Jing Zhao, Ph.D.

Research Scientist
Center for Biostatistics, Department of Biomedical Informatics
The Ohio State University

CONTACT INFORMATION

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EDUCATION

Ph.D., Statistics, 2016
Department of Statistics, the University of Georgia, Athens, GA.
Dissertation: A Probabilistic Model for Gene Family Evolution.

M.S., Statistics, 2015
Department of Statistics, the University of Georgia, Athens, GA.

M.S., Operations Research, 2010
Department of Mathematics, Shandong University, China.

B.S., Applied Mathematics, 2005
Department of Mathematics, Shandong University, China.

PROFESSIONAL EXPERIENCE

01/2019-present, **Research Scientist**
Department of Biomedical Informatics at the Ohio State University

01/2017-01/2019, **Adjunct Assistant Professor**
The Department of Internal Medicine at University of South Dakota Sanford School of Medicine

05/2017-01/2019 **Assistant Research Scientist,**
Population Health Group, Sanford Research
Co-Director
Research Design & Biostatistics Core, Sanford Research

04/2016-05/2017, **Biostatistician**
Population Health Group, Sanford Research

07/2012-04/2016, **Research Assistant**
Department of Statistics, the University of Georgia

RESEARCH INTERESTS

- Biomedical and clinical informatics
  - Identifying disease progression patterns from large-scale Electronic Medical Records
  - Predicting disease risks through mining of Electronic Medical Records and Omics data
- Statistical modeling in molecular phylogenetics and evolution
  - Incorporating phylogenetic approaches to microbe-host interactions analysis

- Investigating impacts of biological and environmental factors on the evolution process of genes or species

RESEARCH SUPPORT

Ongoing (total 6.84 calendar)

NIH/R33CA258016 (PI: Liu) 05/01/2021 - 04/30/2024 0.84 calendar
Validating urine derived cancer cells (UDCC) -- non-invasive and living liquid biopsies -- in bladder cancer clinics
Role: Co-Investigator

American Cancer Society (PI: Hertlein) 01/01/2020-12/31/2023 0.6 calendar
Investigating the role of BCL3 in ibrutinib resistant CLL
Role: Co-Investigator

NIH/R01CA251753 (PI: Miles) 07/14/2020 – 06/30/2025 1.2 calendar
The translational regulation of pro-apoptotic genes
Role: Co-Investigator

NIH/R01NS118200 (PI: Schwab) 07/01/2020 – 06/30/2025 0.6 calendar
Reducing infection susceptibility by immune function restoration in spinal cord injury
Role: Co-Investigator

NIH/R03NS116334 (PI: Otero) 06/01/2020 – 11/30/2021 0.6 calendar
Implementation of Machine Learning Workflows in Primary Brain Tumor Diagnostics
Role: Co-Investigator

DOD/W81XWH2010361 (PI: Karuppaiyah) 06/01/2020 – 05/31/2022 0.6 calendar
Endoplasmin: A Novel Therapeutic Target and Potential Marker of Chemoresistance
Role: Co-Investigator

NIH/K23AR068450 (PI: Hanaoka) 09/01/2019 - 08/30/2021 2.4 calendar
Skeletal muscle in rheumatoid arthritis
Role: Biostatistician

Starting soon (total 3 calendar)

DOD (PI: Karuppaiyah) 07/01/2021-06/30/2023 0.6 calendar
Role of hypoxia and TMEM205 in ovarian clear cell carcinoma progression and outcome
Role: Co-Investigator

NSF/EAGER (PI: Ma) 2021-2023 1.2 calendar
IIBR Informatics: A reinforced imputation framework for accurate gene expression recovery from single-cell RNA-seq data
Role: Co-Investigator

NIH (PI: Karuppaiyah) 2021-2023 1.2 calendar
Highly sensitive, rapid lateral flow immunoassay assay for detection of SARS-CoV-2 using exosomes

enriched from body fluids
Role: Co-Investigator

Completed
NIH/NHGRI/6U01HG007253-03 (PI: Denny / site PI: Wilke) 07/01/18 – 01/06/2019
Integrated Individualized Intelligent Prescribing (I3P)
Role: Co-Investigator

