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 (proficient), Java (moderate), R, C#, JavaScript, Matlab (familiar)

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

Internship

Bosch Automotive Products (Suzhou) | Full stack developer | *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

Research & Projects

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 Accuracy:0.751) and maintained steady performance in generalization ability test.

Kaggle: data analysis projects | *Python, R* | *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*   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 m^6A Reader Sites based on Deep Learning Model | *Python*   Mar 2020 - Sep 2020

- Compared the performance between SVM, CNN and CNN+RNN frameworks in predicting m^6A Reader in Keras
- Quantified each nucleotide contribution by layer-wise relevance calculation with overall high performance (average Accuracy: 0.868)

m^6A 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 Accuracy: 0.947) in predicting the m^6A Reader substrates

PUBLICATION

- Zhen, D., **Wu, Y.**, Zhang, Y., Chen, K., Song, B., Xu, H., Tang, Y., Wei, Z., Meng, J. (2020). m^6A Reader: Epitranscriptome Target Prediction and Functional Characterization of N^6-Methyladenosine (m^6A) 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 m^6A 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