

Michael C. Wu

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

Phone: 206-667-6603
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

2016 –

Assistant Member

2013 – 2016

Department of Biostatistics, University of Washington

Seattle, Washington USA

Affiliate Associate Professor

2017 –

Affiliate Assistant Professor

2015 – 2017

SWOG Statistical Center, Fred Hutchinson Cancer Research Center

Seattle, Washington USA

*Faculty Statistician, Melanoma & Translational
Medicine*

2013 –

Fred Hutchinson/University of Washington Cancer Consortium

Seattle, Washington USA

Member

2013 –

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

Chapel Hill, North Carolina USA

Assistant Professor (Adjunct)

2014 – 2017

Assistant Professor (On Leave)

2013 – 2014

Assistant Professor (Tenure Track)

2009 – 2013

**Carolina Center for Genome Sciences, and Center for Environmental Health and Sus-
ceptibility, The University of North Carolina at Chapel Hill**

Chapel Hill, North Carolina USA

Member

2009 – 2013

Department of Biostatistics, Harvard University
Boston, Massachusetts USA

Graduate Research Assistant

2006 – 2009

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

Graduate Research Assistant, X. Shirley Liu Lab

Spring 2006

Graduate Research Assistant

Summer 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
Biology and Regeneration Branch*

Summer 2000, Summer 2001

**HONORS &
AWARDS**

- Invited Keynote, Japanese Society of Computational Statistics: 2016
- *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) (PA 12-265), 2013.
- Reviewer, NIH, NIEHS: CHEAR Grants, 2015
- *Ad hoc* Reviewer, NIH: DDK-C Study Section: 2015, 2016.
- *Ad hoc* Reviewer, NIH: IRAP Study Section: 2017.
- External Reviewer, Health Effects Institute, 2012, 2013.
- Biostatistical Reviewer, Susan G. Komen Foundation, 2012, 2014, 2015.

Editorial Roles

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

Paper and Conference Review

1. *American Journal of Bioethics*
2. *American Journal of Epidemiology*
3. *American Journal of Human Genetics*
4. *Annals of Applied Statistics*
5. *Annals of Human Genetics*
6. *Annals of Statistics*
7. *Bioinformatics*
8. *Biometrical Journal*
9. *Biometrics*
10. *Biometrika*
11. *Biostatistics*
12. *BMC Bioinformatics*
13. *BMC Genetics*
14. *BMC Genomics*
15. *BMC Medical Genomics*
16. *BMC Medical Research Methodology*
17. *Briefings in Bioinformatics*
18. *Canadian Journal of Statistics*
19. *Cancer*
20. *Carcinogenesis*
21. *Clinical Cancer Research*
22. *Computational and Mathematical Methods in Medicine*
23. *Environment International*
24. *Environmental Health Perspectives*
25. *Epigenetics*
26. *Epigenomics*
27. *European Journal of Human Genetics*
28. *Frontiers in Genetics*
29. *Genetic Epidemiology*
30. *Genetic Medicine*
31. *Genetics*
32. *Genome Biology*
33. *Human Heredity*
34. *Intelligent Systems for Molecular Biology*
35. *Journal of the American Statistical Association*
36. *Journal of Applied Statistics*
37. *Microbiome*
38. *Molecular Psychiatry*
39. *mSystems*
40. *Nature Communications*
41. *The Oncologist*
42. *Oncotarget*
43. *The Pharmacogenomics Journal*
44. *PLOS Computational Biology*
45. *PLOS Genetics*
46. *PLOS One*
47. *Proceedings of the National Academy of Sciences*
48. *Sankhya B*
49. *Scientific Reports*
50. *Statistical Applications in Genetics and Molecular Biology*
51. *Statistics in Medicine*
52. *Technometrics*

Committee Appointments

- Chair, Planning Committee, ENAR Junior Researcher Workshop, 2012 – 2013.
- Member, Planning Committee, ENAR Junior Researcher Workshop, 2011 – 2015.
- Member, Organizing Committee, BIRS Workshop on *Emerging Statistical Challenges and Methods For Analysis of Massive Genomic Data in Complex Human Disease Studies*, 2014.
- JSM Program Chair, ASA Section on Statistics in Genomics and Genetics, 2016 – 2017.
- Chair, Student Paper Competition, ASA Section on Statistics in Genomics and Genetics, 2017 – 2018.
- Member, Organizing Committee, BIRS Workshop on *Emerging Statistical Challenges and Methods for Analysis of Human Microbiome Data*, 2019.

