

# Xiangqin Cui

Department of Biostatistics  
327 Ryals Public Health Building  
1665 University Boulevard  
University of Alabama at Birmingham  
Birmingham, AL 35294

Phone: 205-996-4154  
Fax: 205-975-2540  
Email: xcui@uab.edu

## **EDUCATION AND TRAINING:**

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2001 - 2004, Postdoctoral training in statistical genetics focusing on experimental design and statistical analysis of microarray data, 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

### *Continued Education:*

Short Courses: “Mathematical Genetics” 2001-2003 at the Jackson Lab, Bar Harbor, Maine  
“Missing Data” by Pau Allison, 2006 at UAB  
“International Workshop on Methodology of Twin and Family Studies”, 2005, Boulder, Colorado.  
“Information-theoretic approaches to Empirical Science” 2010 at UAB  
“Parallel Computing Boot Camp”, 2008 at UAB

Online Courses: “Resampling Methods” By Phillip Good  
“Statistical Genetics”

Self-taught: Applied Regression Analysis  
Experimental Designs  
The Analysis of Messy data  
Analysis of Variance  
Variance Components,  
Bioequivalence  
MATLAB, R, LaTeX

Audited at UAB: Statistical Inference  
Bayesian Data Analysis  
Categorical Data Analysis

## **RESEARCH EXPERIENCE:**

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2004-present Assistant Professor (non-tenure track), Section on Statistical Genetics, Department of Biostatistics; Department of Medicine, University of Alabama at Birmingham, Birmingham, AL  
2004-2009 Assistant Professor (non-tenure track), Department of Medicine, Division of Genetic and Translational Medicine, 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

**PUBLICATIONS (First and corresponding/senior author marked with \*\*):**

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**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 Parmigiani G. 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” (Ralph D'Agostino Lisa Sullivan, and Joseph Massaro ed.) Wiley. 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, New Jersey, pp 201-217.
5. Kennedy RE and **Cui X\*\*** (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 new York, 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 in *Vicia 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](https://pubmed.ncbi.nlm.nih.gov/115560/)
4. Skibbe DS, Liu F, Wen TJ, Yandean MD, **Cui X**, Jun Cao J, Simmons CR, 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](https://pubmed.ncbi.nlm.nih.gov/1462470/)
6. **Cui X\*\***, MK Kerr and GA Churchill. Transformations for cDNA microarray data.(2003) *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](https://pubmed.ncbi.nlm.nih.gov/154570/)
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. **Cui X\*\***, J. T.G. Hwang, J. Qiu, N.J. Blades and G. Churchill (2005) Improved statistical tests for differential gene expression by shrinking variance component estimates. *Biostatistics*. 6(1):59-75.
10. Yao H, Guo L, Fu Y, Borsuk LA, Wen TJ, Skibbe DS, **Cui X**, Scheffler BE, Cao J, Emrich SJ, Ashlock DA, Schnable PS. (2005) Evaluation of five ab initio gene prediction programs for the discovery of maize genes. *Plant Mol Biol*. 57(3):445-60.
11. Mrug M., R. Li, **X Cui**, T. R. Schoeb, G. A. Churchill, and L. M. 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.
12. Allison DB, **Cui X**, Page GP, Sabripour M (2006). Microarray data analysis: from disarray to consolidation and consensus. *Nat Rev Genet*. 7:55-65.
13. **Cui, X\*\***. and A. E. 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
14. **Cui, X\*\***, Jason Affourtit, Keith R. Shockley, Yong Woo, and Gary A. Churchill (2006) Inheritance Patterns of Transcript Levels in F1 Hybrid Mice, *Genetics* 174:627-637
15. Laudencia-Chinguanco, Debbie L., Stamova B.S., Laxo G.R., **Cui XQ**, and Anderson OD (2006) Analysis of the wheat endosperm transcriptome, *J. Appl. Genet* 47:287-302.
16. Brand J.P.L., Chen L, **Cui, X.**, Bartolucci, A.A, Page, G.P., Kim, K., Barnes, S., Srinivasasainagendra, V., Beasley, T.M., Allison, D.B. (2007) "An Adaptive Alpha-spending Algorithm Improves the Power of Statistical Inference in Microarray Data Analysis" *Bioinformatics*, 1(10) 384-389. PMID: [PMCID: PMC1896052](#)
17. Ruden, D. M., **X Cui**, A. Loraine, A., Ye, J., Bynum, K., Kim, N. C., De Luca, M., Garfinkel, M. D., Lu, X. (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
18. Wu, X., Wang, J., **Cui, X.**, Maianu, L., Rhees, B., Rosinski, J., So, W.V., Willi, S.M., Osier M.V., Hill, H.S., Page, G.P., Allison, D.B., Martin, M., and Timothy Garvey, WT. (2007) The effect of insulin on expression of genes and biochemical pathways in human skeletal muscle: *Endocrine*; 31: 5 – 17.
19. Gao YZ, Guo SY, Yin QZ, **Cui X**, Hisamitsu T, Jiang XH (2007) Possible involvement of integrin signaling pathway in the process of recovery from restraint stress in rats. *Neurosci Bull*. 23 (4):229-35.
20. Mrug, M., J. Zhou, Y. Woo, **X Cui**, Alexander J. Szalai1, Jan Novak, Gary A. Churchill, and Lisa M. Guay-Woodford (2008) " Overexpression of innate immune response genes in a model of recessive polycystic kidney disease " *Kidney International* 73(1):63-76
21. Mrug, M., J. Zhou, Yong Woo, **X Cui**, A. J. Szalai1, J. Novak, G. A. Churchill, and L. M. 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
22. **Cui X\*\***, and A. E. 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. PMID: [PMCID: PMC2621337](#)
23. P.A. Ioannidis, D. B. Allison, C. Ball, C. Furlanello, J. Mangion, G. P. Page, V. van Noort, I. Coulibaly, **X Cui**, A. Culhane, M. Falci, L. Game, G. Jurman, T. Mehta, E. Petretto, J. Wang, M. Axton (2009) Reproducibility of published microarrays gene expression analyses. *Nature Genetics* 41, 178 – 186.

