

Qiao Liu – Curriculum Vitae

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Research Statement

I'm a Postdoctoral Scholar at Department of Statistics, Stanford University. My research interests cover problems on statistical learning and computational biology problems. In particular, I am interested in developing machine learning algorithms, especially deep learning algorithms with applications in both general statistics and specific problems in computational biology, pharmacopathology, and health care. Related related works have been published in top journals (**PNAS**, **Nature Machine Intelligence**, **Nucleic Acids Research**, **Bioinformatics**) and conferences (**ISMB**, **ECCB**, **NeurIPS**, **MICCAI**).

Academic appointment

2021.06-Present Postdoctoral Scholar - Stanford University, Stanford, USA
Department of Statistics, advised by Prof. **Wing Hung Wong** (NAS member)
Developing ML algorithms for solving problems in general statistics and computational biology.

Education

2019.09-2021.06 Joint Ph.D. student - Stanford University, Stanford, USA
Department of Statistics, advised by Prof. **Wing Hung Wong** (NAS member)
Developing machine learning algorithms with applications in both general statistics and biomedical data

2016.09-2019.09 Ph.D. student in **Control Science and Engineering** - Tsinghua University, Beijing, China
Department of Automation, advised by Prof. **Rui Jiang**
Tsinghua National Laboratory for Informatics and Technology (TNLIST)

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, formerly a.k.a. School of Advanced Engineering)
GPA:**91.5**/100, Rank:**2**/50

Internships

2021.06-2022.02 Part-time Consultant - Shanghai Artificial Intelligence Laboratory, Shanghai, China
Research consulting in the combination of AI, computational biology, and medical health care.

2019.06-2019.09 Research Intern - SenseTime Inc, Beijing, China
AI+Healthcare
Developing ML algorithms for drug sensitivity prediction and novel drug discovery

Publications

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

Preprints

1. **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]. *bioRxiv*, 2022.
2. 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]. *bioRxiv*, 2022.
3. Kexin Ding, Mu Zhou, Zichen Wang, **Qiao Liu**, Corey W. Arnold, Shaoting Zhang*, Dimitri N. Metaxas*. Graph Convolutional Networks for Multi-modality Medical Imaging: Methods, Architectures, and Clinical Applications[J]. *arXiv preprint arXiv:2202.08916*, 2022.
4. Shuang Zhang, Yuti Liu, Shuang Chen, **Qiao Liu**, Wanwen Zeng. Applications of Transformer-based Language Models in Bioinformatics: A Survey[J]. Under Review, 2022.

Peer-reviewed papers

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. 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.
7. 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.
8. 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.
9. Qijin Yin, **Qiao Liu**, Zhuoran Fu, Rui Jiang*. scGraph: a graph neural network-based approach to automatically identify cell types[J]. *Bioinformatics*, 2022.
10. 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.
11. **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.
12. 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%)
13. 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.
14. **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.
15. **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.
16. **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%)
17. 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).

18. 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.
19. 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.
20. 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.
21. 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%)
22. **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 Biologythe 18th European Conference on Computational Biology (ISMB/ECCB)*, 2019. (conference acceptance rate:18.9%)
23. 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.
24. Qijin Yin, Mengmeng Wu, **Qiao Liu**, Rui Jiang^{*}. DeepHistone: a deep learning approach to predicting histone modifications[J]. *BMC Genomics*, 2019,20(2):193.
25. 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.
26. **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.
27. **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.
28. 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.

Invited Talks

2022.08	CEGS 2022 (NIH Centers of Excellence in Genomic Science Annual Meeting), Duke University, USA.
2022.08	JSM 2022 (Joint Statistical Meetings), Wasington DC, USA.
2022.06	CVI 2022 (CVI Early Career Research Roundtable), Stanford University, USA.
2021.12	NeurIPS 2021 (Thirty-fifth Conference on Neural Information Processing Systems), Virtual talk.
2020.09	ECCB 2020 (The 19th European Conference on Computational Biology), Virtual talk.
2020.03	CEGS 2020 (NIH Centers of Excellence in Genomic Science Seminar), Stanford University, USA.
2019.11	BIBM 2019 (2019 IEEE International Conference on Bioinformatics & Biomedicine), San Diego, USA
2019.07	ISMB 2019 (The 27th Conference on Intellegent 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 Fifteenth Asia Pacific Bioinformatics Conference), Shenzhen, China

Selected Honers and Awards

2021.06	Excellent Graduates of Beijing , Beijing Municipal Commission of Education (5% of all graduate students)
2021.06	Excellent Ph.D. Thesis , Tsinghua University (6% of all Ph.D. Thesis)
2021.06	Excellent Graduates of Tsinghua University , Tsinghua University (5% of all graduate students)
2020.08	ECCB Fellowship , International Society for Computational Biology
2019.04	ISMB Travel Fellowship , International Society for Computational Biology
2018.10	National Scholarship , Ministry of Education of China (0.2%)

2016.06 **Excellent Graduates of Beijing**, 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 **1st**/2611 in two Joint Embedding tasks
NeurIPS conference
2021.05 **RNA Unpaired Probability Prediction Competition**, rank **3rd**/1012, Baidu AI Studio,
Baidu Inc
2019.03 **Liver Cancer Image Diagnose Competition**, rank **2nd**/1397, Digital China Innovation Contest,
DCIC 2019
2014.10 **Beijing 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 **Beijing 1st Prize in NCSMC**(The 5th National College Students Mathematical Competition),
Chinese Mathematical Society

Technical Strengths

- **Programming Languages**
Python,C,Shell,R,Matlab
- **Deep learning software stacks**
TensorFlow,Keras,PyTorch,PyTorch Lightning
- **Miscellaneous**
Git,OpenMP,Slurm,Flask,Apache Web Servers

Teaching Experiences

2019.02- **Teaching Assistant**, Fundamental Industry Training Center, Tsinghua University
2019.06 **Smart Things and Intelligent Systems**, Undergraduate Course
2018.09- **Teaching Assistant**, Department of Automation, Tsinghua University
2019.01 **Introduction to Artificial Intelligence**, Undergraduate Course
2017.09- **Teaching Assistant**, Department of Automation, Tsinghua University
2018.01 **Introduction to Artificial Intelligence**, Undergraduate Course
2016.08- **Teaching Assistant**, Department of Automation, Tsinghua University
2016.09 **Project of Electronic Circuits**, Undergraduate Summer Course

Professional Activities

Member of International Society of Computational Biology (ISCB).
Student member of Institute of Electrical and Electronics Engineers (IEEE).
PC member of AAAI 2023.
Reviewer for Statistical Journals: *Journal of the American Statistical Association*, *Computational Statistics*
Reviewer for Bioinfo&Machine Learning Journals: *Nature Machine Intelligence*, *Bioinformatics*, *Briefings in Bioinformatics*, *BMC Genomics*, *BMC Bioinformatics*, *Engineering Applications of Artificial Intelligence*, *Complex & Intelligent Systems*.