Invited Conference Sessions Organized and Chaired

- Organizer and Chair, Session on “Addressing Emerging Statistical Challenges in Microbiome Studies,” JSM 2018, Vancouver, BC.

- 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.
- Session Chair, First Joint Biostatistics Symposium, 2010, Beijing, China.
- Session Chair, ENAR, 2009, San Antonio, TX.
- Session 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, “New Statistical Faculty Translational Medicine Development Award”, The Hope Foundation, 2013-2018.
- Subcontract PI and Co-Investigator, “The Vaginal Microbiome and Racial Disparity in Preterm Delivery,” NIH/NIMHD, R01-MD011504, PI: Stephanie Engel (Epidemiology, UNC), 2017-2021.
- Faculty Biostatistician, “SWOG Statistics and Data Management Center (SDMC),” NIH/NCI, U10 CA180819, PI: Michael LeBlanc (Public Health Sciences, FHCRC), 2014-2019.
- 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 (Public Health Sciences, FHCRC), 2014-2019.
- Co-Investigator, “The Gut Microbiota and Graft versus Host Disease (GVHD),” NIH/NIAID, R01 AI134808. PI: David Fredricks (Vaccine and Infectious Diseases, FHCRC). 2017-2021.
- Biostatistician, “MsFLASH: Living a Healthy Menopause”, NIH/NIA, R01 AG048209, MPIs: Andrea LaCroix (Epidemiology, UCSD), Katherine Guthrie (Public Health Sciences, FHCRC), Susan Reed (Women’s Health, UW). 2017-2020.
- Subcontract PI and Co-Investigator, “Overcoming Primary Resistance to PD1 Inhibitors with Combined Immunotherapy,” SU2C AACR/BMS, Catalyst Grant, PI: Toni Ribas (UCLA/SWOG). 2017-2020.
- Subcontract PI and Co-Investigator, “Investigation of Genetic and Immune Mechanisms of Response to BCG for Non-Muscle Invasive Bladder Cancer: A Translational Study of S1602,” DoD/CDMRP, CA170270, PIs: Joshua Meeks (Lead PI, Northwestern/SWOG), David McConkey (JHU/SWOG), Robert Svatek (UTHSCSA/SWOG). 2018 – 2021.

Completed

- Subcontract PI 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.

- Co-Investigator, “Mucus and Hypoxia in Heterogeneous and Progressive CF Lung Disease,” NIH/NHLBI, R01-HL116228, PI: Marianne Muhlebach (Pediatrics, UNC), 2012-2013.
- 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.
- Co-Investigator, “Design and Analysis of Sequencing-based Studies for Complex Human Traits,” NIH/NHGRI, R01-HG006292, PI: Yun Li (Genetics, UNC), 2011–2013.
- Co-Investigator, “Prenatal Smoking, Maternal and Fetal Genetic Variation and Risk of Preeclampsia,” NIH/NICHHD, R01-HD058008, PI: Stephanie Engel (Epidemiology, UNC), 2011-2013.
- 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.
- Biostatistician, “UNC Clinical Translation Science Award - Biostatistics Core,” NIH/NCRR, UL1 TR000083-05, PI: Marschall Runge (Medicine, UNC), 2009 – 2013.
- 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.

PAPERS &
PUBLICATIONS

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

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

- 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
 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., 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. 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., Midttun, 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

†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”

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., Kohltfar-ber, 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
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., Håberg, 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., Håberg, 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 are associated with term small for gestational age and preeclampsia". *American Journal of Reproductive Immunology*, 71(5): 472-84. PMC4040534
33. Joubert, B.R., Håberg, 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

§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"

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.
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

