

# Qiao Liu – Curriculum Vitae

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## Research Statement

I'm an incoming Assistant Professor at the Department of Biostatistics, Yale University. My primary research interest lies in this multi-disciplinary area where I have been devoting to developing AI-powered computational frameworks with significance in both statistical theory and applications. In particular, I have been exploiting the advances in *generative AI* to tackle important high-dimensional statistical problems, such as *density estimation*, *causal inference*, with wide applications in computational biology, such as *single cell genomics*, *multiomics data integration*, and *genomic large language models*.

## Academic Appointment

<b>2025.08-</b>	Assistant Professor - Yale University, New Haven, CT, USA Department of Biostatistics
<b>2021.06- 2025.07</b>	Postdoctoral Scholar - Stanford University, Stanford, CA, USA Department of Statistics, advised by Prof. <b>Wing Hung Wong</b>

## Education

<b>2019.09- 2021.06</b>	Visiting Ph.D. student - Stanford University, Stanford, CA, USA Department of Statistics, advised by Prof. Wing Hung Wong
<b>2016.09- 2019.09</b>	Ph.D. student - Tsinghua University, Beijing, China Department of Automation, advised by Prof. Rui Jiang
<b>2015.08- 2016.01</b>	Exchange Student - Lund University, Lund, Sweden Department of Computer Science, GPA: <b>5.0</b> /5.0
<b>2012.09- 2016.06</b>	Bachelor in Engineering - Beihang University, Beijing, China ShenYuan Honors College (Special Pilot Class), GPA: <b>91.5</b> /100

## Publications

(†=co-first author; \*=corresponding author)

## Preprints

1. **Qiao Liu**† and Wing Hung Wong. An AI-powered Bayesian generative modeling approach for causal inference in observational studies[J]. arXiv preprint arXiv:2501.00755, 2025.
2. **Qiao Liu**†, Wanwen Zeng†, Hongtu Zhu, Lexin Li\*, Wing Hung Wong\*. Leveraging genomic large language models to enhance causal genotype-brain-clinical pathways in Alzheimer's disease[J]. medRxiv, 2024.
3. Wanwen Zeng, Hanmin Guo, **Qiao Liu**, Wing Hung Wong. How to improve polygenic prediction from whole-genome sequencing data by leveraging predicted epigenomic features?[J]. medRxiv, 2024.
4. Xuejian Cui, Qijin Yin, Zijiang Gao, Zhen Li, Xiaoyang Chen, Shengquan Chen, **Qiao Liu**, Wanwen Zeng\*, Rui Jiang\*. CREATE: cell-type-specific cis-regulatory elements identification via discrete embedding[J]. bioRxiv, 2024.