SA1800299 (PI: Ma) 07/01/2017-01/06/2019
Sanford-South Dakota State University Collaborative Research Seed Grant Program
Elucidate Gut Microbial Biomarkers of Obesity by Metagenome and Metatranscriptome
Role: Co-PI

NIH/NIGMS/P20 GM121341 (PI: Thompson) 07/01/2017-01/06/2019
Transdisciplinary Approaches to American Indian and Rural Population Health Research
Role: Co-Lead, COMMAND Core

NIH/NHGRI/U01 HG007253 (MPI: Denny/Wilke) 07/01/2015-06/30/2018
Sanford Precision Medicine - Integrated Individualized Intelligent Prescribing (I3P)
Role: Biostatistician

NIH/NIMHD/U54 MD008164 (PI: Kenyon) 09/26/2012-07/31/2018
Collaborative Research Center for American Indian Health
Role: Biostatistician, Methodology Core

NSF/DMS-1222745 (PI: Liu) 09/01/2012-08/31/2016
A probabilistic model for gene family evolution
Role: Research Assistant

JOURNAL PUBLICATIONS

First or corresponding author ($ corresponding author)

1. **Jing Zhao$**, Paige Hinton, Junyi Chen and Jing Jiang, “Causal inference for the effect of environmental chemicals on chronic kidney disease”, ***Computational and Structural Biotechnology Journal***. 2019; DOI: 10.1016/j.csbj.2019.12.001.
2. **Jing Zhao$**, Shaopeng Gu, and Adam McDermaid. "Predicting outcomes of chronic kidney disease from EMR data based on Random Forest Regression." ***Mathematical biosciences***, 310 (2019): 24-30. PMCID: PMC6435377.
3. Juan Xie, Anjun Ma, Anne Fennell, Qin Ma, and **Jing Zhao$**, It is time to apply biclustering: A comprehensive review of biclustering applications in biological and biomedical data. ***Briefings in Bioinformatics***, DOI: 10.1093/bib/bby014. 2018. PMID: 29490019.
4. **Jing Zhao**, Ashley Teufel, David Liberles, Jim Leebens-Mack, Liang Liu, A generalized birth and death process for modeling the fates of gene duplication, ***BMC Evolutionary Biology***, DOI: 10.1186/s12862-015-0539-2, 20*15.* PMCID: PMC4672517.

