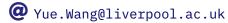
Yue Wang

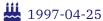












I'm Yue, a Ph.D. candidate studying at the School of Science and Engineering, University of Liverpool. I got my bachelor degree in Applied Mathematics, and have a solid foundation in mathematics, biostatistics, machine learning and artificial intelligence. My Ph.D. project is related to the bioinformatics 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	

d Journal Articles

- 2023 RgnTX: colocalization analysis of transcriptome elements in the presence of isoform heterogeneity and ambiguity. (under review, 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. (under review)
 - > 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

DirectRMDB: a database of post-transcriptional RNA modifications unveiled from direct RNA sequencing technology.

- > 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.

a 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