Feifei Xiao, PhD

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EDUCATION

May 2013	PhD, Biomathematics and Biostatistics Graduate School of Biomedical Sciences, The University of Texas Health Science Center MD Anderson Cancer Center, Houston, TX, USA Mentor: Christopher I. Amos, PhD Dissertation: *Natural and orthogonal interaction framework for modeling gene-gene/gene-environmental interactions and imprinting effects.*
Jun 2009	Master of Science, Microbiology State Key Laboratory of Virology College of Life Sciences, Wuhan University, Wuhan, China
Jun 2006	Bachelor of Science, Biology College of Life Sciences, Wuhan University, Wuhan, China

PROFESSIONAL EXPERIENCE

Aug 2015 - present	**Assistant Professor** Department of Epidemiology and Biostatistics, Cancer Prevention and Control Program, Arnold School of Public Health, University of South Carolina, Columbia, SC, USA
May 2017 – July 2017	**Visiting Assistant Professor** Department of Biomedical Data Science, Geisel School of Medicine at Dartmouth College, Lebanon, NH, USA
Jun 2013 - Jul 2015	**Postdoctoral Research Associate** Department of Biostatistics, Yale School of Public Health, New Haven, CT, USA Mentor: Heping Zhang, PhD

Projects: *Methodology development of copy number variation detection; women and child health.*

Jun 2010 - May 2013 **Graduate Research Assistant**
Department of Genetics/Epidemiology, The University of Texas Health Science Center at Houston MD Anderson Cancer Center, Houston, TX, USA
Mentor: Christopher I. Amos, PhD
Projects: *Natural and orthogonal framework for GxG/GxE interactions and imprinting effects with application to melanoma and lung cancer.*

Sep 2009 - May 2010 **Graduate Research Assistant**
Department of Bioinformatics and Biostatistics/Epidemiology, The University of Texas Health Science Center at Houston MD Anderson Cancer Center, Houston, TX, USA
Project I: *Image annotation tool design for medical diagnosis.*
Supervisor: Jonas Almeida, PhD
Project II: *Segregation and linkage analysis power optimization in parameters selection*.
Supervisor: Christopher I. Amos, PhD
Project III: *Early phase clinical trial design*.
Supervisor: Donald Berry, PhD

Dec 2006 - Nov 2008 **Graduate Research Assistant**
Department of Neuroscience, University of Minnesota, Minneapolis, MN, USA
Project: *Data mining of microRNA/siRNA-target gene interactions and protein-protein interactions.*
Supervisor: Tongbin Li, PhD

MAJOR RESEARCH INTERESTS

Methodology and Application in:

- Big Data Analyses
- Integrative Genomics
- Population Genetics
- Cancer Epidemiology
- Women and Children Health
- Psychiatry and Mental Health

RESEARCH AWARDS AND GRANTS

Ongoing

ASPIRE I Xiao (PI) 07/01/2017 - 9/30/2018
Office of the Vice President for Research, University of South Carolina
Title: Powerful Detection of Genome Structural Change and Its Effect on Cutaneous Melanoma
Role: Principal Investigator
Total Award: $15,000

DMS1722562 Xiao (PI) 07/01/2017 - 6/30/2020
NSF, Division of Mathematical Sciences
Title: Collaborative Research: Scalable and flexible algorithms to detect structural change in complex sequence data.
Role: Principal Investigator
Total Award: $498,229

Pending

12/01/2018 - 11/30/2020
NIH/NCI R21 (PI: Xiao)
Germline Copy Number Variations in Lung Cancer
Role: Principal Investigator (25% of effort)

09/01/2018 - 08/31/2020
USDA (PI: Murphy AE)
Children's dietary inflammatory index-based intervention and products to promote anti-inflammatory-dietary patterns to reduce inflammation and related conditions in children.
Role: Co-Investigator (7.5% of effort)

12/01/2018 - 11/31/2023
NIH/ National Cancer Institute, R01 (PI: Murphy AE)
Dietary Inflammatory Potential, the Colonic Environment, and Adenoma Risk
Role: Co-Investigator (5% of effort)

07/01/2018 - 06/30/2023
NIH/National Cancer Institute, P01 (PI: Hebert JR)
Center for Inflammation, Biobehavioral Risk Factors, and Racial Disparities in Colorectal Cancer
Role: Co-Investigator (15% of effort)

