Feifei Xiao, PhD

CONTACT INFORMATION

Department of Epidemiology and Biostatistics
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Discovery I Building
915 Greene Street, Room 449
Columbia, SC, 29208, USA
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EDUCATION

06/2013 **Ph.D.** in Biomathematics and Biostatistics
The University of Texas Health Science Center MD Anderson Cancer Center, Graduate School of Biomedical Sciences, Houston, TX, USA
Mentor: Christopher I. Amos, PhD
Dissertation: *Natural and orthogonal interaction framework for modeling gene-gene/gene-environmental interactions and imprinting effects.*

06/2009 **M.S.** in Microbiology
Wuhan University, Wuhan, China
State Key Laboratory of Virology
College of Life Sciences

06/2006 **B.S.** in Biology
Wuhan University, Wuhan, China
College of Life Sciences

POST-GRADUATE TRAINING

06/2013 – 07/2015 **Postdoctoral Research Associate**
Yale School of Public Health, New Haven, CT, USA
Department of Biostatistics, School of Public Health
Mentor: Heping Zhang, PhD
Projects: *Algorithms and methods for copy number variation detection; women and children health.*

EMPLOYMENT

07/2021 – present	**Associate Professor (Tenured)** Department of Epidemiology and Biostatistics, Cancer Prevention and Control Program, Arnold School of Public Health, **University of South Carolina**, Columbia, SC, USA
08/2015 – 06/2021	**Assistant Professor** Department of Epidemiology and Biostatistics, Cancer Prevention and Control Program, Arnold School of Public Health, **University of South Carolina**, Columbia, SC, USA
05/2017 – 07/2017	**Visiting Assistant Professor** Department of Biomedical Data Science, Geisel School of Medicine at **Dartmouth College**, Lebanon, NH, USA
06/2010 – 05/2013	**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.*
09/2009 – 05/2010	**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
12/2006 – 11/2008	**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.*

MAJOR RESEARCH INTERESTS

Methodology and Application in:

Statistical Genetics	Single Cell Sequencing
Neuroimaging Data Analyses	Cancer Epidemiology
Integrative Genomics	Machine Learning

RESEARCH AWARDS AND GRANTS

Ongoing

The evolution of copy number variations in the AT-rich Plasmodium genome
R01AI150856 Guler(PI) 04/01/2021 – 03/31/2026
NIH/NIAID
Role: Co-Investigator (15% of effort in first three years, plus 1 RA each year)
Total Award (USC site for Xiao): $219,494

Copy Number Variation and Lung Cancer: Disease Risk and Mechanisms
R21HG010925 Xiao(PI) 09/01/2020 - 08/30/2022
NIH/NHGRI
Role: Principal Investigator (25% of effort, plus 1 RA each year)
Total Award: $426,122

Molecular Basis of Exercise-induced Changes in HDL Function
R01 HL146462 Sarzynski (PI) 04/01/2019 - 03/31/2024
NIH/NHLBI
Role: Co-Investigator (year 1-4: 5%, 5%, 10%, 15% of 9-month, year 5: 25% of 12-month)
Total Award: $3,466,346

A Novel Statistical Algorithm for Copy Number Variation Detection with Application to Lung Cancer
USC Office of the Vice President for Research Xiao (PI) 07/01/2020 - 9/30/2021
ASPIRE-I Innovation grant: Advanced Support for Innovative Research Excellence
Role: Principal Investigator
Total Direct Cost: $14,964

Aging Brain Cohort at the University of South Carolina (ABC@USC)
USC Excellence Initiative Award Fridriksson (PI) 07/01/2019 - 06/30/2023
Role: Co-Investigator (18% of effort)
Total Award: $1,750,000

Mechanisms of Early Onset Colorectal Cancer (EOCRC)
USC Office of the Vice President for Research Hofseth (PI) 07/01/2020 - 9/30/2021
ASPIRE-II Integration grant: Advanced Support for Integration Research Excellence
Role: Co-Investigator
Total Direct Cost: $84,105

Completed

Medicare Shared Savings Cost Determinants Analysis, 2015-2017
ASPH Dean's office Rudisill (PI) 07/01/2020 - 06/30/2021
Role: Co-Investigator (8% of effort)
Total Direct Cost: $14,315

