., Hoyo, C., Middtun, Ø., 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. PMC3491949
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*, 27(2): 106-115. PMC3892431
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*, 227: 442-448. PMC3638946
22. **Wu, M.C.**, Maity, A., Lee, S., Simmons, E.M., Harmon, Q.E., Lin, Xinyi, Engel, S.M., Moll-drem, J.J., Armistead, P.M. (2013). "Kernel machine SNP-set testing under multiple candidate kernels". *Genetic Epidemiology*, 37(3): 267-75. PMC3769109
23. Bencharit, S., Baxter, S.S., Carlson, J., Byrd, W.C., Mayo, M.V., Border, M.B., Kohlfarber, H., Urrutia, E., Saldarriaga, I., Howard-Williams, E.L., Offenbacher, S., **Wu, M.C.**, Buse, J.B. (2013). "Salivary proteins associated with hyperglycemia in diabetes: a proteomic analysis". *Molecular Biosystems*, 9: 2785-97. PMC3888809

[†]THIS PAPER WAS SELECTED BY *AJHG* AS THE "BEST OF" 2011-2012

[‡]THIS PAPER WAS SELECTED BY *EHP* AS THE "2013 PAPER OF THE YEAR"

24. Harmon, Q.E., Engel, S.M., Olshan, A., Moran, T., Stuebe, A., Luo, J., **Wu, M.C.**, Avery, C. (2013). "Association of polymorphisms in natural killer cell-related genes with preterm birth". *American Journal of Epidemiology*, 178(8): 1208-18. PMC3792727
25. Carroll, I.M., Ringel-Kulka, T., Ferrier, L., **Wu, M.C.**, Siddle, J.P., Bueno, L., Ringel, Y. (2013). "Fecal protease activity is associated with compositional alterations in the intestinal microbiota". *PLOS One*, 8(10): e78017. PMC3798377
26. Byrnes, A.E., **Wu, M.C.**, Wright, F.A., Li, M., Li, Y. (2013). "The value of statistical or bioinformatics annotation for rare variant association with quantitative trait". *Genetic Epidemiology*, 37(7): 267-75. PMC4083762
27. Cleary, S.P., Jeck, W.R., Zhao, X., Chen, K., Selitsky, S.R., Savich, G.L., Tan, T.X., **Wu, M.C.**, Getz, G., Lawrence, M.S., Parker, J.S., Li, J., Powers, S., Kim, H., Fischer, S., Giundi, M., Ghanekar, A., Chiang, D.Y. (2013). "Identification of driver genes in hepatocellular carcinoma by exome sequencing". *Hepatology*, 58(5): 1693-1702. PMC3830584
28. Sanders, A.P., Smeester, L., Rojas, D., DeBussycher, T., **Wu, M.C.**, Wright, F.A., Zhou, Y., Laine, J.E., Rager, J.E., Swamy, G.K., Ashley-Koch, A., Miranda, M.L., Fry, R.C. (2014). "Cadmium exposure and the epigenome: exposure-associated patterns of DNA methylation in leukocytes from mother-baby pairs". *Epigenetics*, 9(2): 212-221. PMC3962531
29. **Wu, M.C.**, Joubert, B.R., Kuan, P.F., Häberg, S.E., Nystad, W., Peddada, S.D., London, S.J. (2014). "A systematic assessment of normalization approaches for the Infinium 450k methylation platform". *Epigenetics*, 9(2): 318-329. PMC3962542
- [§]30. Engel, S.M.#, Joubert, B.R.#, **Wu, M.C.#**, Olshan, A.F., Häberg, S.E., Ueland, P.M., Nystad, W., Nilsen, R.M., Vollset, S.E., Peddada, S.D., London, S.J. (2014). "Neonatal genome-wide methylation patterns in relation to birthweight in the Norwegian Mother and Child Birth Cohort". *American Journal of Epidemiology*, 179(7): 834-42. PMC3969535 [# Equal Contribution]
31. Ebert, C.S. Jr., McKinney, K.A., Urrutia, E., **Wu, M.**, Rose, A.S., Fleischman, G.M., Thorp, B., Senior, B.A., Zanation, A.M. (2014). "Expression of protease-activated receptors in allergic fungal rhinosinusitis". *International Forum of Allergy & Rhinology*, 4(4): 266-71. PMID:24500840
32. Harmon, Q.E., Engel, S.M., **Wu, M.C.**, Moran, T., Luo, J., Stuebe, A., Avery, C., Olshan, A. (2014). "Polymorphisms in inflammatory genes associated with term SGA and preeclampsia". *American Journal of Reproductive Immunology*, 71(5): 472-84. PMC4040534
33. Joubert, B.R., Häberg, S.E., Bell, D.A., Nilsen, R.M., Vollset, S.E., Midttun, Ø., Ueland, P.M., **Wu, M.C.**, Nystad, W., Peddada, S.D., London, S.J. (2014). "Maternal smoking and DNA methylation in newborns: *In utero* effects or epigenetic inheritance?". *Cancer Epidemiology, Biomarkers, & Prevention*, 23(6): 1007-17. PMC4140220
34. Nylander-French, L.A., **Wu, M.C.**, Boyner, J., Smeester, L., Sanders, A.P., French, J.E., Fry, R.C. (2014). "DNA methylation modifies urine biomarker levels in 1,6-hexamethylene diisocyanate (HDI) exposed workers: a pilot study". *Toxicology Letters*, 231(2): 217-26. PMID:25445006.
35. Zhao, N., Bell, D.A., Maity, A., Staicu, A.-M., Joubert, B.R., London, S.J., **Wu, M.C.** (2015). "Global analysis of methylation profiles from high resolution CpG data". *Genetic Epidemiology*, 39(2): 53-64. PMC4314375
36. Family, L., Bensen, J.T., Troester, M.A., **Wu, M.C.**, Anders, C.K., Olshan, A.F. (2015). "Single nucleotide polymorphisms in DNA bypass polymerase genes and association with breast cancer and breast cancer subtypes among African Americans and Whites". *Breast Cancer Research and Treatment*, 149(1):181-90. PMC4498665.