¶ AN EARLIER VERSION WON AN ASHG PREDOCTORAL TRAINEE RESEARCH SEMIFINALIST AWARD

- ◇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. PMC4833289
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. PMC4933358
49. 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*, 40(8):722-731. PMC5118060 [# Joint Corresponding Authors]
50. 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. (2016). “Maternal smoking impacts key biological pathways in newborns through epigenetic modification in utero”. *BMC Genomics*, 17(1):976. PMC5124223
51. Zhan, X., Girirajan, S., Zhao, N., **Wu, M.C.**, Ghosh, D. (2016). “A novel copy number variants kernel association test with application to autism spectrum disorders studies”. *Bioinformatics*, 32 (23): 3603-3610. PMC5181531
52. Plantinga, A., Zhan, X., Zhao, N., Chen, J., Jenq, R.R., **Wu, M.C.** (2017). “MiRKAT-S: A community-level test of association between the microbiota and survival times”. *Microbiome* 5(2): 17. PMC5299808
53. Zhan, X., Tong, X., Zhao, N., Maity, A., **Wu, M.C.#**, Chen, J.# (2017). “A small-sample multivariate kernel machine test for microbiome association studies”. *Genetic Epidemiology*, 41(3):210-220. [# Joint Corresponding Authors]
54. Reese, S.E., Zhao, S., **Wu, M.C.**, Joubert, B.R., Parr, C.L., Håberg, S.E., Ueland, P.M., Nilsen, R.M., Middtun, Ø., Vellset, S.E., Peddada, S., Nystad, W., London, S.J. (2017). “DNA methylation score as a biomarker in newborns for sustained maternal smoking during pregnancy”. *Environmental Health Perspectives*, 125(4): 760-766. PMC5381987
55. Zhan, X., Zhao, N., Plantinga, A., Thornton, T.A., Conneely, K.N., Epstein, M.P., **Wu, M.C.** (2017). “Powerful genetic association analysis for common or rare variants with high-dimensional structured traits”. *Genetics*, 206(4): 1779-1790. PMC5560787
56. Mitchell, C.M., Srinivasan, S., Zhan, X., **Wu, M.C.**, Reed, S.D., Guthrie, K.A., LaCroix, A.Z., Fiedler, T., Munch, M., Liu, C., Hoffman, N., Blair, I.A., Newton, K., Freeman, E.W., Joffe, H., Cohen, L., Fredricks, D.N. (2017). “Vaginal microbiota and genitourinary menopausal symptoms: a cross sectional analysis”. *Menopause*, 24(10):1160-1166. PMC5607086
57. Golob, J.L., Pergam, S.A., Srinivasan, S., Fiedler, T.L., Liu, C., Garcia, K., Mielcarak, M., Ko, D., Aker, S., Marquis, S., Loeffelholz, T., Plantinga, A., **Wu, M.C.**, Celustka, K., Morrison, A., Woodfield, M., Fredricks, D.N. (2017). “The stool microbial at neutrophil recovery is predictive for severe acute graft versus host disease after hematopoietic cell transplantation.” *Clinical Infectious Diseases*, 65(12):1984-1991. PMC5850019
- ♣58. Zhan, X., Plantinga, A., Zhao, N., **Wu, M.C.** (2017). “A fast small-sample kernel independence test for microbiome community-level association analysis”. *Biometrics*, 73(4):1453-1463. PMC5592124
59. Bauer, A.E., Avery, C.L., Shi, M., Weinberg, C.R., Olshan, A.F., Harmon, Q.E., Luo, J., Yang, J., Manuck, T., **Wu, M.C.**, Williams, N., McGinnis, R., Morgan, L., K’ungsøyr, K., Trogstad, L., Magnus, P., Engel, S.M. (2018). “A family-based study of carbon monoxide and nitric oxide signaling genes and preeclampsia”. *Paediatric and Perinatal Epidemiology*, 32:1-12. PMC5771849

