OMB No. 0925-0001 and 0925-0002 (Rev. 10/2021 Approved Through 09/30/2024)

BIOGRAPHICAL SKETCH

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NAME: Xiao, Guanghua

eRA COMMONS USER NAME (credential, e.g., agency login): GXIAO1

POSITION TITLE: Professor, Peter J. O’Donnell School of Public Health

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE  (if applicable) | Completion Date  MM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| Tsinghua University, Beijing, China | BE | 06/1997 | Material Science & Engineering |
| Tsinghua University, Beijing, China | MS | 06/2000 | Material Science & Engineering |
| University of Minnesota; Minneapolis, MN | MS | 05/2006 | Electrical Engineering |
| University of Minnesota; Minneapolis, MN | PhD | 08/2006 | Biostatistics |
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**A. Personal Statement**I am a Professor of Data Science and the Mary Dees McDermott Hicks Chair in Medical Science at UT Southwestern Medical Center. I have joint appointment in the Peter O’Donnell Jr. School of Public Health and the Department of Bioinformatics. I am also a member of the Quantitative Biomedical Research Center and the Harold C. Simmons Cancer Center. Currently, I lead the establishment of a Health Data Sciences Ph.D. program at the UT Southwestern.

With training in engineering and statistics, I have an excellent understanding of and deep interest in developing and applying novel computational models to achieve the goal of precision medicine. I have extensive experience in imaging analysis, machine learning/deep learning, predictive modeling, data integration and spatial modeling. My current research includes AI methods for pathology imaging analysis and bioinformatics tools for spatial molecular profiling.

I am the PI or MPI on several research grants, funded by the National Cancer Institute (NCI), the National Institute of General Medical Sciences (NIGMS), the National Institute of Dental and Craniofacial Research (NIDCR), and the Cancer Prevention and Research Institute of Texas (CPRIT).

Key publications:

1. Li Q, Wang X, Liang F, **Xiao G\***, A Bayesian mark interaction model for analysis of tumor pathology images, ***The Annals of Applied Statistics***, 2019 13 (3), 1708-1732
2. Wang S, Rong R, Yang DM, Fujimoto J, Yan S, Cai L, Yang L, Luo D, Behrens C, Parra ER, Yao B, Xu L, Wang T, Wistuba, II, Minna J, Xie Y, **Xiao G**\*. Computational staining of pathology images to study the tumor microenvironment in lung cancer. ***Cancer Res*earch**. 2020. Epub 2020/01/10. PubMed PMID: 31915129.
3. Zhang M, Sheffield T, Zhan X, Li Q, Yang DM, Wang Y, Wang S, Xie Y, Wang T, **Xiao G**\*. Spatial molecular profiling: platforms, applications and analysis tools. ***Briefings in Bioinformatics***. 2020 Aug 6;bbaa145. doi: 10.1093/bib/bbaa145. Online ahead of print.
4. Wang S, Rong R, Zhou Q, Yang DM, Zhang X, Zhan X, Bishop J, Chi Z, Wilhelm CJ, Zhang S, Pickering CR, Kris MG, Minna J, Xie Y, **Xiao G\***. Deep learning of cell spatial organizations identifies clinically relevant insights in tissue images. Nat Commun. 2023 Dec 11;14(1):7872. doi: 10.1038/s41467-023-43172-8. PMID: 38081823

Ongoing projects that I would like to highlight include:

1R01GM140012-01 (Xiao) 01/01/2021-12/31/2024

NIH/NGIMS

Developing computational algorithms for histopathological image analysis

Role: PI

1R01GM141519-01 (Xiao) 08/01/2021-07/31/2025

NIH/NIGMS

Developing novel algorithms for spatial molecular profiling technologies

Role: PI

1R01DE030656-01 (Pickering/Xiao) 06/17/2021-06/16/2026

NIH/NIDCR

Imaging and genomic analysis to improve risk assessment for oral potentially malignant disorders

Role: MPI

1U01CA249245-01A1 (Xiao) 09/01/2021-08/31/2024

NIH/NCI

Informatics tools to analyze and model whole slide image data at the single cell level

Role: PI

RP230330 (Xiao) 03/01/2023-02/28/2027

CPRIT

Integrate whole slide imaging and genomic data to study pediatric rhabdomyosarcoma

Role: PI

**B. Positions, Scientific Appointments, and Honors**

**Positions and Employment**

2022 - Present Co-Lead, Data Science for Precision Health Initiative, UT Southwestern Medical Center, Dallas, TX

2022 - Present Program Director, Ph.D Program in Health Data Science, Peter O’Donnell Jr. School of Public Health, UT Southwestern Medical Center, Dallas, TX

2020 - Present Mary Dees McDermott Hicks Chair in Medical Science, UT Southwestern Medical Center, Dallas, TX

