

# Qiao Liu – Curriculum Vitae

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## Research Statement

I'm a Postdoctoral Scholar at Department of Statistics, Stanford University. My research interests lie on the intersection of machine learning, statistics, and computational biology. I'm especially fascinated in solving several problems in statistics, such as density estimation, causal inference, likelihood-free Bayesian inference, with *deep generative models*. Besides, I'm also interested in various problems in computational biology and biomedical informatics, which involves genomic data, pharmacology data, biomedical data analysis. Related works have been published in top journals (**Nature Machine Intelligence**, **PNAS**, **Genome Biology**, **Nucleic Acids Research**, **Bioinformatics**) and conferences (**ISMB**, **ECCB**, **NeurIPS**, **MICCAI**).

## Academic appointment

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

## Education

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

**2016.09-** Ph.D. student in Control Science and Engineering - Tsinghua University, Beijing, China  
**2019.09** Department of Automation, advised by Prof. **Rui Jiang**

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

**2012.09-** Bachelor in Engineering - Beihang University, Beijing, China  
**2016.06** ShenYuan Honors College (A special Elite Class, formerly a.k.a. School of Advanced Engineering)  
GPA:**91.5**/100, Rank:**2**/50

## 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, 2022.
2. Zijng Gao<sup>†</sup>, **Qiao Liu**<sup>†,\*</sup>, Wanwen Zeng, Wing Hung Wong<sup>\*</sup>, Rui Jiang<sup>\*</sup>. EpiGePT: a Pretrained Transformer model for epigenomics[J]. bioRxiv, 2023.
3. Kexin Ding, Mu Zhou, Zichen Wang, **Qiao Liu**, Corey W. Arnold, Shaoting Zhang<sup>\*</sup>, Dimitri N. Metaxas<sup>\*</sup>. Graph Convolutional Networks for Multi-modality Medical Imaging: Methods, Architectures, and Clinical Applications[J]. arXiv preprint arXiv:2202.08916, 2022.

## Peer-reviewed papers (as lead author)

4. Qijin Yin, Xusheng Cao, Rui Fan, **Qiao Liu**<sup>\*</sup>, Rui Jiang<sup>\*</sup> and Wanwen Zeng<sup>\*</sup>. DeepDrug: A general graph-based deep learning framework for drug-drug interactions and drug-target interactions prediction[J]. *Quantitative biology*, 2023 (in press).
5. **Qiao Liu**<sup>†</sup>, Wanwen Zeng<sup>†</sup>, Wei Zhang, Sicheng Wang, Hongyang Chen, Rui Jiang<sup>\*</sup>, Mu Zhou<sup>\*</sup>, Shaoting Zhang<sup>\*</sup>. Deep generative modeling and clustering of single cell Hi-C data[J]. *Briefings in Bioinformatics*, 2023, 24(1): bbac494.
6. Wanwen Zeng<sup>†</sup>, **Qiao Liu**<sup>†</sup>, Qijin Yin<sup>†</sup>, Rui Jiang<sup>\*</sup>, Wing Hung Wong<sup>\*</sup>. HiChIPdb: a comprehensive database of HiChIP regulatory interactions[J]. *Nucleic Acids Research*. 2022.
7. **Qiao Liu**, Kui Hua, Xuegong Zhang, Wing Hung Wong<sup>\*</sup>, Rui Jiang<sup>\*</sup>. DeepCAGE: incorporating transcription factors in genome-wide prediction of chromatin accessibility[J]. *Genomics, Proteomics & Bioinformatics*, 2022.
8. **Qiao Liu**, Shengquan Chen, Rui Jiang<sup>\*</sup>, Wing Hung Wong<sup>\*</sup>. Simultaneous deep generative modeling and clustering of single cell genomic data[J]. *Nature Machine Intelligence*, 2021, 3(6): 536-544.
9. **Qiao Liu**, Jiaze Xu, Rui Jiang<sup>\*</sup>, Wing Hung Wong<sup>\*</sup>. 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.
10. **Qiao Liu**, Zhiqiang Hu, Rui Jiang<sup>\*</sup>, Mu Zhou<sup>\*</sup>. 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%)
11. **Qiao Liu**, Hairong Lv, Rui Jiang<sup>\*</sup>. 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 Biologythe 18th European Conference on Computational Biology (ISMB/ECCB)*, 2019. (conference acceptance rate:18.9%)
12. Pengyu Chen<sup>†</sup>, **Qiao Liu**<sup>†</sup>, Lan Wei, Beier Zhao, Yin Jia, Hairong Lv<sup>\*</sup>, Xiaolu Fei<sup>\*</sup>. Automatically structuring on Chinese ultrasound report of cerebrovascular diseases via natural language processing[J]. *IEEE Access*, 2019, 7: 89043-89050.
13. **Qiao Liu**, Fei Xia, Qijin Yin, Rui Jiang<sup>\*</sup>. Chromatin accessibility prediction via a hybrid deep convolutional neural network[J]. *Bioinformatics*, 2017, 34(5): 732-738.
14. **Qiao Liu**, Mingxin Gan, Rui Jiang<sup>\*</sup>. 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)

