Xiangqin Cui

Department of Biostatistics and Bioinformatics	Phone:	404-727-3743
Rollins School of Public Health, GCR 214	Fax:	404-727-1370
1518 Clifton Rd., NE	Email:	xiangqin.cui@emory.edu
Emory University	ORCID:	0000-0003-0621-9313
Atlanta, GA 30322		

EDUCATION AND TRAINING

2001–2004, Postdoctoral training. Statistical Genetics/Bioinformatics, The Jackson Laboratory, Bar Harbor, ME (with Dr. Gary Churchill).
1994–2001, Ph.D. Genetics, Iowa State University, Ames, IA (with Dr. Patrick Schnable).
1991–1994, M.S. Molecular and Cytogenetics, Nankai University, Tianjin, P. R. China.
1987–1991, B.A. Biology, Nankai University, Tianjin, P. R. China.

PROFESSIONAL EXPERIENCE

2024 – Present	Professor (Clinic and Research Track), Department of Biostatistics and Bioinformatics, Emory University, Atlanta, GA
2017– Present	Founding Director of Data Analytics Core, Atlanta VA Medical Center, Decatur, GA
2017– 2024	Associate Professor (Clinic and Research Track), Department of Biostatistics and Bioinformatics, Emory University, Atlanta, GA
2012– 2017	Associate Professor, Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL.
2004–2012	Assistant Professor, Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL.
2004–2009	Assistant Professor, Department of Medicine, Division of Genetic and Translational Medicine (later merged into Department of Genetics), University of Alabama at Birmingham, Birmingham, AL.
2001–2004	Postdoctoral associate, The Jackson Laboratory, Bar Harbor, ME.
1994–2001	Graduate Research Assistant, Iowa State University, Ames, IA.
1991–1994	Graduate Research Assistant, Nankai University, Tianjin, China.

LEADERSHIP ROLES

Director of Biostatistics Graduate Studies (DGS) for the Master Program (2021–present)

I took on the director role for the MPH/MSPH program in the Biostatistics Department at Emory University in 2021 after I successfully revamped and streamlined the thesis/capstone structure in the program, which was a major challenge after the program grew into the size of around 100 students. I currently oversee the recruitment, admission, curriculum, student policy, and student services of the program. I also represent the program in the School of Public Health education committee and facilitate the CEPH compliance.

Founding Director of the Data Analytics Core (DAC) at the Atlanta VA Medical Center (2017–present)

I was recruited in 2017 to establish the data analytics core to meet the analytical needs of all investigators in the Atlanta VA Medical Center in study design, data management, data analyses, and grant application. In the past 7 years, the DAC has grown from one person to four staff members (two statisticians, one data manager, and one data scientist) fully funded on research and quality improvement grants. The Data Analytics Core will continue to grow as the needs increase.

Director of the methodology core in Rheumatology NIH P60 program project at UAB (2014–2017).

I took over the directorship when Dr. David Redden became the Biostatistics Department chair in 2014. The methodology core was one of the multiple cores in the P60 grant. It supported 6-7 faculty members with various expertise at 5% -10% effort level and two master-level statisticians. The function of the core was to support the analytic needs of the projects (2 or 3 depending on cycles) and the rheumatology research community. The main tasks were data analyses, grant writing support, study designs, new methods development, new investigator development, and community education. This grant had been funded for more than 10 years by the time I left and it was the third funding cycle under my direction. I had been a member of the core for 6 years before taking on the director role.

RESEARCH AREA

My research career started from molecular and field genetics in plants for my PhD training and went on to genomics/bioinformatics/statistical genetics for gene expression profiling and QTL analyses during my postdoctoral training. After I took on the faculty position in the Biostatistics Department at UAB, my research focused on omics (gene expression profiling, methylation profiling, microbiome etc.) method development and applications through collaborations. Due to the need of UAB O'Brien Center (2008-2017) and UAB CCTS BERD (2010-2017), I started providing general statistical support for the investigators served by these centers. My research switched to clinical trials and observational studies based on electronic health records (EHR) after I moved to Emory University to take on the directorship of the Data Analytics Core at the Atlanta VA Medical Center in 2017. With constant evolvement of my research interests over the past years, one research topic remains to be a stable component. It is renal disease, specifically polycystic kidney disease. My collaboration with Dr. Michal Mrug at UAB on polycystic kidney disease started from gene mapping during our postdoctoral years and continued to present on VA polycystic kidney disease patient cohort building and investigations.

PUBLICATIONS (first and corresponding/senior authorship marked with **)

Book Chapters:

1. Wu H, MK Kerr, **X Cui**, and GA Churchill (2003). MAANOVA: A software package for the analysis of spotted cDNA microarray experiments. Chapter 14 in *The analysis of gene expression data*. Edited by G. Parmigiani et al. Springer, New York, pp. 313–341.
2. **Cui X**** and GA Churchill (2003). How many mice and how many arrays? Replication in mouse cDNA microarray experiments. In *Methods of microarray data analysis III*. Edited by

Kimberly F. Johnson and Simon M. Lin. Kluwer Academic Publishers, Norwell, MA. Pp. 139-154.

3. Page G and **X Cui** (2008). Microarray. In *Wiley encyclopedia of clinical trials*. Edited by Ralph D'Agostino Lisa Sullivan, and Joseph Massaro. Wiley, Noboken, NJ. ISBN: 978-0-471-35203-7.
4. **Cui X.**** (2010). Experimental designs of high throughput biological experiments. Chapter 9 in "Statistical Bioinformatics" edited by Lee, Jae K. John Wiley & Sons, Inc., Hoboken, NJ, pp. 201–217.
5. Kennedy RE, and **X. Cui.**** (2011). Experimental designs and ANOVA for microarray data. Book Chapter 8 in *Hand book of statistical bioinformatics* Edited by Henry Horng-Shing Lu, Bernhard Scholkopf, and Hongyu Zhao. Springer Heidelberg Dordrecht, London, pp. 151-169.

Journal Articles

1. Song WQ, **XQ Cui**, WS Xu, XL Li, YK Peng, and RY Chen (1996). Micro-dissection and amplification of the terminal region from the long arm of the big M chromosome. *Vica faba*. *Chinese Science Bulletin* 41**:** 361–364.
2. **Cui X****, RP Wise, and PS Schnable (1996). The *rf2* nuclear restorer gene of male sterile T-cytoplasm maize. *Science* 272: 1334–1336.
3. Liu F.* **X Cui.*** HT Horner, H Weiner, and PS Schnable (2001). Mitochondrial aldehyde dehydrogenase activity is required for male fertility in maize. *Plant Cell* 13: 1063–1078. * These authors contributed equally to this work. PMCID: PMC135560.
4. Skibbe DS, F Liu, TJ Wen, MD Yandeau, **X Cui**, J Jun Cao, CR Simmons, and PS Schnable (2002). Characterization of the aldehyde dehydrogenase gene families of *Zea mays* and *Arabidopsis. Plant Molecular Biology* 48: 751–764.
5. **Cui X,**** AP Hsia, DA Ashlock, RP Wise, and PS Schnable (2003). Alternative transcription initiation sites and polyadenylation sites are recruited during *Mu* suppression at the *rf2* locus of maize. *Genetics* 163: 685–698. PMCID: PMC1462470.
6. **Cui X,**** MK Kerr, and GA Churchill (2003) Transformations for cDNA microarray data. *Statistical Applications in Genetics and Molecular Biology.* vol 2, issue 1, article 4.
7. **Cui X**** and GA Churchill (2003) Statistical tests for differential expression in cDNA microarray experiments. *Genome Biology*, 4:201. PMCID: PMC154570.
8. Lobenhofer E.K., **X Cui,** L. Bennett, P.L. Cable, G.A. Churchill, and C.A. Afshari (2004) Exploration of Low Dose Estrogen Effects: Identification of No Observed Transcriptional Effect Level (NOTEL). *Toxicol Pathol.* 32(4):482-92.
9. Mrug M, TR Schoeb, R Li, **X Cui**, GA Churchill , and LM Guay-Woodford (2004). Kinesin 12 is predicted to modulate multiple phenotypes in the *cpk* mouse model of ARPKD. *J Am Soc Nephrol* 15:216A.
10. **Cui X,**** JTG Hwang, J Qiu, NJ Blades, and G Churchill (2005). Improved statistical tests for differential gene expression by shrinking variance component estimates. *Biostatistics*. 6(1): 59–75.