24. Zhu, H., G-J Li, L. Ding, **X Cui**, H. Berg, S. M. Assmann, Y. Xia (2009) Arabidopsis Extra Large G Protein 2 (XLG2) interacts with the G $\beta$ subunit of heterotrimeric G protein and functions in disease resistance. *Molecular Plant* 2(3):513-525. PMID: [PMC2902900](#)
25. Chen, L., G. P. Page, T. Mehta, R. Feng, and **X Cui**\*\* (2009). Single Nucleotide Polymorphisms Affect both cis- and trans-eQTLs. *Genomics* 93(6):501-8
26. **Cui, X**\*\*, J. Qiu, J. Zhou, and M. Mrug (2009). Evaluation of house keeping genes as internal control for RT-PCR in polycystic kidney disease study. *The American Journal of Nephrology. Am J Nephrol* 30:413-417.
27. Ulett, G. C., R. I. Webb, K. B. Ulett, **X Cui**, W. H. Benjamin, M. Crowley, and M. A. Schembri.(2010) Group B Streptococcus (GBS) Urinary Tract Infection Involves Binding of GBS to Bladder Uroepithelium and Potent but GBS-Specific Induction of Interleukin-1 $\alpha$ , *The Journal of Infectious Diseases* 201(6):866-70.
28. Thalacker\_Mercer, A., L. J Dell'Italia, **X Cui**, J. M. Cross, and M. M. 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. PMID: [PMC2825766](#)
29. Qiu, J. and **X Cui**\*\* (2010) Evaluation of a Statistical Equivalence Test Applied to Microarray Data. *Journal of Biopharmaceutical Statistics. Journal of biopharmaceutical statistics*, 20(2):240-66.
30. Zhou, J., X. Ouyang, **X Cui**, T. R. Schoeb, L. E. Smythies, M. R. Johnson, L. M. Guay-Woodford, A. B. Chapman, and M. Mrug (2010) Renal CD14 expression correlates with rates of cystic kidney disease progression. *Kidney International*. 78(6):550-60. PMID: [PMC2818397](#)
31. Wu X, Patki A, Lara-Castro C, **Cui X**, Zhang K, Walton R.G, Osier MV, Gadbury GL, Allison DB, Martin M, and WT Garvey. (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, [PMC Journal – In Process](#)
32. Gao L., Fang Z., Zhang K., Zhi D., 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. PMID: [PMC3042188](#)
33. Fang Z. and **X Cui**\*\*. (2011) Design and Validation Issues in Next Generation Sequencing Experiments. *Briefings in Bioinformatics* 12(3) 280-287 PMC Journal-In Process
34. Chen Y, Pat B, Gladden JD, Zheng J, Powell P, Wei C-C, **Cui X**, Husain A, 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.
35. Duell BL, Carey AJ, Tan CK, **Cui X**, Webb RI, Totsika M, Schembri MA, Derrington P, Irving-Rodgers H, Cripps AW, Crowley M, and Ulett GC. (2011) 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* Dec 19. [Epub ahead of print]
36. Moskowitz-Kassai E, Mackelaite L, Chen J, Patel K, Dadhanian DM, Gross SS, Chander P, Delaney V, Deng L, Chen L, **Cui X**, Suthanthiran M, Goligorsky MS. Excretion of anti-angiogenic proteins in patients with chronic allograft dysfunction. *Nephrology Dialysis Transplantation* (in press)
37. Duarte CW, Willey CD, Zhi D, **Cui X**, Harris JJ, Vaughan K, Mehta T, McCbrey RO, Minn AJ, Khodarey NN, Weichselbaum RR, and GY Gillespie. Expression signature of