[§]THIS PAPER WAS SELECTED AS AN *AJE* "EDITOR'S CHOICE" ARTICLE AND WAS ALSO SELECTED AS AN *AJE* AND *SER* "2014 PAPER OF THE YEAR"

37. Hair, B.Y., Troester, M.A., Edmiston, S.N., Parrish, E.A., Robinson, W.R., Wu, M.C., Olshan, A.F., Swift-Scanlan, T., Conway, K. (2015). "Body mass index is associated with gene methylation in estrogen receptor-positive breast tumors". *Cancer Epidemiology, Biomarkers, & Prevention*, 24(3):580-86. PMC4355173
38. Zhao, N., Chen, J., Carroll, I.M., Ringel-Kulka, T., Epstein, M.P., Zhou, H., Zhou, J.J., Ringel, Y., Li, H., Wu, M.C. (2015). "Testing in microbiome profiling studies with MiRKAT, the Microbiome Regression-based Kernel Association Test" *The American Journal of Human Genetics*, 96(5): 797-807. PMC4570290
39. Hair, B.Y., Xu, Z., Kirk, E., Harlid, S., Sandhu, R., Robinson, W.R., Wu, M.C., Olshan, A.F., Conway, K., Taylor, J., Troester, M.A. (2015). "Body mass index associated with genome-wide methylation in breast tissue". *Breast Cancer Research and Treatment*, 151(2): 453-63. PMC4474159.
40. Bohlin, J., Andreassen, B.K., Joubert, B.R., Magnus, M., Wu, M.C., Parr, C.L., Håberg, S.E., Magnus, P., Reese, S.E., Stoltenberg, C., London, S.J., Nystad, W. (2015). "Effect of maternal gestational weight gain on offspring DNA methylation: a follow-up to the ALSPAC cohort study". *BMC Research Notes*, 8:321. PMC4518864
41. Urrutia, E., Lee, S., Maity, A., Zhao, N., Shen, J., Li, Y., Wu, M.C. (2015). "Rare variant testing across methods and thresholds using the multi-kernel sequence kernel association test (MK-SKAT)". *Statistics and Its Interface*, 8: 495-505. PMC4698916
42. Geybels, M.S., Zhao, S., Wong, C., Bibikova, M., Klotzle, B., Wu, M., Ostrander, E.A., Fan, J., Feng, Z., Stanford, J.L. (2015). "Epigenome-wide profiling of DNA methylation in paired prostate cancer versus adjacent benign tissue". *The Prostate*, 75(16): 1941-50. PMC4928710
43. Chen, J., Chen, W., Zhao, N., Wu, M.C., Schaid, D.J., (2016). "Small sample kernel association test for human genetic and microbiome association studies". *Genetic Epidemiology*, 40(1): 5-19. PMC4679685
44. Joubert, B.R., den Dekker, H.T., Felix, J.F., Bohlin, J., Beckett, E., Tiemeier, H., van Meurs, J.B., Uitterlinden, A.G., Hofman, A., Håberg, S.E., Reese, S.E., Andreassen, B.K., Nilsen, R.M., Vollset, S.E., Midttun, Ø., Ueland, P.M., Wu, M.C., Wang, T., Peddada, S.D., Jaddoe, V.W.V., Nystad, W., Dujits, L., London, S.J. (2016). "Maternal plasma folate during pregnancy impacts differential DNA methylation in an epigenome-wide meta-analysis of newborns". *Nature Communications*, 7:10577. PMC474995
45. Suderman, M., Stene, L.C., Bohlin, J., Page, C.M., Holvik, K., Parr, C.L., Magnus, M.C., Håberg, S.E., Joubert, B.R., Wu, M.C., London, S.J., Relton, C., Nystad, W. (2016). "25-hydroxyvitamin D in pregnancy and genome wide cord blood DNA methylation in two pregnancy cohorts (MoBa and ALSPAC)". *The Journal of Steroid Biochemistry and Molecular Biology*, 159:102-109. PMC4829940
46. Lin, Xinyi, Lee, S., Wu, M.C., Wang, C., Chen, H., Li, Z., Lin, X. (2016). "Test for rare variants by environment interactions in sequencing association studies". *Biometrics*, 72: 156-164. PMC4733434
47. Joubert, B.R., Felix, J.F., Yousefi, P., Bakulski, K.M., Just, A.C., Breton, C., Reese, S., Markunas, C., ..., Wu, M.C., ... , London, S.J. (2016). "DNA methylation in newborns and maternal smoking in pregnancy: Genome-wide consortium meta-analysis". *The American Journal of Human Genetics*, 98(4): 680-696. PMC4733434
48. Dai, H., Wu, G., Wu, M., Zhi, D. (2016). "An optimal bahadur-efficient method in detection of sparse signals with applications to pathway analysis in sequencing association studies". *PLOS One*, 11(7):e0152667.
49. Reese, S.E., Zhao, S., Wu, M.C., Joubert, B.R., Parr, C.L., Håberg, S.E., Ueland, P.M., Nilsen, R.M., Midttun, Ø., Vellset, S.E., Peddada, S., Nystad, W., London, S.J. (2016). "DNA methylation score as a biomarker in newborns for sustained maternal smoking during pregnancy". *Environmental Health Perspectives*, In Press.