## Peer-reviewed papers (as lead author)

5. Zijing Gao<sup>†</sup>, **Qiao Liu**<sup>†\*</sup>, Wanwen Zeng, Wing Hung Wong\*, Rui Jiang\*. EpiGePT: a Pretrained Transformer model for human epigenomics[J]. **Genome Biology**, 2024.
6. **Qiao Liu**, Zhongren Chen, Wing Hung Wong\*. An encoding generative modeling approach to dimension reduction and covariate adjustment in causal inference with observational studies [J]. Proceedings of the National Academy of Sciences of the United States of America(**PNAS**), 2024, 121(23), e2322376121.
7. Qijin Yin, Xusheng Cao, Rui Fan, **Qiao Liu**\*, Rui Jiang\* and Wanwen Zeng\*. DeepDrug: A general graph-based deep learning framework for drug-drug interactions and drug-target interactions prediction[J]. **Quantitative Biology**, 2023, 11(3), 260-274.
8. **Qiao Liu**<sup>†</sup>, Wanwen Zeng<sup>†</sup>, Wei Zhang, Sicheng Wang, Hongyang Chen, Rui Jiang\*, Mu Zhou\*, Shaoting Zhang\*. Deep generative modeling and clustering of single cell Hi-C data[J]. **Briefings in Bioinformatics**, 2023, 24(1): bbac494.
9. Wanwen Zeng<sup>†</sup>, **Qiao Liu**<sup>†</sup>, Qijin Yin<sup>†</sup>, Rui Jiang\*, Wing Hung Wong\*. HiChIPdb: a comprehensive database of HiChIP regulatory interactions[J]. **Nucleic Acids Research**. 2022.
10. **Qiao Liu**, Kui Hua, Xuegong Zhang, Wing Hung Wong\*, Rui Jiang\*. DeepCAGE: incorporating transcription factors in genome-wide prediction of chromatin accessibility[J]. **Genomics, Proteomics & Bioinformatics**, 2022.
11. **Qiao Liu**, Shengquan Chen, Rui Jiang\*, Wing Hung Wong\*. Simultaneous deep generative modeling and clustering of single cell genomic data[J]. **Nature Machine Intelligence**, 2021, 3(6): 536-544.
12. **Qiao Liu**, Jiaze Xu, Rui Jiang\*, Wing Hung Wong\*. Density estimation with deep generative neural networks [J]. Proceedings of the National Academy of Sciences of the United States of America(**PNAS**), 2021, 118(15), e2101344118.
13. **Qiao Liu**, Zhiqiang Hu, Rui Jiang\*, Mu Zhou\*. Cancer drug response prediction via a hybrid graph convolutional network[J]. **Bioinformatics**, 2020. 36(Supplement\_2): i911-i918. Also in *Proceedings of the 19th European Conference on Computational Biology (ECCB)*, 2020.(conference acceptance rate:20.2%)
14. **Qiao Liu**, Hairong Lv, Rui Jiang\*. hicGAN infers super resolution Hi-C data with generative adversarial networks. **Bioinformatics**, 2019, 35(14): i99-i107. Also in *Proceedings of the 27th Intelligent Systems for Molecular Biology the 18th European Conference on Computational Biology (ISMB/ECCB)*, 2019. (conference acceptance rate:18.9%)
15. Pengyu Chen<sup>†</sup>, **Qiao Liu**<sup>†</sup>, Lan Wei, Beier Zhao, Yin Jia, Hairong Lv\*, Xiaolu Fei\*. Automatically structuring on Chinese ultrasound report of cerebrovascular diseases via natural language processing[J]. **IEEE Access**, 2019, 7: 89043-89050.
16. **Qiao Liu**, Fei Xia, Qijin Yin, Rui Jiang\*. Chromatin accessibility prediction via a hybrid deep convolutional neural network[J]. **Bioinformatics**, 2017, 34(5): 732-738.
17. **Qiao Liu**, Mingxin Gan, Rui Jiang\*. A sequence-based method to predict the impact of regulatory variants using random forest[J]. **BMC Systems Biology**, 2017, 11(2): 7. Also in *Proceedings of the 15th Asia Pacific Bioinformatics Conference (APBC)*, 2017.

## Peer-reviewed papers (as co-author)

18. Wei Shao, Yuti Liu, Shuang Zhang, Shuang Chen, **Qiao Liu**, Jianyu Zhou, Wanwen Zeng. Inferring gene regulatory network based on scATAC-seq data with gene perturbation[C]. IEEE International Conference on Bioinformatics and Biomedicine (BIBM). 2024.
19. Chuanqi Lao, Pengfei Zheng, Hongyang Chen, **Qiao Liu**, Feng An, Zhao Li. Comprehensive tissue deconvolution of cell-free DNA by deep learning for disease diagnosis and monitoring[J]. **BMC bioinformatics**, 25 (1), 105, 2024.
20. Shuo Li, Weihua Zeng, Xiaohui Ni, **Qiao Liu**,...,Wing Hung Wong\*, Steven M. Dubinett\* and Jasmine Zhou\*. Comprehensive tissue deconvolution of cell-free DNA by deep learning for disease diagnosis and monitoring[J]. Proceedings of the National Academy of Sciences of the United States of America(**PNAS**), 120 (28) e2305236120, 2023.
21. Shuang Zhang, Yuti Liu, Shuang Chen, **Qiao Liu**, Wanwen Zeng. Applications of Transformer-based language models in bioinformatics: A survey[J]. **Bioinformatics Advances**, 2023.
22. Christopher Lance, Malte D Luecken, Daniel B Burkhardt,...,**Qiao Liu**,...,Fabian J Theis\*. Multimodal single cell data integration challenge: results and lessons learned[J]. Proceedings of Machine Learning Research(**PMLR**), 2022.

