







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
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* > <u>Independent first author.</u>
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. > Yiyong Song, Yue Wang* , Xuan Wang, Daiyun Huang, Anh Nguyen, Jia Meng > Briefings in Bioinformatics (IF=13.99) , [10.1093/bib/bbad105] > <u>Independent corresponding author.</u>
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] > <u>Independent first author.</u>
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	<p>DirectRMDb: a database of post-transcriptional RNA modifications unveiled from direct RNA sequencing technology.</p> <ul style="list-style-type: none"> › 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	<p>MetaTX: deciphering the distribution of mRNA-related features in the presence of isoform ambiguity, with applications in epitranscriptome analysis.</p> <ul style="list-style-type: none"> › Yue Wang, Kunqi Chen, Zhen Wei, Frans Coenen, Jionglong Su, Jia Meng* › Bioinformatics (IF = 6.931), 37(9):1285–1291, [10.1093/bioinformatics/btaa938] › <u>Independent first author.</u>

Conference Papers

2020.07	<p>An Improved Algorithm for Estimating the Distribution of RNA-related Genomic Features.</p> <ul style="list-style-type: none"> › Jing Wu, Lihan Zhang, Yuanzhe Wang, Jia Meng, Jionglong Su, Yue Wang* › Proceedings of the Biological Information and Biomedical Engineering, (BIBE), 2020. › <u>Independent corresponding author.</u>
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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