50. He, Q., Cai, T., Liu, Y., Zhao, N., Harmon, Q.E., Almli, L.M., Binder, E.B., Engel, S.M., Ressler, K.J., Conneely, K.N., Lin, X., **Wu, M.C.** (2016). “Prioritizing individual variants after kernel machine testing using variable selection”. *Genetic Epidemiology*, In Press.
51. Zhan, X., Girirajan, S., Zhao, N., **Wu, M.C.**, Ghosh, D. “A novel copy number variants kernel association test with application to autism spectrum disorders studies”. *Bioinformatics*, In Press.

Submitted:

52. **Wu, M.C.**, Kuan, P.F. “Illumina 450K Beadchip Data Analysis”. In: Tost, J. (ed): *DNA Methylation Protocols, 3rd Edition*. Springer Methods in Molecular Biology.
53. **Wu, M.C.** “The dynamic alpha reallocation adaptive signature design”.
- ◇54. Stewart, T.G., **Wu, M.C.**, Zeng, D. “Augmented weighted support vector machines for missing covariates”.
55. Clark, J.J., Maity, A., Harmon, Q.E., Engel, S.M., Epstein, M.P., **Wu, M.C.** “Gene and region based testing of gene-gene interactions for quantitative traits with the SNP-Set Kernel Interaction Test (SKIT)”.
56. Dutcher, J.P., Manola, J., Gordon, M.S., Richardson, R.L., Sosman, J.A., Cella, D., Fairclough, D., Kasimis, B.S., Sledge, G.W., Jr., **Wu, M.C.**, McNeel, D.G., Keefe, S.M., Carducci, M.A., Roach, R.W., Hudes, G.R., Wilding, G. “Phase III randomized trial of interferon alfa-2b (IFN) alone versus interferon alfa-2b plus thalidomide in patients with previously untreated metastatic or unresectable renal cell carcinoma (E2898): a trial of the Eastern Cooperative Oncology Group”.
57. Stewart, T.G., **Wu, M.C.**, Zeng, D. “Doubly robust support vector machines for missing covariates”.
58. Vincent, B.G., Singh, D., **Wu, M.C.**, Hunsucker, S.A., Alatrash, G., Ruisaard, K., Sukhumalchandra, P., Clise-Dwyer, K., Mollndrem, J.J., Prins, J., Armistead, P.M. “Comparative transcriptomics between acute myeloid leukemia stem cell and non-stem cell populations”.
59. Teran Hidalgo, S.J., **Wu, M.C.**, Engel, S.M., Kosorok, M.R. “Goodness-of-fit test for smoothing spline ANOVA models: missing covariates and interaction terms”.
60. Zhan, X., Zhao, N., **Wu, M.C.** “A fast small-sample kernel independence test with application to microbiome association studies”.
61. Zhan, X., Tong, X., Zhao, N., Maity, A., **Wu, M.C.**, Chen, J. # “Regression-based kernel association test in microbiome-profiling studies with multivariate outcomes”. # **Joint Corresponding Authors**
62. Plantinga, A., Zhan, X., Zhao, N., Chen, J., Jenq, R.R., **Wu, M.C.** “MiRKAT-S: A community-level test of association between microbiome composition and survival times”.
63. Rotroff, D.M., Joubert, B.R., Marvel, S.W., Håberg, S.E., **Wu, M.C.**, Nilsen, R.M., Ueland, P.M., Nystad, W., London, S.J., Motsinger-Reif, A. “Maternal smoking impacts key biological pathways in newborns through epigenetic modification in utero”

