Yue Wang

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🏛 University of Liverpool   🎓 Dept of Computer Science•Data Science   👥 1997-04-25

I'm Yue, a Ph.D. candidate studying at the School of Science and Engineering, University of Liverpool. I got my bachelor degree in Applied Mathematics, and have a solid foundation in mathematics, biostatistics, machine learning and artificial intelligence. My Ph.D. project is related to the bioinformatics field, developing statistical and deep learning approaches to characterize high-throughput epitranscriptomics data. I have published papers in renowned journals including *Bioinformatics* and *Briefings in Bioinformatics* as independent first author and independent corresponding author.

For more information on my skills and research projects, please check out my website Link.

🎓 Education

2023.06	**University of Liverpool** •Department of Computer Science
2019.10	Doctor of Philosophy (Ph.D.) •In progress, VIVA examination passed
2019.06	**Xi'an Jiaotong-liverpool University** •Department of Mathematics Science
2015.09	Bachelor degree in Applied Mathematics •first-class degree

💼 Journal Articles

2023	RgnTX: colocalization analysis of transcriptome elements in the presence of isoform heterogeneity and ambiguity. (<u>under review</u>, software accepted by Bioconductor) ❯ **Yue Wang**, Zhen Wei, Jionglong Su, Frans Coenen and Jia Meng* ❯ Independent first author.
2023	m6A-Atlas v2.0: updated resources for unravelling the N6-methyladenosine (m6A) epitranscriptome among multiple species. (<u>under review</u>) ❯ Zhanmin Liang, Haokai Ye, Jiongming Ma, Zhen Wei, **Yue Wang**, Yuxin Zhang, Daiyun Huang, Bowen Song, Jia Meng, Daniel J Rigden*, Kunqi Chen*
2023.03	Multi-task adaptive pooling enabled synergetic learning of RNA modification across tissue, type and species from low-resolution epitranscriptomes. ❯ Yiyou Song, **Yue Wang***, Xuan Wang, Daiyun Huang, Anh Nguyen, Jia Meng ❯ **Briefings in Bioinformatics (IF=13.99)**, [10.1093/bib/bbad105] ❯ Independent corresponding author.
2023.03	Self-attention enabled deep learning of dihydrouridine (D) modification on mRNAs unveiled a distinct sequence signature from tRNAs. ❯ **Yue Wang**, Xuan Wang, Xiaodong Cui, Jia Meng, Rong Rong* ❯ **Molecular Therapy- Nucleic Acids (IF=10.18)**, [10.1016/j.omtn.2023.01.014] ❯ Independent first author.
2023.01	DirectRMDB: a database of post-transcriptional RNA modifications unveiled from direct RNA sequencing technology. ❯ Yuxin Zhang, Jie Jiang, Jiongming Ma, Zhen Wei*, **Yue Wang**, Bowen Song, Jia Meng, Guifang Jia, Joao Pedro de Magalhaes, Daniel J Rigden, Daiyun Hang*, Kunqi Chen* ❯ **Nucleic Acids Research**, 51(D1):D106–D116, [10.1093/nar/gkac1061]

2022.09	RMDisease V2.0: an updated database of genetic variants that affect RNA modifications with disease and trait implication.
	❯ Bowen Song, Xuan Wang, Zhanmin Liang, Jiongming Ma, Daiyun Huang, **Yue Wang**, João Pedro de Magalhães, Daniel J Rigden, Jia Meng, Gang Liu*, Kunqi Chen*, Zhen Wei*
	❯ **Nucleic Acids Research**, 51(D1):D1388–D1396, [10.1093/nar/gkac750]
2021.05	MetaTX: deciphering the distribution of mRNA-related features in the presence of isoform ambiguity, with applications in epitranscriptome analysis.
	❯ **Yue Wang**, Kunqi Chen, Zhen Wei, Frans Coenen, Jionglong Su, Jia Meng*
	❯ **Bioinformatics (IF = 6.931)**, 37(9):1285–1291, [10.1093/bioinformatics/btaa938]
	❯ Independent first author.

💼 Conference Papers

2020.07	An Improved Algorithm for Estimating the Distribution of RNA-related Genomic Features.
	❯ Jinge Wu, Lihan Zhang, Yuanzhe Wang, Jia Meng, Jionglong Su, **Yue Wang***
	❯ Proceedings of the Biological Information and Biomedical Engineering, (BIBE), 2020.
	❯ Independent corresponding author.

‹/› Projects and Codes

❯ `AdaptRM` (Website, Python-Pytorch): A multi-task deep learning model for integrated learning of low- and high- resolution epitranscriptomes.

❯ `RgnTX` (R, Bioconductor): An R/Bioconductor software for the colocalization analysis of transcriptome elements with Monte Carlo permutation tests.

❯ `DPred` (Python-Keras): A novel computational tool for predicting Dihydrouridine (D) sites over mRNA sequences.

❯ `MetaTX` (R package): A statistical model, together with its EM solution, estimating the distribution of mRNA-related features in the presence of isoform ambiguity and differential composition among mRNAs.

⚙ Experiences

❯ Obtained a full scholarship to pursue Ph.D. degree at the University of Liverpool.

❯ Learned online MIT MicroMasters Program in **Statistics and Data Science** and earned certificates.

❯ Invited as reviewer by renowned journals such as *Computational and Structural Biotechnology Journal*.

❯ Worked as a teaching assistant for undergraduate courses: **Introduction to Probability and Statistics**, **Numerical Analysis**, **Statistical Distribution Theory** (in English).

🔧 Skills

❯ **Programming**: Python, R, Matlab, Java, SSH, Git

❯ **Data Mining**: Tensorflow; Pytorch; Pandas; Matplotlib, ggplot2; scikit-learn

❯ **Bioinformatics**: computational genomics, differential methylation analysis, epi-transcriptomics

❯ **Machine Learning**: probability theory, statistical inference theory, Bayesian statistics theory, generalized linear model, generative model, EM algorithm, data clustering and dimension reduction

❯ **Deep Learning**: supervised learning, multi-task learning, weakly-supervised learning