

# Wei Wang

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## EDUCATION

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**Michigan State University, United States**

*Ph.D. in Computer Science*

*Aug. 2013 – Oct. 2021*

GPA: 3.9/4.0

**Institute of Biophysics, Chinese Academy of Sciences, China**

*M.S in Bioinformatics*

*Sep. 2013 – Jun. 2016*

GPA: 3.8/4.0

**Southwest University, China**

*B.E in Software Engineering*

*Sep. 2009 – Jun. 2013*

GPA: 3.5/4.0

## RESEARCH EXPERIENCE

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**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 the estimated support by 10%.
- Developed local genealogy inference approach with the SERES resampling approach.
- Developed non-parametric sequential resampling approach RAWR for the support estimation of phylogenetic trees, which improved the PR-AUC performance by 35%.
- Developed survival prediction model for triple-negative breast cancer based on gene expression data.
- Developing reinforcement learning approach for support estimation of multiple sequence alignment.
- Developing algorithm for phylogenetic inference using RNA-seq reads.
- Developed desktop software, command line tool and online service for phylogenetic support estimation utilizing SERES and RAWR resampling algorithms.

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

*Research Assistant*

*Feb. 2015 – Sep. 2015*

- Developed and refined preprocessing of 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.

## CONFERENCES/TALKS

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- Proceeding talk and poster presentation on 2019 IEEE BIBM 2019 Conference at San Diego, CA, USA (Won Student Travel Award) *Nov 2019*
- Poster presentation on 2019 Evolution Conference at Providence, RI, USA *Jun. 2019*
- Poster presentation on 2019 CRA-W Grad Cohort for Women at Chicago, IL, USA *Apr. 2019*
- Poster presentation on 2019 Engineering Graduate Research Symposium at East Lansing, MI, USA (Won best poster award) *Mar. 2019*
- Proceeding talk and poster presentation on RECOMB-CG 2018 at Magog-Orford (Sherbrooke), Quebec, Canada *Oct. 2018*
- Poster presentation on 2018 BEACON congress at East Lansing, MI, USA *Aug. 2018*
- Poster presentation on 2017 Engineering Graduate Research Symposium at East Lansing, MI, USA (Won 2<sup>nd</sup> poster prize) *Apr 2017*

## TEACHING EXPERIENCE

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- Mentoring graduate student Julia Zhang on the graduate research program *Fall 2020, Spring 2021*
- Mentoring graduate student Ahmad Hejasebazzi on the graduate research program *Spring 2020*
- Mentoring undergraduate student Heather Noonan on the undergraduate research program *Fall 2018*
- Teaching assistant for graduate-level course CSE 841 (Artificial Intelligence) *Fall 2018, Fall 2019*
- Teaching assistant for undergraduate-level course CSE331 (Algorithms and Data Structure). *Fall 2016, Spring 2017*
- Mentoring undergraduate student Jack Smith on his summer research intern. *Summer 2017*

## PUBLICATION

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Julia Zhang, Wei Wang, Meijun Gao, and Kevin J. Liu. "RAWR v1.0: a software suite for sequence-aware phylogenetic support estimation and other RANdom Walk Resampling tasks". *Under review*

Meijun Gao, Wei Wang, and Kevin J. Liu. "The Impact of Multiple Sequence Alignment Error on Summary-based Phylogenetic Network Estimation". *the 13th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, 2022*

Wang, Wei, et al. "Build a better bootstrap and the RAWR shall beat a random path to your door: phylogenetic support estimation revisited." *ISMB/ECCB 2021*

Wei Wang, Qiqige Wuyun, and Kevin Liu. An Application of Random Walk Resampling to Phylogenetic HMM Inference and Learning. *IEEE transactions on nanobioscience, 2020*

Wei Wang, Qiqige Wuyun, and Kevin Liu. "An Application of Random Walk Resampling to Phylogenetic HMM Inference and Learning". *IEEE BIBM 2019 conference*

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". *Algorithms for Molecular Biology, 2020*

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**

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Student travel award of IEEE BIBM 2019 Conference at San Diego, CA, USA	<i>Nov. 2019</i>
The best poster award of the 2019 Engineering Graduate Research Symposium	<i>Mar. 2019</i>
2 <sup>nd</sup> place poster award of the 2017 Engineering Graduate Research Symposium	<i>Apr. 2017</i>
BEACON Top-Up Recruiting Fellowships	<i>2016 - 2019</i>
Outstanding Student, Chinese Academy of Sciences	<i>Apr. 2014</i>
First Class Scholarship of Southwest University	<i>Oct. 2010, 2012</i>