


Yue Wang

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

I'm Yue, a recent graduate from the University of Liverpool with a Ph.D. in Computer Science. I got my bachelor degree in Applied Mathematics, and have a solid foundation in mathematics, biostatistics, machine learning and artificial intelligence. In my doctoral study, I focused on the bioinformatics field, and developed statistical and deep learning approaches to characterize high-throughput epi-transcriptomics 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

2023.07	University of Liverpool •Department of Computer Science
2019.10	Doctor of Philosophy (Ph.D.) •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. (under review , software accepted by Bioconductor) <ul style="list-style-type: none">▶ 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) <ul style="list-style-type: none">▶ Zhanmin Liang, Haokai Ye, Jiongmeng 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. <ul style="list-style-type: none">▶ Yiyong Song, Yue Wang*, Xuan Wang, Daiyun Huang, Anh Nguyen, Jia Meng▶ Briefings in Bioinformatics (IF=13.994), [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. <ul style="list-style-type: none">▶ Yue Wang, Xuan Wang, Xiaodong Cui, Jia Meng, Rong Rong*▶ Molecular Therapy- Nucleic Acids (IF=10.183), [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. <ul style="list-style-type: none">▶ Yuxin Zhang, Jie Jiang, Jiongmeng 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 (IF = 19.160), 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 (IF = 19.160)**, 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

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201334709

03rd July 2023

Dear Yue Wang

Confirmation of Award

I am very pleased to inform you that your award of the degree of Doctor in Philosophy was approved on 03rd July 2023. You will be formally admitted to the degree of Doctor in Philosophy at a graduation ceremony to be held in Liverpool, at which point you will receive your formal award documentation.

The following is a summary of your registration:

You were registered as a candidate for the degree of Doctor in Philosophy from 01st October 2019. On 11th April 2023 you submitted your thesis which was entitled "*Statistical and Deep Learning Approaches for Characterizing RNA Modification with respect to RNA Sequence, Functional Component and Gene Structure*" following which the examiners recommended that you be awarded the degree of Doctor in Philosophy.

If they have not done so already, you will be contacted in due course by the University of Liverpool's Graduation Ceremonies Team with an invitation to register your intentions for your graduation ceremony in Liverpool. Please contact the team at gradenq@liverpool.ac.uk if you have any queries about this.

May I take this opportunity to offer you my congratulations on behalf of the University of Liverpool, and to wish you every success for the future.

Yours sincerely,



Michael Percival
Student Experience Manager (Administrative Services)