

# Ruochi Zhang

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## 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: 4.04) School of Computer Science, <b>Carnegie Mellon University</b> , Pittsburgh, PA, USA. Advisor: Dr. Jian Ma	08/2017 – Present
Master Student in Machine Learning School of Computer Science, <b>Carnegie Mellon University</b> , Pittsburgh, PA, USA.	12/2019 – Present
B.E. in Automation (GPA: 89/100, Top 8.7% of the class) Department of Automation, <b>Tsinghua University</b> , 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

• 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 J. Probing multi-way chromatin interaction with hypergraph representation learning. (*RE-COMB* 2020)
2. Tian D<sup>†</sup>, **Zhang R**<sup>†</sup> (co-first author), Zhang Y, Zhu X, Ma J. MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. *Genome Res*, gr-250316. **[Cover article]**
3. **Zhang R**, Zou Y, Ma J. Hyper-SAGNN: a self-attention based graph neural network for hypergraphs (*ICLR* 2020) *arXiv*:1911.02613.
4. **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.
5. 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.

### Papers in Preparation

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

## 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.