YIFAN DENG

◇ yifand@cs.wisc.edu ◇ Google Scholar

EDUCATION

University of Wisconsin-Madison, Madison *Sept. 2022 - Present*
PhD student in Computer Science
Fudan University, Shanghai *Sept. 2021 - Aug. 2022, Quitted*
MPhil student in Computer Science
Wuhan University, Wuhan *Sept. 2017 - June 2021*
Bachelor in Electronic Engineering

RESEARCH INTERESTS

My research interests mainly lie in the area of AI application in Healthcare and Biology, with a focus on small molecule, protein and genomics problems. I aim to accelerate the development of new drug and find the cause of gene-related diseases like cancer.

SELECTED PUBLICATIONS

1.**Deng Y**, Xu X, Qiu Y, et al. A multimodal deep learning framework for predicting drug-drug interaction events[J]. Bioinformatics, 2020.
2.**Deng Y**, Qiu Y, Xu X, et al. META-DDIE: predicting drugdrug interaction events with few-shot learning[J]. Briefings in Bioinformatics, 2021.
3.Qiu Y, Zhang Y, **Deng Y**, et al. A Comprehensive Review of Computational Methods for Drug-drug Interaction Detection[J]. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020.
4.Liu S, Wang Y, Wang T, **Deng Y**, et al. Improved Drug-Target Interaction Prediction with Inter-Molecular Graph Transformer[J]. Briefings in Bioinformatics, 2022

EXPERIENCE

ByteDance(TikTok) AI Lab, AI Drug team, Research Intern *Apr. 2022 - Present*
We proposed a novel protein design methodology, which improved the sequence recovery rate from 50% to 55%. More details may be disclosed during the interview or after the publication.
CUHK, Department of Computer Science, Research Assistant *July 2021 - Apr. 2022*
Used point cloud transformer and molecular dynamics simulation data to model the protein surface calculation, thus enhancing the performance in several downstream tasks such as protein interaction site identification, protein-protein interaction and ligand-protein interaction.
Microsoft Research Asia, Computational Biology Group, Research Intern *Dec. 2020 - June 2021*
1.Built the dataset of Enhancer-Promoter with cCRE, RNA-seq and ChIP-Seq data and model the gene regulation problem with transformer. Reached a spearman correlation of 0.53 across 11 cell types on gene expression level prediction and successfully identified MYC's nearby cCREs' influences on it.
2.Used Graph Transformer in the prediction of drug-target interaction. By integrating inter-molecular information, we greatly increase model's performance on DUD-E, LIT-PCBA and PBDbind by 9.1% in AUC.
Microsoft Research Asia, Innovation Engineering Group, Research Intern *Sept. 2020 - Dec. 2020*
Based on Qlib, we used AutoML to perform feature engineering automatically, and generate promising new factors, increasing Information Coefficient by 2%, which may contribute to better prediction of stock data.
Wuhan University, School of Computer Science, Research Assistant *Apr. 2020-Aug. 2020*
In order to deal with the imbalanced DDI event distribution, we proposed META-DDIE, a few shot learning framework to predict the rare events, which shows 10% accuracy improvement compared with transfer learning method.
Wuhan University, School of Computer Science, Research Assistant *Mar. 2019 - Jan. 2020*
Collected multiple features of drugs from different resources, building a multimodal deep learning framework to predict drug-drug interaction events, increasing the AUPR from 0.89 to 0.92.

HONORS AND AWARDS

Scholarship
Liu Daoyu's Scholarship (Top 36 out of 21,000 undergraduate in Wuhan University) *Dec. 2020*