11. Yao H, L , Y Fu, LA Borsuk, TJ Wen, DS Skibbe, **X Cui**, BE Scheffler, J Cao, SJ Emrich, DA Ashlock, and PS Schnable (2005). Evaluation of five ab initio gene prediction programs for the discovery of maize genes. *Plant Mol Biol.* 57(3): 445-60.
12. Mrug M, R Li, **X Cui**, TR Schoeb, GA Churchill, and LM Guay-Woodford (2005). Kinesin-related protein 12 is a candidate polycystic kidney disease modifier in the *cpk* mouse**.** *J Am Soc Nephrol*. 16(4): 905–16.
13. Allison DB, **X Cui**, GP Page, and M Sabripour (2006). Microarray data analysis: From disarray to consolidation and consensus. *Nat Rev Genet.* 7: 55–65.
14. **Cui, X,**** and AE Loraine (2006). Global correlation analysis between redundant probe sets using a large collection of arabidopsis ath1 expression profiling data. *Comput Syst Bioinformatics Conf.* 2006: 223–226.
15. **Cui, X,**** J Affourtit, KR Shockley, Y Woo, and GA Churchill (2006). Inheritance patterns of transcript levels in f1 hybrid mice. Genetics 174: 627–637.
16. Laudencia-Chingcuanco, DL., BS Stamova, GR Laxo, XQ **Cui**, and OD Anderson (2006). Analysis of the wheat endosperm transcriptome. *J. Appl. Genet* 47:.287–302.
17. Allison DB, **X Cui**, GP Page, and M Sabripour (2006). Erratum: Microarray data analysis: From disarray to consolidation and consensus (Nature Reviews Genetics (2006) 7 (55-65) DOI: 10.1038/nrg1749). *Nature Review Genetics* 7(5):406.
18. Brand JPL, L Chen, X **Cui,** AA Bartolucci, AA Page, K Kim, K.,S Barnes, S.,V Srinivasasainagendra, TM Beasley, and DB Allison (2007). An adaptive alpha-spending algorithm improves the power of statistical inference in microarray data analysis. *Bioinformation,* 1(10): 384–389. PMCID: PMC1896052.
19. Ye J, Cui X, Loraine A, Bynum K, Kim NC, White G, De Luca M, Garfinkel MD, Lu X, Ruden DM (2007). Methods for nutrigenomics and longevity studies in Drosophila: Effects of diets high in sucrose, palmitic acid, soy, or beef. *Methods Mol Biol.* 371:111–41.
20. Wu, X, J Wang, **X Cui,** L Maianu, B Rhees, J Rosinski, WV So, SM Willi, MV Osier HS Hill, GP Page, DB Allison, M Martin, and WT Garvey (2007). The effect of insulin on expression of genes and biochemical pathways in human skeletal muscle. *Endocrine*; 32(3):356.
21. Gao YZ, SY Guo, QZ Yin, **X Cui**, T. Hisamitsu, and XH Jiang (2007). Possible involvement of integrin signaling pathway in the process of recovery from restraint stress in rats. *Neurosci Bull.* 23(4):22935.
22. Mrug, M., J Zhou, **X Cui**, LM Guay-Woodford, N Hill-Kapturczak (2007). Thrombospondin 1, a latent TGFβ activator, is expressed abnormally in autosomal recessive polycystic kidney disease. *J Am Soc Nephrol* 18:360 A.
23. Mrug, M, J Zhou, Y Woo, **X Cui**, AJ Szalai1, J Novak, GA Churchill, and LM Guay-Woodford (2008). Overexpression of innate immune response genes in a model of recessive polycystic kidney disease. *Kidney International* 73(1):63–76.
24. Mrug, M, J Zhou, Y Woo, **X Cui**, AJ Szalai1, J Novak, GA Churchill, and LM Guay-Woodford (2008). Overexpression of complement-component genes in Han: SPRD rats a model of polycystic kidney disease – Response. *Kidney International* 73(11):1325–1325

25. **Cui, X,**** and AE Loraine (2009) Consistency analysis of redundant probe sets on affymetrix three-prime expression arrays and applications to differential mRNA processing. *PLoS ONE* 4(1):e4229. PMC2621337.
26. PA Ioannidis, DB Allison, C Ball, C Furlanello, J Mangion, GP Page, V van Noort, I Coulibaly, **X Cui**, A Culhane, M Falci, L Game, G Jurman, T Mehta, E Petretto, JWang, M Axton (2009). Reproducibility of published microarrays gene expression analyses. *Nature Genetics* 41:178–186.
27. Zhu, H, G-J Li, L Ding, **X Cui**, H Berg, SM Assmann, and Y Xia (2009) Arabidopsis Extra Large G Protein 2 (XLG2) interacts with the Gβ□subunit of heterotrimeric G protein and functions in disease resistance. *Molecular Plant* 2(3):513–525. PMC2902900.
28. Chen, L, GP Page, T Mehta, R Feng, and **X Cui.**** (2009). Single nucleotide polymorphisms affect both cis- and trans-eQTLs. *Genomics* 93(6):501–8. PMC4041081.
29. **Cui, X,**** J Qiu, J Zhou, and M Mrug (2009). Validation of endogenous internal real-time PCR controls in renal tissues. *Am J Nephrol* 30:413–417. PMC2818397.
30. Ulett, GC, RI Webb, KB Ulett, **X Cui,** WH Benjamin, M Crowley, and MA Schembri. (2010). Group B Streptococcus (GBS) urinary tract infection involves binding of GBS to bladder uroepithelium and potent but GBS-specific induction of Interleukin-1α. *The Journal of Infectious Diseases* 201(6):866–70.
31. Thalacker-Mercer, A, LJ Dell'Italia, **X Cui**, JM Cross, and MM Bamman (2010). Differential Genomic Responses in Old vs. Young Humans Despite Similar Levels of Modest Muscle Damage After Resistance Loading. *Physiological Genomics* 40(3):141–9. PMC2825766.
32. Qiu, J, and **X Cui**.** (2010). Evaluation of a statistical equivalence test applied to microarray data. *Journal of Biopharmaceutical Statistics,* 20(2):240-66.
33. Zhou, J, X Ouyang, **X Cui,** TR Schoeb, LE Smythies, MR Johnson, LM Guay-Woodford, AB Chapman, and M Mrug (2010) Renal CD14 expression correlates with rates of cystic kidney disease progression. *Kidney International* 78(6):550–60. PMC2818397.
34. Garvey WT, Wu X, A Patki, C Lara-Castro, **X Cui**, K Zhang, RG Walton, MV Osier, GL Gadbury, DB Allison, and M Martin M (2011). Genes and biochemical pathways in human skeletal muscle affecting resting energy expenditure and fuel partitioning. *Journal of Applied Physiology* Mar;110(3):746–55. PMC3070475.
35. Gao L, Z Fang, K Zhang, D Zhi, and **X Cui.**** (2011). Length bias correction for RNA-seq data in gene set enrichment analyses. *Bioinformatics* 7(5):662–669. doi: 10.1093/bioinformatics/btr005. PMC3042188.
36. Fang Z, and **X Cui.**** (2011). Design and validation issues in next generation sequencing experiments. *Briefings in Bioinformatics* 12(3):280–287.
37. Chen Y, B Pat, JD Gladden, J Zheng, P Powell, C-C Wei, **X Cui**, A Husain, and LJ Dell'Italia (2011). Dynamic molecular and histopathological changes in extracellular matrix and inflammation in the transition to heart failure in isolated volume overload. *Circulation. AJP-Heart and Circulatory Physiology* 300(6):H2251–60. PMC3119090.

