

Wei Wang

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EDUCATION

Michigan State University, United States

Ph.D. in Computer Science

Degree expected: May, 2021

GPA: 3.9/4.0

Institute of Biophysics, Chinese Academy of Sciences, China

Sep. 2013 – Jun. 2016

M.S in Bioinformatics

GPA: 3.8/4.0

Southwest University, China

Sep. 2009 – Jun. 2013

B.E in Software Engineering

GPA: 3.5/4.0

TECHNICAL STRENGTHS

Proficient in Python, R, Java, C++, MATLAB, JavaScript, PHP, HTML

Have rich experience in algorithm development, statistical model design, data mining with large-scale data, and pattern recognition. Experienced with machine learning theories and algorithms.

RESEARCH EXPERIENCE

Department of Computer Science and Engineering, Michigan State University

Research Assistant

Jul. 2016 – Now

- Designed and developed SERES, a new sequential resampling approach for biological sequences, which has been successfully applied on support estimation of multiple sequence alignment and improved the accuracy of support estimation by 10%.
- Developed local genealogy inference approach with the SERES resampling approach.
- Developed support estimation approach for phylogenetic tree using the SERES resampling approach and improved the performance by 35%.
- Building up statistical model and algorithm for inferring phylogenetic network from large-scale data.
- Building new sampling approach for the support estimation of multiple sequence alignment using reinforcement learning.

System Immunology Lab, Department of Biomedical Engineering, University of Texas at Austin

Research Assistant

Feb. 2015 – Sep. 2015

- Developed and refined preprocessing of r RNA-Seq data using clustering. Reduced sequencing error rate to 0.003%.
- Built up human donor database to manage basic information and sequencing data of human donors.

Key Laboratory of RNA Biology, Institute of Biophysics, Chinese Academy of Science

Research Assistant

Sep. 2013 – Jun. 2016

- Built up classification model for mutation pattern of antibody repertoire of HIV infected patients based on large RNA-Seq data.
- Identified patterns involved in different HIV disease progression from high-dimension gene expression data by clustering methods.

PROJECTS

2019 WiDS Datathon: Identification of The Oil Palm Plantations

Feb. 2019 – Feb. 2019

- Worked in a group of four. Applied se-resnext101 on the problem of identification of the oil palm plantations from the high-resolution satellite imagery.
- Our team won the 4th place of this competition.

Toxic Comment Classification by Deep Learning networks

Feb. 2018 – May. 2018

- Worked in a group of two. Applied LSTM Classifier, GRU Classifier and Gradient Boosting Decision Tree Classifier on the problem of toxic comment classification. The best accuracy achieved 98%.

Automatic Generation of Chinese Song Ci Using RNN

Feb. 2017 – May. 2017

- Worked in a group of three. Applied LSTM, GAN and Genetic Algorithm on learning to write Song Ci with given format and topic. Generated Ci which were meaningful, relevant to the topic and following certain patterns of rhyme.
- Won the most popular project award in 2017 Spring CSE 847 Machine Learning Course.

PUBLICATION

Wei Wang, Jack Smith, Hussein A. Hejase, and Kevin J. Liu. “Non-parametric and semi-parametric support estimation using sequential resampling random walks on biomolecular sequences”. *16th RECOMB Comparative Genomics 2018 (RECOMB CG 2018)*

SELECTED HONORS AND AWARDS

The best poster award of the 2019 Engineering Graduate Research Symposium

Mar. 2019

2nd place poster award of the 2017 Engineering Graduate Research Symposium

Apr. 2017

BEACON Top-Up Recruiting Fellowships

2016 - 2019

Outstanding Student, Chinese Academy of Sciences

Apr. 2014