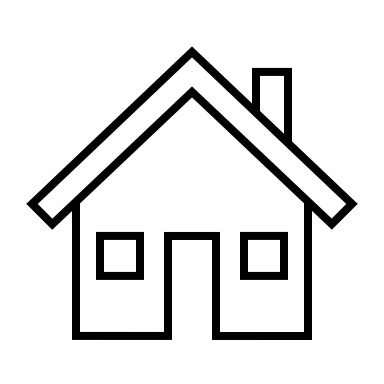
**Yuxuan Wu**

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**EDUCATION**

**Carnegie Mellon University** Aug 2021 - Now Major: Computational Biology GPA: In progressing

**Xi’an Jiaotong-Liverpool University** Sep 2017 - Jun 2021 Major: Bioinformatics GPA: 3.85/4.0

**Professional skills**

**Standardized Test:** TOEFL 106 (Speaking 25) GRE 326 + 3.5 (Quantitative 169)

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

**Programming language:** Python, Java, R, C#, JavaScript, Matlab

**Frameworks & tools:** Tensorflow, MySQL, Bootstrap, Hadoop, Ubuntu, Docker, Git

**Projects**

**Bosch Automotive Products (Suzhou) |** Full stack developer, Internship | *C#, SQL, JavaScript, Bootstrap, Ajax, jQuery*

* Developed an online platform to report and handle the problems about machine downtime Mar 2021- May 2021
* Achieved the real-time data interaction between the web page and Oracle database based on MVC design pattern
* Utilized Bootstrap framework to improve the user interface; Applied ajax and jQuery to transfer information asynchronously

**WeakRM: Viral m6A weakly supervised learning of RNA modification |** *Python, R, Bash* Sep 2020 - May 2021

* Incorporated both sequence-derived and structure-derived features by one-hot encoding methods
* Built a multi-instance learning with gated attention mechanism model which could maximize the feature utilization efficiency
* Achieved state-of-the-art performance (average AUROC:0.83) and maintained steady performance in generalization ability test.

**Kaggle: data analysis projects |** *Python, R |* [*https://www.kaggle.com/yuxuanwu17/code*](https://www.kaggle.com/yuxuanwu17/code)Sep 2020 - Jan 2021

* Explorative data analysis of heart failure and optimization of SVM-based model detection (Python)
* Explorative data analysis of avocado price from 2015 to 2020 in the United States (R)

**Hadoop based big data analysis |** *Java, Maven* |[*https://github.com/yuxuanwu17/Hadoop\_cw2*](https://github.com/yuxuanwu17/Hadoop_cw2)Sep 2020 - Jan 2021

* Configured the Hadoop environment in Ubuntu on the cloud server, Mac environment and Maven
* Learned the mechanisms about Map and Reduce and finished the word analysis in the Hadoop framework

**Predicting** **m6A Reader Sites based on Deep Learning Model |** *Python* Mar 2020 - Sep 2020

* Compared the performance between SVM, CNN and CNN+RNN frameworks in predicting m6A Reader in Keras
* Quantified each nucleotide contribution by layer-wise relevance calculation with overall high performance (average AUROC: 0.942)

**m6A Reader: Epitranscriptome target prediction and functional characterization |** *R*Jun 2019 - Feb 2020

* Built and evaluated the performance in multiple machine learning models (SVM, LR, RF and XGBoost) on sequence & genome data
* Achieved high performance in SVM (average AUROC: 0.9) in predicting the m6A Reader substrates

**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