38. Duell BL, AJ Carey, CK Tan, **X Cui**, RI Webb, M Totsika, MA Schembri, P Derrington, H Irving-Rodgers, AW Cripps, M Crowley, and GC Ulett (2012) Innate transcriptional networks activated in bladder in response to uropathogenic Escherichia coli drive diverse biological pathways and rapid synthesis of IL-10 for defense against bacterial urinary tract infection. *Journal of Immunology* 188(2):781–92.
39. Duarte CW, CD Willey, D Zhi D, **X Cui,** JJ Harris, LK Vaughan, T Mehta, RO McCubrey, NN Khodarev, RR Weichselbaum, and GY Gillespie (2012). Expression signature of ifn/stat1 signaling genes predicts poor survival outcome in Glioblastoma Multiforme in a subtype-specific manner. *PLoS One* 2012; 7(1):e29653. PMC3252343.
40. Reynolds RJ, **X Cui**, LK Vaughan, DT Redden, Z Causey, E Perkins, T Shah, LB Hughes; CLEAR Investigators, A Damle, M Kern, PK Gregersen, MR Johnson, and SL3Bridges Jr (2012). Gene expression patterns in peripheral blood cells associated with radiographic severity in African Americans with early rheumatoid arthritis. *Rheumatology International*. 33(1):129-37. doi: 10.1007/s00296-011-2355-3. PMC3769702.
41. Moskowitz-Kassai E, L Mackelaite, J Chen, K Patel, DM Dadhania, SS Gross, P Chander, V Delaney, L Deng, L Chen, **X Cui**, M Suthanthiran, and MS Goligorsky MS (2012) Excretion of anti-angiogenic proteins in patients with chronic allograft dysfunction. *Nephrology Dialysis Transplantation*. 2012 Feb;27(2):494-7. Epub 2012 Jan 17. PMC3275786.
42. Fang Z., R Du, and **X Cui.**** (2012) Uniform approximation is more appropriate for Wilcoxon Rank-Sum Test in Gene Set Analysis. *PLoS One*. 7(2):e31505 Epub 2012 Feb 7. PMC3274536.
43. Zhou J, Ouyang X, Schoeb TR, Bolisetty S, **Cui X**, Mrug S, Yoder BK, Johnson MR, Szalai AJ, Mrug M (2012) Kidney Injury Accelerates Cystogenesis via Pathways Modulated by Heme Oxygenase and Complement. *J Am Soc Nephrol*. Jul;23(7):1161-71. PMC3380643.
44. Tan CK, AJ Carey, **X Cui**, RI Webb, WH Benjamin Jr., AW Cripps, M Crowley, KB Ulett, and GC Ulett. (2012) Genome-wide mapping of cystitis due to Streptococcus agalactiae and Escherichia coli in mice identifies a unique bladder transcriptome signifying pathogen-specific antimicrobial defense against urinary tract infection. *Infection and Immunity.* 80(9):3145-60. PMC3418756.
45. Wu H, M. Wu, D Zhi, S A Santorico, **X Cui**** (2012) Statistics for Next Generation Sequencing---- Meeting Report. *Frontiers in Statistical Genetics and Methodology* doi:10.3389/fgene.2012.00128. PMC3395795.
46. Krejčí E, Pesevski Z, Dealmeida AC, Mrug M, Fresco VM, Argraves WS, Barth JL, **Cui X**, Sedmera D (2012) Microarray analysis of normal and abnormal chick ventricular myocardial development. *Physiol Res*. 2012 Jul 24;61 Suppl 1:S137-44.
47. Fox ER, Musani SK, Barbalic M, Lin H, Yu B, Ogunyankin KO, Smith NL, Kutlar A, Glazer NL, Post WS, Paltoo DN, Dries DL, Farlow DN, Duarte CW, Kardia SL, Meyers KJ, Sun YV, Arnett DK, Patki AA, Sha J, **Cui X**, Samdarshi TE, Penman AD, Bibbins-Domingo K, Bůžková P, Benjamin EJ, Bluemke DA, Morrison AC, Heiss G, Carr JJ, Tracy RP, Mosley TH, Taylor HA, Psaty BM, Heckbert SR, Cappola TP, Vasan RS (2013) Genome-wide association study of cardiac structure and systolic function in African Americans: The Candidate Gene Association Resource (CARe) Study. *Circ Cardiovasc Genet*. 2013 Feb;6(1):37-46. PMCID:PMC3591479.

48. Thalacker-Mercer A, Stec M, **Cui X**, Cross J, Windham S, Bamman M. (2013) Cluster analysis reveals differential transcript profiles associated with resistance training-induced human skeletal muscle hypertrophy. *Physiological Genomics* 17;45(12):499-507. PMCID:PMC3680779.

49. Johnson SL, SO. Hughes, **X Cui**, X Li, DB Allison, Y Liu, S Goodell, T Nicklas, T Power, KL Vollrath (2014) Portion sizes for children are associated with parental characteristics and the amounts parents serve themselves. The American Journal of Clinical Nutrition. 99(4):763-70. doi: 10.3945/ajcn.113.078311 PMCID: PMC3953879.

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51. Yan Q, Tiwari HK, Yi N, Lin WY, Gao G, Lou XY, **Cui X**, Liu N. (2014) Kernel-machine testing coupled with a rank-truncation method for genetic pathway analysis. *Genetic Epidemiology*, 38(5):447-56. doi: 10.1002/gepi.21813 PMCID: PMC4073214.

52. Qiu J; Qi Y; **Cui X** (2014) Applying shrinkage variance estimators to the TOST test in high dimensional settings. *Statistics in Genetics and Molecular Biology*, 13(3):323-41. doi: 10.1515/sagmb-2013-0045.

53. Peng Y, Song L, Zhao M, Harmelink C, Debenedittis P, **Cui X**, Wang Q, Jiao K. (2014) Critical roles of miRNA-mediated regulation of TGFβ signalling during mouse cardiogenesis. *Cardiovasc Res.* 103(2):258-67. doi: 10.1093/cvr/cvu126. PMCID: PMC4110444.

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metabolite identification, pathway analysis, applications of metabolomics and its future. *Journal of Mass spectrometry*, 51(8):535-548. doi: 10.1002/jms.3780

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and Ulcerative Colitis Patients. *Mucosal Immunology Mucosal Immunol*. 11(5):1487-1495. doi: 10.1038/s41385-018-0046-z.

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84. Zhong H, S Kim, D Zhi, **X Cui**** (2019) Predicting Gene Expression Using DNA methylation in Three Human Populations. *PeerJ* 7:e6757 https://doi.org/10.7717/peerj.6757
85. Behring M, A Vazquez, **X Cui**, M Irvin, A Ojesina, S Agarwal, U Manne, and S Shrestha (2019). Gains of function in somatic TP53 mutations are associated with immune-rich breast tumors and changes in tumor associated macrophages, *Mol Genet Genomic Med*. (12):e1001.
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91. Woodbury A, Krishnamurthy V, Gebre M, Napadow V, Bicknese C, Liu M, Lukemire J, Kalangara J, **Cui X**, Guo Y, Sniecinski R, Crosson B. (2020) Feasibility of Auricular Field Stimulation in Fibromyalgia: Evaluation by Functional Magnetic Resonance Imaging, Randomized Trial. *Pain Med*. 22 (3), 715-726. doi: 10.1093/pm/pnaa317.
92. **Cui X****, JW. Gallini, CL. Jasien, and M Mrug (2021) Autosomal Dominant Polycystic Kidney Disease does not significantly alter major COVID-19 outcomes among veterans. *Kidney 360*, 2 (6) 983-988; DOI: https://doi.org/10.34067/KID.0007282020. PMID: 33269373.

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phenylketonuria. *Orphanet J Rare Dis.* 18(1):222. doi: 10.1186/s13023-023-02842-y. PMID: 37516884; PMCID: PMC10386684.

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110. Hogan K, **Cui X**, Giangiacomo A, Feola AJ. Association of Age of Menopause and Glaucoma Diagnosis in Female Veterans. *Invest Ophthalmol Vis Sci*. 2024 Aug 1;65(10):32. doi: 10.1167/iovs.65.10.32. PubMed PMID: 39172460; PubMed Central PMCID: PMC11346079.

