LEI XIONG

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EDUCATION

Massachusetts Institute of Technology (CSAIL)　　　　　　　Dec 2021 - Present
Broad Institute of MIT and Harvard
Postdoctoral Associate (mentor: Manolis Kellis)

Tsinhua University　　　　　　　　　　　　　　　　　　　Sep 2015 - Oct 2020
Ph.D., Computational Biology (advisor: Qiangfeng Cliff Zhang)

University of Science and Technology of China　　　　　　　Sep 2011 - Jun 2015
B.S., Biology, Shitsan Pai Talent Program in Life Sciences

RESEARCH EXPERIENCE

Tsinghua University　　　　　　　　　　　　　　　　　　　Nov 2020 - Apr 2021
Research Assistant

Tsinghua University　　　　　　　　　　　　　　　　　　　Jul 2014 - May 2015
Research Intern on Bachelor Thesis (advisor: Nieng Yan)

RESEARCH INTERESTS

My research interests are centered on the development and application of innovative deep learning approaches to solve complex biological questions, with a primary focus on advancing our understanding of gene regulation and cellular diversity. To achieve this goal, I build models that can effectively capture and interpret complex features from biological datasets, which provides new insights into fundamental biological processes. Through my work, I aim to drive significant advances in the field of single-cell multiomics, which has the potential to contribute to a better understanding of human health and disease.

HONORS AND AWARDS

Honors
- **Outstanding Doctoral Dissertation**, Tsinghua University (Top 5%, selected in 2021) 2020
- **Outstanding Graduate**, Beijing (Top 5%, selected in 2021)　　　　　　　　　2020
- **Top 10 Advances of Bioinformatics in China** (selected in 2020)　　　　　　　2019
- **Top 10 Algorithms and Tools for Bioinformatics in China** (selected in 2020)　2019
- **iGEM Gold Medal**, USTC-China　　　　　　　　　　　　　　　　　　　2013

Fellowship
- **Outstanding Fellowship**, the Beijing Advanced Innovation Center of Structure Biology (¥ 20k)　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　2019

- **Innovation Fellowship**, the Beijing Advanced Innovation Center of Structural Biology (¥ 30k)   2016

Scholarship
- **Student Scholarship**, University of Science and Technology of China   2012-2013
- **Student Scholarship**, University of Science and Technology of China   2011-2012
- **Freshman Scholarship**, University of Science and Technology of China   2011

PUBLICATIONS

* for equal authorship, # for corresponding authorship.

1. **Xiong, L.**, Xu, K., Tian, K., Shao, Y., Tang, L., Gao, G., Zhang, M., Jiang, T., & Zhang, Q. C. (2019). SCALE method for single-cell ATAC-seq analysis via latent feature extraction. Nature Communications, 10(1), 4576.

2. Zhang, B., Zhang, Y., **Xiong, L.**, Li, Y., Zhang, Y., Zhao, J., Jiang, H., Li, C., Liu, Y., Liu, X., Liu, H., Ping, Y.-F., Zhang, Q. C., Zhang, Z., Bian, X.-W., Zhao, Y., & Hu, X. (2022). CD127 imprints functional heterogeneity to diversify monocyte responses in inflammatory diseases. The Journal of Experimental Medicine, 219(2). https://doi.org/10.1084/jem.20211191

3. **Xiong, L.***, Tian, K*., Li, Y., Ning, W., Gao, X., & Zhang, Q. C. (2022). Online single-cell data integration through projecting heterogeneous datasets into a common cell-embedding space. Nature Communications, 13(1), 6118.

4. Deng, D., Sun, P., Yan, C., Ke, M., Jiang, X., **Xiong, L.**, Ren, W., Hirata, K., Yamamoto, M., Fan, S., & Yan, N. (2015). Molecular basis of ligand recognition and transport by glucose transporters. Nature, 526(7573), 391–396.

PRESENTATIONS

Invited talks
- MAIB-talk, The Artificial Intelligence and Biomedicine Society (IHS)   Mar 2023

Posters
- American Society of Human Genetics (ASHG)   2022

ACADEMIC SERVICE

Referee Sevice
- Bioinformatics
- BMC Bioinformatics
- PLoS ONE (*2)
- Big Data
- Frontiers in Endocrinology

Conference Sevice

- AAAI 2023 Workshop on Representation Learning for Responsible Human-Centric AI (*3), Area Chair

- AMIA 2023 Annual Symposium (*7)