◇ THIS PAPER WAS SELECTED BY *AJHG* AS THE “BEST OF” 2015-2016

♣ AN EARLIER VERSION WON A 2017 ASA BIOMETRICS SECTION PAPER AWARD

- ♣60. Zhao, N., Zhan, X., Huang, Y.-T., Almlı, L.M., Smith, A., Epstein, M.P., Conneely, K.N., **Wu, M.C.** (2018). “Kernel machine methods for integrative analysis of genome-wide methylation and genotyping studies”. *Genetic Epidemiology*, 42(2):156-167.
61. Teran Hidalgo, S.J., **Wu, M.C.**, Engel, S.M., Kosorok, M.R. (2018). “Goodness-of-fit test for nonparametric regression models: smoothing splines ANOVA models as example”. *Computational Statistics and Data Analysis*, 122: 135-155.
62. Fujii, R., Hishida, A., **Wu, M.C.**, Kondo, T., Hattori, Y., Naito, M., Endoh, K., Nakatochi, M., Hamajima, N., Kubo, M., Kuriki, K., Wakai, K. (2018). “Genome-wide association study for pollinosis identified two novel loci in interleukin (IL)-1B in a Japanese population”. *Nagoya Journal of Medical Science*, 80: 109-120. PMC5857507
63. Luo, Y., Maity, A., **Wu, M.C.**, Smith, C., Duan, Q., Li, Y., Tzeng, J.-Y. (2018). “On the sub-structure controls in rare variant analysis — principal components or variance components?”. *Genetic Epidemiology*, 42(3):276-287. PMC5851819
64. Mitchell, C.M., Srinivasan, S., Plantinga, A., **Wu, M.C.**, Reed, S.D., Guthrie, K.A., LaCroix, A.Z., Fiedler, T., Munch, M., Liu, C., Hoffman, N.G., Blair, I.A., Newton, K., Freedman, E.W., Joffe, H., Cohen, L., Fredricks, D.N. (2018). “Associations between improvement in genitourinary symptoms of menopause and changes in the vaginal ecosystem”. *Menopause*, 25(5): 500-507. PMC5898977
65. Stewart, T.G., Zeng, D., **Wu, M.C.** (2018). “Constructing support vector machines with missing data”. *WIREs Computational Statistics*. In Press.
66. Zhan, X., **Wu, M.C.** (2018). “A note on testing and estimation in marker-set association study using semiparametric quantile regression kernel machine”. *Biometrics*, In Press.
67. Manuzak, J.A., Gott, T.M., Kirkwood, J.S., Coronado, E., Hensley-McBain, T., Miller, C., Cheu, R.K., Collier, A.C., Funderburg, N.T., Martin, J.N., **Wu, M.C.**, Isoherranen, N., Hunt, P.W., Klatt, N.R. (2018). “Heavy cannabis use associated with reduction in activated and inflammatory immune cell frequencies in antiretroviral therapy-treated Human Immunodeficiency Virus-infected individuals.” *Clinical Infectious Diseases*, In Press.

Published Book Chapters:

1. **Wu, M.C.**, Kuan, P.F. (2018). “A Guide to Illumina BeadChip Data Analysis”. In: Tost, J. (ed): *DNA Methylation Protocols, 3rd Edition*. Springer Methods in Molecular Biology, vol 1708; 303-330. Humana Press, New York, NY. PMID: 29224151

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.
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”. Technical Report.

♣SELECTED AS THE IGES HIGHLIGHT/PAPER OF THE MONTH

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

♮AN EARLIER VERSION WON AN ENAR DISTINGUISHED 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 Report.
9. Li, L., **Wu, M.C.**, Lin, X. (2012). “Prioritizing phenotype-associated uncommon variants in sequencing association studies”. Technical Report.
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”. Technical Report.