PUBLICATIONS

Published or in press (*corresponding author):

1. Zhao Y, Varn F, Cai G, **Xiao F**, Amos CI, and Cheng C. A P53-deficiency gene signature predicts recurrence risk of patients with early stage lung adenocarcinoma. *Cancer Epidemiology, Biomarkers & Prevention*. 2018; 27(1):86-95.
2. Bukowski R, Sadovsky Y, H. Goodarzi, Zhang H, Biggio JR, Varner M, Parry S, **Xiao F**, and et al. Onset of Human Preterm and Term Birth is Related to Unique Inflammatory Transcriptome Profiles at the Maternal Fetal Interface. *Peer J*. 2017; 5:e3685.
3. Cai G, Zheng X, Liang S, **Xiao F***. Local sequence and sequencing depth dependent accuracy of RNA-seq reads. *BMC Bioinformatics*. 2017; 8(1): 364.
4. **Xiao F**, Niu Y, Hao N, Xu Y, Jin Z, Zhang H. modSaRa: a computationally efficient R package for CNV identification. *Bioinformatics*. 2017; 33(15):2384-2385.
5. Cai G, **Xiao F**, Cheng C, Li Y, Amos CI, Whitfield ML. Population effect model identifies gene expression predictors of survival outcomes in lung adenocarcinoma for both Caucasian and Asian patients. *PLoS One.* 2017; 12(4):e0175850.
6. **Xiao F**, Cai G, Zhang H. Segregation analysis suggests that a genetic reason may contribute to "the dress" colour perception. *PLoS One*. 2016; 11(10):e0165095.
7. **Xiao F**, Min X, Zhang H. Modified screening and ranking algorithm for copy number variant detection. *Bioinformatics*. 2015; 31(9):1341-8.
8. Zhang H, Baldwin DA, Bukowski RK, Parry S, Xu Y, Song C, Andrews WW, Saade GR, Esplin MS, Sadovsky Y, Reddy UM, Ilekis J, Varner M, Biggio JR Jr; Eunice Kennedy Shriver National Institute of Child Health and Human Development (NICHD) Genomic and Proteomic Network for Preterm Birth Research (GPN-PBR) cohort (including **Xiao F**). A genome-wide association study of early spontaneous preterm delivery. *Genet Epidemiol*. 2015; 39(3):217-26.
9. Manuck TA, Esplin MS, Biggio J, Bukowski R, Parry S, Zhang H, Huang H, Varner MW, Andrews W, Saade G, Sadovsky Y, Reddy UM, Ilekis J; Eunice Kennedy Shriver NICHD GPN-PBR cohort (including **Xiao F**). The phenotype of spontaneous preterm birth: application of a clinical phenotyping tool. *Am J Obstet Gynecol*. 2015; 212(4):487.
10. Parry S, Zhang H, Biggio J, Bukowski R, Varner M, Xu Y, Andrews WW, Saade GR, Esplin MS, Leite R, Ilekis J, Reddy UM, Sadovsky Y, Blair IA; Eunice Kennedy Shriver NICHD GPN-PBR cohort (including **Xiao F**). Maternal serum serpin B7 is associated with early spontaneous preterm birth. *Am J Obstet Gynecol*. 2014; 211(6):678.e1-12.
11. **Xiao F**, Ma J, Cai G, Fang S, Lee JE, Wei Q, Amos CI. Natural and orthogonal interaction model for estimating gene-gene interactions: applied to cutaneous melanoma. *Human Genetics*. 2014; 133(5):559-74.
12. **Xiao F**, Ma J, Amos CI. A unified framework integrating parent-of-origin effects for association study. *PLoS ONE*. 2013; 8(8):e72208.
13. Ma J, **Xiao F**, Xiong M, Andrew AS, Brenner H, Duell EJ, Haugen A, Hoggart C, Hung RJ, Lazarus P, Liu C, Matsuo K, Mayordomo JI, Schwartz AG, Staratschek-Jox A, Wichmann E, Yang P, Amos CI. Natural and orthogonal interaction framework for modeling gene-environment interactions with application to lung cancer. *Human heredity*. 2012; 73(4):185-94.