Technical Reports:

All Reports Available Upon Request:

1. **Wu, M.C.**, Lee, J.S. (2006). “Gaussian mixture modeling of polarimetric synthetic aperture radar images for unsupervised terrain classification”. Technical Report.
2. **Wu, M.C.**, Lin, X. (2007). “Adaptively penalized logistic regression for testing the significance of gene pathways”. Technical Report.

◇EARLIER VERSIONS OF THIS WORK WON BOTH THE 2014 ENAR POSTER COMPETITION AND THE 2015 ENAR DISTINGUISHED STUDENT PAPER AWARD

3. 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 Report.
- ♣4. **Wu, M.C.**, Zhang, L., Lin, X. (2008). “Two group classification using sparse linear discriminant analysis”. Technical Report.
- ♠5. **Wu, M.C.**, Cai, T., Lin, X. (2009). “Testing for regression coefficients in LASSO regularized regression”.
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 Report.
9. Li, L., **Wu, M.C.**, Lin, X. (2012). “Prioritizing phenotype-associated uncommon variants in sequencing association studies”.
10. Family, L., Bensen, J.T., Troester, M.A., **Wu, M.C.**, Anders, C.K., Olshan, A.F. (2015). “Single nucleotide polymorphisms in base excision repair pathway genes and association with breast cancer and breast cancer subtypes among African Americans and Whites”.

EXTRAMURAL
TALKS &
PRESENTATIONS

1. “Next Generation Kernel Methods for Now Generation Sequencing Data”, Japanese Society of Computational Statistics. (October 2016). {Invited Keynote}
2. “Statistical Methods for Microbiome Data Analysis”, Department of Lab Medicine, University of Washington, Seattle, WA. (October 2016) {Invited}
3. “Kernel Machine Methods for Genetic Studies with High-Dimensional and Complex Outcomes”, JSM, Chicago, IL. (August 2016). {Invited}
4. “Kernel Machine Methods for Community Level Analysis of Microbiome Data”, ENAR, San Antonio, TX. (March 2016). {Invited}
5. “Kernel Machine Methods for Complex Genomic Data: Integrative Analysis and Accommodating Interactions”, Department of Biomedical Informatics, CHOP/U. Penn., Philadelphia, PA. (October 2015). {Invited}
6. “Next-Generation Statistical Approaches for Now-Generation Sequencing Studies”, Non-Clinical Biostatistics Conference, Philadelphia, PA. (October 2015). {Invited}
7. “Semi-Nonparametric Interaction Analysis via Brownian Distance Covariance”, JSM, Seattle, WA. (August 2015). {Topic Contributed}
8. “Joint Analysis of Genomic Data from Different Sources using Kernel Machine Regression with Multiple Kernels”, ICSA Applied Statistics Symposium, Fort Collins, CO. (June 2015). {Invited}
9. “Flexible Testing Approaches for Microbiome and Multi-omics Analysis”, Department of Biostatistics, University of Washington, Seattle, WA. (October 2014). {Invited}
10. Discussant, “Statistical Methods for Genomics and High Dimensional Data”, JSM, Boston, MA. (August 2014). {Invited Discussant}
11. “Analysis of Complex Genomic Data using Recent Advances in Statistical Science”, West Virginia Clinical and Translational Science Institute, University of West Virginia, Morgantown, WV. (July 2014). {Invited}