EXTRAMURAL
TALKS &
PRESENTATIONS

1. “Microbiome in Cancer Clinical Trials”, NCTN Statistical Group Meeting, Portland, OR. (May 2018). {Invited}
2. “Joint Modeling and Analysis of Microbiome with Other Omics Data”, ENAR, Atlanta, GA. (March 2018). {Invited}
3. “Statistical Methods for Correlating Microbiome and other Omics Data”, Department of Biostatistics, MD Anderson Cancer Center, Houston, TX. (October 2017). {Invited}
4. “Joint Modeling and Analysis of Microbiome with Other Omics Data”, JSM, Baltimore, MD. (August 2017). {Invited}
5. “Kernel Methods for Analysis of High-Dimensional Traits”, ICSA Applied Statistics Symposium, Chicago, IL. (June 2017). {Invited}
6. “Statistical Methods for Microbiome Data Analysis”, Genomics Seminar Series, Penn State University, University Park, PA. (May 2017). {Invited}
7. “Kernel Methods for Correlating Genetic Data with Microbiome and Other -Omic Outcomes”, TopMed Analysis Working Group, University of Washington, Seattle, WA. (March 2017).
8. “Kernel Machine Based Methods for Analyzing Genome Data from Different Sources”, ICSA International Conference, Shanghai, China. (December 2016). {Invited}
9. “Next Generation Kernel Methods for Now Generation Sequencing Data”, Japanese Society of Computational Statistics. (October 2016). {Invited Keynote}
10. “Statistical Methods for Microbiome Data Analysis”, Department of Lab Medicine, University of Washington, Seattle, WA. (October 2016). {Invited}
11. “Kernel Machine Methods for Genetic Studies with High-Dimensional and Complex Outcomes”, JSM, Chicago, IL. (August 2016). {Invited}
12. “Kernel Machine Methods for Community Level Analysis of Microbiome Data”, ENAR, San Antonio, TX. (March 2016). {Invited}
13. “Kernel Machine Methods for Complex Genomic Data: Integrative Analysis and Accommodating Interactions”, Department of Biomedical Informatics, CHOP/U. Penn., Philadelphia, PA. (October 2015). {Invited}
14. “Next-Generation Statistical Approaches for Now-Generation Sequencing Studies”, Non-Clinical Biostatistics Conference, Philadelphia, PA. (October 2015). {Invited}
15. “Semi-Nonparametric Interaction Analysis via Brownian Distance Covariance”, JSM, Seattle, WA. (August 2015). {Topic Contributed}
16. “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}

17. "Flexible Testing Approaches for Microbiome and Multi-omics Analysis", Department of Biostatistics, University of Washington, Seattle, WA. (October 2014). {Invited}
18. Discussant, "Statistical Methods for Genomics and High Dimensional Data", JSM, Boston, MA. (August 2014). {Invited Discussant}
19. "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}
20. "Statistical Methods for Integrative Analysis of Different Types of Genomic Data", IMS Asia Pacific Rim, Taipei, Taiwan. (July 2014). {Invited}
21. "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}
22. "Integrative Genomic Analysis and Detecting Epistasis using Flexible Statistical Methods", Department of Statistics, Oregon State University, Corvallis, OR. (April 2014). {Invited}
23. "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}
24. "Normalization and Related Issues in Analysis of Methylation Data", National Institute of Environmental Health Sciences, Research Triangle Park, NC. (June 2013). {Invited}
25. "Inferential Strategies for High Dimensional -omics Data", Division of Public Health Sciences, Fred Hutchinson Cancer Research Institute, Seattle, WA. (March 2013). {Invited}
26. "Flexible Methods for Testing Interactions in Genetic Association Studies", EITC-Bio 2012: Recent Advances in Biomedical Research, Princeton, NJ. (October 2012). {Invited}
27. "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}
28. "Resampling Based Variable Selection Methods for Next Generation Sequencing Studies", JSM, San Diego, CA. (August 2012). {Topic Contributed}
29. "Estimation and Testing in Genetic Association Studies under the Additive Kernel Machine Model", IMS Asia Pacific Rim, Tsukuba, Japan. (July 2012). {Invited}
30. "Kernel Machine Methods for Assessing Interactions in Genomic Studies", ICSA Applied Statistics Symposium, Boston, MA. (June 2012). {Invited}
31. "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}
32. "Kernel Machine Based Testing of Rare Variant by Environment Interactions", ENAR, Washington D.C. (April 2012). {Invited}
33. "Statistical Issues in Genome Wide Methylation Profiling Studies", Department of Epidemiology and Biostatistics, University of South Carolina, Charleston, SC. (March 2012). {Invited}
34. "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}
35. "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}
36. "Rare Variant Analysis Using the Multi-Kernel Sequence Kernel Association Test", Research Triangle Statistical Genetics Conference, Research Triangle Park, NC. (October 2011). {Invited}