111. Hogan K, **Cui X**, Giangiacomo A, Feola AJ. Postmenopausal Hormone Therapy Was Associated With Later Age of Onset Among Glaucoma Cases. *Invest Ophthalmol Vis Sci*. 2024 Aug 1;65(10):31. doi: 10.1167/iovs.65.10.31. PubMed PMID: 39172461; PubMed Central PMCID: PMC11346078.

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113. Titanji BK, Nagatomi S, Gallini JW, **Cui X**, Hanberg JS, Hsieh E, Marconi VC. The Association Between Rheumatic Disease Therapies and Cardiovascular Outcomes in People with HIV-A Retrospective Cohort Study. J Clin Med. 2024 Oct 18;13(20). doi:

10.3390/jcm13206209. PubMed PMID: 39458159; PubMed Central PMCID: PMC11508247.

114. Li F, Kumar S, Pokutta-Paskaleva A, Kang DW, Kim C, Raykin J, Omojola V, Hoffmann C, Zhao F, Teichmann M, Park C, In Baek K, Sanchez Marrero G, Ma J, Yanigasawa H, Leask A, Timmins L, **Cui X**, Sutliff R, Gleason RL Jr, Jo H, Brewster L. Endothelial cell (EC)-specific CTGF/CCN2 Expression Increases EC Reprogramming and Atherosclerosis. Matrix Biol. 2025 Jan 14:S0945-053X(25)00009-5. doi: 10.1016/j.matbio.2025.01.003. Epub ahead of print. PMID: 39818254.

115. Zhang N, Li Y, Zhang X, Chrenek MA, Wang J, Girardot PE, Sellers JT, Brenner C, **Cui X**, Geisert EE, Nickerson J, Boatright JH. Oral supplementation with Nicotinamide Riboside treatment protects RGCs in DBA/2J mouse model. bioRxiv [Preprint]. 2024 Dec 4:2024.12.03.626460. doi: 10.1101/2024.12.03.626460. PMID: 39677633; PMCID: PMC11642848.

PRESENTATIONS

Talks

“Fertility restoration in cytoplasmic male sterile maize,” at the Interdepartmental Genetics Program Retreat, August 23, 1997.

“Characterization of *rf2*, a maize mitochondrial male sterility restorer gene,” at the All Iowa Genetics Symposium, June 19, 1998.

“Analyze cDNA microarray data using MAANOVA,” invited talk at Amgen, Inc. Thousand Oaks, CA, June 7, 2002.

“How many mice and how many arrays? Replication of cDNA microarray experiment,” invited talk at the CAMDA02 contest, Nov. 14–15, 2002, Durham, NC.

“The inheritance pattern of gene expression in mouse,” at the Microarray Research Coordination Network Retreat, Mohonk, NY, September 27–30, 2004.

“Statistical equivalence testing applied to microarray data,” at the Microarray Research Coordination Network Retreat, Mohonk, NY, September 19–23, 2005.

“Consistency assessment among multiple probe sets interrogating the same gene on the Affymetrix MOE430 GeneChip,” CIS seminar series, Octobor 24, 2007.

“Consistency assessment among redundant probe sets interrogating the same gene on the Affymetrix MOE430 GeneChip,” Fifth Annual Rocky Mountain Bioinformatics, Snow Mass, CO, November 30-December 2, 2007.

“Statistical equivalence testing applied to microarray data,” SSG retreat, January 4 , 2008.

“Statistical equivalence testing applied to microarray data,” ENAR, March 16–19, Washington, D.C., 2008.

“Microarray data analysis – estebalished routines and new directions,” December 5, 2008, Florida State University, Tallahassee, FL.

“Interrogation of alternative splicing using microarray,” May 20, 2009, First International Biomedical Conference at Nankai, Tianjing, China.

“Identifying equivalently expressed genes using DNA microarrays,” May 21, 2009, Department of Statistics, Nankai University, Tianjin, China.

“Experimental design for microarray experiments,” May 23, 2009, Institute of Crop Sciences, the Chinese Academy of Agricultural Sciences, Beijing, China.

“Gene class enrichment analysis for RNA-seq data,” March 23, 2010, ENAR, New Orleans, LA.

“Length bias correction for RNA-seq data in gene set analyses,” March 22, 2011, ENAR, Miami, FL. (Invited)

“Equivalence testing of high dimensional expression data,” November 2011, Emory University, Atlanta, GA. (Invited)

“Equivalence evaluation of GBM primary tumors and xenografts”, August 4th, 2012, JSM San Diego (invited)

“From arrays to NGS - methodology research in Omic equivalence and number crunching in collaboration research”, Feb 5th, 2013, Children’s National Medical Center. Washington DC. (Invited)

“RNA-seq Data for Differential Expression Analysis”, May 13th 2014, Next Generation Sequencing Workshop, UNC Charlotte, NC.

“New Findings for an Old Problem – qRT-PCR Data Normalization” June 25th, 2014. Department of Bioinformatics, Tongjin University. Shanghai, China (invited).

“Uniform Approximation for Wilcoxon Rank-Sum Test in Gene Set Analysis” June 27th, 2014, The Third International Symposium on Biostatistics, Chengdu, China (invited)

“Exploring Immune-Repertoire Sequencing Data” June 13th, 2016. ICSA Applied Statistics Symposium. Atlanta, GA.

“Predicting Gene Expression Using DNA methylation in Three Human Populations”, March 29th, 2019. MCBIOS, Birmingham, GA (Invited).

“From Omics to EHR, Following the Research Calls (Needs)”, Feb 29th, 2020, Statistical Practice in Cancer Conference, Tampa, FL (Keynote Speaker)

“VA Electronic Medical Record for Research – Challenges and Opportunities”, Oct 1st, 2020, Women in Statistics and Data Science, Virtual Conference (Invited).

“VA Electronic Medical Record for Research – Challenges and Opportunities”, November 22, 2021, Biostatistics Program, LSU Health Sciences Center, New Orleans, LA (Invited) Virtual.

“VA Electronic Medical Records for Research – Challenges and Opportunities”, March 28, 2022, Department of Statistics, Iowa State University, Ames, IA (Invited) Virtual.

Posters

Cui X, WJ Chen, RP Wise, and PS Schnable. (1995). The *rf2* nuclear restore of cmsT encodes an aldehyde dehydrogenase, 37 Maize Genetics Conference, March 16–19, Asilomar, CA.

Cui X, F Liu, WJ Chen, RP Wise, and PS Schnable. (1996). The *rf2* nuclear restore of cmsT encodes an aldehyde dehydrogenase, 38th Maize Genetics Conference, March 14–17, St. Charles, IL.

Liu F, **X Cui**, WJ Chen, AP Hsia, RP Wise, and PS Schnable. (1997). The biochemistry characterization of *rf2* protein which is required for cmsT, 39th Maize Genetics Conference, March 13–16, Clearwater Beach, FL.

Cui X, AP Hsia, RP Wise, and PS Schnable. (1998). Suppression of *rf2-m* alleles, 40th Maize Genetics Conference, March 19–20, Lake Geneva, WI.

Cui X, and PS Schnable. (1999). The physiological role of *rf2* independent of its cms-T restorer, 41st Maize Genetics Conference, March 11–14, Lake Geneva, WI.

Cui X, B Scheffler, C Simmons, RB Meely, and PS Schnable. (2000). Mutations in the maize *pdc3* gene cause reduced levels of tolerance to anaerobic stress, annual meeting of the American Society of Plant Physiologists, July 15–19, San Diego, CA.

Cui X, and GA Churchill. (2002). The application of ratio by intensity plot in microarray normalization, MGED IV (Miroarray and Chips: Algorithms and Applications), February 13–16.

Cui X, JTG Hwang, J Qiu, NJ Blade, S-W Tsaih, and GA Churchill. (2004). Improved statistical tests for differential gene expression by shrinking variance components estimates, International Conference on Analysis of Genomic Data, May 10–11, Boston, MA.

Cui X, J Affourtit, Y Woo, and GA Churchill. (2005). Inheritance Patterns of transcript levels in F1 hybrid mice. Plant and Animal Genomic XIII, January 15–19, San Diego, CA.

Cui X, and J Qiu. (2007). Identifying equivalently expressed genes using microarray. Gordon Conference: Toxicogenomics. June 24–29, New London, NJ.

