**Yuxuan Wu**

**yuxuan.wu17@gmail.com | 86 18936148662**

**EDUCATION**

**Xi’an Jiaotong-Liverpool University**  09/2017-07/2021

**Major:** Bioinformatics **GPA:** 3.85/4.0

**Standarized Test:** TOEFL 106 (Speaking 25) GRE 326 + 3.5 (Quantative 169)

**Award:** University Academic Achievement Award of 2017-2018 (Top10%); Silver Award in iGEM competition 2018

**Coursework:** Linear Algebra, Calculus, Introduction to Programming in Java, Database Development and Design, Methods for Analyzing Public Health (I,II): Biostatistics, Bioinformatics (I,II), Artificial Intelligence, Biochemical Methods and Analysis, Advanced Genetics, Molecular and Cell Biology Techniques

**PUBLICATION**

* Zhen, D., **Wu, Y.**, Zhang, Y., Chen, K., Song, B., Xu, H., Tang, Y., Wei, Z., Meng, J. (2020). m6A Reader: Epitranscriptome Target Prediction and Functional Characterization of N6-Methyladenosine (m6A) Readers, *Frontiers in Cell and Developmental Biology*, DOI: 10.3389/fcell.2020.00741 **(IF:5.201)**
* **Wu, Y.**, Zhang, Y., Wang, R., Meng, J., Chen K., Song, Y., Huang, D. (Accept). Prediction of m6A Reader substrate sites using deep convolutional and recurrent neural network, Conference: BIBE 2021- The Fifth International Conference on Biological Information and Biomedical Engineering, July 20-22, 2021 at Hangzhou, China; <https://github.com/yuxuanwu17/m6A_reader>
* Zhang, Y., **Wu**, **Y.**, Zhen, D., Chen, K., Meng, J. (Accept). Meta-analysis for knockdown of METTL3 or METTL14 affecting N6-methyladenosine methylation level, Conference: BIBE 2021- The Fifth International Conference on Biological Information and Biomedical Engineering, July 20-22, 2021 at Hangzhou, China; <https://github.com/yuxuanwu17/meta_analysis>

**RESEARCH**

**Predicting** **m6A Reader Sites based on Deep Learning Model** 03/2020-09/2020

* Compared the performance between SVM, CNN and CNN+RNN frameworks in predicting m6A Reader in Python
* Quantified the contribution of each input nucleotide to the m6A Reader sites by the layer-wise relevance calculation
* Achieved state-of-the-art performance (average AUROC: 0.942) under the CNN+RNN framework

**Meta-Analysis for knockdown of *N*6-Methyladenosine** **(m6A)** **Writer on mRNA** **methylation level** 01/2020-09/2020

* Verified the effectiveness of METTL3 or METTL14 in regulating the m6A methylation level in mRNA
* Constructed the Random-effects meta-analysis model and minimized the existed heterogeneity

**m6A Reader: Epitranscriptome target prediction and functional characterization** 06/2019-02/2020

* Incorporated both sequence-dervied and genome-derived features by 8 encoding methods from preprocessed sequence data
* Applied F-score technique to select significant features, reduce information redundancy and prevent potential overfitting
* Built and evaluated the performance in multiple machine learning models (SVM, LR, RF and XGBoost)
* Achieved high performance in SVM (average AUROC: 0.9) in predicting the m6A Reader substrates

**International Genetically Engineered Machine (iGEM) competition: EXOport**

**Website**: <http://2018.igem.org/Team:XJTLU-CHINA> 12/2017-11/2018

* Designed a special exsosome that could carry therapeutic drugs to cross the blood-brain barrier to relieve neurodegenerative dieases
* Simulated the transported efficiency of exosomes in circulatory system and created the pharmacokinetic model to estimate the drug delivery efficiency of the mRNA packaged into exosomes
* Took responsibility for the wet experiments including molecular cloning, cell culture (HEK293T) and plasmid transfection

**INTERNSHIP**

**Suzhou GeneQuantum Pharmaceuticals Corporation** 05/2018-09/2018

* Joined the Molecular Evolution department and worked as an assistant for molecular cloning
* Designed sequence primers using DNAworks and synthesized target genes using PCR

**SKILLS & INTERESTS**

Programming Language: R (proficient), Python (proficient), Shell (moderate), MATLAB (moderate), Java (moderate), SQL (moderate)

Skills: Adobe Illustrator, Calligraphy (Level 9), roller skating (National second-level athlete)