37. "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}
38. "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}
39. "Analysis of High-throughput Sequencing Data via the Sequence Kernel Association Test", Emerging Information and Technology Conferences (EITC-2011), Chicago, IL. (July 2011). {Invited}
40. "Kernel Machine Tests for Rare Genetic Variants in Sequencing Studies", ICSA, New York, NY. (June 2011). {Contributed}
41. "Kernel Machine Based Analysis of High-throughput Sequencing Data", Division of Public Health Sciences, Fred Hutchinson Cancer Research Institute, Seattle, WA. (April 2011). {Invited}
42. "Rare Variant Association Testing Using the Sequence Kernel Association Test (SKAT)", Statistical Genetics Group, GlaxoSmithKline, Research Triangle Park, NC. (December 2010). {Invited}
43. "Rare Variant Association Testing Using the Sequence Kernel Association Test (SKAT)", Department of Statistics, NC State University, Raleigh, NC. (November 2010). {Invited}
44. "Variable Selection in the Kernel Machine Framework via the Garrote Kernel Selector", JSM, Vancouver, BC Canada. (August 2010). {Invited}
45. "Kernel Machine Based Analysis of Genetic Association Studies", First Joint Biostatistics Symposium, Beijing, China. (July 2010). {Invited}
46. "Variable Selection in the Kernel Machine Framework via the Garrote Kernel Selector", Statistical Analysis of Complex Data, Kunming, Yunnan China. (July 2010). {Contributed}
47. "Kernel Machine Methods for the Analysis of Large Scale Genetic Association Studies", ENAR, New Orleans, LA. (March 2010). {Contributed}
48. "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}
49. "Kernel Machine Approaches for the Analysis of Genome Wide Association Studies", Emerging Information and Technology Conferences (EITC-2009), Cambridge, MA. (August 2009). {Invited}
50. "Kernel Based Variable Selection via the Garrote Kernel Selector", ICSA Applied Statistics Symposium, San Francisco, CA. (June 2009). {Invited}
51. "Variable Selection in the Kernel Machine Framework", ENAR, San Antonio, TX. (March 2009). {Contributed}
52. "Regularization and Variable Selection in Classification and Regression Problems using Omics Data", Department of Statistics, Cornell University, Ithaca, NY. (March 2009). {Invited}
53. "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}
54. "Inferential Strategies for High-dimensional 'Omics' Data", Department of Biostatistics, University of North Carolina - Chapel Hill, Chapel Hill, NC. (February 2009). {Invited}
55. "Inferential Strategies for High-dimensional 'Omics' Data", Department of Epidemiology and Biostatistics, University of Maryland, College Park, MD. (February 2009). {Invited}
56. "Regularization and Variable Selection in Classification and Regression Problems using Omics Data", Department of Statistics, University of Virginia, Charlottesville, VA. (February 2009). {Invited}

57. “Regularization and Variable Selection in Predictive Modeling using Omics Data”, Department of Statistics, North Carolina State University, Raleigh, NC. (February 2009). {Invited}
58. “Regularization and Variable Selection in Predictive Modelling using Omics Data”, Department of Biostatistics, Johns Hopkins University, Baltimore, MD. (January 2009). {Invited}
59. “Inferential Strategies for High-dimensional ‘Omics’ Data”, Department of Biostatistics, Yale University, New Haven, CT. (January 2009). {Invited}
60. “Regularization and Variable Selection in Predictive Modelling using Omics Data”, Department of Statistics, U.C. Davis, Davis, CA. (January 2009). {Invited}
61. “Genomic Feature Based Analysis of Genome Wide Association Studies via Logistic Kernel Machines”, Racebrook Environmental Statistics Symposium, Sheffield, MA. (November 2008).
62. “Identification of Genes and Gene Pathways Associated with Metal Particulate Exposure using Sparse Linear Discriminant Analysis”, GENI, Boston, MA. (October 2008). {Contributed Poster}
63. “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}
64. “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}
65. “Use of Sparse Linear Discriminant Analysis in Testing Gene Pathways”, ICSA Applied Statistics Symposium, Piscataway, NJ. (June 2008). {Invited}
66. “A Parametric Permutation Test for Regression Coefficients in LASSO Regularized Regression for High Dimensional Data”, ENAR, Arlington, VA. (March 2008). {Contributed}
67. “Use of Variable Selection in Testing the Significance of Gene Sets”, ENAR, Atlanta, GA. (March 2007). {Contributed}
68. “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. “Community Level Analysis in Modern Microbiome Studies”, Microbiome Research Initiative, Fred Hutchinson Cancer Research Center, Seattle, WA. (February 2018).
2. “Kernel Methods for Correlating Microbiome and Other Omics Data”. CCSG Biostat & Comp Bio Retreat, Fred Hutchinson Cancer Research Center, Seattle, WA. (October 2017).
3. “Next Generation Methods for Analyzing Now Generation Sequencing Data”, Public Health Sciences All Staff Meeting, Fred Hutchinson Cancer Research Center, Seattle, WA. (April 2017).
4. “Statistical Methods for Correlating Microbiome and Other Genomic Data Types”, Clinical Research Division Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA. (March 2017).
5. Panelist, “No Fishing Allowed! P-Hacking and other Misuses of Statistical Methods in Research”, UW/Hutch Summer Bioethics Series, Fred Hutchinson Cancer Research Center, Seattle, WA. (August 2016).
6. “Statistical (Non?) Issues in Microbiome Association Studies”, VIDC Scientific Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA. (March 2016).
7. “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).
8. “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).