Collaborative Research: Scalable and flexible algorithms to detect structural change in complex sequence data
DMS1722562 Xiao (PI) 07/01/2017 - 6/30/2020
NSF, Division of Mathematical Sciences
Role: Principal Investigator (8% of effort)
Total Award: $498,229

COVID-19 Severe Progression Prediction with AI Approaches from Multi-dimensional Data
USC Office of the Vice President for Research Cai (PI) 05/15/2020 - 12/31/2020
Role: Co-Investigator
Total Direct Cost: $25,000

miRNA bioinformatics of peak VO2 response to exercise training in heart failure
P20GM103499 Sarzynski (PI) 07/01/2019 - 06/30/2020
NIH/NIGMS South Carolina IDeA Network of Biomedical Research Excellence (SC INBRE), Bioinformatics Pilot Project Program
Role: Co-Investigator
Total Direct Cost: $9,984

Powerful Detection of Genome Structural Change and Its Effect on Cutaneous Melanoma
USC Office of the Vice President for Research Xiao (PI) 07/01/2017 - 9/30/2018
ASPIRE-I Innovation grant: Advanced Support for Innovative Research Excellence
Role: Principal Investigator (8% of effort)
Total Award: $15,000

Pending

Autonomic and Sensory Dysfunctions in FMR1 Conditions: Development, Mechanisms and Consequences
R01 Roberts (PI) 09/01/2021 - 08/31/2026
NIH/NIMH
Role: Co-Investigator (7.5% of effort)
Total Requested: $3,720,036 (ranked as 6% percentile)

PUBLICATIONS

Published or in press (***** indicates corresponding author; # indicates advisee):

1. Qin F#, Luo X#, Cai G, **Xiao F***. Shall genomic correlation structure be considered in copy number variation detection? *Briefings in Bioinformatics* (2021). Online.

2. Liang Q, Tan C, **Xiao F**, Yin F, Liu M, Lei L, Wu L, Yang Y, Tan HJ, Liu S, Zeng X. Integrated profiling identifies ITGB3BP as prognostic biomarker for hepatocellular carcinoma. *Bosnian Journal of Basic Medical Sciences* (2021). Online.

3. Cai G, Zhu X, Charvet L, **Xiao F**, Datta A, Androulakis XM. A Systematic review and meta-analysis on the efficacy of transcranial direct current stimulation for migraine. *Journal of Pain Research*. 2021. 14:1171-1183.

4. Luo X#, Qin F#, Cai G, **Xiao F***. Integrating genomic correlation structure improves copy number variations detection. *Bioinformatics*. 2021. 37(3):312-317.

5. Zhou J, Cui X, **Xiao F**, Cai G. A cluster-based approach for identifying prognostic microRNA signatures in digestive system cancers. *International Journal of Molecular Sciences*. 2021. 22(4):1529.

6. Kristinsson S, Zhang W, Rorden C, Newman-Norlund R, Basilakos A, Bonilha L, Yourganov G, **Xiao F***, Hillis A**,** Fridriksson J. Machine learning-based multimodal prediction of language outcomes in chronic aphasia. *Human Brain Mapping*. 2021. 42(6):1682-1698.

7. Hao N, Niu YS, **Xiao F**, Zhang H. A super scalable algorithm for short segment detection. *Statistics in Biosciences*. 2021. 13(1):18-33.

8. Cai G, Bossé Y, **Xiao F**, Kheradmand F, Amos CI. Tobacco smoking increases the lung gene expression of ACE2, the receptor of SARS-CoV-2. *American Journal of Respiratory and Critical Care Medicine*. 2020. 201(12):1557-1559.

9. Wang L#, Luo X#, Cheng C, Amos CI, Cai G, **Xiao F***. A gene expression based immune signature for lung adenocarcinoma prognosis. *Cancer Immunology and Immunotherapy*. 2020. 69(9):1881-1890.

10. Deng S, Hardin J, Amos CI, **Xiao F***. Joint modeling of eQTLs and parent-of-origin effects using an orthogonal framework with RNA-seq data. *Human Genetics*. 2020.139(8):1107-1117.