Cui X, and A Loraine. (2007). Consistency assessment among redundant probe sets interrogating the same gene on the Affymetrix MOE430 GeneChip. Fifth Annual Rocky Mountain Bioinformatics, November 30–December 2, Snow Mass, CO.

Mirel B, B J Keller, M Peleg, **X Cui**, and R Altman. (2009). Design of integrated translational bioinformatics systems. 2009. AMIA summit on translational bioinformatics (STB 2009), March 15–17, 2009.

Kennedy R, and **X Cui.** (2009). Searching for efficient experimental design for differential DNA methylation studies, at ENAR 2009, March 15–18. San Antonio, TX.

Cui X, M Cook, Z Li, R Williams, K Hamre, and L Lu. (2010). Genetic and stress influence on DNA methylation in mouse hippocampus, at the 9th Complex Trait Community Conference (CTC 2010), May 7–10, Chicago, IL.

Yang, C, and **X Cui.** (2011). Multi-group tests of equivalence for microarray data, ENAR, March 20–23, Miami, FL.

Cuna, A., B. Halloran, O. Faye-Petersen, D. Kelly, D. Crossman, **X. Cui**, K. Pandit, N. Kaminski, S. Bhattacharya, A. Ahmad, T.J. Mariani and N. Ambalavanan. Alterations in Gene Expression and DNA Methylation during Murine and Human Lung Alveolar Septation. Octobr 23 2015, AAP Experience Nation Conference & Exhibition, Washington, DC.

Wilson L, G. Trivedi; A. Sreedasyam;H. Kim; **X. Cui**; L. J Cseke; S. Barnes. Quantitative SWATH Proteomics Analysis of Tree Fungal Interactions under Nutrient Limiting Conditions. 63rd American Society for Mass Spectrometry (ASMS) Conference. May 31st - June 4th, 2015, St. Louis, MO.

Brewer R. A., **Cui X.**, Liu N., Miyasaki N. D., Ptacek T., Kumar R., Morrow C. D, Smith, D. L. Jr. Acarbose treatment and the gut microbiota. Gerontological Society of America Annual Scientific Meeting. Nov 18-22 2015; Orlando, FL.

Ma E., Kang M., **Cui X.**, Zhang W., Fu Y., Garvey W.T., Circulating MicroRNA Species and Role in Human Insulin Resistance. American Diabetes Association conference. June 5-9, 2015; Boston, MS.

McLean M, Bates GW, **Cui X**, Barnes S, Harper L. Peri-conception metabolomics in serum and follicular fluid of obese versus non-obese women undergoing IVF, at 63rd Annual Scientific Meeting of Society for Reproductive Investigation, Mar 16, 2011-18, 2016

Cui X, J. Meng, J. Gallini, C. Jasien, M. Mrug “ADPKD patients and risk to severe COVID-19 illnesses” at PKD Connections conference, June 25, 2021, Virtual.

TEACHING AND ADVISING

Courses Taught at Emory:

BIOS 598 “Thesis Mentorship”, Department of Biostatistics and Bioinformatics
  Spring 2019 with 40 students
  Spring 2020 with 54 students
BIOS 581 “Statistical Practice II”, Department of Biostatistics and Bioinformatics
  Spring 2021 with 28 students
  Spring 2022 with 24 students
  Spring 2023 with 24 students
  Spring 2024 with 30 students
BIOS 580 “Statistical Proactice I”, Department of Biostatistics and Bioinformatics
  Fall 2021 with 30 students
  Fall 2022 with 44 students
  Fall 2023 with 49 students
BIOS 599R “Thesis” (Monitoring), Department of Biostatistics and Bioinformatics
  Spring 2022 with 6 students
  Spring 2023 with 20 students
  Spring 2024 with 17 students

Courses Taught at UAB:

BST 675 “Instroduction to Statistical Genetics” Department of Biostatistics
  Spring 2009
  Spring 2011
  Spring 2013
BST 676 “Genomic Data Analysis” Department of Biostatistics (revised course)
  Spring 2010
  Spring 2012
BST 611 “Intermediate Statistical Analysis I” Department of Biostatistics
  Spring 2015 online
  Fall 2015 in person
BST 626 “Data Management/Reporting with R and SAS”
  Fall 2016
BST 690 “Biostatic Consult and App Pro” (directed study) Department of Biostatistics
  Summer 2009
  Summer 2010
  Summer 2011
BST 698 “Non-disertation Research” Department of Biostatistics
  Spring 2015,
  Summer 2015

Guest Lectures at UAB:

“Introduction to Microarray Technology (Biology and Experimental Design),” CS640 (course title: Bioinformatics; primary instructor: Chengcui Zhang). Fall 2004.

“Image processing,analysis,QC and normalization—Two Color,” in NSF Plant Microarray Short Course, June 14, 2005, Madison, WI; June 13, 2006.

“Inferential Statistical Procedures - Linear Models,” in NSF Plant Microarray Short Course, June 14, 2005, Madison, WI.

NIDDK short course at UAB: “Demonstration and Supervised Practice (Microarray).” May 4, 2005. Birmingham, AL.

“Genomics, Bioinformatics, and Medicine,” in UAB K30 genetics lectures (organizer: Bruce Korf), Spring 2005, 2006, 2007, 2008.

“Inferencial Statistical Procedures—Linear Models” in the 2nd NSF Plant Microarray Short Course, August 2, 2006. Boston, MA.

“Statistical Analysis of Microarray Data: Design, Normalization, and Statistical Inference” in Genet702 (course title: Animal Model Systems for Genetic and Genomic Analyses). Spring 2005, Spring 2007.

“Design of Microarray Experiments,” in International Microarray Workshop, January 11, 2007; January 10, 2008, Tucson, AZ.

“Statistical Aspects for the Polycystic Kidney Study,” in HMG703 (Title: Hughes Med-Grad “Quantitative Methods”). March 28, 2007; April 1, 2009.

“Basic Statistics,” in Genetics Core Lecture Series (organizer: Scott Austin). August 17, 2007; Fall 2008.

“Introduction to QTL Mapping,” in NSF Statistical Genetics Short Course, July 12, 2008, Birmingham, AL.

“Software Demonstration of MAANOVA Package,” in the NSF Statistical Genetics Short Course, July 12, 2008, Birmingham, AL.

“Permutation Methods,” in BST 765 (course name: Advanced Computational Methods; primary instructor: Rui Feng). Oct 1, 2008.

“Arrays and Bioinformatics,” in Combined Fellow’s Physiology Conference (organizer: James Hagood), February 19, 2009.

“Microarray Analysis and Related Topics,” in EPI 788 (course name: Molecular Epidemiology; primary instructor: Elizabeth Brown). Summer 2009, Summer 2011.

“Introduction to Epigenetics/Epigenomics,” in Introduction to Statistical Genetics Workshop. New Orleans, LA., Feb 12, 2009.

“Bioinformatics, Genomics, and Medicine,” in Vocabulary of Clinical & Translational Science (organizer: Jacqueline Ann Moss). Sep 18, 2009.

“Analysis Issues of Microarray and Next-Generation Sequencing Data,” in the Genomics Block of GBS 722 (course name: GGS Bioinformatics: course master: Michael Crowley). Jan 26, 2011.

“Microarray Data Analysis Software—R Based,” in the Bioinformatics Block of GBS 722 (course name: GGS Bioinformatics: course master: Chiquito Crasto). Feb 28, 2011.

“Statistical Analyses of RNA-seq Data,” in BST 695 (course name: Special Topics; primary instructor: Degui Zhi). April 6, 2011.

“Software Packages Affy, MAANOVA, and PowerAtlas,” in the NIGMS short course, Birmingham, AL, July 20, 2011.

“Analysis of Whole Genome Transcriptome Sequencing Data,” in the NHGRI short course on Next Generation Sequencing, Birmingham, AL. December 19, 2011.

“Introduction to R & Bio-conductor”. For NIGMS short course at UAB 7/9/2012

“Affy, RMANOVA package demo”. For NIGMS short course at UAB 7/11/2012

“Analysis of Whole Genome Transcriptome Sequencing Data,” in the NHGRI short course on Next Generation Sequencing, Birmingham, AL. December 12, 2012.