IFN/STAT1 signaling genes predicts poor survival outcome in Glioblastoma Multiforme in a subtype-specific manner. *PLoS One* (in press)

38. Fang Z., R. Du, and **X. Cui\*\***. Uniform Approximation Is More Appropriate for Wilcoxon Rank-Sum Test in Gene Set Analysis. *PLoS One* (in press)
39. Reynolds, RJ, **Cui X**, Vaughan LK, Redden DT, Causey Z, Perkins E, Shah T, Hughes LB, Damle A. Kern M, Gregersen PK, Bridges SL. Gene Expression patterns in peripheral blood cells associated with radiographic severity in African-Americans with early rheumatoid arthritis. *Rheumatology International* (accepted)

#### ***Published abstracts:***

1. Mrug M , Schoeb TR, Li R, **Cui X**, Churchill GA , Guay-Woodford LM (2004) Kinesin 12 is predicted to modulate multiple phenotypes in the *cpk* mouse model of ARPKD. *J Am Soc Nephrol* **15**:216A.
2. Mrug, M., Zhou, J., **Cui, X.**, Guay-Woodford, L.M., Hill-Kapturczak, N., and J.E., M.-U. 2007. Thrombospondin 1, a latent TGF $\beta$  activator, is expressed abnormally in autosomal recessive polycystic kidney disease. *J Am Soc Nephrol* **18**:360 A

#### ***Articles submitted/under revision***

- Fang Z and **X Cui\*\***. Statistical tests for detecting differentially expressed genes in RNA-seq experiments. *Computational Statistics and Data Analysis* (under revision)
- Chee K. Tan, Alison J. Carey, Xiangqin Cui, Richard I. Webb, William H. Benjamin Jr., Allan W. Cripps, Michael Crowley, Kimberly B. Ulett, and Glen C. Ulett. Temporal genome-wide mapping of innate immune activation during streptococcal cystitis reveals delayed inflammation amid diverse host response pathways in urinary tract infection due to Gram-positive bacteria. *Journal of Immunology* (submitted)
- Zhou J, Ouyang X, Schoeb TR, Bolisetty S, **Cui X**, Johnson MR, Szalai AJ, Mrug M. *CysI*<sup>cpk</sup> mutation-induced injury accelerates renal cystogenesis *via* heme oxygenase- and complement-regulated pathways (submitted)
- Fox ER, Musani SK, Barbalic M, Lin H, Ogunyankin KO, Smith NL, Kutlar, A, Glazer NL, Post WS, Paltoo DN, Dries DL, Farlow F, Duarte D, Kardia S, Meyers K, Sun Y, Arnett D, Patki A, Samdarshi TE, Penman AD, Bibbins-Domingo K, Bužková P, Benjamin EJ, Bluemke DA, Morrison AC, Gerardo Heiss G, Carr J, Tracy RP, PhD<sup>4</sup>, Taylor HA, **Cui X**, Psaty B, Heckbert SR, Cappola TP, Vasan RS. Genome-wide Association Study of Cardiac Structure and Systolic Function in African Americans: the Candidate Gene Association Resource (CARE) Study (submitted)
- Thalacker-Mercer A, **Cui X**, Stec M, Merritt E, Bamman. Genetic Regulation of Myofiber Hypertrophy. (submitted)
- Mrug M, Zhou J, C Yang C, Aronow BJ, Cui X, and Guay-Woodford LM. Kinesin family member 12 is a candidate *Mpkd2* locus modifier gene and encodes a cilia-associated protein. (submitted to *Journal of the American Society of Nephrology*)

