

# Weihua Guan

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## EDUCATION

University of Michigan, Ann Arbor, MI

*Ph.D. in Biostatistics*

Thesis: "Models and methods for genome-wide association studies"

May 2010

Advisor: Michael Boehnke

Texas A&M University, College Station, TX

*M.S. in Statistics*

August 2001

Advisor: P. Fred Dahm

Peking University, Beijing, China

*B.S. in Chemistry*

June 1997

Advisor: Weixiao Cao

*Advanced Education Program in Science*

1993-1995

## RESEARCH INTERESTS

Genome-wide association studies of complex diseases; statistical issues in association studies, statistical methods for DNA methylation and sequence data analysis.

## EXPERIENCE

Associate Professor, Division of Biostatistics, School of Public Health University of Minnesota

June 2016-current

Assistant Professor, Division of Biostatistics, School of Public Health University of Minnesota

May 2010-May 2016

Statistician, Stata Corporation, College Station, TX

May 2001-August 2003

## PUBLICATIONS

1. Chong W, Demerath EW, Pankow JS, Bressler J, Fornage M, Grove ML, Chen W, **Guan W**. 2016. Imputation of Missing Covariate Values in Epigenome-Wide Analysis of DNA Methylation Data. *Epigenetics*. 11:132-139.
2. Joehanes R\*, Just AC\*, Marioni RE\*, Pilling LC\*, Reynolds LM\*, Mandaviya PR\*, **Guan W\***, Xu T\*, Elks CE\*, Aslibekyan S\*, Moreno-Macias H\*, Smith JA\*, Brody JA\*, Dhingra R\*, Yousefi P, Pankow JS, Kunze S, Shah SH, McRae AF, Lohman K, Sha J, Absher DM, Ferrucci L, Zhao W, Demerath EW, Bressler J, Grove ML, Huan T, Liu C, Mendelson MM, Yao C, Kiel DP, Peters A, Wang-Sattler R, Visscher PM, Wray NR, Starr JM, Ding J, Rodriguez CJ, Wareham NJ, Irvin MR, Zhi D, Barrdahl M, Vineis P, Ambatipudi S, Uitterlinden AG, Hofman A, Schwartz J, Colicino E, Hou L, Vokonas PS, Hernandez DG, Singleton AB, Bandinelli S, Turner ST, Ware EB, Smith AK, Klengel T, Binder EB, Psaty BM, Taylor KD, Gharib SA, Swenson BR, Liang L, DeMeo DL, O'Connor GT, Herceg Z, Ressler KJ, Conneely KN, Sotoodehnia N, Kardina SL, Melzer D, Baccarelli AA, van Meurs JB, Romieu I, Arnett DK, Ong KK, Liu Y, Waldenberger M,