“Introduction to R and Bioconductor”, in the NIGMS short course on Statistical Genetics and Genomics, Birmingham, AL, 7/8/2013

“RNAseq: Experimental Design and Data Analysis”, in the NIGMS short course on Statistical Genetics and Genomics, Birmingham, AL, 7/11/2013

“Bowtie/TopHat, SAMTools, IGV, R packages for RNA-seq and ChIP-seq”, together with Hao Wu in the NIGMS short course on Statistical Genetics and Genomics, Birmingham, AL, 7/11/2013

“Transcriptome Analysis” in 3rd Short Course on Next-Generation Sequencing: Technology and Statistical Methods, Birmingham, Al, 12/18/2013

“Software Demonstration (RNA-Seq & Galaxy)” in 3rd Short Course on Next-Generation Sequencing: Technology and Statistical Methods, Birmingham, Al, 12/18/2013

“About RNA-seq” in WINGS Workshop in Next Generation Science, UNC Charlotte, May 13-14, 2014

“Introduction to R & Bio-conductor” in Short Course on Statistical Genetics and Genomics. Birmingham, AL, 4th 7/7/2014, 5th 7/27/2015, 6th 7/13/2016

“Transcriptome Analyses: Microarray and RNAseq” in Short Course on Statistical Genetics and Genomics. Birmingham, AL, 4th 7/10/2014, 5th 7/29/2015, 6th 7/11/2016

“Introduction to R & Bio-conductor” in Short Course on Next-Generation Sequencing: Technology and Statistical Methods. Birmingham, AL, 4th 12/15/2014, 5th 12/14/2015

“Transcriptome Analysis Using NGS” in Short Course on Next-Generation Sequencing: Technology and Statistical Methods. Birmingham, AL, 4th 12/17/2014, 5th 12/19/2015

“Experimental Design of Omics Experiments” in GBS 748: Advanced Graduate Course in Metabolomics, January 17th 2015; January 6th, 2016

“Interpretation of Metabolomics Analysis Results” in GBS 748: Advanced Graduate Course in Metabolomics, Feb. 9th 2015;

“Introduction to R and Bioconductor” in GBS 722: Bioinformatics, Feb. 11th-12th 2015; March 8-9, 2-016.

“Training in Experimental Design” 6/15/2015 in 3rd and 7/18/2016 4th Annual Workshop on Metabolomics.

“Statistical analysis using metaboanalyst” 7/20/2016 in 4th Annual Workshop on Metabolomics.

“Designing a Metabolomics Experiment” 12/2/2015 in One-Day Metabolomics Workshop

“Experimental Design & Statistics” 9/11/2015 in MIC 741:Topics in Professional Development

Guest lectures at the Jackson Laboratory:

“Data Quality Control and Normalization,” in the Workshop on Techniques in Gene Microarray

“Development and Analysis: Approaches to Heart, Lung, Blood, and Sleep Disorders.” Jackson Lab, Bar Harbor, ME April 24-28, 2002

“Data Transformation of cDNA Microarray,” in the Short Course on Mathematical Approaches to the Analysis of Complex Phenotypes. Bar Harbor, ME, September 23, 2002

At Iowa State University:

Genetics Lab (Bio 301L)

Student and Post-doctoral Fellow advised:

Summer interns

Tarik Trend, Emery Univresity, (2007) Intern advisor

Master students

--- Served as academic advisor

Liyan Gao	(2009–2010)
Luqin Deng	(2009–2012)
Shaohua Yu	(2013-2014)
Justin Leach	(2014-2016)
Lauren Wood	(2015-2017)
Jiaying Hao	(2016-2017)
Fuchenchu Wang	(2016-2017)
Mofei Liu	(2018-2020)
Shiyu Chen	(2018-2020)
Xinhang Wang	(2018-2020)
Chen Zhao	(2018-2020)
Jiaxi Gen	(2020-2022)
Qing Zhang	(2020-2022)
Jiali Lu	(2022-2023)
Zhuoyang Zhang	(2023- present)
Chiao Yu Huang	(2023- present)

--- Served as thesis/capstone/research advisor

Kathakali Ghosh	(2005–2006)	research advisor
Liyan Gao	(2009–2010)	research advisor
Luqin Deng	(2009–2012)	research advisor
Ligong Chen	(2010–2012)	research advisor
Xuelin Li	(2013)	research advisor
Amanda Chou Sue	(2014)	thesis committee, Epidemiology
Shaohua Yu	(2013-2014)	research advisor
Holly Hartman	(2015)	research advisor
Jiaying Hao	(2016-2017)	research advisor
Fuchenchu Wang	(2016-2017)	research advisor
Mofei Liu	(2018-2020)	thesis advisor
Shiyu Chen	(2018-2020)	thesis advisor
Xinhang Wang	(2018-2020)	thesis advisor
Jiawei Meng	(2019-2021)	research/capstone advisor
Yue Xie	(2019-2021)	research/advisor
Jiaxi Gen	(2020-2022)	capstone advisor
Lei Wang	(2020-2022)	research advisor
Sihong Li	(2020-2022)	research advisor
Chenyang Jiang	(2021-2022)	capstone advisor
Angelo Marra	(2021-2023)	research/captone advisor

Alex Klimek	(2022-2024)	research/captone advisor
Jonathan Lin	(2023-2024)	research advisor
Yu Zhang	(2023-2024)	capstone advisor
Haihui (Sabrina) Yan	(2023-2024)	capstone advisor
Yimeng Zhang	(2023-2024)	capstone advisor
Dongchen Cai	(2023-2024)	capstone advisor
Xiaxian Ou	(2024- present)	research advisor
Zhengyi Ou	(2024- present)	research advisor
Zhuoyang Zhang	(2024- present)	research advisor
Chiao Yu Huang	(2024- present)	research advisor

Ph.D students:

Lang Chen	(2006-2008)	disertation Co-chair
Celeste Yang	(2010-2013)	disertation Chair
Henry Roberson	(2005–2008)	academic advisor
Jun Li	(2005–2011)	academic advisor
Guoqiao Wang	(2010–2013)	academic advisor
Amanda H. Pendegraft	(2014- 2017)	academic and research advisor
Rachel Parker	(2019- 2022)	academic advisor

Ph.D disertation committees:

Hong Gao Ph.D.	(2007-2009)	Department of Vision Science, UAB
Jacquelyn Zimmerman Ph.D.	(2009–2012)	Department of Medicine, Division of Hematology & Oncology, UAB
Elizabeth Perkins Ph.D.	(2011–2012)	Clinical Immunology and Rheumatology, UAB
Kathryn Royse Ph.D.	(2011–2014)	Epidemiology, UAB
Lindsy Jones Ph.D	(2013-2015)	Biostatistics, UAB
Michael Behring Ph.D	(2015- 2018)	Epidemiology, UAB
Stephen Gragg MD/Ph.D	(2016-2017)	NIH Medical Scientist Training, UAB
Yogasudha Veturi Ph.D	(2016-2017)	Biostatistics, UAB
Meriah Schoen Ph.D	(2019 -2022)	Nutrition, Emory

Postdocs

Richard Kennedy	(2008–2011)	Co-mentor
Armrit Karki	(2012-2012)	mentor
Jason Guichard	(2012-2015)	Co-mentor

Junior faculty (NIH K awardees or VA CDA awardees) mentored:

Tomi Akinyemiju (K award)	(2016-2017)
Yuanyuan Li (K award)	(2016-2017)
Ida Fonkoue (KL2 training grant)	(2021)
Aaron Trammel (KL2 training grant)	(2019-present)
Arash Harzand (VA CDA-2 training grant awarded)	(2019-present)
Anna Woodbury (VA CDA-2 training grant awarded)	(2018-present)

Veronica Rowe (VA CDA-2 training grant application)	(2020-2021)
Sunil Agarwal (co-mentor for TL1 grant)	(2022)
Shreya Raja (VA CDA-2 training grant application)	(2021)
Jinhee Jeong (KL2 training grant application)	(2022)
Justin Sprik (AHA Career Development Awarded)	(2021)
Ryan Smith (CDA2 training grant application)	(2021)
Joseph Roberts (CDA1 training grant application awarded)	(2021)
Olamide Alabi (CDA1 training grant application awarded)	(2024)