11. Liu M, Liu X, Liu S, **Xiao F**, Guo E, Qin X, Wu L, Liang Q, Liang Z, Li K, Zhang D, Yang Y, Luo X, Lei L, Tan HJ, Yin F, Zeng X. Big data-based identification of multi-gene prognostic signatures in liver cancer. *Frontiers in Oncology*. 2020. 10:847.

12. Kristinsson S, **Xiao F**, Yourganov G, Bonilha L, Stark BC, Rorden C, Basilakos A, Fridriksson J. BDNF Genotype Specific Differences in Cortical Activation in Chronic Aphasia. *Journal of Speech, Language, and Hearing Research*. 2019. 62(11):3923-3936.

13. Xiao F*, Luo X#, Hao N, Niu YS, Xiao X, Cai G, Amos CI, Zhang H. An accurate and powerful method for copy number variation detection. *Bioinformatics.* 2019. 35(17):2891-2898.

14. 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.

15. 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.

16. 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.

17. 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.

18. 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.

19. 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.

20. Xiao F, Min X, Zhang H. Modified screening and ranking algorithm for copy number variant detection. *Bioinformatics*. 2015; 31(9):1341-8.

21. 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.

22. 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.

23. 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.

24. **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.

25. **Xiao F**, Ma J, Amos CI. A unified framework integrating parent-of-origin effects for association study. *PLoS ONE*. 2013; 8(8):e72208.

26. 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.

27. 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.
28. **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.

29. 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.

30. 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 submitted (***** indicates corresponding author; # indicates advisee):

31. Luo X#, Cai G, McClain A, Amos CI, Cai B, **Xiao F***. BMI-CNV: a Bayesian framework for multiple sample copy number variation detection. *Bioinformatics*. Under Review.

32. Qin F#, Luo X#, **Xiao F**, Cai G. SCRIP: an accurate simulator for single-cell RNA sequencing data. *Bioinformatics*. Under Revision.

33. Sun Z, Neelon B, Ethier SP, **Xiao F**, Wallace K, Chung D. A Bayesian framework for pathway-guided identification of cancer subgroups by integrating multiple types of genomic data. *Statistics in Medicine*. Under Review.

34. Cai G, **Xiao F***. SARS-CoV-2 Impair Dendritic Cells and Regulate DC-SIGN Expression in Tissues. *Cell Reports*. Submitted.

35. Cai G, **Xiao F***. SCANNER: A web server for annotation, visualization and sharing of single cell RNA-seq data. bioRxiv. doi: https://doi.org/10.1101/2020.01.25.919712.

HONORS AND AWARDS

- North Coast Conference on Precision Medicine Travel Award, 2018
- March of Dimes Award for Best Research in Prematurity, SMFM's Meeting, 2015
- NIGMS Short Course on Statistical Genetics & Genomics Travel Award, 2014
- City Federation of Women's Clubs Endowed Scholarship in Biomedical Sciences, 2013
- Summer Institute of Statistical Genetics (SISG) Travel Award, 2011
- Scholarship for Excellent Graduate Students, Wuhan University, 2006-2009
- Outstanding Undergraduate Student Scholarship, Wuhan University, 2005 & 2006
- Superior Academic Activities Award, Wuhan University, 2004
- Outstanding Freshman Scholarship, Wuhan University, 2002

SHORT COURSES/EDUCATIONAL WORKSHOPS

- USC Center for Teaching Excellence Workshop: *Active Learning Made Easy*. Columbia, SC, November 2018.
- Educational Workshop on Genetic Epidemiology: *Fundamentals for Precision Medicine*, IGES meeting, Cambridge, UK, September 2017
- USC Center for Teaching Excellence New Faculty Academy Workshop: *Stress Reduction and Resilience: Strategies for Busy Faculty Member*. Columbia, SC, December 2016
- Educational Workshop*: Big data phenotyping: opportunities, analytic challenges and solutions*, IGES meeting, Toronto, ON, Canada, October 2016
- Statistical Genetics and Genomics, University of Alabama, Birmingham, AL, July 2014
- Summer Institute in Statistical Genetics, University of Washington, Seattle, WA, May 2011