- Deary IJ, Fornage M, Levy D, London SJ. 2016. Epigenetic Signatures of Cigarette Smoking. *Circ Cardiovasc Genet.* 9:436-447. (co-first author)
3. Chen BH, Marioni RE, Colicino E, Peters MJ, Ward-Caviness CK, Tsai PC, Roetker NS, Just AC, Demerath EW, **Guan W**, Bressler J, Fornage M, Studenski S, Vandiver AR, Moore AZ, Tanaka T, Kiel DP, Liang L, Vokonas P, Schwartz J, Lunetta KL, Murabito JM, Bandinelli S, Hernandez DG, Melzer D, Nalls M, Pilling LC, Price TR, Singleton AB, Gieger C, Holle R, Kretschmer A, Kronenberg F, Kunze S, Linseisen J, Meisinger C, Rathmann W, Waldenberger M, Visscher PM, Shah S, Wray NR, McRae AF, Franco OH, Hofman A, Uitterlinden AG, Absher D, Assimes T, Levine ME, Lu AT, Tsao PS, Hou L, Manson JE, Carty CL, LaCroix AZ, Reiner AP, Spector TD, Feinberg AP, Levy D, Baccarelli A, van Meurs J, Bell JT, Peters A, Deary IJ, Pankow JS, Ferrucci L, Horvath S. 2016. DNA methylation-based measures of biological age: meta-analysis predicting time to death. *Aging (Albany NY).* 8:1844-1865.
  4. Shabani E, Opoka RO, Bangirana P, Park GS, Vercellotti GM, **Guan W**, Hodges JS, Lavstsen T, John CC. 2016. The endothelial protein C receptor rs867186-GG genotype is associated with increased soluble EPCR and could mediate protection against severe malaria. *Sci Rep.* 6:27084.
  5. Tsai MY, Cao J, Steffen BT, Weir NL, Rich SS, Liang S, **Guan W**. 2016. 5-lipoxygenase gene variants are not associated with atherosclerosis or incident coronary heart disease in the Multi-Ethnic Study of Atherosclerosis cohort. *Journal of the American Heart Association.* 5:e002814.
  6. McMahon SK, Lewis B, Oakes M, Guan W, Wyman JF, Rothman AJ. 2016. Older Adults' Experiences Using a Commercially Available Monitor to Self-Track Their Physical Activity. *JMIR Mhealth Uhealth.* 4:e35.
  7. Wu J, Li Y, **Guan W**, Viken K, Perlman DM, Bhargava M. 2016. FCGR3A and FCGR3B copy number variations are risk factors for sarcoidosis. *Human Genetics.* 135:715-725.
  8. Crabtree JN, He W, **Guan W**, Flage M, Miller MS, Peterson EJ. 2016. Autoimmune variant PTPN22 C1858T is associated with impaired responses to influenza virus vaccination. *The Journal of Infectious Diseases.* 214:248-257.
  9. Arora M, Lee S, Spellman S, Weisdorf D, **Guan W**, Haagenon M, Wang T, Horowitz M, Verneris M, Fleischhauer K, Hsu K, Thyagarajan B. 2016. Validation Study of the Role of Base Excision Repair Pathway as a Predictor of TRM and Relapse post HCT. *Biology of Blood and Marrow Transplantation.* 22:1531-1532.
  10. Zhang G, Huang KC, Xu Z, Tzeng JY, Conneely KN, **Guan W**, Kang Km Li Y. 2016. Across-platform imputation of DNA methylation levels incorporating non-local information using penalized functional regression. *Genet Epidemiol.* 40:333-340.
  11. Cao J, Steffen BT, Budoff M, Post WS, Thanassoulis G, Kestenbaum B, McConnell JP, Warnick R, **Guan W**, Tsai MY. 2016. Lipoprotein(a) levels are associated with subclinical calcific aortic valve disease in Caucasian and Black individuals: The Multi-Ethnic Study of Atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology.* 36:1003-1009.
  12. Wu B, **Guan W**, Pankow JS. 2016. On Efficient and Accurate Calculation of Significance P-Values for Sequence Kernel Association Testing of Variant Set. *Ann Hum Genet.* 80:123-135.
  13. Wu B, Pankow JS, **Guan W**. 2015. Sequence kernel association analysis of rare variant set based on the marginal regression model for binary traits. *Genet Epidemiol.* 39:399-405.