PROFESSIONAL SOCIETIES

American Association for the Advancement of Science (AAAS)	1997–2011
International Society for Computational Biology (ISCB)	2007–2012
The American Society of Human Genetics (ASHG)	2011–2015
American Statistical Association (ASA)	2002–present
International Chinese Statistical Association (ICSA)	2013–present
Caucus for Women in Statistics (CWS)	2016–present

PROFESSIONAL SERVICES

Editorial board: Associate editor for *Frontiers in Epigenomics* (2011 - present)

Associate editor for *PeerJ* (Oct 2014 – present)

Appointed microarray referee: Plant Cell (2008–2011)

Add hoc Referee for:

Bioinformatics, Nature Genetics, Biostatistics, BioTechniques, Physiological Genomics, Theoretical and Applied Genetics, Computational Statistics & Data Analysis, JASA, BMC-Bioinformatics, BMC Evolutionary Biology Genetics, Euphytica, International Journal of Plant Genomics, Biometrical Journal of Biological Chemistry, The Annals of Statistics, Plant Physiology, Journal of Applied Statistics, Journal of the American Society of Nephrology, Frontier Journals, BMC-Genomics, npj-Digital Medicine

National services:

Professional Committees:

Financial Advisory Committee, International Chinese Statistics Association (ICSA), (2018-present)
First Responder for the Mentor on the GO program of the "Caucus of Women in Statistics" (2018–2023)
ASA Georgia Chapter representative (2020–2023)
PKD Foundation Data Sharing Advisory Committee (2021–2022)

National conferences:

Organizer of the NHGRI-funded "Statistical Analysis for Next Generation Sequencing," Birmingham, AL, (Sept. 26–27, 2011)
Co-organizer of the 2nd NSF Plant Microarray Short Course (2006)

Scientific Committee member for annual Critical Assessment of Massive Data Analysis (CAMDA) conferences (2009–2014)

ENAR session chair for “Experimental Design, Power/Sample Size, and Survey Research” New Orleans, LA. (March 2010)

Organizer for invited session “Next Generation Sequencing,” at ENAR 2, Miami, FL. (2011)

Program committee member for “Workshop on Computational Advances in Molecular Epidemiology (CAME),” Atlanta, GA. (2011)

ICSA chair for Session 57: Recent Method Developments on Quantile Regression” Tianjin, China. (July 2nd, 2019)

Grant Reviews:

NSF Ad-hoc grant reviewer (2008)

NIH/NHLBI study section for RFA HL-11-002, "Common Pathogenetic Mechanisms of Lung Cancer and COPD" (2010)

NSFC grant review (May 2011)

NIH ZRG1_HDM study section (May 2014) “Gene and environment interaction”

European Transnational Call for Proposals (E-RARE-3 2018) “ Transnational research projects on hypothesis-driven use of multi-omic integrated approaches for discovery of diseases causes and/or functional validation in the context of rare diseases.” (July 2018)

Canada CIHR “Operating Grant: Clinical Trials Projects” (July 2022)

NIH-NIDDK RFA DK22-018 Human Islet Research Network (HIRN) Pancreas Knowledgebase Program (PanKbase) (U24 – Clinical Trial Not Allowed) (August 2023)

Others:

DNA Day Essay Contest judge (third annual essay contest for U.S./Canadian students in grades 7–12), (April 2008)

Birmingham UseR group organizer (2014–2017)

University Services:

UAB University Level:

UAB Faculty Senate	(2013–2015)
UAB Grievance and Termination Hearing Panel	(2016–2017)
HSF-GEF Grant Review Committee	(2010–2017)

UAB School of Public Health:

Admission and Graduation Committee	(2011–2015, chair 2013-2015)
Award Nomination Committee	(2012–2016)
Norwood Award Selection Committee	(2005–2013)
Public Health Practice Committee	(2016–2017)

UAB Department of Biostatistics:

Co-organizer for SSG Seminar	(2005–2008)
Department of Medicine Ph.D. Faculty Advisory Group	(2007–2008)
IGGP Graduate Program Admission Committee	(2007–2009)

Chair of the SSG StatGen Software Training Committee	(2008)
Organizer of the SSG Monthly Research Update Seminar	(2009)
Postdoctoral Trainee Research Day judge	(2010)
Organizer of the Bimonthly Biostatistics social event (SMA)	(2007–2011)
SSG Faculty Recruiting Committee	(2007–2012)
SSG Curriculum Committee	(2008–2014)
SSG programmer recruiting committee chair	(2015)
Biostatistics social chair	(2012–2015)
Graduate Student Admission Committee chair	(2016–2017)

Emory Department of Biostatistics and Bioinformatics:

Master Program Curriculum Committee	(2018–2020)
Master Student Admission Committee	(2018–present)
Master Student Recruitment Committee	(2018–2020)
PhD Exam Committee	(2021)
PhD Curriculum Committee	(2020–2021)
Chair Search Committee	(2019–2020)
Faculty Search Committee	(2020–2021)
Director of Mater Graduate Program	(2021–present)
Data Science Certificate Initiative	(2022–present)

Emory School of Public Health:

Education Committee	(2021–present)
CRT faculty Committee	(2021–2023)
Academic Standard Committee	(2021–present)

Atlanta VA Medical Center

Directory of the Data Analytics Core	(2017-present)
R&D committee member	(2019-present)

HONORS

Nankai University Scholarship, China	1988
Guanghua Scholarship, China	1992
Wang Kechang Scholarship, China	1993
Phi Kappa Phi, Iowa State University Chapter	1996
Fung Fellowship	1998
Stadler Research Fellowship	1999
1st Runner up for CAMDA (Critical Assessment of Microarray Data Analysis) competition	2002
Best Paper Award, Science Unbound Foundation	2012

GRANTS:

Newly Funded and Ongoing:

Otsuka Pharmaceutical (Mrug and Cui) 10/1/2023-11/30/2024
Extraction of real-time ADPKD outcomes from a large electronic health record dataset.

Role: mPI

VA 150RX004845-01 (Mauck and Drissi) 01/01/2024-12/31/2028
CReATE Motion Center: Cartilage Regeneration using Advanced Technologies to Enable Motion
Role: co-I

VA I01RX004537 (Krishnamurthy) 01/2024-12/2027
What makes a responder, a responder? Biomarkers to help identify responders and resistors to high-intensity interval training for lower extremity chronic stroke (BReaTHE)
Role: co-I

VA RX005050 (Woodbury) 10/1/2024-9/31/2027
Auricular Neuromodulation in Veterans with Fibromyalgia
Role: co-I

00003431, University of Alabama at Birmingham (Cui) 9/17/2018–8/31/24
Biological Comparisons among Three Derivative Models of Glioma Patient Cancers.
Role: mPI of the NIH P60

I01CX001065, VA Merit (Park) 07/01/2015 – 06/30/2024
Mechanisms of Sympathetic Overactivity in Post-traumatic Stress Disorder (PTSD).
Role: Co-I

1I01BX004232-01A2, VA Merit (Mrug) 10/01/2019 – 09/30/2023
Intra-renal T-cell heterogeneity in ADPKD patients
Role: Co-I

HX001025, VA Merit (Wilson) 4/01/2021 – 3/31/2025
Investigation of Heart and Vascular Outcomes in Older Veterans
Role: Co-I

OT2HL161847-01, NIH/NHLBI (Ighovwerha Ofotokun; VA subrecipient PI: Sushma Cribbs)
10/01/2021 – 5/23/2023
RECOVER: A Multi-site Observational Study of Post-Acute Sequelae of SARS-CoV-2 Infection in Adults
Role: Co-I

R01MD017046-01, NIH/NIMHHD (Lynch) 12/01/2021–11/30/2026
Veteran Access and Limitations to Organ Recovery (VALOR)
Role: Co-I

00107978, DoD, (Park) 7/01/2022–6/30/2026
Elucidating Mechanisms of Hypertension Risk in Post-Traumatic Stress Disorder
Role: Co-I