TEACHING EXPERIENCE

Instructor

BIOS 894	Topics: Statistical Methods in Bioinformatics	*Spring 2021*
BIOS 805	Categorical Data Analysis	*Fall 2020*
STAT 770	Categorical Data Analysis	*Fall 2020*
BIOS 794	Topics: Biostatistical Modeling in Genetic Data Analysis	*Fall 2019*
BIOS 757	Intermediate Biostatistics	*Fall 2017, 2018, 2019*
BIOS J757	Intermediate Biostatistics (Distance)	*Spring 2018, 2019*
BIOS 890	Independent Study of Teaching Practicum	*Fall 2017, Fall 2019*
BIOS 890	Independent Study of Research Practicum	*Summer 2018*, Spring 2021
BIOS 794	Special topics in Biostatistics-Statistical Genetics	*Spring 2017*
BIOS 700	Introduction to Biostatistics	*Spring 2016, Fall 2016*

Guest Lectures

EPID 777	Fundamentals of Genetic Epidemiology	Spring 2021
EPID 800	Epidemiology Methods II	*Fall 2015, 2016, 2017, 2019*
BIOS 745	Seminar in Biostatistics	*Spring 2018*
ENHS 793	Bioinformatics and Computational Biology	*Fall 2018, Fall 2019*

MENTORING EXPERIENCE

PhD Dissertation Advisee

Completed

- Xizhi Luo, PhD in Biostatistics Defense: 07/2021
  Topic: *Accurate and integrative detection of copy number variants with high-throughput data*

Ongoing

- Xuanxuan Yu, PhD candidate in Biostatistics 08/2019 – now
- Fei Qin, PhD candidate in Biostatistics 08/2018 – now

Doctoral Dissertation Committee

Completed

- Rahimi Gelareh, PhD in Biostatistics (advisor: James Hardin) Defense: 08/2018
  Topic: *Adjusting for mis-reporting in count data*
- Xiangyang Cao, PhD in Statistics (U of SC, advisor: Dr. Karl Gregory), Defense: 08/2018
  Topic: *High-dimensional inference based on the Leave-One-Covariate-Out LASSO path*.
- Yuan Hong, PhD candidate in Biostatistics (advisor: Dr. Alexander Mclain),
  Defense: 11/2020
  Topic: *Incorporation and Measurement of Uncertainty in Longitudinal and Spatial Data*
- Zequn Sun, PhD candidate in Biostatistics (MUSC, advisor: Dr. Dongjun Chung),
  Defense: 07/2021
  Topic: *Bayesian latent factor model by integrating multiple types of genomic data*

Ongoing

- Farahnaz Islam, PhD candidate in Biostatistics (advisor: Dr. James Hardin), 08/2019 – now
- Ian Palmer, PhD candidate in Biology (advisor: Dr. Zhengqing Fu) 05/2017 – now
  Topic: *Effects of the Pseudomonas syringae effector HopAA1-2 on salicylic acid-mediated plant defense*
- Andrés Gaviria, PhD candidate in Environmental Health and Epidemiology (advisor: Drs. Jim Burch; Sean Norman) 05/2016 – now
  Topic: *Describing the Impact of Antibiotic Resistant Bacteria in the Environment and on Population Health in South Carolina*

