YUXUAN WU

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EDUCATION

Carnegie Mellon University - School of Computer Science   Pittsburgh, PA

Master of Science in Computational Biology | GPA: 4.0/4.0   Aug 2021 – May 2023

Courseworks: Algorithms and Data Structures, Statistics, Computational Medicine, Genomic, Deep Learning

Xi'an Jiaotong-Liverpool University   Suzhou, China

Bachelor of Science in Bioinformatics | GPA: 3.88/4.0 (Top 5%)   Sep 2017 - Jun 2021

Honors: University Academic Achievement Award of 2017-2018 (Top 10%); Silver Award in iGEM competition 2018

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

TECHNICAL SKILLS

Programming Languages: Python, Java, Golang, R , SQL, C#, HTML/CSS/JavaScript, Matlab

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

PROFESSIONAL EXPERIENCE

CyLab Biometrics Center | Research Assistant Intern | Weapon Image Classification | MMPose   Apr 2022 – Aug 2022

- Conducted cleaning and analysis of the images and segmented the tasks into 3 difficulty levels by blurry and occlusion
- Generated and optimized corresponding hand-region cropped image datasets with pose information by MMPose
- Incorporated ResNet18 for weapon classification problem and achieved a 0.809 accuracy in real-time testing

Bosch Automotive Products | Full-stack developer | *C#, SQL, JavaScript, Bootstrap, Ajax, jQuery*   Mar 2021- May 2021

- Developed a web platform to report and handle the problems about machine downtime
- 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

PROJECTS & RESEARCHES

Kaggle Competition:11785 Deep Learning (A$^+$) | *Pytorch* | *https://www.kaggle.com/yuxuanwucmu* Mar 2022 – May 2022

- Implemented the SOTA ConvNext with data augmentation to achieve 0.893 accuracy in image classification task (Top 10%)
- Fine-tuned and trained the saved model with Triplet loss to achieve 0.962 AUC in image verification task (Top 25%)
- Incorporated CTC loss and Beam Search based on RNN model for automatic speech recognition (Top 10%)
- Implemented attention-based speech recognition (ASR) in Seq-to-Seq fashion with Teaching-force, LockedDropout (Top 10%)

Semantic Supervision Paradigm | *Pytorch* | *https://github.com/yuxuanwu17/Semantic_Supervision* Mar 2022 – May 2022

- Implemented SemSup which leverages semantic information of labels to boost classification accuracy by multi-modality
- Deployed a label description encoder by pre-trained Bert, an image encoder by ResNet, and a MLP scorer for fusion
- Enabled generalization and high accuracy on cifar100: Unseen Description (0.71), Unseen Class (0.63), Unseen Superclass (0.66)

WeakRBP: Weakly supervised learning of RNA-protein binding preference | *Python, R, Bash*   Sep 2021 - May 2022

- Incorporated both sequence and structure-derived instance features by stride and a sliding window to satisfy multi-instance learning
- Upgraded pooling and feature merging methods by gated-attention to dynamically learn and quantify instance significance
- Achieved SOTA performance (Accuracy:0.751) with robust generalization ability and visualized the attention map for interpretability

Epitranscriptome target prediction and functional characterization of m^{6}A Reader | *Python, R*   Mar 2019 - Sep 2020

- Compared the performance between SVM, CNN and CNN+RNN frameworks in predicting m^{6}A Reader in Keras
- Collaboratively built and evaluated multiple machine learning models (SVM, LR, RF and XGBoost) on sequence & genome data
- Quantified each nucleotide contribution by layer-wise relevance calculation with overall high performance (average Accuracy: 0.868)

PUBLICATIONS

- **Wu, Y.**, Zhang, Y., Wang, R…. (2021). Prediction of m^{6}A Reader substrate sites using deep convolutional and recurrent neural network, *BIBE 2021*, DOI: https://doi.org/10.1145/3469678.3469706
- Zhen, D., **Wu, Y.**, Zhang, Y…(2020). m^{6}A Reader: Epitranscriptome Target Prediction and Functional Characterization of N^6-Methyladenosine (m^{6}A) Readers, *Frontiers in Cell and Developmental Biology*, DOI: 10.3389/fcell.2020.00741 **(IF:5.201)**