

# ZIQI ZHANG

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## EDUCATION

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| <b>Georgia Institute of Technology, GA, USA</b><br><i>Ph.D. in Computational Science and Engineering</i> <ul style="list-style-type: none"><li>• Advisor: Prof. Xiuwei Zhang</li></ul>  | <i>Sep 2020 - present</i>   |
| <b>Georgia Institute of Technology, GA, USA</b><br><i>Master of Computational Science and Engineering</i> <ul style="list-style-type: none"><li>• Advisor: Prof. Xiuwei Zhang</li></ul> | <i>Sep 2020 - Dec 2023</i>  |
| <b>Georgia Institute of Technology, GA, USA</b><br><i>Master of Electrical and Computer Engineering</i>   | <i>Sep 2019 - present</i>   |
| <b>Beihang University, Beijing, China</b><br><i>Bachelor of Electronic and Information Engineering</i>  | <i>Sep 2015 - July 2019</i> |

## WORK EXPERIENCE

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| <b>Computational Research Intern</b><br><i>Department of Cellular and Tissue Genomics, Genentech, CA, USA</i> <ul style="list-style-type: none"><li>• Advisor: Dr. Runmin Wei, Dr. Bo Li</li></ul> | <i>May 2024 - August 2024</i> |
| <b>Graduate Research Assistant</b><br><i>Georgia Institute of Technology, GA, USA</i>  | <i>May 2020 - Present</i>     |

## PUBLICATION

### Journal & Conference papers

1. Hechen Li, **Ziqi Zhang**, Michael Squires, Xi Chen, Xiuwei Zhang<sup>†</sup>, “scMultiSim: simulation of multi-modality single cell data guided by cell-cell interactions and gene regulatory networks”, *Nature Methods*, 2025
2. **Ziqi Zhang**, and Xiuwei Zhang<sup>†</sup>. “Data-driven batch detection enhances single-cell omics data analysis.” *Cell Systems* 2024.
3. **Ziqi Zhang**, Xinye Zhao, Mehak Bindra, Peng Qiu, and Xiuwei Zhang<sup>†</sup>. “scDisInFact: disentangled learning for integration and prediction of multi-batch multi-condition single-cell RNA-sequencing data”, *Nature Communications*, 2024
4. **Ziqi Zhang**, Haoran Sun, Ragunathan Mariappan, Xinyu Chen, Xi Chen, Mika S Jain, Mirjana Efremova, Sarah A Teichmann, Vaibhav Rajan, Xiuwei Zhang<sup>†</sup>. “scMoMaT jointly performs single cell mosaic integration and multi-modal bio-marker detection”, *Nature Communications*, 2023
5. **Ziqi Zhang**, Chengkai Yang, and Xiuwei Zhang<sup>†</sup>. “scDART: integrating unmatched scRNA-seq and scATAC-seq data and learning cross-modality relationship simultaneously” *Genome Biology*, 2022
6. **Ziqi Zhang** and Xiuwei Zhang<sup>†</sup>. “Inference of high-resolution trajectories in single-cell RNA-seq data by using RNA velocity”, *Cell Reports Methods*, 2021
7. Vaibhav Rajan, **Ziqi Zhang**, Carl Kingsford, and Xiuwei Zhang<sup>†</sup>. “Maximum likelihood reconstruction of ancestral networks by integer linear programming”, *Bioinformatics*, 2021

### Preprints & Working papers

1. **Ziqi Zhang**, Chandra Sekhar Reddy E, Chao Zhang, and Xiuwei Zhang<sup>†</sup>. “scREBOUND: An Efficient Design of single-cell Foundation Model with Batch Representation”, *in submission to NeurIPS*, 2025

2. Macrina Lobo, **Ziqi Zhang**<sup>†</sup>, and Xiuwei Zhang<sup>†</sup>. “SpaDecoder: Decoding Spatial Transcriptomes at Single Cell Resolution Leveraging Tissue Structure”, *working paper*, 2025
3. **Ziqi Zhang**, Jongseok Han, Le Song, and Xiuwei Zhang<sup>†</sup>. “CeSpGRN: Inferring cell-specific gene regulatory networks from single cell multi-omics and spatial data”, *under revision at Bioinformatics*, 2025
4. **Ziqi Zhang** and Xiuwei Zhang<sup>†</sup>. “Velosim: Simulating single cell gene-expression and RNA velocity”, *BioRxiv*, 2021

## Workshop

1. **Ziqi Zhang** and Xiuwei Zhang. “Integrating unmatched scRNA-seq and scATAC-seq data and learning cross-modality relationship simultaneously” **Spotlight**, *16th Machine Learning in Computational Biology (MLCB)*, 2021
2. **Ziqi Zhang**, Haoran Sun, Ragunathan Mariappan, Xi Chen, Mika S Jain, Mirjana Efremova, Sarah A Teichmann, Vaibhav Rajan, Xiuwei Zhang. “Integrating unpaired scRNA-seq and scATAC-seq with unequal cell type compositions” *ICML workshop on Computational Biology*, 2021