Master's Thesis Committee

Completed

- Andrew Fogner, MPH in Epidemiology (advisor: Dr. Myriam Torres), Defense: 05/2016
  Thesis title: *Prenatal Depression in South Carolina Latinos*
- Danielle Sill, MSPH in Epidemiology (advisor: Dr. Myriam Torres), Defense: 03/2017
  Thesis title: *The association between sexual risk behaviors of Latinos and HIV Knowledge in South Carolina*
- Amanda Collins, MSPH in Epidemiology (advisor: Dr. Anwar Merchant),Defense: 07/2018
  Topic: *Effect Modification of Stroke in The Relationship Between Tooth Loss and Cognitive Functioning*
- Diana Diaz, MPH in Epidemiology (advisor: Dr. Susan Steck), Defense: 07/2019
  Topic: *Association between SNPs in the vitamin D binding protein, vitamin D status, and aggressive prostate cancer by race*
- Brittany Crawford, MSPH in Epidemiology (advisor: Dr. Susan Steck), Defense: 03/2020
  Topic: *Serum Calcium, Phosphorus, and PTH and Prostate Cancer Aggressiveness*
- Haley Davis-Martin, MSPH in Epidemiology (advisor: Dr. Matthew Lohman), Defense: 04/2020
  Topic: *The interaction between caffeine consumption, alcohol use, and amount of sleep on bone health*
- Marie Knoll, MSPH in Epidemiology (advisor: Dr. Susan Steck) Defense: 06/2020
  Topic: *Association between urinary enterolignans as a marker for gut microbiome diversity and depression in NHANES*
- Huizhong Yang, MPH in Biostatistics (advisor: Dr. Bo Cai) Defense: 06/2020
  Topic: *Bayesian Zero Inflation Model for Ordinal Data*

Ongoing

- Wanfang Zhang, MPH candidate in Biostatistics (advisor: Dr. Bo Cai) 01/2019 – now

Academic Advisor (for advice on courses and other academic activities)

- Nichlas Yell, PhD candidate in Biostatistics
- Xuanxuan Yu, PhD candidate in Biostatistics
- Fei Qin, PhD candidate in Biostatistics
- Huizhong Yang, MS in Biostatistics

Undergraduate Thesis Advisee (Visiting scholars from Nanjing Medical University, China)

- Zilong Bian, Title: *DNA methylation-based signature prediction model for cancer* 02/2020-06/2020
- Jingting Lu, Title: *CNV based signature prediction model for cancer*. 02/2020-06/2020
- Jiani Xu, Title: *Comprehensive Analysis of Somatic Copy Number Aberrations and Gene Expression in Lung Adenocarcinoma* 01/2018-06/2018

- Yaqian Liu, Title: *Integrative analysis of Copy number aberrations in Esophageal Cancer* 01/2018-06/2018
- Lijuan Wang, Title: *Differential expression of immunology pathway related genes in Lung carcinoma* 01/2017-06/2017
- Lu Xu, Title: *Implications of immunotherapy in breast cancer treatment*. 01/2017-06/2017

CONFERENCE PRESENTATIONS

1. Data-led policy design using Medicare Shared Savings Program (MSSP) health care cost trajectories. *Abstract.* Academy Health, 2021.
2. Multimodal neuroimaging prediction models carry complementary information that can be harnessed to enhance prediction of language function in aphasia. *Abstract.* Society for the Neurobiology of Language, 2020.
3. Joint modeling of eQTLs and parent-of-origin effects with RNA-seq data. *Contributed*. JSM Virtual Meeting, August 2020.
4. Adjusting for misreporting in count data. *Abstract*. ASA Women in Statistics and Data Science Conference, Bellevue, Washington, October 2019.
5. An accurate and powerful method for copy number variation detection. *Invited Poster Presentation*. Houston, TX, October 2019.
6. Assessment of Statistical Batch Effect Correction Methods for Different RNA Sequencing Data Types. *Abstract*. Houston, TX, October 2019.
7. BDNF Genotype Specific Differences in Cortical Activation in Chronic Aphasia. *Abstract*. Society for the Neurobiology of Language, Helsinki, Finland, August 2019.
8. LDSaRa: A Powerful Method for High Resolution Copy Number Variation Detection. *Invited talk*. International Chinese Statistical Association (ICSA), June 2019.
9. Common genetic variations in the calcium sensing receptor (CaSR) gene, plasma 25-hydroxyviamin D and aggressive prostate cancer in the North Carolina-Louisiana Prostate Cancer (PCaP) study. *Abstract.* Annual Meeting-American Society of Preventive Oncology, March 2019.
10. LDSaRa: a powerful tool for high resolution copy number variation detection. *Abstract*. South Carolina Chapter American Statistical Association Annual Meeting, March 2019.
11. Copy number variation detection with complex genetic data. *Invited talk*, American Statistics Association South Carolina Chapter, Clemson, SC, October 2018.
12. Improving copy number estimation by incorporating BAF using modSaRa. *Contributed talk*, Joint Statistical Meeting (JSM), Vancouver, Canada, August 2018.
13. Integrating genetic source improves power for copy number variation detection. *Invited talk*, ICSA, Qingdao, China, July 2018.
14. Integrating genetic source boosts power for copy number variation detection. *Invited talk, International Statistics Forum*, Beijing, China, July 2018.