14. Ma Y, Follis JL, Smith CE, Tanaka T, Manichaikul AW, Chu AY, Samieri C, Zhou X, **Guan W**, Wang L, Biggs ML, Chen YD, Hernandez DG, Borecki I, Chasman DI, Rich S, Ferrucci L, Irvin MR, Aslibekyan S, Zhi D, Tiwari HK, Claas SA, Sha J, Kabagambe EK, Lai CQ, Parnell LD, Lee YC, Amouyel P1, Lambert JC, Psaty BM, King IB, Mozaffarian D, McKnight B, Bandinelli S, Tsai MY, Ridker PM, Ding J, Mstat KL, Liu Y, Sotoodehnia N, Barberger-Gateau P, Steffen LM, Siscovick DS, Absher D, Arnett DK, Ordovás JM, Lemaitre RN. 2016. *Am J Clin Nutr.* 103:567-578.
15. Oetting WS, Schladt DP, **Guan W**, Miller MB, Remmel RP, Dorr C, Sanghavi K, Mannon RB, Herrera B, Matas AJ, Salomon DR, Kwok PY, Keating BJ, Israni AK, Jacobson PA; DeKAF Investigators. 2016. Genomewide Association Study of Tacrolimus Concentrations in African American Kidney Transplant Recipients Identifies Multiple CYP3A5 Alleles. *Am J Transplant.* 16:574-582.
16. Thyagarajan B, **Guan W**, Fedirko V, Barcelo H, Tu H, Gross M, Goodman M, Bostick RM. 2016. No association between mitochondrial dna copy number and colorectal adenomas. *Mol Carcinogen.* 1290-1296.
17. Wang T\*, **Guan W\***, Lin J, Boutaoui N, Canino G, Luo J, Celedon JC, Chen W. 2015. A systematic study of normalization methods for Infinium 450K methylation data using whole-genome bisulfite sequencing data. *Epigenetics.* 10:662-669. (\*co-first author)
18. Sanghavi K, Brundage RC, Miller MB, Schladt DP, Israni AK, **Guan W**, Oetting WS, Mannon RB, Remmel RP, Matas AJ, Jacobson PA. 2015. Genotype-guided tacrolimus dosing in African-American kidney transplant recipients. *Pharmacogenomics J.* NIHMSID: NIHMS735273.
19. Dorajoo R, Sun Y, Han Y, Ke T, Burger A, Chang X, Low HQ, **Guan W**, Lemaitre RN, Khor CC, Yuan JM, Koh WP, Ong CN, Tai ES, Liu J, van Dam RM, Heng CK, Friedlander Y. 2015. A genome-wide association study of n-3 and n-6 plasma fatty acids in a Singaporean Chinese population. *Genes Nutr.* 10:53.
20. Li YR, van Setten J, Verma SS, Lu Y, Holmes MV, Gao H, Lek M, Nair N, Chandrupatla H, Chang B, Karczewski KJ, Wong C, Mohebnasab M, Mukhtar E, Tragante V, Li C, Steel L, Garifallou J, Guettouche T, Almoguera B, Cao H, **Guan W**, Himes A, van Houten J, Pasquier A, Yu R, Carrigan E, Miller MB, Schladt D, Akdere A, Gonzalez A, Llyod KM, McGinn D, Michaud, Z, Colasacco A, Snyder J, Thomas K, Wang T, Wu B, Alzahrani AJ, Al-Ali AK, Al-Muhanna FA, Al-Rubaish AM, Al-Mueilo S, Monos DS, Murphy B, Olthoff KM, Wijmenga C, Webster T, Kamou M, Balasubramanian S, Lanktree MB, Oetting WS, Garcia-Pavia P, MacArthur DG, Hakonarson H, Jacobson PA, Birdwell KA, Ritchie MD, Asselbergs FW, Israni AK, Shaked A, Keating BJ. 2015. Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. *Genome Medicine.* 7:90.

21. International Genetics & Translational Research in Transplantation Network (iGeneTRaiN). 2015. Design and Implementation of the International Genetics and Translational Research in Transplantation Network. *Transplantation*. 99:2401-2412.
22. Jia C\*, **Guan W\***, Yang A, Xiao R, Tang WH, Moravec CS, Margulies KB, Cappola TP, Li M, Li C. 2015. MetaDiff: differential isoform expression analysis using random-effects meta-regression. *BMC Bioinformatics*. 16:208. (\*.co-first author)
23. Huang X, Jennings SF, Bruce B, Buchan A, Cai L, Chen P, Cramer CL, Guan W, Hilgert UK, Jiang H, Li Z, McClure G, McMullen DF, Nanduri B, Perkins A, Rekepalli B, Salem S, Specker J, Walker K, Wunsch D, Xiong D, Zhang S, Zhang Y, Zhao Z, Moore JH. 2015. Big data-a 21st century science Maginot Line? No-boundary thinking: shifting from the big data paradigm. *BioData Min*. 8:7.
24. Pulk RA, Schladt DS, Oetting WS, **Guan W**, Israni AK, Matas AJ, Rimmel RP, Jacobson PA. 2015. Multigene predictors of tacrolimus exposure in kidney transplant recipients. *Pharmacogenomics*. 12:1-14.
25. Demerath EW, **Guan W**, Grove ML, Aslibekyan S, Mendelson M, Zhou YH, Hedman AK, Sandling JK, Li L, Irvin MR, Zhi D, Deloukas P, Liang L, Liu C, Bressler J, Spector TD, North K, Li Y, Absher DM, Levy D, Arnett DK, Fornage M, Pankow JS, Boerwinkle E. 2015. Epigenome-wide association study (ewas) of bmi, bmi change, and waist circumference in african american adults identifies multiple replicated loci. *Hum Mol Genet*. 24:4464-4479.
26. Aslibekyan S, Demerath EW, Mendelson M, Zhi D, **Guan W**, Liang L, Sha J, Pankow JS, Liu C, Irvin MR, Fornage M, Hidalgo B, Lin L, Thibeault KS, Bressler J, Tsai MY, Grove ML, Hopkins PN, Boerwinkle E, Borecki IB, Ordovas JM, Levy D, Tiwari HK, Absher DM, Arnett DK. 2015. Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. *Obesity*. 23: 1493-1501.
27. Dorr C, Wu B, **Guan W**, Muthusamy A, Sanghavi K, Schladt DP, Maltzman JS, Scherer SE, Brott MJ, Matas A, Jacobson PA, Oetting WS, Israni AK. 2015. Differentially expressed gene transcripts using RNAsequencing from the blood of immunosuppressed kidney allograft recipients. *PLoS One*. In press.
28. **Guan W**, Cao J, Steffen BT, Post WS, Stein JH, Tattersall MC, Kaufman JD, McConnell JP, Hoefner DM, Warnick RW, Tsai MY. 2015. Race is a key variable in assigning lipoprotein(a) cut points for coronary heart disease risk assessment: the Multi-Ethnic Study of Atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*. 35:996-1001.
29. Satzer D, Maurer EW, Lanctin D, **Guan W**, Abosch A. 2015. Anatomic correlates of deep brain stimulation electrode impedance. *J Neurol Neurosurg Psychiatry*. 86:398-403.
30. Wu B, **Guan W**. 2015. Reader reaction on the generalized Kruskal-Wallis test for genetic association studies incorporating group uncertainty. *Biometrics*. 71:556-557.