Contributing author

5. Leigh Hartog, **Jing Zhao**, Jerry Reynolds, Gabrielle Brokamp, Ferdinand Vilson, W. David Arnold, Samantha LoRusso, “Factors Influencing the Severity and Progression of Respiratory Muscle Dysfunction in Myotonic Dystrophy Type 1”, ***Frontiers in Neurology***, 2021, in press.
6. Jessica Blackburn, Valeria F. Chapur, Julie A. Stephens, **Jing Zhao**, Anne Shepler, Christopher R. Pierson, Jose J. Otero, “Revisiting the Neuropathology of Sudden Infant Death Syndrome (SIDS)”, ***Frontiers in Neurology***, 11 (2020).
7. Wesley Wang, Diego Alzate-Correa, Michele Joana Alves, Mikayla Jones, Alfredo J. Garcia III, **Jing Zhao**, Catherine Miriam Czeisler, Jos´e Javier Otero, “Machine Learning-based Data Analytic Approaches for Evaluating Post-natal Mouse Respiratory Physiological Evolution”, ***Respiratory Physiology & Neurobiology***, 283 (2020): 103558.
8. Jessica Blackburn, Michele Joana Alves, **Jing Zhao**, Catherine M. Czeisler, José Javier Otero, “Astrocyte Regional Heterogeneity Revealed Through Machine Learning ‐ based Glial Neuroanatomical Assays”, ***The FASEB Journal,*** 34.S1 (2020): 1-1.
9. Parker, Camille, **Zhao, Jing**, Pearce, David A., Kovács, Attila D..” Comparative analysis of the gut microbiota composition in the Cln1R151X and Cln2R207X mouse models of Batten disease and in three wild-type mouse strains.” ***Archives of Microbiology.*** 2020; DOI: 10.1007/s00203-020-02007-6.
10. Ming Yin, **Jing Zhao**, Paul Monk, Douglas Martin, Edmund Folefac, Monika Joshi, Ning Jin, Amir Mortazavi, Claire Verschraegen, Steven Clinton. “Comparative effectiveness of surgery versus external beam radiation with/without brachytherapy in high-risk localized prostate cancer.” ***Cancer Medicine***, 2019;00:1-8. DOI: 10.1002/cam4.2605.
11. Tyler B. Johnson, Logan M. Langin, **Jing Zhao**, Jill M. Weimer, David A. Pearce, and Attila D. Kovács. "Changes in motor behavior, neuropathology, and gut microbiota of a Batten disease mouse model following administration of acidified drinking water." ***Scientific Reports***, 9, no. 1 (2019): 1-16. PMID: 31628420. PMCID: PMC6802212.
12. Yan Wang, Sen Yang, **Jing Zhao**, Wei Du, Yanchun Liang, Cankun Wang, Fengfeng Zhou, Yuan Tian, and Qin Ma. "Using Machine Learning to Measure Relatedness Between Genes: A Multi-Features Model." ***Scientific reports***, 9, no. 1 (2019): 4192.
13. Russell A. Wilke, Mohammad Qamar, Roxana A. Lupu, Shaopeng Gu, and **Jing Zhao**. "Chronic Kidney Disease in Agricultural Communities." ***The American Journal of Medicine***, (2019). PMID: 30998912.
14. Sen Liang, Sen Yang, Dayang Liang, Jiechao Ma, Yuan Tian, **Jing Zhao**, Xu Zhang, Ying Xu, and Yan Wang. "A novel matched-pairs feature selection method considering with tumor purity for differential gene expression analyses." ***Mathematical Biosciences***, 311 (2019): 39-48.
15. Natasha Petry, Roxana Lupu, Ahmed Gohar, Eric A. Larson, Carmen Peterson, Vanessa Williams, **Jing Zhao**, Russell A. Wilke, and Lindsay J. Hines. "CYP2C19 genotype, physician prescribing pattern, and risk for long QT on serotonin selective reuptake inhibitors." ***Pharmacogenomics***, 0 (2019). PMCID: PMC6562837.
16. **Jing Zhao**, Tess Weber, Jessica Hanson, Chad Birger, Morgan Nelson, and Susan Puumala, “A County-Level Health Index to Capture Geographic Variation in Health Conditions in North Dakota, South Dakota, and Minnesota.” ***South Dakota Medicine***, 2019 May; 72(5):206-213. PMID:31454473.
17. Adam McDermaid, Brandon Monier, **Jing Zhao**, Bingqiang Liu, and Qin Ma, Interpretation of differential gene expression results of RNA-seq data: review and integration. ***Briefings in Bioinformatics***, DOI:10.1093/bib/bby067, 2018. PMID: 30099484.
18. Marianna Madeo, Paul L. Colbert, Daniel W. Vermeer, Christopher T. Lucido, Jacob T. Cain, Elisabeth G. Vichaya, Aaron J. Grossberg, DesiRae Muirhead, Alex P. Rickel, Zhongkui Hong, **Jing**

Zhao, Jill M. Weimer, William C. Spanos, John H. Lee, Robert Dantzer, DVM, Paola D. Vermeer, Cancer exosomes induce tumor innervation, ***Nature Communications***, DOI: 10.1038/s41467-018-06640-0, 2018.

