

Zhihan Zhou

Add: Dorm 1, Yuquan Campus, Zhejiang University, Hangzhou, China

Tel: (86) 17816872057 E-mail: zzh760998379@163.com

EDUCATION

Zhejiang University, School of Mathematical Sciences

Hangzhou, China

Bachelor of Science in Mathematics and Applied Mathematics

expected 6.2018

- GPA: 3.42, major GPA: 3.62 (top 50%)
- Awarded third prize in College Math Competition

RESEARCH EXPERIENCE

Joint Speaker Diarization and Recognition Using Convolutional and Recurrent Neural Networks

U.S.

Advisor: Zhiyao Duan, Assistant Professor in Dept. of ECE, University of Rochester

First Author

7 – 9.2017

- Designed a system to simultaneously complement speaker diarization and recognition to identify specific speakers and estimated corresponding time boundaries; being accepted by ICASSP 2018 for publishing
- Segmented conversational files into non-overlapping 0.2-sec time frames; transformed time frames into log-mel spectrograms, then categorized these spectrograms into a Convolutional Neural Network (CNN1)
- Initiated another Convolutional Neural Network (CNN2) to process regression to detect speaker change probability in order to utilize the continuity between chronologically distributed time frames
- Integrated the outputs of CNN1 and CNN2 with a Recurrent Neural Network (RNN) that elicited improvements in specifying identity with corresponding time periods simultaneously
- Verified performance of the developed method in two data sets with accuracy above 83% in the first set, followed by a recall over 0.8 and precision over 0.7 in the second set, proving the method's plausibility
- Programmed the entire project using Python, leveraging the Librosa module to transform frames into spectrograms and construct 3 neural networks with different structures based on the Keras module

Ensemble Learning and Link Prediction for miRNA-Disease Association prediction

Hangzhou, China

Joint First Author

3 – 6.2017

- Predicted potential miRNA-disease associations by identifying the models in MATLAB; the completed article is currently under review and expected to be published in RNA Biology, a peer-reviewed journal
- Constructed known miRNA-disease association network matrix based on the data set HMDD v2.0 (Li et al., 2014) and verified the results by applying the network matrix to irrelevant data sets
- Built miRNA functional similarity network and disease semantic similarity network matrices to quantify the connectivity and relevancy between diseases and miRNAs
- Calculated Gaussian interaction profile kernel similarity for miRNAs and diseases based on the assumption that functional similar miRNAs tend to be associated with similar diseases as well as the topologic information of known miRNA-disease associations network
- Integrated the aforementioned 5 networks into a comprehensive similarity network and used 3 similarity-based algorithms to predict potential associations between the miRNA-disease and 14 disease states (kidney neoplasms, lymphoma, etc.) by pinpointing 50 relevant miRNAs, then cross checked the relevancy by confirming results of 2 other data sets
- Derived weighted average of the three algorithms using ensemble learning based on the experiment above, and sorted all combinations among 383 diseases and 495 miRNAs by the probability of existence
- Utilized results of LOOCV and 5-fold CV methods to draw a Receiver Operating Characteristics (ROC) curve and calculated the area under ROC, revealing AUC=0.9181(LOOCV), AUC=0.8181(5-fold CV) with an enhanced precision
- Programmed the entire experiment process in MATLAB with a matrix transformation based on the integration of 4 similarity network matrices

OTHERS

- Proficient in Python, C and MATLAB
- Completed courses including Machine Learning, Data Structure and Operating Systems on Coursera