14. Zhou S, Xiao W, Wan Q, Yi C, **Xiao F**, Liu Y, Qi Y. Nogo-B mediates HeLa cell adhesion and motility through binding of Fibulin-5. *Biochemical and biophysical research communications*. 2010; 398(2):247-53.
15. **Xiao F**, Zuo Z, Cai G, Kang S, Gao X, Li T. miRecords: an integrated resource for microRNA-target interactions. *Nucleic acids research.* 2009; 37:D105-10.
16. Ren Y, Gong W, Zhou H, Wang Y, **Xiao F**, Li T. siRecords: a database of mammalian RNAi experiments and efficacies. *Nucleic acids research*. 2009; 37: D146-9.
17. Gong W, Zhou D, Ren Y, Wang Y, Zuo Z, Shen Y, **Xiao F**, Zhu Q, Hong A, Zhou X, Gao X, Li T. PepCyber: P~PEP: a database of human protein-protein interactions mediated by phosphoprotein-binding domains. *Nucleic acids research*. 2008; 36: D679-83.

Under review or in preparation (*****corresponding author**)**:

18. Xiao F, Luo X, Hao N, Niu Y, Cai G, Amos CI, Zhang H. An accurate and powerful method for copy number variation detection. *Bioinformatics*. Submitted
19. Sill DN, Torres ME, **Xiao F**, Ingram LA. Study to Assess Beliefs and Evaluate Risks (SABER): identifying the impact of HIV knowledge on sexual risk behaviors among South Carolina Latinos. *Journal of Immigrant and Minority Health*. Submitted.
20. Biggio RJ, **Xiao F**, Baldwin D, Bukowski R, Parry S, Esplin MS, Andrews WW, Saade GR, Varner M, Sadovsky Y, Reddy UM, Ilekis J, Zhang H. Maternal and neonatal copy number variants and the association with early spontaneous preterm birth. *The Journal of the American Medical Association*. Under Revision.
21. Cai G, **Xiao F***. RNA-seq differential expression detection and its study specific strategy. Manuscript.
22. Cai G, Qiu P, Verhaak RG, Chen T, **Xiao F***, Liang S. Expression regulatory methylator phenotype in breast cancer. Manuscript.
23. **Cai G**, Xiao F, Liang S. A new bias in RNA-seq. Manuscript.
24. Steck SE, Woloszynska-Read A, Antwi SO, Zhang H, Arab L, Fontham E, Mohler JL, Su LJ, **Xiao F**, Smith GJ, Trump D, Johnson C, Bensen JT. SNPs in vitamin D-related genes are associated with prostate cancer aggressiveness in the North Carolina-Louisiana Prostate Cancer Project (PCaP). Manuscript.
25. Parry S, **Xiao F**, Leite R, Biggio JR, Bukowski R, Varner M, Zhang H, Andrews W, Saade G, Esplin MS. MicroRNA as biomarkers of spontaneous preterm birth. Manuscript.
26. **Xiao F,** Deng S, Cai G, Amos CI. Imprinting effect detection using an orthogonal framework for eQTL mapping with RNA-seq data. In preparation.

HONORS AND AWARDS

March of Dimes Award for Best Research in Prematurity, SMFM's Meeting, 2015

NIGMS Short Course on Statistical Genetics & Genomics Travel Fellowship Award, 2014

City Federation of Women's Clubs Endowed Scholarship in Biomedical Sciences, 2013

Summer Institute of Statistical Genetics (SISG) Travel Scholarship, 2011

Outstanding Undergraduate Student Scholarship, Wuhan University, 2005 & 2006

Special Contribution Award in Academic Activities, Wuhan University, 2004

Outstanding Freshman Scholarship, Wuhan University, 2002

SHORT COURSES/EDUCATIONAL WORKSHOPS

Educational Workshop on Genetic Epidemiology: Fundamentals for Precision Medicine, Cambridge, UK *Sep 2017*

Big data phenotyping: opportunities, analytic challenges and solutions, Toronto, ON, Canada *Oct 2016*

Statistical Genetics and Genomics, University of Alabama, Birmingham, AL *Jul 2014*

Summer Institute in Statistical Genetics, University of Washington, Seattle, WA *May 2011*

TEACHING EXPERIENCE

Instructor

BIOS794	Special topics in Biostatistics-Statistical Genetics	*Spring 2017*
BIOS700	Introduction to Biostatistics	*Spring 2016, Fall 2016*
BIOS 757	Intermediate Biostatistics	*Fall 2017*
BIOS J757	Intermediate Biostatistics (Distance)	*Spring 2018*
BIOS890	Independent Study	*Fall 2017, Summer 2018*