VA Merit (Marconi) 7/01/2022–6/30/2026
Host Genetic and Epigenetic Factors of the Progression, Comorbidities and Outcomes of Viral Infection
Role: Co-I

Completed:

GRANTS AS PI or Co-PI:

247G20a, PKD Foundation (Cui) 7/1/2020 –4/30/2024
Machine Learning for Predicting eGFR Decline in CRISP Study Patients
Role: PI

RTI (Cui) subcontract of NSF grant 10/1/2020–6/30/2021
Convergence Accelerator – Track D: Application of sequential inductive transfer learning for experimental metadata normalization to enable rapid integrative analysis.
Role: mPI of the NSF grant

2P60AR048095-06A1 NIH (Cui) 9/1/15–6/30/18
NIAMS Multidisciplinary Clinical Research Center—Methodology Core
Role: PI of Methodology Core

NIH 1R13HG005792 (Cui) 1/1/11–11/30/12
Statistical Analyses for Next Generation Sequencing (national conference)
Role: PI

UAB CAEG Partnership Pilot Program (Cui) 8/15/10–8/14/11
Unmasking Novel Cystogenic Pathways: Biological Knowledge-Based Statistical Pathway Analyses of Genome-Wide Gene Expression and DNA Methylation Data
Role: PI

UAB Faculty Development Grant (Cui) 8/1/08–7/31/09
Toward the Integration of Genomics and Epigenomics—a Pilot Genome-wide Methylation Study to Characterize the Relationship Between DNA Methylation and Marker Genotype, Gene Expression, and Phenotype in Mouse RI Lines.
Role: PI

UAB Center of Nutrition Research Pilot (Cui) 8/1/05–7/31/06
Characterizing the Diet/Nutrition Effect on Gene Alternative Transcripts Using Affymetrix Microarray Data.
Role: PI

GRANTS AS CO-I:

NIH/NIDDK P30 DK07022 (Agarwal) 07/01/08–06/30/18
UAB-UCSD O'Brien Core Center for Acute Kidney Injury Research
Role: Primary co-investigator in the Biostatistics/Bioinformatics Resource

8UL1TR000165-05 (Kimberly) 09/01/2015 – 8/31/2020
UAB Center for Clinical and Translational Science
Role: Co-Investigator (major player in BERD)

NIH/NIDDK R01DK097107 (Mannon) 08/01/13 – 06/30/17
Ulcerative Colitis – Regulation of the IL-13 Receptor System
Role: Co-Investigator for data analysis

NIH/NCI R01CA186646 (MPI, Brown/Vachon) 07/01/2014 – 03/31/2019
Molecular characterization of myeloma and related asymptomatic precursor states
Role: Co-Investigator for data analysis

NIH/NIGMS R25 GM093044 (Tiwari) 08/01/10 – 05/31/17
Short Course on Statistical Genetics and Genomics
Role: co-director mainly in charge of hands-on component.

NIH/NCI R01CA178441 (Tollefsbol) 04/01/2014 – 02/28/2019
Combinatorial Epigenetic-Based Prevention of Breast Cancer
Role: Co-Investigator for data analysis

NIH/NIDDK R01DK097423 (Mrug) 08/05/2013 – 06/30/2018
Mechanisms of C3 Effects in ARPKD Pathogenesis
Role: Co-Investigator for data analysis

NIH/NCI R21CA205501 (Yoon) 04/01/2016 – 03/31/2018
Developing Therapy for the Treatment of Cholangiocarcinoma Nutritional deficiencies and environmental.

NIH/NIGMS R01GM085105 (Miller) 05/01/2014 – 02/28/2016
Prostaglandins in C. Elegans Fertilization
Role: Co-Investigator for data analysis

NIH/NCI AICR 316184 (Tollefsbol) 01/01/2015 – 12/31/2016
Epigenetics of Early Life Exposure to Cancer Preventive Cruciferous Vegetables
Role: Co-Investigator for data analysis

NIH/NCI R21CA182861 (MPI, Brown/Sanderson) 07/01/2014 – 06/30/2016
The Role of Exosome Heparanase and miRNAs as Biomarkers for Myeloma
Role: Co-Investigator for data analysis

1R01HL109785-01A1 (Dell'Ialia) 04/01/12–03/31/16
Mitochondrial Haplotype Influences LV Dysfunction in Heart Failure.
Role: minor co-Investigate for supervising postdoc on the data analysis

NIH/NINDS R21NS085497 (King) 09/01/13 – 08/31/15

Molecular Signatures of Amyotrophic Lateral Sclerosis in Skeletal Muscle
Role: Co-Investigator for data analysis

NIH/NIGMS R25 GM093044 (Tiwari) 08/01/10 – 07/31/15
Short Course on Statistical Genetics and Genomics
Role: Deputy Director and teaching

NIH/NIDDK 1R01DK085027-01A1 (Allon) 7/1/2010–6/30/2014
Vascular Abnormalities in Patients Receiving a Dialysis Access.
Role: Co-I

DHHS SRI S10-005 (Gillespie) 6/30/2010–12/30/2013
Interrogation of Key Genomic Alterations in Glioblastoma Multiforme (GBM) for Identification of Molecular Pathways Critical to GBM Tumorigenesis and Progression
Role: Co-I

NSF/USF UF11080 (Allison) 3/01/11–3/31/14
Integrating physiological and genetic mechanisms to understand the evolution of cold tolerance
Role: Co-I

NIH/NIDDK 5R01DK083562 (Garvey) 8/1/2009–7/31/2013
NR4A Orphan Receptors and Insulin Resistance
Role: Co-I

VA RR&D Merit Review F7226R (Bamman) 3/1/10–6/30/13
Understanding Muscle Regeneration Impairment in Aging Veterans
Role: Co-I

NIH 2P30HD038985-06A2 (Percy) 9/1/08–6/30/13
UAB Mental Retardation Research Center
Role: Co-I

AIFCR 10A020 (Tollefsbol) 1/01/11–12/31/12
Green Tea Polyphenols in the Prevention of Breast Cancer Initiation

NIH/NHLBI P50 HL77100 (Dell'Italia) 2/9/2005–12/31/2010
SCCOR in Cardiac Dysfuction and Disease—Biostatistics Core
Role: Co-I

NIH U54CA100949 (Barnes) 9/9/2003–8/31/2010
Center for Gene-Nutrient Interaction (CNGI)
Role: Co-I

NIH/NIDDK 1 P30 DK074038-02 (Guay-Woodford) 9/30/2005–8/31/2010
UAB Recessive PKD Research and Translational Core Center
Role: Co-I

NIH/NIDDK R01DK68261 (Nagy) 7/1/2004–6/3020/09
Antipsychotic Drug-Induced Weight Gain
Role: Co-I

Susan G. Komen Breast Cancer Foundation (Frost) 12/1/2007–11/30/2009
Targeting the Hedgehog Pathway in the Treatment of Breast Cancer
Role: Co-I

NIH/NIDDK 1 R21 DK078522 (Guay-Woodford) 6/1/2006–5/30/11
Genetics and Pharmacogenetics in FSGS (PPG Project 4)
Role: Co-I

NIH/NHLBI 5 R01 HL075211 (Oparil) 7/1/2004–6/30/2008
Estrogen Modulates Injury-Induced Inflammation
Role: Co-I

NIH/NIA R01AG020681 (Prolla) 3/15/2003–1/31/2008
Gene Expression Profiling, Caloric Restriction and Aging.
Role: Co-I

NSF 0217651 (Allison) 10/01/02–08/31/06
Design and Analysis of Microarray Gene Expression Studies in Plants: Toward Sound Statistical Procedures
Role: Co-I

NIH/NIEHS R01ES12933-01A1 (Ruden) 04/01/05–03/31/10
QTL and Microarray Mapping Lead Sensitivity Genes
Role: Co-I

Burroughs Welcome Fund (Guay-Woodford) 07/01/01–06/30/06
Genetic Modifiers of Recessive Polycystic Kidney Disease: Implications for Pathogenesis and Therapeutics
Role: Co-I

NIH 1 R21 HL72871 (Matalon) 10/01/01–09/30/06
Modulation of Innate Immunity in Lung Transplantation
Role: Co-I