

CURRICULUM VITAE

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EDUCATION

2015-2020	Ph.D. in Computational Biology, Tsinghua University
2011-2015	B.Sc. in Biology , Shitsan Pai Talent Program in Life Sciences, Univ. of Science and Technology of China

RESEARCH EXPERIENCE

2021.12-	Postdoctoral Associate, Computer Science and Artificial Intelligence Laboratory (CSAIL), Massachusetts Institute of Technology ; Broad Institute of MIT and Harvard
2020.11-2021.4	Research Assistant, School of Life Sciences, Tsinghua University
2015-2020	Ph.D. student supervised by Prof. Qiangfeng Cliff Zhang , School of Life Sciences, Tsinghua University Topics: <ul style="list-style-type: none"> Develop artificial intelligence algorithm SCALEX that projects cells into a shared batch-invariant cell-embedding space for single-cell data integration, demonstrate its integration accuracy and efficiency, especially on partial-overlapping and large-scale datasets for linking heterogeneous single-cell datasets and accurate label transfer, and application on construction of continuously expandable single-cell atlases. Develop artificial intelligence algorithm SCALE that combines the deep generative variational autoencoder (VAE) framework with Gaussian Mixture Model for single-cell ATAC-seq analysis and demonstrate its remarkably improved performance including visualization, clustering, imputation and downstream motif identification by extensive comparisons with other tools. Set up a structure-enabled protein-protein interaction (PPI) database with mapped 3D cancer mutations and drug targets, construct a 3D PPI network and design network diffusion algorithm to find hotspots and modules enriched cancer mutation or drug target. Identify candidate driver mutations, core cancer-driving modules and propose new cancer drug targets. (Bayer-Tsinghua Collaboration, BTC-PPI).
2014-2015	Undergraduate student, Bachelor thesis supervised by Prof. Nieng Yan , School of Medicine, Tsinghua University Topics:

- Determine the structure of human GLUT3 in complex with D-glucose at 1.5 Å resolution in an outward-occluded conformation and provided insights into the alternating access cycle for GLUTs. I was responsible for comparison of glucose uptake efficiency among different mutated proteins. I cloned over 200 plasmids of different point mutations, constructed the bacmids and expressed in insect cells, purified the proteins and assayed their glucose transporting efficiency.
- 2013-2014 Undergraduate Research Program supervised by Prof. **Jianye Zang**, School of Life Sciences, **Univ. of Science and Technology of China**
Topics:
 - Structure and function research of ubiquitin ligase TRAF1 (TRAF-interacting protein) including molecular clone, protein expression and purification, pull down, inclusion body denaturation and renaturation experiments.
- 2012-2013 Member of 2013 USTC-China iGEM Team, School of Life Sciences, **Univ. of Science and Technology of China**
Topics:
 - In Situ Transdermal Vaccine. We constructed a macromolecule transdermal delivery system with the support of TD-1 polypeptide in *Bacillus subtilis*. We also designed a reporter system and a kill switch for usability and biosafety.

AWARDS AND HONORS

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| 2021 | Outstanding Doctoral Dissertation Award of Tsinghua University |
| 2021 | Outstanding Graduate of Beijing |
| 2020 | SCALE method was selected as
“ Top Ten Advances in Bioinformatics in China ” in 2019 and
“ Top Ten Algorithms and Tools for Bioinformatics in China ” in 2019
by <i>Genomics, Proteomics & Bioinformatics</i> |
| 2019 | Outstanding Fellowship of
the Beijing Advanced Innovation Center of Structure Biology at Tsinghua University |
| 2016 | Innovation Fellowship of
the Beijing Advanced Innovation Center of Structural Biology at Tsinghua University |
| 2013 | 2013 USTC-China iGEM Team won Gold Medal |
| 2011-2013 | Student Scholarship, Univ. of Science and Technology of China |

PUBLICATIONS

* for equal authorship, # for corresponding authorship.

1. **Lei Xiong***, Kang Tian*, Yuzhe Li, Weixi Ning, Xin Gao & Qiangfeng Cliff Zhang#. (2022). Online single-cell data integration through projecting heterogeneous datasets into a common cell-embedding space. **Nature Communications** 13:6118.
2. Bin Zhang*, Yuan Zhang*, **Lei Xiong**, Yuzhe Li, Yunliang Zhang, Jiuliang Zhao, Hui Jiang, Can Li, Yunqi Liu, Xindong Liu, Haofei Liu, Yi-Fang Ping, Qiangfeng Cliff Zhang, Zheng Zhang, Xiu-Wu Bian#, Yan Zhao# & Xiaoyu Hu#. (2021). CD127 imprints functional heterogeneity to diversify monocyte responses in human inflammatory diseases. **JEM**
3. **Lei Xiong**, Kui Xu, Kang Tian, Yanqiu Shao, Lei Tang, Ge Gao, Michael Zhang, Tao Jiang & Qiangfeng Cliff Zhang#. (2019). SCALE method for single-cell ATAC-seq analysis via latent feature extraction. **Nature Communications** 10:4576.

4. Dong Deng*, Pengcheng* Sun, Chuangye Yan, Meng Ke, Xin Jiang, **Lei Xiong**, Wenlin Ren, Kunio Hirata, Masaki Yamamoto, Shilong Fan, Nieng Yan#. (2015) Molecular basis of ligand recognition and transport by glucose transporters. *Nature* 526:391-396.

SKILLS

1. Designing artificial intelligence algorithm for biological problems
2. Biological data mining
3. Single-cell data analysis
4. Network analysis