Guest Lectures

EPID800	Epidemiology Methods II (Guest lecturer)	*Fall 2015, 2016, 2017*
BIOS745	Seminar in Biostatistics	*Spring 2018*

MENTORING EXPERIENCE

Doctoral dissertation and Master's Thesis Committee (Completed):

- Andrew Fogner – Thesis Committee Member
  MPH in Epidemiology (advisor: Myriam Torres), Defense on May 3, 2016
  Thesis title: *Prenatal Depression in South Carolina Latinos*
- Danielle Sill – Thesis Committee Member
  MSPH in Epidemiology (advisor: Myriam Torres), Defense on March 3, 2017
  Thesis title: *The association between sexual risk behaviors of Latinos and HIV Knowledge in South Carolina*

Doctoral dissertation and Master's Thesis Committee (Current):

- Rahimi Gelareh – Dissertation Committee Member
  PhD candidate in Biostatistics (advisor Dr. James Hardin)
- Amanda Collins – Thesis Committee Member

MSPH in Epidemiology (advisor Dr. Anwar Merchant)
Topic: *Effect Modification of Stroke in The Relationship Between Tooth Loss and Cognitive Functioning*

- Andrés Gaviria – Dissertation Committee Member
  PhD candidate in Environmental Health and Epidemiology (advisor Dr. Jim Burch)
  Topic: *Describing the Impact of Antibiotic Resistant Bacteria in the Environment and on Population Health in South Carolina*

Undergraduate students:

- Lijuan Wang – Thesis advisor
  Visiting student from Nanjing Medical University, China
  Title: Differential expression of immunology pathway related genes in Lung carcinoma
- Lu Xu – Thesis advisor
  Visiting student from Nanjing Medical University, China
  Title: Implications of immunotherapy in breast cancer treatment

INVITED TALKS AND SEMINARS

1. Integrating genetic source boosts power for copy number variation detection. Department of Statistics, University of South Carolina, Columbia, SC, April 2018.
2. A powerful statistical framework for copy number variation detection with application to melanoma. Medical University of South Carolina, Charleston, SC, April 2018.
3. Copy number variations, parent-of-origin effects and cancer. Nanjing Medical University, Nanjing, Jiangsu, China, Jul 2017.
4. Imprinting effect detection and copy number variation in cancer. Wuhan University, Wuhan, Hubei, China, Jul 2017.
5. Copy number variations, epigenetics and cancer. Dartmouth College, Hanover, NH, USA, Feb 2017.
6. Testing of parent-of-origin effect in eQTL mapping using RNA-seq data. University of South Carolina, Columbia, SC, USA, Nov 2016.
7. A statistical framework for copy number variation detection with application to melanoma study. Wuhan University, Wuhan, China, June 2016.
8. A framework of testing interactions and parent-of-origin effect with application to cancer studies. Moffitt Cancer Center, Tampa, FL, USA, Dec 2015.
9. Testing of interactions and parent-of-origin effect using orthogonal models. University of South Carolina, Columbia, SC, USA, Nov 2015.
10. Modified Screening and Ranking Algorithm for Copy Number Variation Detection. City University of New York, New York, NY, USA, Apr 2015.
11. A new change-point model based method for copy number variation detection. University of Massachusetts Amherst, Amherst, MA, USA, Mar 2015.

12. Modified Screening and Ranking Algorithm for Copy Number Variation Detection. University of South Carolina, Colombia, SC, USA, Feb 2015.
13. Modified Screening and Ranking Algorithm for Copy Number Variation Detection. *Seminar*, University of Colorado Boulder, Boulder, CO, USA, Jan 2015.
14. Natural and Orthogonal Model for Gene-Gene interactions Applied to Cutaneous Melanoma. Geisel School of Medicine at Dartmouth College, Lebanon, NH, USA, Jul 2013.

