Stanford

Qiao Liu

Postdoctoral Scholar, Statistics

📄 Curriculum Vitae available Online

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BIO

I am currently a postdoctoral scholar at the Department of Statistics, Stanford University, advised by Prof. Wing Hung Wong (NAS member). Prior to that, I was a PhD student at Tsinghua University, where I spent two years at Stanford University, jointly advised by Prof. Wing Hung Wong. My research interests lie in the intersection of machine learning, statistics, and computational biology. I'm especially fascinated by solving several problems in statistics, such as density estimation, causal inference, and likelihood-free Bayesian, with deep generative models. Besides, I'm also interested in various problems in computational biology and biomedical informatics, which involve genomic data, pharmacology data, and biomedical data analysis.

STANFORD ADVISORS

- Wing H Wong, Postdoctoral Faculty Sponsor

LINKS

- Personal website: http://liuqiao.me

Research & Scholarship

LAB AFFILIATIONS

- Wing H Wong, Wong Lab (9/1/2019)

Publications

PUBLICATIONS

- **Comprehensive tissue deconvolution of cell-free DNA by deep learning for disease diagnosis and monitoring.** *Proceedings of the National Academy of Sciences of the United States of America*
  Li, S., Zeng, W., Ni, X., Liu, Q., Li, W., Stackpole, M. L., Zhou, Y., Gower, A., Krysan, K., Ahuja, P., Lu, D. S., Raman, S. S., Hsu, et al
  2023; 120 (28): e2305236120

- **Deep generative modeling and clustering of single cell Hi-C data.** *Briefings in bioinformatics*
  Liu, Q., Zeng, W., Zhang, W., Wang, S., Chen, H., Jiang, R., Zhou, M., Zhang, S.
  2022

- **HiChIPdb: a comprehensive database of HiChIP regulatory interactions.** *Nucleic acids research*
  Zeng, W., Liu, Q., Yin, Q., Jiang, R., Wong, W. H.
  2022

- **DeepCAGE: Incorporating transcription factors in genome-wide prediction of chromatin accessibility.** *Genomics, proteomics & bioinformatics*
  Liu, Q., Hua, K., Zhang, X., Wong, W. H., Jiang, R.
  2022

- **OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions.** *Nucleic acids research*
  Chen, S., Liu, Q., Cui, X., Feng, Z., Li, C., Wang, X., Zhang, X., Wang, Y., Jiang, R.
  2021; 49 (W1): W483-W490

- **Simultaneous deep generative modeling and clustering of single cell genomic data.** *Nature machine intelligence*
  Liu, Q., Chen, S., Jiang, R., Wong, W. H.
  2021; 3 (6): 536-544

- **Simultaneous deep generative modelling and clustering of single-cell genomic data** *NATURE MACHINE INTELLIGENCE*
  Liu, Q., Chen, S., Jiang, R., Wong, W.
  2021

- **Density estimation using deep generative neural networks.** *Proceedings of the National Academy of Sciences of the United States of America*
  Liu, Q., Xu, J., Jiang, R., Wong, W. H.
  2021; 118 (15)

- **DeepCDR: a hybrid graph convolutional network for predicting cancer drug response**
  Liu, Q., Hu, Z., Jiang, R., Zhou, M.
  OXFORD UNIV PRESS.2020: I911-I918

- **hicGAN infers super resolution Hi-C data with generative adversarial networks**
  Liu, Q., Lv, H., Jiang, R.
  OXFORD UNIV PRESS.2019: I99-I107

- **Chromatin accessibility prediction via a hybrid deep convolutional neural network** *BIOINFORMATICS*
  Liu, Q., Xia, F., Yin, Q., Jiang, R.
  2018; 34 (5): 732–38

- **Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG.** *Genome biology*
  Duren, Z., Chang, F., Naqing, F., Xin, J., Liu, Q., Wong, W. H.
  2022; 23 (1): 114

- **DualGCN: a dual graph convolutional network model to predict cancer drug response.** *BMC bioinformatics*
  Ma, T., Liu, Q., Li, H., Zhou, M., Jiang, R., Zhang, X.
  2022; 23 (Suppl 4): 129

- **scGraph: a graph neural network-based approach to automatically identify cell types.** *Bioinformatics (Oxford, England)*
  Yin, Q., Liu, Q., Fu, Z., Zeng, W., Zhang, B., Zhang, X., Jiang, R., Lv, H.
  2022

- **DeepHistone: a deep learning approach to predicting histone modifications**
  Yin, Q., Wu, M., Liu, Q., Lv, H., Jiang, R.
  BMC.2019: 193

- **A sequence-based method to predict the impact of regulatory variants using random forest** *BMC SYSTEMS BIOLOGY*
  Liu, Q., Gan, M., Jiang, R.
  2017; 11: 7