


Stanford

Qiao Liu

Postdoctoral Scholar, Statistics

 Curriculum Vitae available Online

Bio

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

- **Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG.** *Genome biology*
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- **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.
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- **scGraph: a graph neural network-based approach to automatically identify cell types.** *Bioinformatics (Oxford, England)*
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- **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.
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- **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.
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- **Simultaneous deep generative modeling and clustering of single cell genomic data.** *Nature machine intelligence*
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- **Simultaneous deep generative modelling and clustering of single-cell genomic data** *NATURE MACHINE INTELLIGENCE*
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- **Density estimation using deep generative neural networks.** *Proceedings of the National Academy of Sciences of the United States of America*

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● **DeepCDR: a hybrid graph convolutional network for predicting cancer drug response**

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● **hicGAN infers super resolution Hi-C data with generative adversarial networks**

Liu, Q., Lv, H., Jiang, R.
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● **DeepHistone: a deep learning approach to predicting histone modifications**

Yin, Q., Wu, M., Liu, Q., Lv, H., Jiang, R.
BMC.2019: 193

● **Chromatin accessibility prediction via a hybrid deep convolutional neural network** *BIOINFORMATICS*

Liu, Q., Xia, F., Yin, Q., Jiang, R.
2018; 34 (5): 732–38

● **A sequence-based method to predict the impact of regulatory variants using random forest** *BMC SYSTEMS BIOLOGY*

Liu, Q., Gan, M., Jiang, R.
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