

YUXUAN WU

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EDUCATION

Carnegie Mellon University

Aug 2021 – May 2023

Master of Science in Computational Biology

Xi'an Jiaotong-Liverpool University

Sep 2017 - Jun 2021

Bachelor of Science in Bioinformatics

GPA: 3.88/4.0 (Top 5%)

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

Coursework: Java Programming, Artificial Intelligence, Databases Design, Big Data Analysis, Data Mining, Web Development

TECHNICAL SKILLS

Programming language: Java, Python, R, C#, HTML/CSS/JavaScript, Matlab

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

PROFESSIONAL EXPERIENCE

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

- Developed a web 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
- Independently utilized Bootstrap to enhance the user interface; Applied ajax and jQuery to transfer information asynchronously

RESEARCHES & 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

- Detected the existing heart failure disease globally and optimized the SVM-based model to achieve average accuracy in 0.833
- Independently visualized and analyzed avocado price patterns from 2015 to 2020 in the United States by ggplot2

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 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 Accuracy: 0.868)

m⁶A Reader: Epitranscriptome target prediction and functional characterization | *R*

Jun 2019 - Feb 2020

- Collaboratively built and evaluated 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 m⁶A Reader substrates

PUBLICATIONS

- Zhen, D., Wu, Y., Zhang, Y... (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.... (2021). [Prediction of m⁶A Reader substrate sites using deep convolutional and recurrent neural network](#), Conference: BIBE 2021