19. Brandon Monier, Adam McDermaid, Cankun Wang, **Jing Zhao**, Allison Miller, Anne Fennell, Qin Ma, IRIS-EDA: An integrated RNA-Seq interpretation system for gene expression data analysis. ***PLoS Computational Biology***, in press, 2018. PMCID: PMC6392338.
20. Fang Fang, Ashley VanCleave, Ralph Helmuth, Haydee Torres, Kirby Rickel, Hannah Wollenzien, Hongli Sun, Erliang Zeng, **Jing Zhao**, and Jianning Tao. "Targeting the Wnt/β-catenin pathway in human osteosarcoma cells." ***Oncotarget*** 9, no. 95 (2018): 36780.
21. Yu Zhang, Sha Cao, **Jing Zhao**, Burair Alsaihati, Qin Ma, and Chi Zhang, MRHCA: a nonparametric statistics based method for hub and co-expression module identification in large gene co-expression network, ***Quantitative Biology***, Quantitative Biology 6, no. 1 (2018): 40-55.
22. David Whitesock, **Jing Zhao**, Kristen Goettsch, Jessica Hanson, Validating a Survey for Addiction Wellness: The Recovery Capital Index. ***South Dakota Medicine***, PMID: 29999606, 2018.
23. Sheng-Yong Niu, Jinyu Yang, Adam McDermaid, **Jing Zhao**, Yu Kang, and Qin Ma, Bioinformatics tools for quantitative and functional metagenome and metatranscriptome data analysis in microbes, ***Briefings in Bioinformatics***, DOI: 10.1093/bib/bbx051, 2017. PMID: 28481971.
24. Xiao-Ran Xin, Yong Chen, Di Chen, Fa Xiao, Laurence D. Parnell, **Jing Zhao**, Liang Liu, Jose M. Ordovas, ChaoQiang Lai, and Lirong Shen, Supplementation with Major Royal-Jelly Proteins Increases Lifespan, Feeding, and Fecundity in *Drosophila*, ***Jounral of Agriculture and Food Chemistry***, , DOI: 10.1021/acs.jafc.6b00514, 2016.
25. Talaysha Lingham, Mu Ye, Haiqiang Chen, Karuna Chintapenta, **Jing Zhao**, and Gulnihal Ozbay, Effects of high hydrostatic pressure on the physical, microbial, and chemical attributes of oysters (Crassostrea virginica), ***Journal of Food Science***, DOI: 10.1111/1750-3841.13290, 2016.
26. Ashley Teufel, **Jing Zhao**, Malgorzata O'Reilly, Liang Liu and David A. Liberles , On Mechanistic Modeling of Gene Content Evolution: Birth-Death Models and Mechanisms of Gene Birth and Gene Retention, ***Computation***, DOI:10.3390/computation2030112, 2014.
27. Qin Ma, Jaxk Reeves, David A. Liberles, Lili Yu, Zheng Chang, **Jing Zhao**, Juan Cui, Ying Xu, Liang Liu, A phylogenetic model for understanding the effect of gene duplication on cancer progressing. ***Nucleic Acids Research***, DOI:10.1093/nar/gkt1320, 1-9, 2013.

Under review

1. Barbara A. Gower PhD, Marcas Bamman PhD, **Jing Zhao** PhD, Kristen Heitman MS RDN LD, Fahad Khan MD, Beatriz Y. Hanaoka MD MPH, "Resting energy expenditure and the interplay among insulin resistance, inflammation and protein intake in patients with rheumatoid arthritis", **Arthritis Care & Research**, under review.
2. Steven H Sun, Debasish Sundi, David Abood, Brooke Benner, Mallory DiVincenzo, Megan Duggan, Fouad Choueiry, Thomas Mace, Prashant Trikha, Lianbo Yu, **Jing Zhao**, William E. Carson, "Targeting Myeloid Derived Suppressor Cells Enhances Therapeutic Response of Anti-PD-L1 Immune Checkpoint Blockade", **Annals of Medical Oncology**, under review.