CONFERENCE PRESENTATIONS

1. Analyses of germline copy number variation and gene expression in cutaneous melanoma. *Contributed talk*, International Genetic and Epidemiology Society (IGES), Cambridge, UK, Sep 2017.
2. Efficient epigenetic effect identification in eQTL mapping with RNA-seq data. *Invited talk*, International Conference on Computational Methods (ICCM), Guilin, Guangxi, China, July 2017.
3. Modeling parent-of-origin effect in eQTL mapping using RNA-seq data. *Invited talk*, International Chinese Statistical Association (ICSA), Chicago, IL, June 2017.
4. Testing of parent-of-origin effect in eQTL mapping using RNA-seq data. *Contributed talk*, IGES, Toronto, ON, Canada, Oct 2016.
5. A change-point based method for copy number variation detection with application to melanoma. *Contributed talk*, ICSA, Atlanta, GA, June 2016.
6. SNPs in vitamin D-related genes are associated with prostate cancer aggressiveness in the North Carolina-Louisiana Prostate Cancer Project (PCaP). *Abstract*, American Association for Cancer Research, New Orleans, LA, April 2016.
7. A new change-point model based method for copy number variation detection. *Poster presentation*, American Society of Human Genetics (ASHG), Baltimore, MD, USA, Oct 2015.
8. Modified screening and ranking algorithm for copy number variation detection. *Poster presentation*, IGES, Baltimore, MD, USA, Oct 2015.
9. Using expression data to define patient specific predictors for survival outcomes in lung adenocarcinoma. *Abstract*, ASHG, Baltimore, MD, USA, Oct 2015.
10. MicroRNA as biomarkers of spontaneous preterm birth. *Abstract*, Society for Maternal-Fetal Medicine (SMFM). March 2015.
11. Neonatal, not Maternal, Copy Number Variants are Associated with Spontaneous Preterm Birth. *Abstract*, SMFM. March 2015.
12. Natural and orthogonal model for gene-gene interactions applied to cutaneous melanoma. *Poster presentation*, IGES, Chicago, IL, USA, Sep 2013.
13. Natural and orthogonal association framework to detect parent-of-origin effects. *Poster presentation*, IGES, Stevenson, WA, USA, Oct 2012.

14. Natural and orthogonal interaction framework for modeling GxG and GxE interactions. *Poster presentation*, IGES, Stevenson, WA, USA, Oct 2012.

INSTITUTIONAL SERVICES

- Chair of the Biostatistics Forum for the Department of Epidemiology and Biostatistics (2017)
- Division of Biostatistics Admissions Committee (2016-)
- Department of Epidemiology and Biostatistics Search Committee (Fall 2017 – Spring 2018)
- Chair of the Graduate Exam Committee for the Department of Epidemiology and Biostatistics (2017 - 2018)
- Member of the Book Store Committee for the University of South Carolina (2017 - now)
- Member of the Graduate Exam Committee for the Department of Epidemiology and Biostatistics (2016 - 2017)

EXTERNAL SERVICES and MEMBERSHIP

- Platform session chair: International Conference on Computational Methods (ICCM), Guilin, Guangxi, China, 2017
- Platform session chair: International Chinese Statistical Association, Atlanta, GA, 2016
- Program committee: European Conference on Computational Biology (ECCB), 2016
- *Ad hoc* reviewer for *Biomedical Sciences*, *BioData Mining*, *Bioinformatics*, *BMC Cancer*, *Clinical Genetics*, *European Conference on Computational Biology 2014 and 2016*, *Frontier in Genetics*, *Genetic Epidemiology*, *Human Genetics, IEEE Signal Processing Letters, Journal of Theoretical Biology, Nutrition & Metabolism, PLoS ONE, Plos Computational Biology, Peer J, Scientific Report and Statistics & Its Interface*.
- Invited reviewer for *Annals of Public Health and Research* and *Human Genetics*
- Member of the International Genetic Epidemiology Society (IGES)
- Member of the American Society of Human Genetics (ASHG)
- Member of the American Association of Cancer Research (AACR)
- Member of the International Chinese Statistical Association (ICSA)

SOFTWARE

modSaRa

- An R package for a change-point model based method for copy number variation detection.
  http://c2s2.yale.edu/software/modSaRa

miRecords

- An integrated resource for animal microRNA-target interactions providing both computational predicted and experimental validated miRNA-target interactions.
  http://c1.accurascience.com/miRecords/

COMPUTER SKILLS

Computational Programming:

- R/S-plus
- Unix Shell Script
- SAS
- Stata
- JavaScript
- C