15. A super scalable algorithm for short segment detection. *Abstract.* International Conference on Econometrics and Statistics, Hongkong, China. June 2018.
16. Analyses of germline copy number variation and gene expression in cutaneous melanoma. *Invited talk*, International Genetic and Epidemiology Society (IGES), Cambridge, UK, Sep 2017.
17. Efficient epigenetic effect identification in eQTL mapping with RNA-seq data. *Invited talk*, International Conference on Computational Methods (ICCM), Guilin, Guangxi, China, July 2017.
18. Modeling parent-of-origin effect in eQTL mapping using RNA-seq data. *Invited talk*, ICSA, Chicago, IL, June 2017.
19. Testing of parent-of-origin effect in eQTL mapping using RNA-seq data. *Invited talk*, IGES, Toronto, ON, Canada, Oct 2016.
20. A change-point based method for copy number variation detection with application to melanoma. *Invited talk*, ICSA, Atlanta, GA, June 2016.
21. 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.
22. A new change-point model based method for copy number variation detection. *Invited Poster presentation*, American Society of Human Genetics (ASHG), Baltimore, MD, USA, Oct 2015.
23. Modified screening and ranking algorithm for copy number variation detection. *Invited Poster presentation*, IGES, Baltimore, MD, USA, Oct 2015.
24. Using expression data to define patient specific predictors for survival outcomes in lung adenocarcinoma. *Abstract*, ASHG, Baltimore, MD, USA, Oct 2015.
25. MicroRNA as biomarkers of spontaneous preterm birth. *Abstract*, Society for Maternal-Fetal Medicine (SMFM). March 2015.
26. Neonatal, not Maternal, Copy Number Variants are Associated with Spontaneous Preterm Birth. *Abstract*, SMFM. March 2015.
27. Natural and orthogonal model for gene-gene interactions applied to cutaneous melanoma. *Poster presentation*, IGES, Chicago, IL, USA, Sep 2013.
28. Natural and orthogonal association framework to detect parent-of-origin effects. *Poster presentation*, IGES, Stevenson, WA, USA, Oct 2012.
29. Natural and orthogonal interaction framework for modeling GxG and GxE interactions. *Poster presentation*, IGES, Stevenson, WA, USA, Oct 2012.

INVITED TALKS AND SEMINARS

30. Identification and characterization of genomic features from high throughput data. UCLA, March 2021.

31. Copy number variation, epigenetics and cancer. School of Medicine, Wuhan University, China, July 2019.
32. Genetics and Environment Factors in Complex Diseases. School of Public Health, Guangxi Medical University, China, June 2019.
33. An accurate and powerful method for copy number variation detection. Department of Biology, Fudan University, China, June 2018.
34. Integrating genetic source boosts power for copy number variation detection. Department of Statistics, University of South Carolina, Columbia, SC, April 2018.
35. A powerful statistical framework for copy number variation detection with application to melanoma. Medical University of South Carolina, Charleston, SC, April 2018.
36. Copy number variations, parent-of-origin effects and cancer. Nanjing Medical University, Nanjing, Jiangsu, China, Jul 2017.
37. Imprinting effect detection and copy number variation in cancer. Wuhan University, Wuhan, Hubei, China, Jul 2017.
38. Copy number variations, epigenetics and cancer. Dartmouth College, Hanover, NH, USA, Feb 2017.
39. Testing of parent-of-origin effect in eQTL mapping using RNA-seq data. University of South Carolina, Columbia, SC, USA, Nov 2016.
40. A statistical framework for copy number variation detection with application to melanoma study. Wuhan University, Wuhan, China, June 2016.
41. A framework of testing interactions and parent-of-origin effect with application to cancer studies. Moffitt Cancer Center, Tampa, FL, USA, Dec 2015.
42. Testing of interactions and parent-of-origin effect using orthogonal models. University of South Carolina, Columbia, SC, USA, Nov 2015.
43. Modified Screening and Ranking Algorithm for Copy Number Variation Detection. City University of New York, New York, NY, USA, April 2015.
44. A new change-point model based method for copy number variation detection. University of Massachusetts Amherst, Amherst, MA, USA, March 2015.
45. Modified Screening and Ranking Algorithm for Copy Number Variation Detection. University of South Carolina, Colombia, SC, USA, February 2015.
46. Modified Screening and Ranking Algorithm for Copy Number Variation Detection. *Seminar*, University of Colorado Boulder, Boulder, CO, USA, January 2015.
47. Natural and Orthogonal Model for Gene-Gene interactions Applied to Cutaneous Melanoma. Geisel School of Medicine at Dartmouth College, Lebanon, NH, USA, July 2013.