#### **PRESENTATIONS:**

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##### ***Talks***

Fertility restoration in cytoplasmic male sterile maize, Interdepartmental Genetics Program Retreat, August 23<sup>rd</sup>, 1997

Characterization of *rf2*, a maize mitochondrial male sterility restorer gene, All Iowa Genetics Symposium, June 19<sup>th</sup>, 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. CAMDA02 contest, Nov. 14-15 2002, Durham, NC.

The inheritance pattern of gene expression in mouse. Microarray Research Coordination Network Retreat, Mohonk, NY, September 27-30, 2004

Statistical Equivalence Testing Applied to Microarray Data, 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, October 24<sup>th</sup>, 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<sup>th</sup>-December 2<sup>nd</sup>, 2007

Statistical Equivalence Testing Applied to Microarray Data, SSG retreat, January 4<sup>th</sup>, 2008.

Statistical Equivalence Testing Applied to Microarray Data, ENAR, March 16-19, Washington DC, 2008

Microarray Data Analysis – Established Routines and New Directions, December 5<sup>th</sup> 2008, Florida State University, Tallahassee, FL.

Interrogation of Alternative Splicing Using Microarray, May 20<sup>th</sup>, 2009, First International Biomedical Conference at Nankai, Tianjing, China

Identifying Equivalently Expressed Genes using DNA Microarrays, May 21<sup>st</sup>, 2009, Department of Statistics, Nankai University, Tianjin, China

Experimental Design for Microarray Experiments, May 23<sup>rd</sup>, 2009, Institute of Crop Sciences, the Chinese Academy of Agricultural Sciences. Beijing, China

Gene Class Enrichment Analysis for RNA-seq Data, March 23<sup>rd</sup>, 2010, ENAR, New Orleans, LA

Length bias correction for RNA-seq Data in Gene set analyses, March 22<sup>nd</sup>, 2011, ENAR, Miami, FL

Equivalence testing of high dimensional expression data, November 2011, Emory University, Atlanta, GA.

### **Posters**

**Cui X**, WJ Chen, RP Wise and PS Schnable (1995) The *rf2* nuclear restore of *cmsT* encodes an aldehyde dehydrogenase, 37<sup>th</sup> maize genetics conference, 16-19 March, Asilomar, CA.

**Cui X**, F Liu, WJ Chen, RP Wise, PS Schnable (1996) The *rf2* nuclear restore of *cmsT* encodes an aldehyde dehydrogenase, 38<sup>th</sup> maize genetics conference, 14-17 March, ST Charles, IL

Liu F, **X Cui**, WJ Chen, AP Hsia, RP Wise, PS Schnable (1997) The biochemistry characterization of *rf2* protein which is required for *cmsT*, 39<sup>th</sup> maize genetics conference, 13-16 March, Clearwater Beach, FL

**Cui X**, AP Hsia, RP Wise and PS Schnable (1998) Suppression of *rf2-m* alleles, 40<sup>th</sup> maize genetics conference, 19-20 March, Lake Geneva, WI

**Cui X** and PS Schnable (1999) The physiological role of *rf2* independent of its *cms-T* restorer, 41<sup>st</sup> maize genetics conference, 11-14 March, Lake Geneva, WI