2019 - Present Professor (with tenure), Peter O’Donnell Jr. School of Public Health, UT Southwestern Medical Center, Dallas, TX

2019 - Present Professor, Department of Bioinformatics, UT Southwestern Medical Center, Dallas, TX

2015-2019 Associate Professor (with tenure), Department of Bioinformatics, UT Southwestern Medical Center, Dallas, TX

2013-2019 Associate Professor (with tenure), Department of Population & Data Sciences, UT Southwestern Medical Center, Dallas, TX

2006-2013 Assistant Professor, Department of Population & Data Sciences, UT Southwestern Medical Center, Dallas, TX

**Honors**

2006 Delta Omega National Society, Pi Chapter

2004-2006 Merck Doctoral Fellowship

2004 New Student Scholarship, Division of Biostatistics, University of Minnesota

1997 Graduate with Honors, Tsinghua University

1997 Outstanding Undergraduate Thesis Award, Tsinghua University

1993-1997 Honor Student, Tsinghua University

1993-1997 Outstanding Student Scholarship, Tsinghua University

**Grant Review:**

2023 NIH CDMA (Clinical Data Management and Analysis) study section

2023 NIH special emphasis panel: Topics in Clinical Informatics and Data Analytics

2023 NIH/NCI NCI Program Project (P01) Review Panel

2022 NIH/NCI ITCR (Informatics Tools for Cancer Research) R21/U01/U24

2022 NIH CDMA (Clinical Data Management and Analysis) study section

2022 NIH/NIAID Data Science Tools for Infectious and Immune-Mediated Diseases R21/U01/U24

2021 NIH/NCI ITCR (Informatics Tools for Cancer Research) U01/U24

2021 NIH/NIAID Data Science Tools for Infectious and Immune-Mediated Diseases R21/U01/U24

2021 NIH/NCI SBIR Phase IIB Bridge Award

2020 NIH/NIAID COVID-19 Emergency FOAs

2020 NIH/NCI ITCR (Informatics Tools for Cancer Research) U01/U24

2020 NIH/NCI NCI SPORE (Specialized Programs of Research Excellence) P50

2020 NIH CDMA (Clinical Data Management and Analysis) study section

2019 NIH/NCI ITCR (Informatics Tools for Cancer Research) U01/U24

2016 NIH/NCI, ZCA1 SRB-5 (J1)

2019 NIH/NCI, ZCA1 SRB-P (M2)

**C. Contributions to Science**

**1.** **Tissue imaging data analysis**. My lab has developed novel algorithms for cell segmentation, cell type classification, micro-blood-vessel prediction and tumor region detection. Our study was highlighted on the cover page of the May 2020 issue of *Cancer Research*.

1. Yi F, Huang J, Yang L, Xie Y, Xiao G. Automatic extraction of cell nuclei from H&E-stained histopathological images. ***Journal of Medical Imaging.*** 2017 Apr;4(2):027502. PMID: 28653017
2. Yi F, Yang L, Wang S, Lei G, Huang C; Xie Y, **Xiao G\*.** Micro-vessel Prediction in H&E Stained Pathology Images using Fully Convolutional Neural Networks. ***BMC Bioinformatics***2018, 19:64. PMC5828328.
3. Wang S, Wang T, Yang L, Yang DM, Fujimoto J, Yi F, Luo X, Yang Y, Yao B, Lin S, Moran C, Kalhor N, Weissferdt A, Minna J, Xie Y, Wistuba II, Mao Y, Xiao G. ConvPath: A Software Tool for Lung Adenocarcinoma Digital Pathological Image Analysis Aided by Convolutional Neural Network. ***EBioMedicine.*** 2019, 50:103-110. PMID: 31767541.
4. Wang S, Rong R, Yang DM, Fujimoto J, Yan S, Cai L, Yang L, Luo D, Behrens C, Parra ER, Yao B, Xu L, Wang T, Wistuba, II, Minna J, Xie Y, **Xiao G**\*. Computational staining of pathology images to study the tumor microenvironment in lung cancer. ***Cancer Research***. 2020. PubMed PMID: 31915129.

**2. Machine learning and deep learning.** My lab has developed machine learning algorithms and deep learning models to predict clinical outcomes.

1. **Xiao G,** Ma S, Minna J, Xie Y. Adaptive prediction model in prospective molecular-signature-based clinical studies, ***Clin. Cancer Res.*** 2014, Feb 1;20(3):531-9. PMC3946561.
2. Luo X, Zang X, Yang L, Huang J, Liang F, Rodriguez Canales J, Wistuba, II, Gazdar A, Xie Y, **Xiao G\***. Comprehensive Computational Pathological Image Analysis Predicts Lung Cancer Prognosis. ***J. Thoracic Oncol.*** 2017, 12:3, 501–509. PMC5462113.
3. Huang C, Zhang A, **Xiao G\*.** Deep Integrative Analysis for Survival Prediction. ***Pac Symp Biocomput***. 2018; 23:343-352. PMID: 29218895.
4. Wang S, Yang DM, Rong R, Zhan X, **Xiao G\*.** Pathology image analysis using segmentation deep learning algorithms. ***American Journal of Pathology****.* 2019, Jun 11. PMC6723214.

