

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: 4.01) 08/2017 – Present
School of Computer Science, **Carnegie Mellon University**, Pittsburgh, PA, USA.
Advisor: Dr. Jian Ma

B.E. in Automation (GPA: 89/100, Top 8.7% of the class) 08/2013 – 07/2017
Department of Automation, **Tsinghua University**, Beijing, China
Advisor: Dr. Jianyang Zeng, Dr. Rui Jiang

- 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. (Accepted by **RECOMB 2020**)
2. Tian D[†], **Zhang R**[†] (co-first author), Zhang Y, Zhu X, Ma J. MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. (Accepted by **Genome Res**) **bioRxiv**, 2019: 542092.
3. **Zhang R**, Zou Y, Ma J. Hyper-SAGNN: a self-attention based graph neural network for hypergraphs (Accepted by **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.