- Cui X**, B Scheffler, C Simmons, RB Meely and PS Schnable (2000) Mutations in the maize *pd3* gene cause reduced levels of tolerance to anaerobic stress, annual meeting of the American Society of Plant Physiologists, 15-19 July, San Diego, CA
- Cui X**, G.A. Churchill (2002) The application of ratio by intensity plot in microarray normalization, MGED IV (Microarray and Chips: Algorithms and Applications), 13-16 Feb, 2002
- Cui X**, J.T.G Hwang, J. Qiu, N. J. Blade, S.-W. Tsaih and G.A. 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 G. A. 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 Jing Qiu (2007) Identifying equivalently expressed genes using microarray. Gordon Conference: Toxicogenomics. June 24-29, New London, NJ.
- Cui X** and Ann Loraine (2007) Consistency Assessment among Redundant Probe Sets Interrogating the Same Gene on the Affymetrix MOE430 GeneChip. Fifth Annual Rocky Mountain Bioinformatics, November 30<sup>th</sup>-December 2<sup>nd</sup>, Snow Mass, CO
- Mirel B., B. J. Keller, M. Peleg, **X Cui**, 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** "Searching for efficient experimental design for Differential DNA Methylation studies" at ENAR 2009, March 15-18, 2009. 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 9<sup>th</sup> 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<sup>th</sup> -23<sup>rd</sup>, Miami, FL.

## **TEACHING AND ADVISING:**

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### ***Courses taught at UAB:***

- BST 675 "Introduction to Statistical Genetics", Department of Biostatistics (spring 2009, spring 2011)
- BST 690 "Biostatic Consult and App Pro.", Department of Biostatistics (summer 2009, summer 2010, summer 2011)
- BST 676 "Genomic Data Analysis", Department of Biostatistics (spring 2010). Newly revised course.

### ***Guest Lectures at UAB:***

- "Introduction to Microarray Technology (Biology and Experimental Design)", CS640: Fall 2004
- "Image processing, analysis, QC and normalization -Two color". NSF Plant Microarray Short Course, June 14, 2005, Madison, WI. 6/13/06
- "Inferential Statistical Procedures - Linear Models" NSF Plant Microarray Short Course, June 14, 2005, Madison, WI
- NIDDK short course at UAB: Demonstration and Supervised Practice(Microarray). 5/49/05

“Genomics, Bioinformatics, and Medicine”. UAB K30 genetics lectures, Spring 05, 06,07, 08  
“Inferencial Statistical Procedures--Linear Models” 2<sup>nd</sup> NSF Plant Microarray Short Course,  
August 2, 2006. Boston, MA.  
“Statistical Analysis of Microarray Data: Design, Normalization, and Statistical Inference”  
Genet702 Spring 05, 07  
“Design of microarray experiments” International Microarray Workshop, January 11, 2007.  
January 10<sup>th</sup> 2008, Tucson, Arizona.  
Statistical Aspects for the polycystic kidney study, HMG703. March 28, 2007, April 1<sup>st</sup> 2009  
Basic Statistics, Genetics Core Lecture Series. August 17, 2007.  
Introduction to QTL mapping, at NSF Statistical Genetics Short Course, July 12<sup>th</sup> 2008,  
Birmingham, AL  
Software Demonstration of MAANOVA package, at NSF Statistical Genetics Short Course, July  
12<sup>th</sup> 2008, Birmingham, AL  
Permutation Methods. In BST course “Advanced Statistical Computing” Oct 1<sup>st</sup> 2008  
Arrays and Bioinformatics, Combined Fellow’s Physiology Conference, February 19, 2009  
Microarray Analysis and Related Topics, in Molecular Epidemiology, June, 2009, 2011.  
Introduction to Epigenetics/Epigenomics, in Introduction to Statistical Genetics Workshop (New  
Orleans, Feb 12th 2009)  
Bioinformatics, Genomics, and Medicine, in Vocabulary of Clinical & Translational Science,  
Sep 18<sup>th</sup>, 2009  
Analysis Issues of Microarray and Next-Generation Sequencing Data, in the Genomics Block of  
GBS 722, Jan 26<sup>th</sup>, 2011.  
Microarray Data Analysis Software – R Based, in the Bioinformatics Block of GBS 722, Feb  
28<sup>th</sup>, 2011  
Statistical Analyses of RNA-seq Data, for Degui’s calss, April 6<sup>th</sup>, 2011-10-11  
Analysis of Gene Expression Data, for Epi course “Molecular Epidemiology”, June 29<sup>th</sup>, 2011.  
Software packages “Affy, maanova, and PowerAtlas” the NIGMS short course, July 20<sup>th</sup>, 2011.