23. Zhana Duren, Fengge Chang, Fnu Naqing, Jingxue Xin, **Qiao Liu**, Wing Hung Wong\*. Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG[J]. **Genome Biology**, 2022, 23(1): 1-19.
24. Jinxiang Ou, Yunheng Shen, Feng Wang, **Qiao Liu**, Xuegong Zhang, Hairong Lv\*. AggEnhance: Aggregation enhancement by class interior points in federated learning with non-IID data[J]. ACM Transactions on Intelligent Systems and Technology (**TIST**), 2022.
25. Qijin Yin, **Qiao Liu**, Zhuoran Fu, Rui Jiang\*. scGraph: a graph neural network-based approach to automatically identify cell types[J]. **Bioinformatics**, 2022.
26. Tianxing Ma, **Qiao Liu**, Haochen Li, Mu Zhou, Rui Jiang, Xuegong Zhang\*. DualGCN: a dual graph convolutional network model to predict cancer drug response[J]. **BMC bioinformatics**, 2022, 23(4): 1-13.
27. Feng Wang, Guoyizhe Wei, **Qiao Liu**, Jinxiang Ou, Xian Wei, Hairong Lv\*. Boost neural networks by checkpoints [C]. Conference on Neural Information Processing Systems (**NeurIPS**), 2021, 33. (acceptance rate:26%)
28. Shengquan Chen, **Qiao Liu**, Xuejian Cui, Rui Jiang\*. OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions[J]. **Nucleic Acids Research**, 2021, 49(W1): W483-W490.
29. Kexin Ding, **Qiao Liu**, Edward Lee, Mu Zhou, Aidong Lu, Shaoting Zhang\*. Feature-enhanced graph networks for genetic mutational prediction using histopathological images in colon cancer[C]. International Conference on Medical Image Computing and Computer Assisted Intervention (**MICCAI**), 2020, (pp. 294-304).
30. Qingzhu Yang, **Qiao Liu**, Hairong Lv\*. A decentralized system for medical data management via blockchain [J]. **Journal of Internet Technology**, 2020, 21(5): 1335-1345.
31. Junfeng Liu, **Qiao Liu**, Qingzhu Yang\*. Mstree: a multispecies coalescent approach for estimating ancestral population size and divergence time during speciation with gene flow [J]. **Genome Biology and Evolution**, 2020, 12(5): 715-719.
32. Chencheng Xu, **Qiao Liu**, Jianyu Zhou, Minzhu Xie, Jianxing Feng, Tao Jiang\*. Quantifying functional impacts of regulatory variants with multi-task Bayesian neural network[J]. **Bioinformatics**, 2020, 36(5): 1397-1404.
33. Chencheng Xu, **Qiao Liu**, Minlie Huang, Tao Jiang\*. Reinforced molecular optimization with neighborhood-controlled grammars[C]. Conference on Neural Information Processing Systems (**NeurIPS**), 2020, 33. (acceptance rate:20.1%)
34. Qijin Yin, Mengmeng Wu, **Qiao Liu**, Rui Jiang\*. DeepHistone: a deep learning approach to predicting histone modifications[J]. **BMC Genomics**, 2019,20(2):193.
35. Shaoming Song, Hongfei Cui, Shengquan Chen, **Qiao Liu**, Rui Jiang\*. EpiFIT: Functional interpretation of transcription factors based on combination of sequence and epigenetic information[J]. **Quantitative Biology**, 2019, 1-11.
36. Bai Li, Mu Lin, **Qiao Liu**, Ya Li\*, Changjun Zhou\*. Protein folding optimization based on 3D off-lattice model via an improved artificial bee colony algorithm[J]. **Journal of Molecular Modeling**, 2015, 21(10): 261.

## Funding

NIH 1K99HG013661 (Pathway to Independence Award). Role: PI(sole)

Start/End: Sep 2024 - Sep 2029. Total cost: \$1,068,930

Title: Bridging the gap between genetic variants and radiomic phenotypes via genomic large language models

## Invited Talks

2024.11	USC Quantitative and Computational Biology, Los Angeles, USA
2024.10	ICIBM 2024(International Conference on Intelligent Biology and Medicine), Houston, TX, USA
2023.10	UNC Biostats Seminar, remote talk
2023.04	UC Berkeley Biostats Seminar, UC Berkeley, USA
2023.04	Tsinghua Statistical Seminar, Tsinghua University, China (remote)
2022.08	NIH CEGS Annual Meeting, Duke University, USA
2022.08	JSM 2022(Joint Statistical Meetings), Washington DC, USA
2022.06	CVI Early Career Research Roundtable, Stanford University, USA
2021.12	NeurIPS 2021(The 35th Conference on Neural Information Processing Systems), remote talk
2020.09	ECCB 2020(The 19th European Conference on Computational Biology), remote talk