♣ THIS PAPER WON A 2008 ASA STATISTICAL COMPUTING & GRAPHICS SECTION STUDENT PAPER AWARD

♠ AN EARLIER VERSION WON AN ENAR DISTINGUISHED STUDENT PAPER AWARD

12. “Statistical Methods for Integrative Analysis of Different Types of Genomic Data”, IMS Asia Pacific Rim, Taipei, Taiwan. (July 2014). {Invited}
13. “Kernel Machine Methods for Gene-Gene Interaction Testing”, Workshop on Emerging Statistical Challenges and Methods For Analysis of Massive Genomic Data in Complex Human Disease Studies, Banff International Research Station, Banff, Canada. (June 2014). {Invited}
14. “Integrative Genomic Analysis and Detecting Epistasis using Flexible Statistical Methods”, Department of Statistics, Oregon State University, Corvallis, OR. (April 2014). {Invited}
15. “Kernel Machine Methods for Gene-Gene Interaction Testing and for Integrative Genomic Analysis”, Cardiovascular Health Research Unit, University of Washington, Seattle, WA. (January 2014). {Invited}
16. “Normalization and Related Issues in Analysis of Methylation Data”, National Institute of Environmental Health Sciences, Research Triangle Park, NC. (June 2013). {Invited}
17. “Inferential Strategies for High Dimensional -omics Data”, Division of Public Health Sciences, Fred Hutchinson Cancer Research Institute, Seattle, WA. (March 2013). {Invited}
18. “Flexible Methods for Testing Interactions in Genetic Association Studies”, EITC-Bio 2012: Recent Advances in Biomedical Research, Princeton, NJ. (October 2012). {Invited}
19. “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}
20. “Resampling Based Variable Selection Methods for Next Generation Sequencing Studies”, JSM, San Diego, CA. (August 2012). {Topic Contributed}
21. “Estimation and Testing in Genetic Association Studies under the Additive Kernel Machine Model”, IMS Asia Pacific Rim, Tsukuba, Japan. (July 2012). {Invited}
22. “Kernel Machine Methods for Assessing Interactions in Genomic Studies”, ICSA Applied Statistics Symposium, Boston, MA. (June 2012). {Invited}
23. “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}
24. “Kernel Machine Based Testing of Rare Variant by Environment Interactions”, ENAR, Washington D.C. (April 2012). {Invited}
25. “Statistical Issues in Genome Wide Methylation Profiling Studies”, Department of Epidemiology and Biostatistics, University of South Carolina, Charleston, SC. (March 2012). {Invited}
26. “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}
27. “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}
28. “Rare Variant Analysis Using the Multi-Kernel Sequence Kernel Association Test”, Research Triangle Statistical Genetics Conference, Research Triangle Park, NC. (October 2011). {Invited}
29. “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}
30. “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}
31. “Analysis of High-throughput Sequencing Data via the Sequence Kernel Association Test”, Emerging Information and Technology Conferences (EITC-2011), Chicago, IL. (July 2011). {Invited}