***Guest lectures at the Jackson Laboratory:***

Data quality control and normalization. Workshop on Techniques in Gene Microarray  
Development and Analysis: Approaches to Heart, Lung, Blood and Sleep Disorders. Jackson  
Lab, Bar Harbor, Maine April 24-28, 2002  
Data Transformation of cDNA microarray. Short Course on Mathematical Approaches to the  
Analysis of Complex Phenotypes. Bar Harbor, Maine, September 23, 2002

***At Iowa State University:***

Teaching Assistant for Genetics Lab (Bio 301L)

***Student and Post-doctoral Fellow Advising:***

Kathakali Ghosh (2005-2006) MS student research project advisor  
Tarik Trend, Emery Univresity, (2007) summer intern advisor  
Jun Li (2005-2011) Ph.D student academic advisor  
Henry Roberson (2005-2008) Ph.D student academic advisor  
Lang Chen (2006-2008) Co-mentor for Ph.D disertation  
Liyang Gao (2009- 2010 ) MS student academic and research advisor  
Luqin Deng (2009-) MS student academic and research advisor

Ligong Chen (2010-) MS student research advisor  
Guoqiao Wang (2010-) Ph.D student academic advisor  
Celeste Yang (2010-) Ph.D student disertation mentor  
Richard Kennedy (2008-2011) Co-mentor for post-doctoral training

***Graduate disertation committees:***

Hong Gao (Ph.D), Department of Vision Science (graduated 2009)  
Jacquelyn Zimmerman (Ph.D) Department of Medicine, Division of Hematology & Oncology (2009- present)  
Kathryn Royse (Ph.D) Department of Epidemiology (2011-present)  
Elizabeth Perkins (Ph.D) Clinical Immunology and Rheumatology (2011-present)

**PROFESSIONAL SOCIETIES:**

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American Association for the Advancement of Science (AAAS)	1997-2011
American Statistical Association (ASA)	2002-present
International Society for Computational Biology (ISCB)	2007-present
The American Society of Human Genetics (ASHG)	2011-

**PROFESSIONAL SERVICES:**

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***Editorial board:*** Associate editor for *Frontiers in Epigenomics*

***Appointed microarray specialty 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  
Journal of Biological Chemistry          The Annals of Statistics

***National services:***

National conferences:

- Organizer of the NHGRI funded “Statistical Analysis for Next Generation Sequencing”, Birmingham, Sept 26-27, 2011.
- Co-organizer of the 2<sup>nd</sup> NSF Plant Microarray Short Course (2006).
- Scientific Committee member for annual Critical assessment of Massive Data Analysis (CAMDA) conferences (2009- present).
- ENAR session chair for “Experimental Design, Power/Sample Size, and Survey Research” (March 2010), New Orleans, LA.
- Organizer for invited session “next generation sequencing” at ENAR 2011, Miami, FL.
- Program committee member for “Workshop on Computational Advances in Molecular Epidemiology (CAME)”, Atlanta, GA. 2011.

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)

Others

DNA Day Essay Contest judge (The third annual essay contest for US/Canadian students from grades 7-12.) April 2008

***University Services:***

HSF-GEF grant review committee (2010-present)  
School of Public Health Admission and Graduation Committee (2011-present)  
Postdoctoral Trainee Research Day judge (2010).  
Norwood Award Selection Committee (2005-present)  
IGGP graduate program admission committee (2007-2009)  
Department of Medicine Ph.D faculty Advisory Group (2007-2008)  
Organizer of the bimonthly Biostatistics Social event (SMA) (2007-2011)  
Co-organizer for SSG seminar (2005-2008)  
Organizer of the SSG monthly research update seminar (2009)  
Chair of the SSG StatGen software training committee (2008)  
SSG Faculty Recruiting Committee (2007- 2011)  
SSG curriculum committee (2008-present)

**HONORS:**

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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

**GRANTS:**

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***Active***

GRANTS AS PI:

NIH 1R13HG005792 12/1/10-11/30/11 \$20,000

*Statistical Analyses for Next Generation Sequencing*

Organizing a two-day conference for biologists, bioinformaticians, and statisticians to discuss challenges and strategies in the next generation sequencing data analysis

