Guohao Wang

(+86)15269353128 | ■ truman@nwafu.edu.cn | ♠ https://trumanphd.github.io/ | ♠ TrumanPhd/ | ♠ Guohao03 | ♥

@TrumanPhd | ♠ Yangling, Shaanxi, China

Education

Sep. 2021 - Jun. 2025 currently sophomore

Northwest AF University (NWAFU) Yangling, Shaanxi BS in EE Sep. 2021 - Jun. 2025 currently sophomore GPA 3.91 (92.15, top3)

Technical Skills

Programming Python (Pytorch, keras, numpy, pandas), shell, Matlab, C, HTML,

Professional Softwares Vscode (-ssh), Anaconda, Docker, Remote collaboration software, ChatGPT prompt, CAD, AD,.....

Drawing & Typesetting Visio, Photoshop, Office, LATEX,

Languages English(oral&paper writing), Chinese(native)

Publications _____

[1] Guohao Wang, Ze Liu*, Ting Liu, et al. "F5C-finder: combining language model with multi-head attention for predicting 5-Formylcytidine modifications on mRNA" prepare submit to Briefings in Bioinformatics

Research Projects _____

Research on Genomics (single cell ATAC-seq) with Deep learning (Swin transformer)

Yangling

Project supported by the Young Scientists Fund of the National Natural Science Foundation of China (Grant No.

61902323) Research assistant

Dec. 2023.Mar -

- · Multi-GPU model training on Linux
- Nueral network based models to denoise and peak calling for m6A data from m6A-seq
- Read and debugged models from classic papers in the field of computer vision presented at top conferences after 2015.

Research on epigenetic modification identification with LLM and webserver implemention

Yangling

Research assistant in NWAFU

Dec. 2022 - May. 2023

July. 2022 - Nov. 2022

- Improved fusion model with RNN and multi-head attention to recognize 5-Formylcytidine modifications on mRNA
- Developed SOTA models and implemented on webserver
- Finished a paper for Briefings in Bioinformatics as first author supervised by Prof. Ze liu

Research on Oxidoreductase protein identification with machine learning

Yangling

Research assistant in NWAFU

Design new feature engineering methods for bio-sequences

- HAO selection: an improved feature selection methods with better performances than MRMD on epigenetic modification
- All the code and methods has been open sourced on Git-hub

References _

Prof. Ze Liu