ZIYUE WANG

Biostatistics and Computational Biology Branch, National Institute of Environmental Health Sciences

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CURRENT POSITION

Postdoctoral Fellow, 2020-present
Biostatistics and Computational Biology Branch, National Institute of Environmental Health Sciences, National Institutes of Health
Advisors: Alison Motsinger-Reif and Shanshan Zhao

EDUCATION

Ph.D. in Statistics and Minor in Quantitative Biology, 2015-2020
Department of Statistics, University of Wisconsin-Madison
Advisor: Christina Kendziorski
Dissertation: Statistical Methods for Genomics and Genetics Data Analysis

B.S in Mathematics and Applied Mathematics and B.S in International Economy and Trade, 2010-2014
Department of Mathematics, Shanghai Jiao Tong University, Shanghai, China

RESEARCH INTERESTS

Statistical genetics, genomics and microbiomics analysis
Cross species and multi-omics data integration
High-throughput sequencing data

PROFESSIONAL EXPERIENCE

Postdoctoral Fellow, 2020-present
Biostatistics and Computational Biology Branch, National Institute of Environmental Health Sciences
Advisors: Alison Motsinger-Reif and Shanshan Zhao

· Development of bioinformatics pipeline and normalization methods for microbiome data
· Development of integration methods for cross-species multi-omics data
· Collaboration with multi-disciplinary scientists on analysis of environmental and mouse microbiome data

Research Assistant, 2016-2020
Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison
Advisor: Christina Kendziorski

· Development of network reconstruction method using regularized algorithm for single cell RNA-seq data
· Built and maintained RNA-sequencing data analysis pipeline from quality control to advanced downstream analysis.
· Led collaborative projects with various laboratories on biomedical and genomics data

Research Assistant, 2018-2020
Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison
Advisor: Christina Kendziorski; Collaborator: Mark Keller

· Built a cross species genetic signal integration pipeline

- Developed an iterative mapping procedure for narrowing down genetic region of interest
- Conducted QTL mapping for genetic architecture profiles on diversity outbred mouse data

Research Assistant, 2017-2018
Morgridge Institute for Research, University of Wisconsin-Madison
Advisor: Christina Kendziorski; Collaborator: Li-Fang Chu

- Built polynomial and segmented regression models to characterize dynamic activity of microRNAs and mRNAs over time
- Identified microRNAs and mRNAs with similar expression pattern across human and mouse data

Junior Biostatistician, 2014-2015
Medical Research and Biometrics Center, National Center for Cardiovascular Diseases, affiliated with Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, China

- Conducted data management using SQL, statistical analysis and reviewed reports for multiple registered clinical trials in China
- Collaborated onsite with hospital doctors and provided consulting in China Acute Myocardial Infarction Registry project

Trainee, 2012-2013
Department of Computer Science and Engineering, Shanghai Jiao Tong University
Advisor: Wujun Li

- Discussed on convex optimal models applied to social network data in weekly seminars

PUBLICATIONS

Peer-Reviewed

Maitre L, Guimbaud JB, Warembourg C, Gil-Oumrait N, Petrone PM, Chadeau-Hyam M, Vrijheid M, Gonzalez JR, Basagaa X, Exposome Data Challenge Participant Consortium. State-of-the-Art Methods for Exposure-Health Studies: results from the Exposome Data Challenge Event. *Environment International.* 2022 Aug 27:107422.

Emfinger CH, de Klerk E, Schueler KL, Rabaglia ME, Stapleton DS, Simonett SP, Mitok KA, **Wang Z**, Liu X, Paulo JA, Yu Q. β Cell-specific deletion of Zfp148 improves nutrient-stimulated β cell Ca^{2+} responses. *JCI insight.* 2022 May 23;7(10).

De I, Maklakova V, Litscher S, Boyd MM, Klemm LC, **Wang Z**, Kendziorski C, Collier LS. Microglial responses to CSF1 overexpression do not promote the expansion of other glial lineages. *Journal of Neuroinflammation.* 2021 Dec;18(1):1-3.

Foote AG, **Wang Z**, Kendziorski C, Thibeault SL. Tissue specific human fibroblast differential expression based on RNAsequencing analysis. *BMC Genomics.* 2019 Dec 1;20(1):308.

Lungova V, Chen X, **Wang Z**, Kendziorski C, Thibeault SL. Human induced pluripotent stem cell-derived vocal fold mucosa mimics development and responses to smoke exposure. *Nature Communications.* 2019 Sep 24;10(1):1-6.

Keller MP, Rabaglia ME, Schueler KL, Stapleton DS, Gatti DM, Vincent M, Mitok KA, **Wang Z**, Ishimura T, Simonett SP, Emfinger CH. Gene loci associated with insulin secretion in islets from nondiabetic mice. *The Journal of Clinical Investigation.* 2019 Sep 9;129(10).