32. "Kernel Machine Tests for Rare Genetic Variants in Sequencing Studies", ICOSA, New York, NY. (June 2011). {Contributed}
33. "Kernel Machine Based Analysis of High-throughput Sequencing Data", Division of Public Health Sciences, Fred Hutchinson Cancer Research Institute, Seattle, WA. (April 2011). {Invited}
34. "Rare Variant Association Testing Using the Sequence Kernel Association Test (SKAT)", Statistical Genetics Group, GlaxoSmithKline, Research Triangle Park, NC. (December 2010). {Invited}
35. "Rare Variant Association Testing Using the Sequence Kernel Association Test (SKAT)", Department of Statistics, NC State University, Raleigh, NC. (November 2010). {Invited}
36. "Variable Selection in the Kernel Machine Framework via the Garrote Kernel Selector", JSM, Vancouver, BC Canada. (August 2010). {Invited}
37. "Kernel Machine Based Analysis of Genetic Association Studies", First Joint Biostatistics Symposium, Beijing, China. (July 2010). {Invited}
38. "Variable Selection in the Kernel Machine Framework via the Garrote Kernel Selector", Statistical Analysis of Complex Data, Kunming, Yunnan China. (July 2010). {Contributed}
39. "Kernel Machine Methods for the Analysis of Large Scale Genetic Association Studies", ENAR, New Orleans, LA. (March 2010). {Contributed}
40. "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}
41. "Kernel Machine Approaches for the Analysis of Genome Wide Association Studies", Emerging Information and Technology Conferences (EITC-2009), Cambridge, MA. (August 2009). {Invited}
42. "Kernel Based Variable Selection via the Garrote Kernel Selector", ICOSA Applied Statistics Symposium, San Francisco, CA. (June 2009). {Invited}
43. "Variable Selection in the Kernel Machine Framework", ENAR, San Antonio, TX. (March 2009). {Contributed}
44. "Regularization and Variable Selection in Classification and Regression Problems using Omics Data", Department of Statistics, Cornell University, Ithaca, NY. (March 2009). {Invited}
45. "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}
46. "Inferential Strategies for High-dimensional 'Omics' Data", Department of Biostatistics, University of North Carolina - Chapel Hill, Chapel Hill, NC. (February 2009). {Invited}
47. "Inferential Strategies for High-dimensional 'Omics' Data", Department of Epidemiology and Biostatistics, University of Maryland, College Park, MD. (February 2009). {Invited}
48. "Regularization and Variable Selection in Classification and Regression Problems using Omics Data", Department of Statistics, University of Virginia, Charlottesville, VA. (February 2009). {Invited}
49. "Regularization and Variable Selection in Predictive Modelling using Omics Data", Department of Statistics, North Carolina State University, Raleigh, NC. (February 2009). {Invited}
50. "Regularization and Variable Selection in Predictive Modelling using Omics Data", Department of Biostatistics, Johns Hopkins University, Baltimore, MD. (January 2009). {Invited}
51. "Inferential Strategies for High-dimensional 'Omics' Data", Department of Biostatistics, Yale University, New Haven, CT. (January 2009). {Invited}
52. "Regularization and Variable Selection in Predictive Modelling using Omics Data", Department of Statistics, U.C. Davis, Davis, CA. (January 2009). {Invited}

53. “Genomic Feature Based Analysis of Genome Wide Association Studies via Logistic Kernel Machines”, Racebrook Environmental Statistics Symposium, Sheffield, MA. (November 2008).
54. “Identification of Genes and Gene Pathways Associated with Metal Particulate Exposure using Sparse Linear Discriminant Analysis”, GENI, Boston, MA. (October 2008). {Contributed Poster}
55. “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}
56. “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}
57. “Use of Sparse Linear Discriminant Analysis in Testing Gene Pathways”, ICSA Applied Statistics Symposium, Piscataway, NJ. (June 2008). {Invited}
58. “A Parametric Permutation Test for Regression Coefficients in LASSO Regularized Regression for High Dimensional Data”, ENAR, Arlington, VA. (March 2008). {Contributed}
59. “Use of Variable Selection in Testing the Significance of Gene Sets”, ENAR, Atlanta, GA. (March 2007). {Contributed}
60. “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 (Non?) Issues in Microbiome Association Studies”, VID D Scientific Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA. (March 2016).
2. “Statistical Issues in Analyzing DNA Methylation Data”, Analysis Tools and Methods for High-throughput Genomic Data (ATME) Affinity Group, Fred Hutchinson Cancer Research Center, Seattle, WA. (January 2015).
3. “Kernel Machine Methods for Analysis of -Omics Data from Different Sources”, Computational Biology Program Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA. (August 2014).
- #4. “SKAT for Scat: Analysis of Fecal Microbiome Profiles”, UW Biostatistics Department Retreat, Leavenworth, WA. (September 2013).
5. “Statistical Issues in the Analysis of Genome Wide Methylation Data”, NC TRaCS Biostatistics Grand Rounds, UNC, Chapel Hill, NC. (April 2013).
6. “Career Development for Students and How to Properly do Crap Research”, Biostatistics Students Association Seminar, UNC, Chapel Hill, NC. (March 2013).
7. “Statistical Methods for the Analysis of Sequencing Data”, NC TRaCS Biostatistics Grand Rounds, UNC, Chapel Hill, NC. (January 2012).
8. “Environmentally Friendly Approaches for the Analysis of Genomic Data”, Department of Biostatistics Colloquium, UNC, Chapel Hill, NC. (January 2012).
9. “Analysis of Genome Wide Expression Profile Experiments”, NC TRaCS Biostatistics Seminar Series, UNC, Chapel Hill, NC. (September 2010).
10. “A Direct and Powerful Approach for Testing Rare Variants”, Mini-Symposium on Next-Generation Sequencing and Analysis, UNC, Chapel Hill, NC. (May 2010).
11. “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).
12. “HD-TVs: An overview of High Dimensional Testing and Variable Selection”, (First) Biostatistics Student Invited Seminar, UNC, Chapel Hill, NC. (January 2010).