9. “SKAT for Scat: Analysis of Fecal Microbiome Profiles”, UW Biostatistics Department Retreat, Leavenworth, WA. (September 2013).
10. “Statistical Issues in the Analysis of Genome Wide Methylation Data”, NC TRaCS Biostatistics Grand Rounds, UNC, Chapel Hill, NC. (April 2013).
11. “Career Development for Students and How to Properly do Crap Research”, Biostatistics Students Association Seminar, UNC, Chapel Hill, NC. (March 2013).
12. “Statistical Methods for the Analysis of Sequencing Data”, NC TRaCS Biostatistics Grand Rounds, UNC, Chapel Hill, NC. (January 2012).
13. “Environmentally Friendly Approaches for the Analysis of Genomic Data”, Department of Biostatistics Colloquium, UNC, Chapel Hill, NC. (January 2012).
14. “Analysis of Genome Wide Expression Profile Experiments”, NC TRaCS Biostatistics Seminar Series, UNC, Chapel Hill, NC. (September 2010).
15. “A Direct and Powerful Approach for Testing Rare Variants”, Mini-Symposium on Next-Generation Sequencing and Analysis, UNC, Chapel Hill, NC. (May 2010).
16. “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).
17. “HD-TVs: An overview of High Dimensional Testing and Variable Selection”, (First) Biostatistics Student Invited Seminar, UNC, Chapel Hill, NC. (January 2010).
18. “Gene Set Analysis using Sparse Linear Discriminant Analysis”, NC TRaCS Biostatistics Grand Rounds, UNC, Chapel Hill, NC. (November 2009).
19. “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).
20. “Sparse Linear Discriminant Analysis for Testing Differential Gene Pathway Activity Induced by Metal Particulate Exposure”, Environmental Statistics Seminar Series, HSPH, Boston, MA. (May 2008).
21. “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. VanderWalde, A., Latkovic-Taber, M., Hu-Lieskovan, S., Grossmann, K., Sosman, J., Campos, D., **Wu, M.**, Ribas, A. “Combining ipilimumab (ipi) and nivolumab (nivo) in advanced melanoma following progression on a PD-1 inhibitor (SWOG S1616)”, *ASCO 2018*, Chicago, IL. (June 2018).
2. Hu-Lieskovan, S., Moon, J., Lau Clark, A.M., Grossmann, K., Sosman, J., Campos, D., **Wu, M.C.**, Ryan, C., Ribas, A. “Reversing resistance to PD-1 blockade by combination of talimogene laherparepvec (T-VEC) with pembrolizumab (pembro) in advanced melanoma patients following progression on a prior PD-1 inhibitor: SWOG S1607 (NCT#02965716)”, *ASCO 2018*, Chicago, IL. (June 2018).
3. Kendra, K., Moon, J., Hu-Lieskovan, S., Carson III, W., Campos, D., Cochran, A., **Wu, M.**, Ribas, A. “SWOG S1512: A phase II and pilot trial of PD-1 blockade with pembrolizumab in patients with resectable or unresectable desmoplastic melanoma (DM)”, *ASCO 2018*, Chicago, IL. (June 2018).
4. Fujii, R., Hishida, A., **Wu, M.C.**, Kondo, T., Naito, M., Hattori, Y., Nakatochi, M., Kuriki, K., Hamajima, N., Wakai, K. “Genome wide association study on pollinosis in a Japanese population: The J-MICC Study”, *World Congress of Epidemiology 2017*, Saitama, Japan. (August 2017).