Karim AS, Yan A, Ocotl E, Bennett DD, **Wang Z**, Kendziorski C, Gibson AL. Discordance between histologic and visual assessment of tissue viability in excised burn wound tissue. *Wound Repair and Regeneration.* 2019 Mar;27(2):150-61.

Karim A, **Wang Z**, Glover CR, Kendziorski C, Gibson A. 40 M2 Macrophages May Mitigate Burn Inflammation and Promote Wound Healing. *Journal of Burn Care & Research.* 2019 Mar 9;40 (Supplement 1):S29-30.

Zhao Y, Zhao W, **Wang Z**, Li W, Wang Y. Time related receiver operation characteristic curves and its application in clinical trials and diagnostic analysis. *Chinese Journal of Epidemiology.* 2016 Jun;37(6):891-4.

Wang Y, Wang X, **Wang Z**. Estimation of Parameters based on Type-II Hybrid Censored Data by EM Algorithm. *Chinese Journal of Applied Probability and Statistics.* 2016, 32(2): 121-131.

Preprints

Wang Z, Zhao S, Motsinger-Reif1 A, TaxaNorm: A Novel Taxa-specific Normalization Approach for Microbiome Data. (submitted to Bioinformatics)

Wang Z, Dalton K, Lee M, Zhao S, Motsinger-Reif A, London S, Farm Exposures Associate with House Dust Microbiome using Whole Genome Shotgun Sequencing. (submitted to Environmental International)

Wang Z, Keller MP, Kendziorski C. *CSI*: a statistical pipeline for cross species integration of genetic data. (submitted to G3: Genes, Genomes, Genetics)

HONORS AND AWARDS

Fellows Award for Research Excellence (FARE), National Institutes of Health, 2022

Best Undergraduate Degree Essay (Top 10), Shanghai Jiao Tong University, 2014

The Third Prize Scholarship, Shanghai Jiao Tong University, 2012 - 2014

The Second Prize in the China Mathematical Contest in Modeling, 2012

PRESENTATIONS

Invited Talks

Research on microbiome, invited presentation to top NIH leadership, Aug, 2022

Contributed Talks

Novel Taxa-Specific Normalization Method for Microbiome Sequencing Count Data, JSM, Aug, 2022

A novel normalization method for microbiome data, ENAR, Mar, 2022

Big Picture, Small Talk competition, National Institute of Environmental Health Sciences, Feb, 2022

Integrative Analysis of Exposome and Transcriptome for Asthma, Exposome Data Challenge Event, ISGlobal, Apr, 2021

Contributed Posters

Novel Taxa-Specific Normalization Method for Microbiome Sequencing Count Data, JSM, Aug, 2022

A novel normalization method for microbiome data, NCBC Microbiome Symposium, May, 2022

A statistical approach for association mapping across multiple species, Fourth Annual Center for Predictive Computational Phenotyping Retreat, May, 2018

MENTORING AND TEACHING EXPERIENCE

Mentor - Katelyn Mclnerney, NIH Summer Internship Student, May-Jul, 2022
Biostatistics and Computational Biology Branch, National Institute of Environmental Health Sciences
· Supervised the project on benchmarking microbiome normalization methods and reviewed posters on NIEHS poster day
· Provided consultation on graduate school application

Instructor, Summer 2022, Statistical Inference
Biostatistics and Computational Biology Branch, National Institute of Environmental Health Sciences
· Prepare lectures, held help sessions and formulated exam solutions

Teaching Assistant, Summer 2021, Regression Models
Biostatistics and Computational Biology Branch, National Institute of Environmental Health Sciences
· Held help sessions and formulated exam solutions

Teaching Assistant, Spring 2019, Statistical Methods for Molecular Biology (STAT 877)
Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison
· Held office hours, graded assignments, formulated exam solutions
· Co-supervised final projects

Tutor, 2012-2013, Probability Theory and Stochastic Process (MA 227)
Department of Mathematics, Shanghai Jiao Tong University
· Helped with homework questions and led review sessions before final exams

EDITORIAL ACTIVITIES

Ad hoc reviewer
Genome Biology, Bioinformatics

SERVICES

Judge, NIH Graduate Student Research Symposium, National Institutes of Health, Feb 2022

Leader and Organizer, NIH Summer Journal Club, National Institutes of Health, Jun-Jul 2022

PROFESSIONAL MEMBERSHIPS

American Statistical Association (ASA)

The International Biometric Society (ENAR)

SOFTWARE AND PROGRAMMING SKILLS

R packages

TaxaNorm: Taxa-specific normalization for microbiome data

CSI: Cross-species integration pipeline

scNBN: Negative binomial graphical model for network analysis in single cell RNA-seq data

Programming Skills

R, MATLAB, SAS; Shell Scripts; Unix Platform; High-performance computing clusters (SLURM)