

# Ruochi Zhang

Eric and Wendy Schmidt Center  
The Broad Institute of MIT and Harvard  
415 Main St  
Cambridge, MA 02142

Phone: (412) 929-1061  
E-mail: zhangruo@broadinstitute.org  
Homepage: <http://ruochiz.com>

## Research Interests

- Computational Genomics and Systems Biology
- Graph Representation Learning
- Deep Learning Methods for Biomedical Data

## Education and Training

- Eric and Wendy Schmidt Center Postdoctoral Fellow 09/2022 – Present  
**The Broad Institute of MIT and Harvard**, Boston, MA, USA.  
Advisor: Bonnie Berger, and Jason D. Buenrostro
- Ph.D. in Computational Biology (GPA: 3.91) 08/2017 – 08/2022  
School of Computer Science, **Carnegie Mellon University**, Pittsburgh, PA, USA.  
Thesis Advisor: Jian Ma  
Committee: Jian Ma, Ziv Bar-Joseph, Ruslan Salakhutdinov, Jure Leskovec, Ivet Bahar  
– Thesis: Charting the landscape of 3D genome organization with graph representation learning
- Master in Machine Learning 12/2019 – 08/2021  
School of Computer Science, **Carnegie Mellon University**, Pittsburgh, PA, USA.
- B.E. in Automation (GPA: 89/100) 08/2013 – 07/2017  
Department of Automation, **Tsinghua University**, Beijing, China  
Thesis Advisor: Jianyang Zeng, Rui Jiang  
– Thesis: Uncovering sequence determinants of RNA-editing with deep learning

## Honors and Recognition

- Outstanding Research Accomplishment Award, CBD, Carnegie Mellon University 2020
- Excellent Graduate of Department of Automation, Tsinghua University 2017
- Second Prize in Challenge Cup, Tsinghua University 2015
- Bronze Medal in iGEM competition 2015
- Academic Scholarship, Tsinghua University 2014, 2015
- Second Place in C Programming Competition, Tsinghua University 2013

## Peer-reviewed Publications

(†=co-first author; \*=co-corresponding author)

### *Representative publications*

1. Xiong K<sup>†</sup>, **Zhang R**<sup>†</sup>, Ma J\*. scGHOST: Identifying single-cell 3D genome subcompartments. *Nature Methods* (accepted in principle).
2. **Zhang R**<sup>†,\*</sup>, Zhou T<sup>†</sup>, and Ma J\*. Ultrafast and Interpretable Single-cell 3D Genome Analysis with Fast-Higashi. *Cell Systems*, 13(10):P798-807.E6, 2022 [**Cover article**] (Early version in *RECOMB* 2022).
3. **Zhang R**, Zhou T, and Ma J. Multiscale and integrative single-cell Hi-C analysis with Higashi. *Nature Biotechnology*, 40:254–261, 2022.
4. **Zhang R**, Ma JZ, and Ma J. DANGO: Predicting higher-order genetic interactions. In *RECOMB* 2021.
5. **Zhang R** and Ma J. Probing multi-way chromatin interaction with hypergraph representation learning.

*Cell Systems*, 10(5):397-407.E5, 2020 (Early version in *RECOMB* 2020).

6. Tian D<sup>†</sup>, **Zhang R**<sup>†</sup>, Zhang Y, Zhu X, and Ma J. MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. *Genome Research*, 30(2):227-238, 2020. [Cover article]
7. **Zhang R**, Zou Y, and Ma J. Hyper-SAGNN: a self-attention based graph neural network for hypergraphs. In *ICLR* 2020.
8. **Zhang R**, Wang Y, Yang Y, Zhang Y, and Ma J. Predicting CTCF-mediated chromatin loops using CTCF-MP. *Bioinformatics* (Proceedings of *ISMB* 2018), 34(13):i133-i141, 2018.

#### **Publications as contributing author**

9. Wang Y, Zhang Y, **Zhang R**, Zhang L, Chen Y, Schaik T, Hupkes D, Sasak T, Gilbert D, Steensel B, Belmont A, and Ma J. SPIN reveals genome-wide landscape of nuclear compartmentalization. *Genome Biology*, 22:36, 2021.
10. Lazzarotto CR, Malinin NL, Li Y, **Zhang R**, Yang Y, Lee G, Cowley E, He Y, Lan X, Jividen K, Katta V, Kolmakova NG, Petersen CT, Qi Q, Strelcov E, Maragh S, Krenciute G, Ma J, Cheng Y, and Tsai SQ. Large-scale CHANGE-seq CRISPR-Cas9 profiling reveals genetic and epigenetic determinants of genome-wide nuclease activity. *Nature Biotechnology*, 38(11):1317-1327, 2020.
11. Yang Y, **Zhang R**, Singh S, and Ma J. Exploiting sequence-based features for predicting enhancer-promoter interactions. *Bioinformatics* (Proceedings of *ISMB* 2017), 33(14):i252-i260, 2017.

