Qiao Liu – Curriculum Vitae

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Research Statement

I'm a Postdoctoral Scholar at Department of Statistics, Stanford University working with Prof. Wing Hung Wong. My primary research interest lies in this multi-disciplinary area where I have been devoting to developing practical statistical and machine learning tools with significance in both statistical theory and applications. In particular, I have been exploiting the advances in *generative artificial intelligence (AI)* to tackle several fundamental statistical problems, such as *density estimation*, *causal inference*, with wide applications in computational biology.

Academic Appointment

2021.06-
Present
Postdoctoral Scholar - Stanford University, Stanford, CA, USA
Department of Statistics, advised by Prof. **Wing Hung Wong**

Education

2019.09-
2021.06
Joint Ph.D. student - Stanford University, Stanford, CA, USA
Department of Statistics, advised by Prof. Wing Hung Wong

2016.09-
2019.09
Ph.D. student - Tsinghua University, Beijing, China
Department of Automation, advised by Prof. Rui Jiang

2015.08-
2016.01
Exchange Student - Lund University, Lund, Sweden
Department of Computer Science, GPA:**5.0**/5.0

2012.09-
2016.06
Bachelor in Engineering - Beihang University, Beijing, China
ShenYuan Honors College (Special Pilot Class)
GPA:**91.5**/100

Publications

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

Preprints

1. **Qiao Liu**, Zhongren Chen, Wing Hung Wong*. CausalEGM: a general causal inference framework by encoding generative modeling [J]. arXiv, 2023 (under review at *Journal of the American Statistical Association*).

2. Zijing Gao†, **Qiao Liu**†*, Wanwen Zeng, Wing Hung Wong*, Rui Jiang*. EpiGePT: a Pretrained Transformer model for epigenomics[J]. bioRxiv, 2023 (under review at *Nature Methods*).

Peer-reviewed papers (as lead author)

3. 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.

4. **Qiao Liu**†, Wanwen Zeng†, 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.

5. Wanwen Zeng†, **Qiao Liu**†, Qijin Yin†, Rui Jiang*, Wing Hung Wong*. HiChIPdb: a comprehensive database of HiChIP regulatory interactions[J]. ***Nucleic Acids Research***. 2022.

6. **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.

7. **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.

8. **Qiao Liu**, Jiaze Xu, Rui Jiang*, Wing Hung Wong*. Density estimation with deep generatative neural networks [J]. Proceedings of the National Academy of Sciences of the United States of America(***PNAS***), 2021, 118(15), e2101344118.

9. **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%)

10. **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%)

11. Pengyu Chen†, **Qiao Liu**†, 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.

12. **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.

13. **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)

14. 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.

15. Shuang Zhang, Yuti Liu, Shuang Chen, **Qiao Liu**, Wanwen Zeng. Applications of Transformer-based language models in bioinformatics: A survey[J]. ***Bioinformatics Advances***, 2023.

16. 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.

17. 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.

18. 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.

19. Qijin Yin, **Qiao Liu**, Zhuoran Fu, Rui Jiang*. scGraph: a graph neural network-based approach to automatically identify cell types[J]. ***Bioinformatics***, 2022.

20. 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.

21. 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%)

22. 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.

23. 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).

24. 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.

25. 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.

26. 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.

27. 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%)

28. Qijin Yin, Mengmeng Wu, **Qiao Liu**, Rui Jiang*. DeepHistone: a deep learning approach to predicting histone modifications[J]. *BMC Genomics*, 2019,20(2):193.

29. 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.

30. 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

Invited Talks

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

Selected Honers and Awards

2022.12	**Outstanding Ph.D. Thesis Award**, Beijing Municipal Commission of Education
2021.06	**Outstanding Graduates Award**, Beijing Municipal Commission of Education
2021.06	**Tsinghua Outstanding Ph.D. Thesis Award**, Tsinghua University
2021.06	**Tsinghua University Outstanding Graduates Award**, Tsinghua University
2020.08	**ECCB Fellowship**, International Society for Computational Biology (ISCB)
2019.04	**ISMB Travel Fellowship**, International Society for Computational Biology (ISCB)
2018.10	**National Scholarship**, Ministry of Education of China (**0.2**% domestically)
2016.06	**Outstanding Graduates Award**, Beijing Municipal Commission of Education
2015.06	**Microsoft Young Fellowship**, Microsoft Research Asia (**40** winners nationwide)

Selected Competitions

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

Teaching Experiences

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

Mentoring Experiences

2023.08-Present   Justin He, undergrad student at UCSD (ongoing)
2023.07-Present   Yuyan Liu, undergrad student at Peking University (ongoing)
2022.03-Present   Zijin Gao, Ph.D. student at Tsinghua w/ Prof. Rui Jiang (ongoing)
2021.08-2022.12   Zhongren Chen, master student at Stanford w/ Prof. Wing Wong (now Ph.D. student at Yale)
2021.06-2021.08   Silu Li, undergrad at Tsinghua w/ Prof. Wing Wong (now Ph.D. student at Harvard)
2019.02-2019.07   Chenghao Wang, undergrad student at Tsinghua (now Master student at UCLA)
2018.02-2018.07   Jiawei Huang, undergrad student at Tsinghua (now Ph.D. student at USC)

Professional Activities

Member   *American Statistical Association (ASA),International Society of Computational Biology (ISCB)*
Reviewer   Stats Journals: *Journal of the American Statistical Association (JASA), Journal of Causal Inference*
ML Journals: *Nature Methods, Nature Machine Intelligence*
Engineering Applications of Artificial Intelligence, Complex & Intelligent Systems
Bioinformatics Journals: *Bioinformatics, Briefings in Bioinformatics, Bioinformatics Advances*
Genomics, Proteomics & Bioinformatic, BMC Genomics, BMC Bioinformatics,
Computational Biology, Drug Discovery Today, NAR Genomics and Bioinformatics
Biomedical Journals: *IEEE Transactions on Medical Imaging*
PC member   ML conferences *AAAI 2023, 2024*