2020.03	<b>Center for Personal Dynamic Regulomes Seminar</b> , Stanford University, USA
2019.11	<b>BIBM 2019</b> (IEEE International Conference on Bioinformatics & Biomedicine), San Diego, USA
2019.07	<b>ISMB 2019</b> (The 27th Conference on Intelligent Systems for Molecular Biology), Basel, Switzerland
2019.03	<b>BUAFAI 2019</b> (The First Beijing Universities Academic Forum of Artificial Intelligence), Beijing, China
2017.01	<b>APBC 2017</b> (The 15th Asia Pacific Bioinformatics Conference), Shenzhen, China

## Selected Honers and Awards

2024.08	<b>Pathway to Independence Award K99/R00</b> , NIH NHGRI
2022.12	<b>Outstanding Ph.D. Thesis Award</b> , Beijing Municipal Commission of Education
2021.06	<b>Outstanding Graduates Award</b> , Beijing Municipal Commission of Education
2021.06	<b>Tsinghua Outstanding Ph.D. Thesis Award</b> , Tsinghua University
2021.06	<b>Tsinghua University Outstanding Graduates Award</b> , Tsinghua University
2020.08	<b>ECCB Fellowship</b> , International Society for Computational Biology (ISCB)
2019.04	<b>ISMB Travel Fellowship</b> , International Society for Computational Biology (ISCB)
2018.10	<b>National Scholarship</b> , Ministry of Education of China ( <b>0.2%</b> domestically)
2016.06	<b>Outstanding Graduates Award</b> , Beijing Municipal Commission of Education
2015.06	<b>Microsoft Young Fellowship</b> , Microsoft Research Asia ( <b>40</b> winners nationwide)

## Selected Competitions

2021.12	<b>NeurIPS 2021 Competition, Multimodal Data Integration</b> , rank <b>1<sup>st</sup></b> /2611 in two Joint Embedding Tasks, NeurIPS conference
2021.05	<b>RNA Unpaired Probability Prediction Competition</b> , rank <b>3<sup>rd</sup></b> /1012, Baidu AI Studio, Baidu Inc
2019.03	<b>Liver Cancer Image Diagnose Competition</b> , rank <b>2<sup>nd</sup></b> /1397, Digital China Innovation Contest
2014.10	<b>1<sup>st</sup> Prize in NCSMC</b> (The <b>6<sup>th</sup></b> National College Students Mathematical Competition), Chinese Mathematical Society
2014.09	<b>National 1<sup>st</sup> Prize in CUMCM</b> (Contemporary Undergraduate Mathematical Contest in Modeling), China Society for Industrial and Applied Mathematics
2013.10	<b>1<sup>st</sup> Prize in NCSMC</b> (The <b>5<sup>th</sup></b> National College Students Mathematical Competition), Chinese Mathematical Society

## Teaching Experiences

2024 Spring	Teaching Assistant, <i>Literature of Statistics</i> Department of Statistics, Stanford University
2023 Summer	Teaching Assistant, <i>Introduction to Generative Models</i> Institute for Computational& Mathematical Engineering (ICME), Stanford University
2019 Fall	Teaching Assistant, <i>Intelligent Algorithms and Systems</i> Fundamental Industry Training Center, Tsinghua University
2018 Fall	Teaching Assistant, <i>Statistical Methods with Applications</i> Department of Automation, Tsinghua University
2017 Fall	Teaching Assistant, <i>Introduction to Artificial Intelligence</i> Department of Automation, Tsinghua University

## Professional Activities

Member	<i>American Statistical Association (ASA), International Society of Computational Biology (ISCB)</i>
Reviewer	Stats Journals: <i>Journal of the American Statistical Association (JASA), Journal of Causal Inference</i> <i>Journal of Computational and Graphical Statistics, Computational Statistics</i> Comput. Biol. Journals: <i>Nature Methods, Nature Machine Intelligence, Nature Communications, Genome Biology, Bioinformatics, Briefings in Bioinformatics, iScience, Bioinformatics Advances, Genomics, Proteomics &amp; Bioinformatic, BMC Genomics, BMC Bioinformatics, Patterns, Computational Biology, Drug Discovery Today, NAR Genomics and Bioinformatics, Engineering Applications of Artificial Intelligence, Complex &amp; Intelligent Systems,</i>

