CURRICULUM VITAE

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## EDUCATION

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

## RESEARCH EXPERIENCE

2015-2020  Ph.D. student supervised by Prof. **Qiangfeng Cliff Zhang**,
School of Life Sciences, **Tsinghua University**
**Topics:**

- Develop artificial intelligence algorithm **SCALEX** that projects cells into a shared batch-invariant space for single-cell data integration, demonstrate its integration accuracy especially on partial-overlapping datasets for linking heterogeneous single-cell datasets and fast label transferring, and apply to tumor microenvironment of pan-cancer for interpreting cancer heterogeneity.

- 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 TRAIP (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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| 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 *Genomics, Proteomics & Bioinformatics* |
| 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, Qiangfeng Cliff Zhang#. (2020). SCALEX: Single-cell analysis via latent feature extraction universally. (Manuscript)
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#. (2020). CD127 imprints functional heterogeneity to diversify monocyte responses in human inflammatory diseases. (Submitted)
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
5. Python programming & Linux