15. Shuo Li, Weihua Zeng, Xiaohui Ni, **Qiao Liu**,..., Wing Hung Wong<sup>\*</sup>, Steven M. Dubinett<sup>\*</sup> and Xianghong Jasmine Zhou<sup>\*</sup>. 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.
16. Shuang Zhang, Yuti Liu, Shuang Chen, **Qiao Liu**, Wanwen Zeng. Applications of Transformer-based Language Models in Bioinformatics: A Survey[J]. *Bioinformatics Advances*, 2023.
17. Christopher Lance, Malte D Luecken, Daniel B Burkhardt,...,**Qiao Liu**,...,Fabian J Theis<sup>\*</sup>. Multimodal single cell data integration challenge: results and lessons learned[J]. Proceedings of Machine Learning Research(*PMLR*), 2022.
18. Zhana Duren, Fengge Chang, Fnu Naqing, Jingxue Xin, **Qiao Liu**, Wing Hung Wong<sup>\*</sup>. Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG[J]. *Genome Biology*, 2022, 23(1): 1-19.
19. Jinxiang Ou, Yunheng Shen, Feng Wang, **Qiao Liu**, Xuegong Zhang, Hairong Lv<sup>\*</sup>. AggEnhance: Aggregation Enhancement by Class Interior Points in Federated Learning with Non-IID Data[J]. ACM Transactions on Intelligent Systems and Technology (*TIST*), 2022.

20. Qijin Yin, **Qiao Liu**, Zhuoran Fu, Rui Jiang<sup>\*</sup>. scGraph: a graph neural network-based approach to automatically identify cell types[J]. *Bioinformatics*, 2022.
21. Tianxing Ma, **Qiao Liu**, Haochen Li, Mu Zhou, Rui Jiang, Xuegong Zhang<sup>\*</sup>. DualGCN: a dual graph convolutional network model to predict cancer drug response[J]. *BMC bioinformatics*, 2022, 23(4): 1-13.
22. Feng Wang, Guoyizhe Wei, **Qiao Liu**, Jinxiang Ou, Xian Wei, Hairong Lv<sup>\*</sup>. Boost Neural Networks by Checkpoints [C]. Conference on Neural Information Processing Systems (*NeurIPS*), 2021, 33. (acceptance rate:26%)
23. Shengquan Chen, **Qiao Liu**, Xuejian Cui, Rui Jiang<sup>\*</sup>. OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions[J]. *Nucleic Acids Research*, 2021, 49(W1): W483-W490.
24. Kexin Ding, **Qiao Liu**, Edward Lee, Mu Zhou, Aidong Lu, Shaoting Zhang<sup>\*</sup>. 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).
25. Qingzhu Yang, **Qiao Liu**, Hairong Lv<sup>\*</sup>. A Decentralized System for Medical Data Management via Blockchain [J]. *Journal of Internet Technology*, 2020, 21(5): 1335-1345.
26. Junfeng Liu, **Qiao Liu**, Qingzhu Yang<sup>\*</sup>. 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.
27. Chencheng Xu, **Qiao Liu**, Jianyu Zhou, Minzhu Xie, Jianxing Feng, Tao Jiang<sup>\*</sup>. Quantifying functional impacts of regulatory variants with multi-task Bayesian neural network[J]. *Bioinformatics*, 2020, 36(5): 1397-1404.
28. Chencheng Xu, **Qiao Liu**, Minlie Huang, Tao Jiang<sup>\*</sup>. Reinforced molecular optimization with neighborhood-controlled grammars[C]. Conference on Neural Information Processing Systems (*NeurIPS*), 2020, 33. (acceptance rate:20.1%)
29. Qijin Yin, Mengmeng Wu, **Qiao Liu**, Rui Jiang<sup>\*</sup>. DeepHistone: a deep learning approach to predicting histone modifications[J]. *BMC Genomics*, 2019,20(2):193.
30. Shaoming Song, Hongfei Cui, Shengquan Chen, **Qiao Liu**, Rui Jiang<sup>\*</sup>. EpiFIT: Functional interpretation of transcription factors based on combination of sequence and epigenetic information[J]. *Quantitative Biology*, 2019, 1-11.
31. Bai Li, Mu Lin, **Qiao Liu**, Ya Li<sup>\*</sup>, Changjun Zhou<sup>\*</sup>. 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.