31. Steffen BT, **Guan W**, Remaley AT, Paramsothy P, Heckbert SR, McClelland RL, Greenland P, Michos ED, Tsai MY. 2015. Use of Lipoprotein Particle Measures for Assessing Coronary Heart Disease Risk Post-American Heart Association/American College of Cardiology Guidelines: the Multi-Ethnic Study of Atherosclerosis. *Arterioscl Throm Vas.* 35:448-54.
32. Maier R, Moser G, Chen GB, Ripke S; Cross-Disorder Working Group of the Psychiatric Genomics Consortium, et al. 2015. Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. *Am J Hum Genet.* 96:283-94.
33. Network and Pathway Analysis Subgroup of Psychiatric Genomics Consortium. 2015. Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nat Neurosci.* 18:199-209.
34. Lemaitre RN, King IB, Kabagambe EK, Wu JH, McKnight B, Manichaikul A, **Guan W**, Sun Q, Chasman DI, Foy M, Wang L, Zhu J, Siscovick DS, Tsai MY, Arnett DK, Psaty BM, Djousse L, Chen YD, Tang W, Weng LC, Wu H, Jensen MK, Chu AY, Jacobs DR Jr, Rich SS, Mozaffarian D, Steffen L, Rimm EB, Hu FB, Ridker PM, Fornage M, Friedlander Y. 2015. Genetic loci associated with circulating levels of very long-chain saturated fatty acids. *J Lipid Res.* 56:176-184.
35. **Guan W**, Li C. 2014. Design of DNA pooling to allow incorporation of covariates in rare variants analysis. *PLoS One.* 9(12):e114523.
36. Bose M, Wu C, Pankow JS, Demerath EW, Bressler J, Fornage M, Grove ML, Mosley TH, Hicks C, North K, Kao WH, Zhang Y, Boerwinkle E, **Guan W**. 2014. Evaluation of microarray-based DNA methylation measurement using technical replicates: the Atherosclerosis Risk In Communities (ARIC) Study. *BMC Bioinformatics.* 15:312.
37. **Guan W**, Steffen BT, Steffen LM, Lemaitre RN, Wu J, Tanaka T, Manichaikul A, Foy M, Rich SS, Wang L, Nettleton JA, Tang W, Ferrucci L, Gu X, Bandinelli S, King IB, McKnight B, Psaty BM, Siscovick D, Djousse L, Chen Y, Fornage M, Mozaffarian D, Tsai MY. 2014. Genome-wide association study of plasma n6 polyunsaturated fatty acids within the CHARGE consortium. *Circ Cardiovasc Genet.* 7: 321-331.
38. Adhikari N, **Guan W**, Capaldo B, Mackey AJ, Carlson M, Ramakrishnan S, Walek D, Gupta M, Mitchell A, Eckman P, John R, Ashley E, Barton PJ, Hall JL. 2014. Identification of a new target of miR-16, Vacuolar Protein Sorting 4a. *PLoS One.* 9(7):e101509.
39. Lamba V, Ghodke Y, **Guan W**, Lamba JK. 2014. Identification of suitable reference genes for hepatic microRNA quantitation. *BMC Res Notes.* 7:129.
40. Wu J, Lin R, Huang J, **Guan W**, Oetting WS, Sriramarao P, Blumenthal MN. 2014. Functional Fcγ receptor polymorphisms are associated with human allergy. *PLoS One.* 9(2):e89196.
41. Adhikari N, Billaud M, Carlson M, Lake SP, Montaniel KR, Staggs R, **Guan W**, Walek D, Desir S, Isakson BE, Barocas VH, Hall JL. 2014. Vascular biomechanical properties in mice with smooth muscle specific deletion of *Ndst1*. *Molecular and Cellular Biochemistry.* 385: 225-238.