#WON BEST FACULTY PRESENTATION (VOTED BY STUDENTS)

13. “Gene Set Analysis using Sparse Linear Discriminant Analysis”, NC TRaCS Biostatistics Grand Rounds, UNC, Chapel Hill, NC. (November 2009).
14. “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).
15. “Sparse Linear Discriminant Analysis for Testing Differential Gene Pathway Activity Induced by Metal Particulate Exposure”, Environmental Statistics Seminar Series, HSPH, Boston, MA. (May 2008).
16. “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. Hishida, A., Zhao, N., **Wu, M.C.**, Nakatochi, M., Naito, M., Sasakabe, T., Hattori, Y., Suma, S., Okada, R., Kawai, S., Morita, E., Hamajima, N., Tanaka, H., Wakai, K. “A SNP-set Kernel Association Test detected genetic pathway involved in persistent *Helicobacter pylori* infection”. *Annual Meeting of the Japanese Epidemiological Association*, Nagoya, Japan (January 2015).
2. Hattori, Y., Hishida, A., Morita, E., Nakatochi, M., Zhao, N., **Wu, M.C.**, Sasakabe, T., Suma, S., Okada, R., Kawai, S., Naito, M., Hamajima, N., Tanaka, H., Wakai, K. “SNP-set Kernel Association Test Identified Two Biological Pathways Associated with Cedar and Hinoki Pollen Allergy”. *Annual Meeting of the Japanese Epidemiological Association*, Nagoya, Japan (January 2015).
3. Dhramsiri, U., Hunsucker, S.A., Vincent, B.A., **Wu, M.**, Collins, E.J., Liang, S., Molldrem, J.J. “UNC-GRK4-1: An Allele Specific Cancer Testis Antigen Identified Through Genomic Screening”. *American Society of Hematology*, New Orleans, LA. (December 2013).
4. Vincent, B., Singh, D., **Wu, M.C.**, Hunsucker, S.A., Alatrash, G., Ruisaard, K., Sukhumalchandra, 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).
5. 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).
6. 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).
7. 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).
8. 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).
9. Glickman, S.W., Shofer, F.S., **Wu, M.C.**, Scholer, M.J., Ndubizu, 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).
10. Ter-Minassian, M., Wang, Z., Asomaning, K., **Wu, M.C.**, Liu, C.Y., Paulus, J., Liu, G., Bradbury, P.A., Zhai, R., Su, L., Fraunhoffer, 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).

11. Ter-Minassian, M., Wang, Z.M., Asomaning, K., **Wu, M.C.**, Liu, C.Y., Su, L., Fraumeni, 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**]
12. 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).
13. 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**]
14. 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**]

STUDENT
ADVISING

Doctoral Dissertations Directed

1. Jennifer J. Clark, Ph.D., Biostatistics (UNC). 2009 – 2013.
Dissertation: *Estimation and Hypothesis Testing with Additive Kernel Machines for High-Dimensional Data*
Current Position: Mathematical Statistician, Food and Drug Administration
2. Eugene Urrutia, Ph.D., Biostatistics (UNC). 2010 – 2013.
Dissertation: *Statistical Analysis of Genetic Sequencing and Rare Variant Association Studies*
His dissertation won the *2011 American Society of Human Genetics Trainee Research Semifinalist Award*.
Current Position: Independent Biostatistician
3. Ni Zhao, Ph.D., Biostatistics (UNC). 2012 – 2013.
Dissertation: *Kernel Machine Methods for Analysis of Genomic Data from Different Sources*
Current Position: Tenure Track Assistant Professor, The Johns Hopkins University
4. Thomas G. Stewart, Ph.D., Biostatistics (UNC). 2011 – 2015. (Co-advisor: Donglin Zeng)
Dissertation: *Statistical Learning with Missing Data*
His dissertation won the *2014 ENAR Poster Competition* and the *2015 ENAR Distinguished Student Paper Award*.
Current Position: Assistant Professor, Vanderbilt University
5. Sebastian Teran Hidalgo, Ph.D., Biostatistics (UNC). 2012 – Present. (Co-advisor: Michael R. Kosorok)
Dissertation: *Applications of Independence Statistics to Goodness-of-Fit, Clustering of Variables and Multivariate Change-Point Estimation*
Current Position: Post-Doctoral Fellow, Yale University
6. Anna Plantinga, Ph.D., Biostatistics (UW). 2015 – Present.

