Jiawei Zhang 🏅

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🎓 EDUCATION

CIVIL AVIATION UNIVERSITY OF CHINA   *Tianjin, China*
Faculty of Economics and Management, Bachelor of Business Administration   *Sep. 2016 – Jul. 2020*
GPA: 3.67/4.0 (85.4/100)

Key courses: Advanced Mathematics/92 (89+95); Probability-and-Statistics/80; Business Statistics and Forecasting/89

📖 PUBLICATION

Jiawei Zhang, Wang Ma, Hui Yao, "Accurate TCR-pMHC interaction prediction using a BERT-based transfer learning method", Briefings in Bioinformatics, Volume 25, Issue 1, January 2024, bbad436 (IF=6.8/Q1)

Wang Ma, **Jiawei Zhang**, Hui Yao. "NeoMUST: an accurate and efficient multi-task learning model for neoantigen presentation" Life Science Alliance Jan 2024, 7 (4) e202302255 (IF=3.3/Q1)

🔬 RESEARCH EXPERIENCES

DEVELOP AN LLM-BASED BIOLOGICAL AGENT

Westlake University Hangzhou, China
Research Assistant   *May. 2024 – Present*
- Project content: Design and develop an LLM-based agent system that automatically executes corresponding AI models and bioinformatic tools based on the user's needs.
- Main responsibilities: Construct the agent framework; Deploy some of the deep learning models

DEVELOP COLABSAPROT AND SAPROTHUB

Westlake University Hangzhou, China
Research Assistant   *Apr. 2024 – Aug. 2024*
- Project content: Develop ColabSaprot and SaprotHub to support scientific research, allowing biologists to easily train and use Protein Language Models. SaprotHub is widely used for protein-related tasks, with wet lab experiments validating its results.
- Main responsibilities: Test and optimize the function of ColabSaprot; Assist in building ColabSaprot and SaprotHub
- Completed a paper as the OPMC author: "SaprotHub: Making Protein Modeling Accessible to All Biologists". (Under Review at ***Nature Methods***)
- Open-source address: https://github.com/westlake-repl/SaprotHub

RESEARCH AN LLM-BASED WEB3 AGENT

The Hong Kong University of Science and Technology, China
Research Assistant (Remote)   *Apr. 2024 – Present*
- Project content: Design an agent that can decompose user requirements and then select and execute the appropriate tool for each step of the task.
- Main responsibilities: Design the agent framework; Investigate appropriate fine-tuning algorithms

PREDICT TCR-PMHC BINDING USING DEEP LEARNING

Fresh Wind Biotechnologies Inc. Tianjin, China

Assistant Bioinformatics R&D Engineer   *Apr. 2022 – Apr. 2024*

- Project content: Predict the binding of TCR peptide-MHC-1 complexes by BERT-based deep learning model with transfer learning.
- Main responsibilities: Data collection and organization; Modification of model structure; Code writing and Github repository creation; Model training and testing; Writing of the paper
- Results: Completed paper as the first author: "Accurate TCR-pMHC Interaction Prediction Using a BERT-based Transfer Learning Method". (Published in ***Briefings in Bioinformatics***)
- Open-source address: https://github.com/Freshwind-Bioinformatics/TABR-BERT

IDENTIFY NEOANTIGENS USING DEEP LEARNING

Fresh Wind Biotechnologies Inc. Tianjin, China

Assistant Bioinformatics R&D Engineer   *Apr. 2022 – Apr. 2024*

- Project content: Accurate identification of neoantigens by multi-task learning architecture with LSTM as the feature extractor.
- Main responsibilities: Data collection and organization; Assist in Github repository creation; Assist in model testing; Assist in writing of the paper
- Results: Completed paper as the second author: "Neo-MUST: an Accurate and Efficient Multi-Task Learning Model for Neoantigen Presentation". (Published in ***Life Science Alliance***)
- Open-source address: https://github.com/Freshwind-Bioinformatics/NeoMUST

🎈 AWARD & ACTIVITY

2017-2018 Renmin Third-Class Scholarship
National Innovation and Entrepreneurship Project / Team member
Director of the Communication Club of the Student Union of the University
Undergraduate class monitor
School Library, Kindergarten Outstanding Volunteer
Summer Social Practice Advanced Individual

💡 SKILLS AND OTHERS

Skills: Python, Liunx, Docker, R
Interest: Photography📷, Reading🌊