42. Oetting WS, **Guan W**, Schladt DP, Wildebush WA, Becker J, Thyagarajan B, Jacobson PA, Matas AJ, , Israni AK. 2014. Telomere Length of Recipients and Living Kidney Donors and Chronic Graft Dysfunction in Kidney Transplants. *Transplantation*. 97:325-329.
43. Mitchell A, **Guan W**, Staggs R, Hamel A, Hozayen S, Adhikari N, Grindle S, Jall JH, Eckman P. 2013. Identification of differentially expressed transcripts and pathways in blood one week and six months following implant of left ventricular assist devices.. *PLoS One*. 8(10):e77951.
44. Tsai MY, Steffen BT, **Guan W**, McClelland RL, Warnick R, McConnell J, Hoefner D, Remaley AT. 2013. A new automated assay of small dense LDL cholesterol identifies risk of coronary heart disease: the Multi-Ethnic Study of Atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*. 34:196-201.
45. Wang C, Kane RL, Xu D, Li L, **Guan W**, Li H, Meng Q. 2013. Maternal Education and Micro-Geographic Disparities in Nutritional Status among School-Aged Children in Rural Northwestern China. *PLoS One*. 8(12):e82500.
46. Cross-Disorder Group of the Psychiatric Genomics Consortium, et. al. 2013. Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*. 45:984-994.
47. Liang S, Steffen LM, Steffen BT, **Guan W**, Weir NL, Rich SS, Manichaikul A, Vargas JD, Tsai MY. 2013. APOE genotype modifies the association between plasma omega-3 fatty acids and plasma lipids in the Multi-Ethnic Study of Atherosclerosis (MESA). *Atherosclerosis*. 228:181-187.
48. Israni A, Riad SM, Leduc R, Oetting WS, **Guan W**, Schladt D, Matas AJ, Jacobson PA. 2013. Tacrolimus trough levels after month 3 as a predictor of acute rejection following kidney transplantation; a lesson learned from DEKAF genomics. *Transplantation*. 26:982-989.
49. Thyagarajan B, Arora M, **Guan W**, Barcelo H, Jackson S, Kumar S, Gertz M. 2013. Genetic variants in DNA repair pathways are not associated with disease progression among multiple myeloma patients. *Leuk Res*. 37:1527-1531.
50. Zhang Y, **Guan W**, Pan W. 2013. Adjustment for population stratification via principal components in association analysis of rare variants. *Genetic Epidemiology*. 37:99-109.
51. Israni A, Leduc R, Jacobson PA, Wildebush W, **Guan W**, Schladt DP, Matas AJ, Oetting WS. 2013. Inflammation in the setting of chronic allograft dysfunction post-kidney transplant: phenotype & genotype. *Clinical Transplantation*. 27:348-358.
52. Wu JH, Lemaitre RN, Manichaikul A, **Guan W**, Tanaka T, Foy M, Kabagambe EK, Djousse L, Siscovick D, Fretts AM, Johnson C, King IB, Psaty BM, McKnight B, Rich SS, Chen YI, Nettleton JA, Tang W, Bandinelli S, Jacobs DR Jr, Browning BL, Laurie CC, Gu X, Tsai MY, Steffen LM, Ferrucci L, Fornage M, Mozaffarian D. 2012. Genome-wide association study identifies novel loci associated with concentrations of plasma phospholipid fatty acids in the de novo lipogenesis pathway: results from the CHARGE consortium. *Circulation: Cardiovascular Genetics*. 6:171-183.