## Presentations

1. Poster presentation: *scDisInFact: the disentangled learning for integration and prediction of multi-batch multi-condition single-cell RNA sequencing data*, MCBIOS, 2024 [**Best poster presentation award**]
2. Poster presentation: *CeSpGRN: Inferring cell-specific gene regulatory network from single cell multi-omics data and spatial data*, CSHL Single Cell Analysis, 2023
3. Talk: *Inferring GRNs and CCIs using single-cell sequencing data*, InQuBETA workshop: Computational Problems in Single Cell Transcriptomics and Multi-omics, 2023
4. Talk: *scDisInFact: the disentangled learning for integration and prediction of multi-batch multi-condition single-cell RNA sequencing data*, AWSOM-Atlanta Workshop on Single-cell Omics, 2023 [**Best oral presentation award**]
5. Poster presentation: *scDisInFact: the disentangled learning for integration and prediction of multi-batch multi-condition single-cell RNA sequencing data*, RSGDREAM, 2022
6. Talk: *scDisInFact: the disentangled learning for integration and prediction of multi-batch multi-condition single-cell RNA sequencing data*, HotCSE, School of Computational Science and Engineering, Georgia Institute of Technology, 2022
7. Talk: *scMoMaT: Multimodal Data Integration Software*, AWSOM-Atlanta Workshop on Single-cell Omics, 2022
8. Talk: *Integrating unmatched scRNA-seq and scATAC-seq data and learning cross-modality relationship simultaneously*, MLCB, 2021 [**Spotlight presentation**]
9. Flash talk: *Learning latent embedding of multi-modal single cell data and cross-modality relationship simultaneously*, CSHL, 2021
10. Poster presentation: *CeSpGRN: Inferring cell-specific gene regulatory networks from single cell gene expression data*, RECOMB, 2022
11. Poster presentation: *scMoMaT: Integrating arbitrary number of single-cell multi-omics matrices using matrix-trifactorization*, USC-QCB, 2022
12. Poster presentation: *Inference of multiple trajectories in single-cell RNA-Seq data from RNA-velocity*, VIB, 2020
13. Poster presentation: *Inference of multiple trajectories in single-cell RNA-Seq data from RNA-velocity*, RSGDREAM, 2020
14. Poster presentation: *Inference of multiple trajectories in single-cell RNA-Seq data from RNA-velocity*, CSHL-Asia, 2020
15. Flash talk: *Computational methods to study cell mechanisms from single cell data*, Georgia Scientific Computing Symposium (GSCS), 2020

## TEACHING

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### Courses

1. **Head Teaching Assistant:** *CSE 6140 Algorithm* 2021Fall
2. **Teaching Assistant:** *CSE 8803 Machine learning in Computational Biology* 2021Spring
3. **Teaching Assistant:** *CSE 6140 Algorithm* 2020Fall

### Advisee

1. **Macrina M Lobo:** Ph.D. student Sept 2024-Now  
**Project:** *SpaDecoder: Decoding Spatial Transcriptomes at Single Cell Resolution Leveraging Tissue Structure*
2. **Chandra Sekhar Reddy E:** Master student Sept 2023-Now  
**Project:** *Efficient design of single-cell foundation model*
3. **Xinye Zhao:** Master student Nov 2021-Oct 2022  
**Project:** *scDisInFact: disentangled learning for integration and prediction of multi-batch multi-condition single cell RNA-sequencing data*
4. **Xinyu Chen:** Ph.D. student August 2021-Nov 2021  
**Project:** *scMoMaT: Mosaic integration of single cell multi-omics data using matrix tri-factorization*
5. **Jongseok Han:** Master student Jun 2021-Nov 2021  
**Project:** *Inferring cell-specific gene regulatory networks from single cell gene expression data*
6. **Chengkai Yang:** undergraduate student Jun 2020-Jan 2021  
**Project:** *Learning latent embedding of multi-modal single cell data and cross-modality relationship simultaneously*

## AWARD

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### Ph.D. in Georgia Tech

1. Thanks a teacher award *as teaching assistant in CSE6140* Nov 2020

### Undergraduate in Beihang University

1. Outstanding Undergraduate in Beihang University 2019
2. Chinese Graduate Entrance Exam Waiver 2019
3. Learning Merit Scholarship in Beihang University 2018
4. Scholarship for student excellent in Science and Technology competition 2018
5. The Third Prize of National Undergraduate Electronic Design Contest 2017
6. The First Prize of BUAA Physics competition 2015

## SERVICE

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<b>Program Committee:</b>	<i>MLCB 2025</i>
<b>Journal reviewer:</b>	<i>Nature Communications, Patterns, Bioinformatics, Cell Reports Methods, Bioinformatics advance, BMC Bioinformatics, BMC Endocrine Disorders, Journal of Agricultural, Biological, and Environmental Statistics</i>
<b>Conference reviewer:</b>	<i>RECOMB2024, MLCB2023, ISMB2023, RECOMB 2022, ISMB 2022</i>