GRANTS AS CO-I:

P30 DK07022 (Agarwal) 07/01/08-06/30/13  
NIH/NIDDK Total Direct Costs \$3,750,000

*“UAB-UCSD O’Brien Core Center for Acute Kidney Injury Research”*

Core Center will establish an interdisciplinary center of excellence in AKI-related research

2P30HD038985-06A2 (Percy) 9/1/08-6/30/13  
UAB Mental Retardation Research Center Total cost \$5,773,543

This project provides the environment and support for clinical and genetic study of mental diseases.

2P60AR048095-06A1 NIH (Redden) 9/1/08-6/30/13  
*NIAMS Multidisciplinary Clinical Research Center - Methods Core* Total cost \$ 963,354

The objectives of the Methodology Core are: (1) to conduct cutting-edge research in arthritis and MSD by providing statistical, epidemiological, outcomes, and health service expertise and leadership; (2) to support data collection, management, and analytic efforts of the four MCRC projects; (3) to develop original research in methodology applicable to clinical research in arthritis and MSD; and (4) to nurture and support new investigators in arthritis and MSD.

AR055583 (Banman) 4/1/2009-3/31/2014  
NIH Total direct cost \$1,812,500.00  
“*Understanding Muscle Regeneration Impairment Across the Human Age Span*”

This project is to better understand the principal mechanisms driving muscle stem (satellite) cell recruitment and net muscle protein synthesis during skeletal muscle regeneration/growth in aging muscle that cause disruption.

1UL1RR025777-03 (Guay-Woodford) 5/19/08-4/30/13  
NIH/NCRR \$4,231,544

*UAB Center for Clinical and Translational Science*

To 1) establish a centralized communication structure to enhance collaboration between our research centers and programs across all fields of clinical and translational research, including pediatric and community groups; 2) train and develop clinical and translational investigators to become principal investigators and productive members of research teams; 3) facilitate utilization of existing resources and provide new resources; 4) emphasize novel interdisciplinary research that is important given our geographic location and history (i.e., health disparities research) and that utilizes our unique strengths (i.e., outcomes research and drug discovery); and 5) assess the progress of the CCTS toward its goals.

1R01DK085027-01A1 (Allon) 7/1/2010-6/30/2014  
NIH/NIDDK total cost: \$ 2,280,406

*Vascular Abnormalities in Patients Receiving a Dialysis Access.*

This grant is to quantify preoperative arterial medial fibrosis in CKD patients receiving a fistula, and correlate it with fistula non-maturation

S10-005 6/30/2010-12/31/2011  
DHHS SRI (Gillespie) total cost: \$ 991,421

*Interrogation of Key Genomic Alterations in Glioblastoma Multiforme (GBM) for Identification of Molecular Pathways Critical to GBM Tumorigenesis and Progression*

This project is to profile global gene expression, SNP genotype, and kinase activities in the GBM xenograph lines and compare them with the primary tumors.

5R01DK083562 (Garvey) 8/1/2009-7/31/2013  
NIH/NIDDK Total: 2,560,059

*NR4A Orphan Receptors and Insulin Resistance*

10A020 (Tollefsbol) 1/01/11-12/31/12

AIFCR

Green Tea Polyphenols in the Prevention of Breast Cancer Initiation

***Completed:***

GRANTS AS PI:

UAB CAEG Partnership Pilot Program 8/15/10 -8/14/11 \$10,000

*Unmasking novel cystogenic pathways: Biological knowledge-based statistical pathway analyses of genome-wide gene expression and DNA methylation data*

UAB faculty Development Grant 8/1/08-7/31/09 \$30,000

*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.*

UAB Center of Nutrition Research 8/1/05-7/31/06 \$10,000

*Characterizing the Diet/Nutrition Effect on Gene alternative Transcripts Using Affymetrix Microarray Data.*

GRANTS AS CO-I:

P50 HL77100 (Dell'Italia) 2/9/2005 – 12/31/2010

NIH/NHLBI total costs: \$12,009,731

*SCCOR in Cardiac Dysfunction and Disease – Biostatistics Core*

To unravel mechanisms of LV remodeling in three disparate forms of heart disease—volume overload of mitral regurgitation (MR), primary aldosteronism, and diabetic cardiomyopathy—that are resistant to standard medical therapy.

