

Ruochi Zhang

Computational Biology Department
School of Computer Science
Carnegie Mellon University
5000 Forbes Avenue
Pittsburgh, PA 15213

Phone: (412) 929-1061
Office: 7409 Gates-Hillman Complex
E-mail: ruochiz@andrew.cmu.edu
Homepage: <http://cs.cmu.edu/~ruochiz>

Research Interests

- Computational Genomics and Systems Biology
- Graph Representation Learning
- Application of Deep Learning in Genomics Data

Skills

- Programming Languages: Python, C++, MATLAB, C#, Java, JavaScript
- Scientific Computing Libraries: Numpy, Tensorflow, Pytorch, Theano
- Software Development: HTML/XML GUI Development, Qt, Unity 3d
- Bioinformatics Software: Bowtie, GATK toolkit, Samstool

Education and Training

PhD Student in Computational Biology (GPA: 4.03) School of Computer Science, Carnegie Mellon University , Pittsburgh, PA, USA. Advisor: Dr. Jian Ma	08/2017 – Present
Master Student in Machine Learning School of Computer Science, Carnegie Mellon University , Pittsburgh, PA, USA.	12/2019 – Present
B.E. in Automation (GPA: 89/100, Top 8.7% of the class) Department of Automation, Tsinghua University , Beijing, China Advisor: Dr. Jianyang Zeng, Dr. Rui Jiang	08/2013 – 07/2017
• Thesis: Uncovering sequence determinants of RNA-editing by 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

Professional Experience

- Research Assistant 07/2017 – Present
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 – 5/2018
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

Publications

Peer-Reviewed Articles

1. **Zhang R**, Ma JZ*, and Ma J*. DANGO: Predicting higher-order genetic interactions. *Accepted by RE-COMB2021*
2. Wang Y, Zhang Y, **Zhang R**, Zhang L, Chen Y, Schaik T, Hupkes D, Sasak T, Gilbert D, Steensel B, Belmont A, Ma J. SPIN reveals genome-wide landscape of nuclear compartmentalization. *Accepted by Genome Biology*
3. 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, in press, 2020*
4. **Zhang R**, Ma J. Probing multi-way chromatin interaction with hypergraph representation learning. (*RE-COMB 2020*), *Cell Systems*, 10(5):397-407.E5, 2020.
5. Tian D[†], **Zhang R**[†] (co-first author), Zhang Y, Zhu X, Ma J. MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. *Genome Research*, 30(2):227-238, 2020. **[Cover article]**
6. **Zhang R**, Zou Y, Ma J. Hyper-SAGNN: a self-attention based graph neural network for hypergraphs (*ICLR 2020*) *arXiv*:1911.02613.
7. **Zhang R**, Wang Y, Yang Y, Zhang Y, and Ma J. Predicting CTCF-mediated chromatin loops using CTCF-MP. In *Proceedings of the 26th Conference on Intelligent Systems for Molecular Biology (ISMB 2018)*, *Bioinformatics*, 34(13):i133-i141, 2018.
8. Yang Y, **Zhang R**, Singh S, and Ma J. Exploiting sequence-based features for predicting enhancer-promoter interactions. In *Proceedings of the 25th Conference on Intelligent Systems for Molecular Biology (ISMB 2017)*, *Bioinformatics*, 33(14):i252-i260, 2017.

Preprint

1. **Zhang R**, Zhou T, and Ma J. Multiscale and integrative single-cell Hi-C analysis with Higashi. *bioRxiv*, doi: <https://doi.org/10.1101/2020.12.13.422537>

Papers in Preparation

1. **Zhang R**, Ma J. Integrating graph neural network and HMM for genome segmentation

Conference Presentations

- Predicting CTCF-mediated chromatin loops using CTCF-MP. 07/09/2018
Talk presentation. **ISMB 2018: RegSys COSI**, Chicago, USA.
- MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. 12/05/2018
Poster presentation. **4DN Annual Meeting 2018**, San Diego, CA, USA.
- Analyzing single-cell chromatin interaction via hypergraph representation learning. 12/05/2019
Poster presentation. **4DN Annual Meeting 2019**, Washington, USA.
- Probing multi-way chromatin interaction with hypergraph representation learning. . 06/24/2020
Talk presentation. **RECOMB 2020**, Virtual Meeting.