53. **Guan W**, Boehnke M, Pluzhnikov A, Cox NJ, Scott LJ. 2012. Identifying plausible genetic models based on association and linkage results: application to type 2 diabetes. *Genetic Epidemiology*. 36:820-828.
54. Passey C, Birnbaum AK, Brundage RC, Schladt D, Oetting W, Leduc R, Israni A, **Guan W**, Matas A, Jacobson P. 2012. Validation of tacrolimus equation to predict troughs using genetic and clinical factors. *Pharmacogenomics*. 13:1141-1147.
55. Jacobson PA, Schladt D, Israni A, Oetting W, Lin YC, Leduc R, **Guan W**, Lamba V, Matas AJ. 2012. Genetic and clinical determinants of early, acute calcineurin inhibitor-related nephrotoxicity: results from a kidney transplant consortium. *Transplantation*. 93:624-631.
56. Oetting W, **Guan W**, Schladt D, Leduc R, Jacobson P, Matas A, Chinnakotla S, Schröppel B, Murphy B, Israni A. 2012. Donor polymorphisms of tlr4 associated with graft failure in liver transplant recipients. *Liver Transplantation*. 18:1399-1405.
57. Oetting WS, Schladt DP, Leduc R, Jacobson PA, **Guan W**, Matas AJ, Israni A. 2011. Validation of single nucleotide polymorphisms (SNPs) associated with acute rejection in kidney transplant recipients using a large multi-center cohort. *Transplant International*. 24:1231-1238.
58. Psychiatric GWAS Consortium Bipolar Disorder Working Group. 2011. Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. *Nature Genetics* 43:977-983.
59. Jacobson PA, Schladt D, Oetting W, Leduc R, **Guan W**, Lamba V, Matas A, Mannon R, Julian BA, Israni A. 2011. Genetic determinants of mycophenolate related anemia and leukopenia following transplantation. *Transplantation* 91:309-316.
60. Ramsuran V, Kulkarni H, He W, Mlisana K, van Loggerenberg F, Wright EJ, Werner L, Castiblanco-Quinche J, Dolan MJ, **Guan W**, Weiss RA, Clark RA, Abdool Karim SS, Ahuja SK, Ndung'u T. 2011. Duffy-null-associated low neutrophil counts influence hiv-1 susceptibility in high-risk south african black women. *Clinical Infectious Diseases* 52:1248-1256.
61. Israni A, Leduc R, Holmes J, Jacobson P, Lamba V, **Guan W**, Schladt D, Chen J, Matas A, Oetting W. 2010. Single nucleotide polymorphisms, acute rejection and severity of tubulitis in kidney transplantation, accounting for center-to-center variation. *Transplantation*. 90:1401-1408.
62. Scott LJ, Muglia P, Kong XQ, **Guan W**, Flickinger M, Upmanyu R, Tozzi F, Li JZ, Burmeister M, Absher D, Thompson RC, Francks C, Meng F, Antoniadis A, Southwick AM, Schatzberg AF, Bunney WE, Barchas JD, Jones EG, Day R, Matthews K, McGuffin P, Strauss JS, Kennedy JL, Middleton L, Roses AD, Watson SJ, Vincent JB, Myers RM, Farmer AE, Akil H, Burns DK, Boehnke M. 2009. Genome-wide association and meta-analysis of bipolar disorder in European ancestry samples. *Proceedings of the National Academy of Sciences-USA* 106:7501-7506.
63. **Guan W\***, Liang L\*, Boehnke M, Abecasis GR. 2009. Genotype-based matching to correct for population stratification in large-scale case-control genetic association studies. *Genetic Epidemiology* 33:508-517. (\*co-first author)
64. **Guan W**, Pluzhnikov A, Cox NJ, Boehnke M. for the International Type 2 Diabetes Linkage Analysis Consortium, 2008. Meta-analysis of 23 type 2 diabetes linkage studies from the international type 2 diabetes linkage analysis consortium. *Human Heredity* 66:35-49.
65. Li M, Li C, **Guan W**. 2008. Evaluation of coverage variation of SNP chips for genome-wide association studies. *European Journal of Human Genetics* 16:635-643.

66. The International HapMap Consortium, 2005. A haplotype map of the human genome. *Nature* 437:1299-1320.
67. Drukker DM and **Guan W.** 2003. Replicating the results in “on efficient estimation with panel data: an empirical comparison of instrumental variables estimators”. *Journal of Applied Economics* 18:119.