**3. Developing computational algorithms, and bioinformatics tools for complex biomedical data.** We are actively developing new bioinformatics tools and computational algorithms for big data, such as genome-wide RNAi screening data and next-generation sequencing data.

1. Wang T, Xie Y, **Xiao G\***. dCLIP: a computational approach for comparative CLIP-seq analyses. ***Genome Biology.*** 2014, Jan 7;15(1):R11.7. PMC4054096.
2. Cai L, Li Q, Du Y, Yun J, Xie Y, DeBerardinis R, **Xiao G\***. Genomic Regression Analysis of Coordinated Expression, ***Nature Communications****.* 2017, Dec 19;8(1):2187. PMC5736603.
3. Zhang M, Li Q, Yu D, Yao B, Guo W, Xie Y, **Xiao G\***. GeNeCK: a web server for gene network construction and visualization. ***BMC Bioinformatics.*** 2019 Jan 7;20(1):12. PMID: 30616521.
4. Zhang M, Sheffield T, Zhan X, Li Q, Yang DM, Wang Y, Wang S, Xie Y, Wang T, **Xiao G**\*. Spatial molecular profiling: platforms, applications and analysis tools. ***Briefings in Bioinformatics.*** 2020; In Press.

**4. Developing spatial models for biological data.** We have developed computational methodologies for Bayesian analysis, spatial modeling, and integrative analysis of different biological datasets, especially pathological imaging data**.**

1. Zhong R, Kim M, White M, Yang X, **Xiao G\***. Spatial background noise correction for high-throughput RNAi screening. ***Bioinformatics***2013, 29(17):2218-20. PMC3740628.
2. Yu D, Won S, Lim J, **Xiao G\***. Statistical completion of a partially identified graph with applications for the estimation of gene regulatory networks. ***Biostatistics,*** 2015, doi:10.1093/biostatistics/kxv013. PMC4570579.
3. Li Q, Wang X, Liang F, Yi F, Xie Y, Gazdar A, **Xiao G\***. A Bayesian hidden Potts mixture model for analyzing lung cancer pathology images. ***Biostatistics*** 2018, May 18. doi: 10.1093/biostatistics/kxy019. PMC6797059.
4. Li Q, Wang X, Liang F, **Xiao G\***, A Bayesian mark interaction model for analysis of tumor pathology images, ***The Annals of Applied Statistics****,* 2019 13 (3), 1708-1732.

**5. Computational applications in biomedical research.** Besides my research in developing computational methodology, I am also devoted to applying state-of-art computational methods in biomedical research. Collaborating with scientists at UT Southwestern Medical Center, I have co-authored more than 120 biomedical research publications, including eight publications in *Nature, Science,* and *Cell*.

* 1. Wang R, Wei Y, An Z, Zou Z, **Xiao G**, Bhagat G, White M, Reichelt J, Levine B. Akt-Mediated regulation of autophagy and tumorigenesis through beclin 1 phosphorylation. ***Science*** 2012, 338(6109):956-959. PMC3507442.

1. Han T, Kato M, Xie S, Wu L, Mirzaei H, Pei J, Chen M; Xie Y, Allen J; **Xiao G**, McKnight SL. Cell-free formation of RNA granules: bound RNAs identify features and components of cellular assemblies. ***Cell***(2013) [149(4](http://www.cell.com/issue?pii=S0092-8674(12)X0010-2)): 768-779. PMID: 22579282.
2. Xue Z, Ye Q, Anson SR, Yang J, **Xiao G**, Kowbel D, Glass NL, Crosthwaite SK, Liu Y. Transcriptional interference by antisense RNA is required for circadian clock function. ***Nature*** 2014, 514(7524):650-3. PMC4214883.
3. Liu Y, Nguyen PT, Wang X, Zhao Y, Meacham CE, Zou Z, Bordieanu B, Johanns M, Vertommen D, Wijshake T, May H, Xiao G, Shoji-Kawata S, Rider MH, Morrison SJ, Mishra P, Levine B. TLR9 and Beclin 1 Crosstalk Regulates Muscle AMPK Activation in Exercise, ***Nature****.* 2020, 578(7796):605-609. PMID: 32051584PMID: 31821614

**Complete List of Published Work in PubMed:**

[**https://www.ncbi.nlm.nih.gov/myncbi/guanghua.xiao.1/bibliography/public/**](https://www.ncbi.nlm.nih.gov/myncbi/guanghua.xiao.1/bibliography/public/)

**https://scholar.google.com/citations?user=2Lm2u\_oAAAAJ&hl=en**