INSTITUTIONAL SERVICES

- USC Office of the Vice President for Research ASPIRE II Grant Reviewer Committee (2021)

- AI Institute and Center of Excellence in Autism & Neurodevelopment Disorder joint position search committee (2020-2021)
- Department of Epidemiology and Biostatistics Students Handbook Committee (2020)
- Member of USC Faculty Senate Committee (2019 - present)
- USC Office of the Vice President for Research ASPIRE I Reviewer Committee (2019)
- Chair of the Biostatistics Forum for the Department of Epidemiology and Biostatistics (2017-2019)
- Department of Epidemiology and Biostatistics Search Committee (2017 – 2018)
- Member of the Book Store Committee for the University of South Carolina (2017 – 2020)
- Chair of the Graduate Exam Committee for the Department of Epidemiology and Biostatistics (2017 - 2018)
- Member of the Graduate Exam Committee for the Department of Epidemiology and Biostatistics (2016 - 2017)
- Division of Biostatistics Admissions Committee (2016 - present)
- Grader of the Graduate Students Qualifying and Comprehensive Exams (2016 – present)

EXTERNAL SERVICES and MEMBERSHIP

- ASPH NIH grant writing bootcamp. University of South Carolina. 2020-2021
- Early Career Reviewer Panel for NIH Cancer Genetic Study Section, June 2020
- Chair and Organizer, *Statistical learning advancement for inference with complex biomedical data*. International Chinese Statistical Association (ICSA) 2020 Applied Statistics Symposium, Houston, TX, 2020
- Chair and Organizer, *New developments in High Dimensional Data Analysis*. ICSA 2019 Applied Statistics Symposium, Raleigh, NC, 2019
- Platform session chair of International Conference on Computational Methods (ICCM), Guilin, Guangxi, China, 2017
- Platform session chair ICSA, Atlanta, GA, 2016
- Program committee: European Conference on Computational Biology (ECCB), 2016
- *Ad hoc* reviewer for *American Journal of Human Genetics, Biomedical Sciences, BioData Mining, Bioinformatics, BMC Cancer, BMC Medical Genomics, Clinical Genetics, European Conference on Computational Biology, Environmental Science and Pollution Research, Frontier in Genetics, Genetic Epidemiology, Genomics, Human Genetics, Human Heredity, IEEE Signal Processing Letters, Journal of Nervous and Mental Disease, Journal of Theoretical Biology, Molecular Genetics and Genomics, Neoplasia, Nutrition & Diabetes, Nutrition & Metabolism, PLoS ONE, PLoS Computational Biology, PLoS Genetics, Peer J, Scientific Report, Statistics & Its Interface, Environmental Science and Pollution Research.*
- 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

CORRseq and SARAseq

- R packages for copy number variation detection with whole exome sequencing data. https://github.com/FeifeiXiaoUSC/CORRseq-and-SARAseq.

LDcnv

- A R package for whole genome correlation struction integrated copy number variation detection with SNP array data. https://github.com/FeifeiXiaoUSC/LDcnv.

modSaRa2

- An R package for accurate and powerful method for copy number variation detection with SNP array data by integrating relative allele frequencies. https://github.com/FeifeiXiaoUSC/modSaR2.

modSaRa

- An R package for a change-point model based method for copy number variation detection with SNP array data. https://github.com/FeifeiXiaoUSC/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