CONFERENCE POSTERS & ABSTRACTS

1. Hisham Hussan, **Jing Zhao**, Peter P. Stanich, Fred Tabung, Darrell M. Gray, Qin Ma, Steven Clinton, Application of machine learning to enhance colorectal cancer diagnosis and prevention strategies for young adults aged 35-50 years, *Digestive Disease Week (DDW) 2021*.

2. Beatriz Hanaoka, **Jing Zhao**, Heitman K, Goss A and Gower BA, Impact of Insulin Resistance on Energy Expenditure in Individuals with Rheumatoid Arthritis, *The American College of Rheumatology Annual Meeting, Atlanta, GA, 2019 (Abstract #2154).*
3. Juan Xie, Anjun Ma, Anne Fennell, Qin Ma, and **Jing Zhao**, It is time to apply biclustering: a comprehensive review of biclustering applications in biological and biomedical data, *26th Conference on Intelligent Systems for Molecular Biology, 2018.*
4. **Jing Zhao**, Quantifying Toxic Nephropathy in the Great Plains, *Workshop on Chronic Kidney Diseases in Agricultural Communities at NIH, 2018.*
5. Susan E. Hoover and **Jing Zhao**, *Clostridium difficile* Toxin Testing Affects the Treatment Decision, *ASM Microbe 2018*.

PROFESSIONAL PRESENTATIONS

2018, Poster presentation, *It is time to apply biclustering: a comprehensive review of biclustering applications in biological and biomedical data*, Eastern South Dakota Research Symposium, Sioux Falls, SD.
2018, Presentation at Sanford Research Data Club, *Differential Gene Expression Analysis*, Sioux Falls, SD.
2017, Poster presentation, *A Health Index to Capture Geographic Variation in Health Conditions in ND, SD, and MN*, 5th Annual CRCAIH Summit, Sioux Falls, SD.
2017, Presentation on Research & Career for Sanford Research PROMISE Scholars, *Careers in Statistics*, Sioux Falls, SD.
2013, Invited Speaker, *A Phylogenetic Model for Cancer Evolution, SMBE Satellite Meeting on Mechanisms of Protein Evolution*, Denver, CO.

PROFESSIONAL MEMBERSHIPS

Membership

- Member, American Statistical Association (ASA), 2013-present
- Member, Clinical Scientific Review Committee at OSU, 2019-present
- Member, International Society for Computational Biology, 2018-2019
- Member, International Chinese Statistical Association, 2017-2018
- Member, Sanford Health Institutional Review Board, 2018
- Member, Sanford Health Imagenetics Research Committee, 2016-2017

Reviewership

- Peer Reviewer for Journals:
    - *Nucleic Acids Research*
    - *GigaScience*
    - *Computational Biology and Chemistry*
    - *BMC Public Health*
    - *BMC Genomics*
    - *Mathematical BioSciences*
    - *PLOS ONE*
    - *Scientific Reports*
- External reviewer of the Translational Research Institute Pilot Grant Award program at the University of Arkansas for Medical Sciences

- Program Committee Member, Gene family evolution workshop, 2014, Science Hall, New Mexico State University (Las Cruces, NM, USA)

TEACHING EXPERIENCE

2018, **Introduction to Statistics,** Guest Lecturer
Summer Students at Sanford Research
2018, **Clinical Testing and Probability,** Guest Lecturer
Augustana University genetic counseling class
2016, **Bioinformatics**, Guest Lecturer (Dr. Xijin Ge)
Department of Mathematics and Statistics, South Dakota State University
2016, **Next Generation Sequencing Data Analysis**, Guest Lecturer (Dr. Qin Ma)
Department of Mathematics and Statistics, South Dakota State University
2015, **Statistical Phylogenetics**, Guest Lecturer (Dr. Liang Liu)
Department of Statistics, the University of Georgia
2015, **Stochastic Process**, Guest Lecturer (Dr. William McCormick)
Department of Statistics, the University of Georgia