#### **Review articles**

12. Zhou T<sup>†</sup>, **Zhang R**<sup>†</sup>, and Ma J. The 3D genome structure of single cells. *Annual Review of Biomedical Data Science*, Vol. 4:21-41, 2021.

#### **Workshops**

13. Bafna M, Keerthipati V, Kanaparthi S, **Zhang R**. DiffRNAFold: Generating RNA Tertiary Structures with Latent Space Diffusion. NeurIPS 2023, MLSB.

#### **Preprint & Submitted manuscripts**

14. Deng Y<sup>†</sup>, **Zhang R**<sup>†</sup>, Xu P, Ma J\*, and Gu Q\*. PhyGCN: Pre-trained gypergraph convolutional neural networks with self-supervised learning. doi: 10.1101/2023.10.01.560404.
15. Zhou T, **Zhang R**, Jia D, Doty RT, Munday AD, Gao D, Xin L, Abkowitz JL, Duan Z\*, and Ma J\*. Concurrent profiling of multiscale 3D genome organization and gene expression in single mammalian cells. doi: 10.1101/2023.07.20.549578.
16. Hu Y, Ma S, Kartha VK, Duarte FM, Horlbeck M, **Zhang R**, Shrestha R, Labade A, Kletzien H, Meliki A, Castillo A, Durand N, Mattei E, Anderson LJ, Tay T, Earl AS, Shoresh N, Epstein CB, Wagers A, Buenrostro JD\*. Single-cell multi-scale footprinting reveals the modular organization of DNA regulatory elements. bioRxiv, doi: 10.1101/2023.03.28.533945.

#### **Professional Experience**

- Research Assistant 08/2017 – 08/2022  
Computational Biology Department, School of Computer Science  
Carnegie Mellon University, Pittsburgh, PA
- Research Assistant 01/2015 – 05/2017  
Machine Learning and Computational Biology Group  
Institute of Interdisciplinary Information  
Tsinghua University, Beijing, China
- Software Developer 12/2014 – 02/2015  
AR/VR Lab, CIMS Center, Department of Automation  
Tsinghua University, Beijing, China

## Teaching Experience

- Teaching Assistant, School of Computer Science, Carnegie Mellon University. 01/2018 – 05/2018  
Course: Computational Genomics
- Teaching Assistant, School of Computer Science, Carnegie Mellon University. 08/2018 – 12/2018  
Course: Algorithms & Advanced Data Structures
- Teaching Assistant, Dragon Star Program 2017, Harbin, China. 08/2017 – 08/2017  
Course: Bioinformatics

## Talks & Conference Presentations

- Efficient and interpretable single-cell 3D genome analysis with Higashi and Fast-Higashi. 05/23/2022  
Talk presentation. **RECOMB** 2022, San Diego, USA.
- Interpretable single-cell 3D genome analysis reveals nuclear structure and function in mammalian brain tissues. 05/04/2022  
Poster presentation. **Genome Organization & Nuclear Function** 2022, CSHL, USA.
- Efficient and interpretable single-cell 3D genome analysis with Higashi and Fast-Higashi. 12/08/2021  
Poster presentation. **4DN Annual Meeting** 2021, Virtual Meeting.
- DANGO: Predicting higher-order genetic interactions. 08/29/2021  
Talk presentation. **RECOMB** 2021, Virtual Meeting.
- Multiscale and integrative single-cell Hi-C analysis. 07/23/2021  
Talk presentation. **4DN Scientific Webinar**, Virtual Meeting.
- Probing multi-way chromatin interaction with hypergraph representation learning. 06/24/2020  
Talk presentation. **RECOMB** 2020, Virtual Meeting.
- Hyper-SAGNN: a self-attention based graph neural network for hypergraphs. 04/28/2020  
Talk presentation. **ICLR** 2020, Virtual Meeting.
- Analyzing single-cell chromatin interaction via hypergraph representation learning. 12/05/2019  
Poster presentation. **4DN Annual Meeting** 2019, Washington DC, USA.
- MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. 12/05/2018  
Poster presentation. **4DN Annual Meeting** 2018, San Diego, CA, USA.
- Predicting CTCF-mediated chromatin loops using CTCF-MP. 07/09/2018  
Talk presentation. **ISMB** 2018: RegSys COSI, Chicago, USA.

## Professional Service

- PC Member: AAI 2022
- Conference Reviewer: ISMB 2018-2021; RECOMB 2020-2022; APBC 2019
- Journal Reviewer: Bioinformatics; PLOS Computational Biology; IEEE/ACM Transactions on Computational Biology and Bioinformatics; IEEE Transactions on Pattern Analysis and Machine Intelligence; Nature Machine Intelligence