[%]WON BEST FACULTY PRESENTATION (VOTED BY STUDENTS)

5. Manuzak, J.A., Gott, T.M., Kirkwood, J.S., Coronado, E., Hensley-McBain, T., Miller, C., Collier, A., **Wu, M.C.**, Martin, J.N., Isoherranen, N., Hunt, P.W., Klatt, N.R. "High cannabis levels associated with decreased T cell activation in HIV-infected individuals". *IAS 2017*, Paris, France. (July 2017).
6. C. Mitchell, S. Srinivasan, X. Zhan, **M. Wu**, S. Reed, K. Guthrie, A. LaCroix, T. Fiedler, M. Munch, C. Liu, N. Hoffman, I. Blair, K. Newton, E. Freeman, H. Joffe, L. Cohen, and D. Fredricks. "Associations Between Serum Estrogen, Vaginal Microbiota and Vaginal Glycogen in Postmenopausal Women". *IDSOG 2016*, Annapolis, MD (August 2016).
7. 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 Pathways Involved in Persistent Helicobacter pylori Infection". *Annual Meeting of the Japanese Epidemiological Association*, Nagoya, Japan (January 2015).
8. 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).
9. 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).
10. 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).
11. 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).
12. 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).
13. 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).
14. 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).
15. 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).
16. Ter-Minassian, M., Wang, Z., Asomaning, K., **Wu, M.C.**, Liu, C.Y., Paulus, J., Liu, G., Bradbury, P.A., Zhai, R., Su, L., Fraumeni, 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).
17. 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**]

18. 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).
19. 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**]
20. 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: Post-Doctoral Fellow, UNC
3. Ni Zhao, Ph.D., Biostatistics (UNC). 2012 – 2013[&].
Dissertation: *Kernel Machine Methods for Analysis of Genomic Data from Different Sources*
Current Position: 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 – 2016. (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 – 2018.
Dissertation: *Statistical Methods for Analysis of Microbiome Data*
Current Position: Assistant Professor, Williams College

[&] Ni started working with me immediately before I moved to the FHCRC. Thus, she completed her formal dissertation requirements in <1 yr and continued working with me as a post-doc.

7. Nanxun Ma, Ph.D., Biostatistics (UW). 2017 – Present.

Post Doctoral Fellows Supervised:

1. Ni Zhao, 2014 – 2016. (FHCRC) [**** See footnote above ****]
2. Xiang Zhan, 2015 – 2017. (FHCRC)
His post-doc work won a *2017 ASA Biometrics Section Paper Award*.
Current Position: Assistant Professor, Penn State University

Undergraduate Research Mentor

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

Rotational Research Assistants

1. Yatong Li, 2015-2016. (UW)
2. Yezi (Zora) Yang, 2017. (UW)

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 – 2016. (Advisor: Tim Thornton, UW)
5. Anya Mikhaylova, 2016 – 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)
6. Kristina Jordahl, 2016 – 2018. (Epidemiology, UW; Advisor: Parveen Bhatti)
7. Cameron Haas, 2018 – Present. (Epidemiology, UW; Advisor: Sara Lindstroem)
8. Dan Lachance, 2018 – Present. (Molecular Engineering, UW; Advisor: Neel Dey)

Masters Dissertation Committee Membership

1. Yichen Jia, 2016 – 2017. (Biostatistics, UW; Advisor: Tim Thornton)

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.
- Computational Biology Faculty Search Committee: 2016 – 2017.

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: Georgetown, NYU, UCLA, VCU.
- 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, “Rare Variant Analysis”, *6th NIGMS short course on Statistical Genetics and Genomics*, University of Alabama at Birmingham, Birmingham, AL. — July 2016.
- Instructor, “Association Mapping: GWAS and Sequencing Data”, *Summer Institute in Statistical Genetics*, University of Washington, Seattle, WA — July 2016.
- Instructor, “Rare Variant Analysis”, *6th NHGRI short course on Next Generation Sequencing: Technology and Statistical Methods*, University of Alabama at Birmingham, Birmingham, AL. — December 2016.
- Instructor, “Association Mapping: GWAS and Sequencing Data”, *Summer Institute in Statistical Genetics*, University of Washington, Seattle, WA — July 2017.
- Instructor, “Rare Variant Analysis”, *7th NHGRI short course on Next Generation Sequencing: Technology and Statistical Methods*, University of Alabama at Birmingham, Birmingham, AL. — December 2017.

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.