## Invited Talks

<b>2023.04</b>	<b>UC Berkeley Biostats Seminar</b> , UC Berkeley, USA.
<b>2023.04</b>	<b>Tsinghua Stats Seminar</b> , Tsinghua University, China (remote talk).
<b>2022.08</b>	<b>CEGS 2022</b> (NIH Centers of Excellence in Genomic Science Annual Meeting), Duke University, USA.
<b>2022.08</b>	<b>JSM 2022</b> (Joint Statistical Meetings), Wasington DC, USA.
<b>2022.06</b>	<b>CVI 2022</b> (CVI Early Career Research Roundtable), Stanford University, USA.
<b>2021.12</b>	<b>NeurIPS 2021</b> (Thirty-fifth Conference on Neural Information Processing Systems), remote talk.
<b>2020.09</b>	<b>ECCB 2020</b> (The 19th European Conference on Computational Biology), remote talk.
<b>2020.03</b>	<b>CEGS 2020</b> (NIH Centers of Excellence in Genomic Science Seminar), Stanford University, USA.
<b>2019.11</b>	<b>BIBM 2019</b> (2019 IEEE International Conference on Bioinformatics & Biomedicine), San Diego, USA
<b>2019.07</b>	<b>ISMB 2019</b> (The 27th Conference on Intellegent Systems for Molecular Biology), Basel, Switzerland
<b>2019.03</b>	<b>BUAFAI 2019</b> (The First Beijing Universities Academic Forum of Artificial Intelligence), Beijing, China
<b>2017.01</b>	<b>APBC 2017</b> (The Fifteenth Asia Pacific Bioinformatics Conference), Shenzhen, China

## Selected Honers and Awards

<b>2022.12</b>	<b>Outstanding Ph.D. Thesis Award</b> , Beijing Municipal Commission of Education
<b>2021.06</b>	<b>Outstanding Graduates Award</b> , Beijing Municipal Commission of Education (5% of all graduate students)
<b>2021.06</b>	<b>Tsinghua Outstanding Ph.D. Thesis Award</b> , Tsinghua University (6% of all Ph.D. Thesis)
<b>2021.06</b>	<b>Tsinghua University Outstanding Graduates Award</b> , Tsinghua University (5% of all graduate students)

<b>2020.08</b>	<b>ECCB Fellowship</b> , International Society for Computational Biology
<b>2019.04</b>	<b>ISMB Travel Fellowship</b> , International Society for Computational Biology
<b>2018.10</b>	<b>National Scholarship</b> , Ministry of Education of China ( <b>0.2%</b> )
<b>2016.06</b>	<b>Outstanding Graduates Award</b> , Beijing Municipal Commission of Education
<b>2015.06</b>	<b>Microsoft Young Fellowship</b> , Microsoft Research Asia ( <b>40</b> winners nationwide)

## Selected Competitions

<b>2021.12</b>	<b>NeurIPS 2021 Competition, Multimodal Data Integration</b> , rank <b>1<sup>st</sup></b> /2611 in two Joint Embedding tasks NeurIPS conference
<b>2021.05</b>	<b>RNA Unpaired Probability Prediction Competition</b> , rank <b>3<sup>rd</sup></b> /1012, Baidu AI Studio, Baidu Inc
<b>2019.03</b>	<b>Liver Cancer Image Diagnose Competition</b> , rank <b>2<sup>nd</sup></b> /1397, Digital China Innovation Contest, DCIC 2019
<b>2014.10</b>	<b>1<sup>st</sup> Prize in NCSMC</b> (The 6 <sup>th</sup> National College Students Mathematical Competition), Chinese Mathematical Society
<b>2014.09</b>	<b>National 1<sup>st</sup> Prize in CUMCM</b> (Contemporary Undergraduate Mathematical Contest in Modeling), China Society for Industrial and Applied Mathematics
<b>2013.10</b>	<b>1<sup>st</sup> Prize in NCSMC</b> (The 5 <sup>th</sup> National College Students Mathematical Competition), Chinese Mathematical Society

## Teaching Experiences

<b>2023 Summer</b>	<b>Teaching Assistant</b> , ICME Data Science Summer Workshop, Stanford University <b>Introduction to Generative Models</b>
<b>2019.02- 2019.06</b>	<b>Teaching Assistant</b> , Fundamental Industry Training Center, Tsinghua University <b>Smart Things and Intelligent Systems</b>
<b>2018.09- 2019.01</b>	<b>Teaching Assistant</b> , Department of Automation, Tsinghua University <b>Introduction to Artificial Intelligence</b>
<b>2017.09- 2018.01</b>	<b>Teaching Assistant</b> , Department of Automation, Tsinghua University <b>Introduction to Artificial Intelligence</b>

## Professional Activities

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