NIH U54CA100949 (Barnes) 9/9/03-8/31/2010

*Center for Gene-Nutrient Interaction (CNGI)* \$13,809,062 Total

This Center will focus on the identification of genetic pathways that may distinguish cancer cells from normal cells, and the extent to which dietary polyphenols with documented chemo preventive activity modulate these pathways.

1 P30 DK074038-02 (Guay-Woodford) 9/30/05 – 8/31/10

NIH/NIDDK total cost \$3,941,048

*UAB Recessive PKD Research and Translational Core Center*

This center integrates existing intellectual and technological resources of the University and provides a set of services/resources to enable innovative investigations in the four thematic areas related to recessive PKD pathogenesis - 1) cilia-related biology; 2) regulation of epithelial transport pathways; 3) signaling pathways in epithelial differentiation; and 4) matrix biology and fibrosis

R01DK68261 (Nagy) 7/1/04 to 6/30/09

NIH/NIDDK \$1,086,126 Total

*Antipsychotic Drug-Induced Weight Gain*

The specific aim of this project is to determine the mechanism(s) by which the new atypical antipsychotic drugs induce weight gain using a mouse model system.

Susan G Komen Breast Cancer Foundation (Frost) 12/1/07-11/30/09  
*Targeting the Hedgehog Pathway in the Treatment of Breast Cancer* Total cost \$ 300,000

1 R21 DK078522 (Guay-Woodford)  
NIH/NIDDK 6/1/06-5/30/11  
*Genetics and Pharmacogenetics in FSGS (PPG Project 4)* \$862,690 (total direct cost).

5 R01 HL075211 (Oparil)  
NIH/NHLBI 7/1/04-6/30/08  
*Estrogen Modulates Injury-Induced Inflammation*

Utilize a well characterized rodent model to elucidate the fundamental cellular/molecular mechanisms by which ovarian hormones, particularly estrogen, modulate the inflammatory response to acute endoluminal vascular injury.

NIH R01AG020681 (Prolla) 3/15/03 - 1/31/08  
NIH/NIA \$250,000 (1st yr direct) \$1,250,000 (Total costs)  
*Gene expression profiling, caloric restriction and aging.*

To use microarrays for gene expression studies to understand the role of caloric restriction in promoting longevity in mice.

NSF 0217651 (Allison) 10/01/02 – 08/31/06  
NSF \$519,635 (Annual Directs) \$2,220,275  
*Design and Analysis of Microarray Gene Expression Studies in Plants: Toward Sound Statistical Procedures*

To develop statistical methods from a strong epistemological foundation for analysis of microarray data from plants.

NIH R01ES12933-01A1 (Ruden) 04/01/05 - 03/31/10  
NIH/NIEHS \$250,000 (Annual Directs) \$1,598,750  
*QTL and Microarray Mapping Lead Sensitivity Genes*

The hypothesis for this proposal is that one can identify some of the "protective genes" that make an organism resistant to the behavioral and developmental effects of lead toxicity using quantitative trait loci (QTL) mapping techniques combined with microarray and sophisticated genetic analyses.

Burroughs Welcome Fund (Guay-Woodford) 07/01/01 – 06/30/06  
\$150,000 (Direct Annual) \$750,000  
*Genetic Modifiers of Recessive Polycystic Kidney Disease: Implications for Pathogenesis and Therapeutics*

The specific aims of this project are 1) map QTL that modulate *cpk* renal cystic disease and those QTL that unmask and modulate the biliary phenotype in the mouse *cpk* model; 2) determine whether these same QTL modulate *bpk*-associated renal and biliary traits; and 3) test

patients enrolled in our ARPKD Clinical Database to determine whether the human homologues of these renal and biliary QTL modulate disease expression in human ARPKD.

NIH 1 R21 HL72871 (Matalon)

10/01/01 – 09/30/06

\$225,000 (Annual Directs)

*Modulation of Innate Immunity in Lung Transplantation*

The major goal of this project is to identify differences in the ability of Ams to kill gram-positive and gram-negative bacterial pathogens in lung transplant patients.