### **NON-REFEREED JOURNAL ARTICLES OR BOOK CHAPTERS**

2003. Stochastic frontier models. *Stata 8 Reference Manual (Volume 1)*, Stata Press.
2003. Stochastic frontier models for panel-data. *Stata 8 Reference Manual (Cross-Sectional Time-Series)*, Stata Press.
2003. Hausman-Taylor estimator for error component models. *Stata 8 Reference Manual (Cross-Sectional Time-Series)*, Stata Press.
- Guan W** and Gutierrez RG. 2002. Programmable GLM: two user-defined links. *The Stata Journal* 2:378-390.
- Guan W.** 2003. From the help desk: bootstrapping standard errors. *The Stata Journal* 3:71-80.

### **GRANTS AND CONTRACT SUPPORT**

#### Active:

1. Title: Genomics of Kidney Transplantation  
Source: NIH/NIAID  
Period: 8/01/11-7/31/16  
Role: Statistician. (PI: Dr. Arthur Matas)
2. Title: An Integrated Study of Mitochondrial Pathways in Colorectal Cancer  
Source: NIH  
Period: 8/1/13-7/31/16  
Role: Co-Investigator. (PI: Dr. Myron Gross)
3. Title: Epidemiology of Venous Thromboembolism and Pulmonary Embolism (LITE)  
Source: NIH  
Period: 4/15/13-3/31/17  
Role: Co-Investigator. (PI: Dr. Aaron Folsom)
4. Title: Atherosclerosis Risk in Communities (ARIC) study  
Source: NIH  
Period: 10/2/12-10/1/16  
Role: Co-Investigator. (PI: Dr. Aaron Folsom)
5. Title: University of Minnesota Clinical and Translational Science Institute  
Source: NIH  
Period: 6/01/11-5/31/16  
Role: Co-Investigator. (PI: Dr. B. Blazar)
6. Title: Transcriptomic and Epigenetic Signatures of Tobacco Exposure.  
Source: AHA  
Period: 2/1/15-1/31/17  
Role: PI (subcontract to Boston University)
7. Title: Live Cell Auto reactive B Cell Capture for Advanced Analytics in RA.



Source: Rheumatology Research Foundation  
Period: 07/01/2015-06/30/2017  
Role: Co-Investigator. (PI: Dr. Daniel Mueller)

Past:

1. Title: Genome-Wide SNP Data  
Source: Genentech, Inc  
Period: 12/15/07-12/31/10  
Role: Co-Investigator. 10% effort. (PI: Dr. Emily Gillespie)
2. Title: Multi-Marker test for genetic association  
Source: SPH/Minnesota Medical Foundation (MMF) Faculty Research Grant  
Period: 09/01/10-09/01/11  
Role: PI
3. Title: Genomics of Kidney Transplantation  
Source: NIH/NIAID  
Period: 8/01/06-7/31/11  
Role: Statistician. 5% effort. (PI: Dr. Arthur Matas)
4. Title: Multi-Ethnic Study of Atherosclerosis (MESA) 2 Laboratory Center  
Source: Univ of Vermont (NIH prime)  
Period: 08/15/08-08/14/15  
Role: Statistician. 3% effort. (PI: Dr. Michael Tsai)
5. Title: Multi-Ethnic Study of Atherosclerosis (MESA) 2 Lipid Analysis Laboratory  
Source: Univ of Washington (NIH prime)  
Period: 08/15/08-08/14/15  
Role: Statistician. 5% effort. (PI: Dr. Michael Tsai)
6. Title: Design of DNA pooling to allow incorporation of covariates in rare variants analysis  
Source: University of Minnesota (Grant-in-Aid)  
Period: 1/1/13-4/30/14  
Role: PI
7. Title: Identifying Epidemiological Risk Factors for Abdominal Aortic Aneurysm  
Source: NIH  
Period: 04/1/11-03/31/16  
Role: Co-Investigator. 10% effort. (PI: Dr. Weihong Tang)
8. Title: Mitochondria as a novel-biomarker predictor of colorectal adenoma  
Source: NIH  
Period: 04/1/13-03/31/15  
Role: Co-Investigator. 5% effort. (PI: Dr. Bharat Thyagarajan)

**COURSE INSTRUCTION**

Division of Biostatistics, School of Public Health – University of Minnesota  
PUBH 8401: Linear Models (Falls 2009 – current)  
PUBH 7402: Biostatistics Modeling and Methods (Springs 2011 – current)

**PROFESSIONAL MEMBERSHIPS**

American Society of Human Genetics

American Statistical Association

International Biometric Society