Zhuosheng Liu

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Experience

Information Fusion and Mining Lab, Graduate Research Assistant co-advised by Dr. Jiawei Zhang

May 2023 - Now

- Developed and optimized classic machine learning and deep learning models for microbial pangenome, achieving rapid and accurate pathogenicity assessment of pathogenic bacteria.
- Drove advanced solutions and compared different parameter efficient-fine-tuning methods for vision language model.

Data-intensive Biology Lab: Graduate Research Assistant co-advised by Dr. Titus Brown

March 2021 - Now

- Conducted and analyzed large-scale transcriptomics data of microbial-system by building high-throughput and fully automatic bioinformatics pipelines
- Organized and maintained large scientific projects on **High Performance Computer** over the cloud and kept **git version control** up-to-date

Food Microbiology Lab: Graduate Research Assistant advised by Dr. Luxin Wanq

• Conducted experiments using both culture-dependent and next-generation sequencing biotechnology to characterize fitness and behaviors of pathogenic foodborne pathogens

UC Davis FST, MIC and ECS department *Graduate Teaching Assistant*

June 2020 - Now

- Graduate tutor for ECS 122A algorithm analysis and design, holding two hours office hours/week to answer undergraduate questions regarding course material
- Graduate TA for MIC 103L and FST 104L, teaching students in microbiology lab practice and guiding students in journal club

Education

3.97/4.0 PhD. in Food Science, UC Davis | California, USA

CVPR 2024 (Submitted) | PNAS (ready to submit)

2020-25

3.93/4.0 Master's degree in Computer Science, UC Davis | California, USA

2023-25

3.84/4.0 Master's degree in Biotechnology, Columbia University | New York, USA

2019-20

Research Focus: Food Microbiology | Microbial Genomics & Transcriptomics | Applied Bioinformatics | Applied ML/AI International Publications: Microbiology Spectrum(IF9.1) | Food Research International (IF8.1) | Food Control (IF6.1) | LWT (IF6.0) |

Courses: ECS 271 Advanced Machine Learning (A+) | ECS 174 Computer Vision (A) | ECS 122A Algorithm Analysis and Design (A) | ECS 124 Bioinformatics Theory and Practice (A) STA 141 Advanced Statistical Computing A-B-C (A) ECS 201A Computer Architecture

Skills

Software

Programming Python (NumPy, SciPy, pandas, Matlotlib, Jupyter), C/C++, Java, Perl, R, CUDA, CMake, Git, Bash Scripting, LaTeX

Linux, Tensorflow, Pytorch, OpenCV, Snakemake, scikit-learn,

Bioinformatic skills

Automatic workflow construct using Snakemake, 16s rRNA-sequencing analysis, RNA-sequencing analysis, Whole-genome sequencing analysis, Pangenome construction and analysis

Projects

Virulence prediction of pathogenic foodborne pathogens using ML/DL based on Pangenome

June 2023 - Now

Manuscript in preparation

- Constructed pangenome (100,000 unique gene feature) using fully integrated and scalable bioinformatics pipeline (automation achieved using Snakemake)
- Visualized high-dimensional pangenomic gene feature using dimensional reduction PCA
- Trained, optimized, validated and statistically compared fundamental unsupervised and supervised machine learning model performance, including Kmean, GMM, KNN, SVM, RF, Naive Baye
- Trained and validated deep neural network (MLP and CNN) and achieved 93% virulence prediction accuracy

Parameter-Efficient Fine-Tuning for Vision-Language Models

June 2023 - Now

Preliminary report available at *Here*

- Conducted an extensive study on the application of **Parameter-Efficient Fine-Tuning** (PEFT) methods to vision-language models, particularly focusing on the **CLIP**.
- Conducted comprehensive empirical analysis across various datasets, such as VTAB-1K, to understand the adaptability and effectiveness of PEFT methods in different scenarios.
- Investigated the effectiveness of prompt engineering and adapter technique such as LoRA in improving model performance
- Implemented and optimized various hyperparameters through systematic grid search methods to ascertain the most effective settings for the models.
- Demonstrated the potential of PEFT in vision-language models through empirical studies, highlighting the need for enhanced approaches in complex multimodal scenarios.

Transcriptomic analysis of pathogenic Vibrio parahaemolyticus

June 2021 - June 2023

Paper has been accepted and published in Microbiology Specturm *Here*

- Obtained biological insights of Vibrio parahaemolyticus using RNA-seq data analysis (genome reference-free Salmon pipeline)
- Python-oriented web-script extracting essential information gene annotation from JSON-based KEGG database
- Conducted statistical differential expression gene analysis over 4000 unique genes using Deseq2