

Yue Hu | Ph.D.

✉ huyue@picb.ac.cn • 🌐 <https://jechia.github.io/> • in Yue Hu
🐙 jechia • 📧 Yue Hu • 📄 Yue Hu • 🆔 0000-0002-2858-0831

Education

Beijing Jiaotong University
Bachelor, Bioinformatics

Beijing, P.R.China
2013–2017

University of North Carolina at Chapel Hill
Visiting Ph.D student, Department of Pharmacology
Adviser: Dr. Daniel Dominguez

Chapel Hill, NC
2019–2021

Shanghai Institute of Nutrition and Health, CAS
Ph.D, Computational Biology
Adviser: Dr. Zefeng Wang

Shanghai, P.R.China
2017–2023

Research Projects

RNA-binding protein splicing activity prediction model 2016.11-2018.11

- Developed a machine learning method to predict the splicing regulatory activities based on amino acid sequence of RNA-binding proteins

Systematic survey of PRMTs interactome 2018.5-2021.7

- Analyzed the differential splicing of PRMTs' RNA-seq data and found their regulatory roles in splicing

Extensive Dysregulation of SLK Splicing in Cancers Impacts Metastasis 2021.10-2023.3

- Conducted large-scale analysis of cancer-related splicing events, and found SLK's downstream target through RNA-seq analysis

Integrative language model for RBP-RNA interactions 2019.11-2023.7

- Developed a prediction model based on BERT to integrate both *in vivo* and *in vitro* binding experimental data of RBPs, successfully found RBPs' regulatory roles in RNA splicing and translation

Skills

- R
- Bash
- transcriptomic data analysis
- C
- Python
- Pytorch
- Statistical analysis
- MySQL

Model developments

Pytorch - iBindNet: author & maintainer (<https://github.com/jechia/iBindNet>)

Conference presentations

The 4th National Ribonucleic Acid RNA Youth Academic Conference

Lanzhou, P.R.China

Talk,

April, 2023

iBindNet - Integrative language model for RBP-RNA interactions

RNA 2023

Singapore

Talk,

June, 2023

iBindNet - Integrative language model for RBP-RNA interactions

Publications

- Miaowei Mao, Yue Hu, Yun Yang, Yajie Qian, Huanhuan Wei, Wei Fan, Yi Yang, Xiaoling Li, Zefeng Wang. **Modeling and predicting the activities of trans-acting splicing factors with machine learning** *Cell systems* 7 (5), 510-520. e4,2018. doi: 10.1016/j.cels.2018.09.002
- Huan-Huan Wei, Xiao-Juan Fan, Yue Hu, Xiao-Xu Tian, Meng Guo, Miao-Wei Mao, Zhao-Yuan Fang, Ping Wu, Shuai-Xin Gao, Chao Peng, Yun Yang, Zefeng Wang. **A systematic survey of PRMT interactomes reveals the key roles of arginine methylation in the global control of RNA splicing and translation.** *Science Bulletin* 66 (13), 1342-1357,2021. doi: 10.1016/j.scib.2021.01.004

Pre-print Publications

- Ying-Qun Yang, Yue Hu*, Si-Rui Zhang*, Jie-Fu Li, Jia-Wen Guan, Wen-Jing Zhang, Yu Sun, Xiao-Yan Feng, Jing Sun, Yun Yang, Zefeng Wang, Huan-Huan Wei. **Extensive Dysregulation of SLK Splicing in Cancers Impacts Metastasis.** *bioRxiv* 2022.10.28.514146. doi: 10.1101/2022.10.28.514146

References

Zefeng Wang

Shanghai Institute of Nutrition and Health, CAS

wangzefeng@picb.ac.cn

Daniel Dominguez

Department of Pharmacology, School of Medicine, University of North Carolina at Chapel Hill

didoming@email.unc.edu

Zhen Shao

Shanghai Institute of Nutrition and Health, CAS

shaozhen@picb.ac.cn