Post Doctoral Fellows Supervised:

1. Ni Zhao, 2014 – 2016. (FHCRC)
2. Xiang Zhan, 2015 –

Undergraduate Research Mentor

1. Elizabeth Simmons, 2009 – 2011. (UNC)

Biostatistics Doctoral Committee Membership

1. Qianchuan Chad He, 2011 – 2012. (Advisor: Danyu Lin, UNC)
2. Andrea Byrnes, 2011 – 2013. (Advisor: Yun Li, UNC)
3. Xiaoxi Liu, 2012 – 2014. (Advisor: Donglin Zeng, UNC)
4. Jennifer Kirk, 2015 – Present. (Advisor: Tim Thornton, UW)

Non-Biostatistics Doctoral Committee Membership

1. Christopher Cabanski, 2010 – 2012. (Statistics, UNC; Advisor: Steve Marron)
2. Quaker Harmon, 2011 – 2012. (Epidemiology, UNC; Advisor: Stephanie Engel)
3. Jeremy Sabourin, 2011 – 2013. (Statistics, UNC; Advisor: Will Valdar & Andrew Nobel)
4. Leila Family, 2012 – 2014. (Epidemiology, UNC; Advisor: Andy Olshan)
5. Brionna Hair, 2012 – 2014. (Epidemiology, UNC; Advisor: Melissa Troester)

Academic/Course Advisor

- 2010: Jung In Kim, Maria Reynolds
- 2012: Brian Barkley

SERVICE

Fred Hutchinson Cancer Research Center:

- Biostat. & Biomath. Faculty Search Committee: 2014 – 2015.
- Biostat. & Biomath. Seminar Organizer: 2015 – 2016.

Lineberger Comprehensive Cancer Center, The University of North Carolina at Chapel Hill:

- Lineberger Data Warehouse and Biorepository Data Sharing Committee: 2012 – 2013.

Department of Biostatistics, The University of North Carolina at Chapel Hill:

- Awards Committee: 2009 – 2012.
- Masters Examinations Committee: 2010 – 2013.
- Information Technology Committee: 2012 – 2013.

Department of Biostatistics, Harvard University:

- Student Admissions Committee: 2004 – 2005
- Departmental Representative, Graduate Student Council: 2006 – 2009

Other Service:

- Tenure/Promotion Review Service: UCLA, Virginia Commonwealth University
- Judge, ENAR Regional Advisory Board Poster Competition 2012

Community:

- Volunteer martial arts and self-defense instructor

TEACHING
EXPERIENCE

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

2013-2014: BIOS 740

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.

Other Teaching

Short Courses

- Instructor, "Rare Variant Analysis", *3rd NHGRI short course on Next Generation Sequencing: Technology and Statistical Methods*, University of Alabama at Birmingham, Birmingham, AL. — December 2013.
- Instructor, "Rare Variant Analysis", *4th NIGMS short course on Statistical Genetics and Genomics*, University of Alabama at Birmingham, Birmingham, AL. — July 2014.
- Instructor, "Analysis of Genome-wide Sequencing Association Studies", JSM, Boston, MA. — August 2014.
- Instructor, "Rare Variant Analysis", *4th NHGRI short course on Next Generation Sequencing: Technology and Statistical Methods*, University of Alabama at Birmingham, Birmingham, AL. — December 2014.

- Instructor, “Association Mapping: GWAS and Sequencing Data”, *Summer Institute in Statistical Genetics*, University of Washington, Seattle, WA — July 2015.
- Instructor, “Rare Variant Analysis”, *5th NIGMS short course on Statistical Genetics and Genomics*, University of Alabama at Birmingham, Birmingham, AL. — July 2015.
- Instructor, “Human Association Mapping”, *Taipei 2015 Summer Institute in Statistical Genetics*, Taipei, Taiwan — August 2015.
- Instructor, “Rare Variant Analysis”, *5th NHGRI short course on Next Generation Sequencing: Technology and Statistical Methods*, University of Alabama at Birmingham, Birmingham, AL. — December 2015.
- Instructor, “Association Mapping: GWAS and Sequencing Data”, *Summer Institute in Statistical Genetics*, University of Washington, Seattle, WA — July 2016.

Guest Instructor (Extramural)

- Guest Lecturer, BIOS 775, “Statistical Methods for Analysis of Large Scale Epigenetic Profiling Studies”, Department of Biostatistics, University of South Carolina, Columbia, SC. — March 2012.

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.