

**Cankun Wang**

Biomedical Informatics Shared Resource  
Department of Biomedical Informatics  
The Ohio State University

**CONTACT INFORMATION**

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**EDUCATION**

M.S., Plant Science, 2019  
Department of Agronomy, Horticulture & Plant Science, South Dakota State University, SD  
B.S., Software Engineering, 2017  
Department of Software Engineering, Beijing Jiaotong University, China.

**PROFESSIONAL EXPERIENCE**

09/2019-present, **Biomedical Informatics Specialist**  
Department of Biomedical Informatics at the Ohio State University

- Led the development of Azure and AWS cloud computing platforms for the Department of Biomedical Informatics, guaranteeing dependable and efficient cloud-based solutions for vital research and clinical projects involving PHI and HIPAA compliance.
- Conducted cutting-edge analysis of single-cell multi-omics data and next-generation sequencing data to gain insights into complex biological systems and diseases.
- Designed and implemented highly integrated bioinformatics web applications, packages, and databases to streamline data analysis and accelerate research.
- Utilized clinical variables extracted from electronic medical/health records (EMR/EHR) to study the activities of intensive care patients with critical illnesses, leading to improved understanding and treatment of these conditions.
- Developed deep learning frameworks to study transcriptional regulation using single-cell multiomics data, providing new avenues for investigating gene expression patterns and regulation mechanisms.

05/2019-07/2019, **Student Intern**

Department of Biomedical Informatics at the Ohio State University

- Developed an R package for identification of regulatory DNA motifs using ChIP-exo data

01/2018-05/2019 **Graduate Research Assistant**

Department of Plant Science, South Dakota State University, SD

- Conducted a research project in the identification of DNA transcription factors motif
- Developed a web server based on cell-type-specific regulon inference from single-cell RNA-Sequencing

09/2017-12/2017, **Research Assistant**

Department of Mathematics, Shandong University, China

- Established test modules for evaluation DNA motif finding efficiency and explored the optimization as well as the feasibility of further iterations

02/2014-07/2014, **Data Analyst Intern**

Hexin technology, Beijing, China

- Development of the software on automatic generating students' wrong answers collections from the collecting of handing-writing test paper
- Monitor and modify the training datasets on the natural language processing algorithm based on deep learning

## JOURNAL PUBLICATIONS

Full list: <https://scholar.google.com/citations?user=MCccvxgAAAAJ>

First and co-first author (\*)

1. **Cankun Wang**, Anjun Ma, Megan E. Mcnutt, Rebecca Hoyd, Caroline E. Wheeler, Lary A. Robinson, Carlos H.F. Chan, Yousef Zakharia, Rebecca D. Dodd, Cornelia M. Ulrich, Sheetal Hardikar, Michelle L. Churchman, Ahmad A. Tarhini, Eric A. Singer, Alexandra P. Ikeguchi, Martin D. Mccarter, Nicholas Denko, Gabriel Tinoco, Marium Husain, Ning Jin, Afaf E.G. Osman, Islam Eljilany, Aik Choon Tan, Samuel S. Coleman Iv, Louis Denko, Gregory Riedlinger, Bryan P. Schneider, Daniel Spakowicz, & Qin Ma. (2023). A bioinformatics tool for identifying intratumoral microbes from the ORIEN dataset. *bioRxiv*, 2023.2005.2024.541982. doi:10.1101/2023.05.24.541982
2. Shiqiao Ye\*, **Cankun Wang\***, Zhaohui Xu\*, Hui Lin, Xiaoping Wan, Yang Yu, Subhodip Adhichary, Joe Z. Zhang, Yang Zhou, Chun Liu, Matthew Alonzo, Jianli Bi, Angelina Ramirez-Navarro, Isabelle Deschenes, Qin Ma, Vidu Garg, Joseph C. Wu, & Ming-Tao Zhao. Impaired Human Cardiac Cell Development due to NOTCH1 Deficiency. *Circulation Research*, 0(0). doi:10.1161/CIRCRESAHA.122.321398
3. Xiaoying Wang\*, **Cankun Wang\***, Lang Li, Qin Ma, Anjun Ma, & Bingqiang Liu. (2022). DESSO-DB: A web database for sequence and shape motif analyses and identification.

*Computational and Structural Biotechnology Journal*, 20, 3053-3058.

doi:<https://doi.org/10.1016/j.csbj.2022.06.031>

4. **Cankun Wang**, Yujia Xiang, Hongjun Fu, & Qin Ma. (2021). Use of scREAD to explore and analyze single-cell and single-nucleus RNA-seq data for Alzheimer's disease. *STAR Protocols*, 2(2), 100513. doi:10.1016/j.xpro.2021.100513
5. Jing Jiang\*, **Cankun Wang\***, Ren Qi, Hongjun Fu, & Qin Ma. (2020). scREAD: A Single-Cell RNA-Seq Database for Alzheimer's Disease. *iScience*, 23(11), 101769. doi:10.1016/j.isci.2020.101769
6. Anjun Ma\*, **Cankun Wang\***, Yuzhou Chang, Faith H Brennan, Adam Mcdermaid, Bingqiang Liu, Chi Zhang, Phillip G Popovich, & Qin Ma. (2020). IRIS3: integrated cell-type-specific regulon inference server from single-cell RNA-Seq. *Nucleic Acids Research*, 48(W1), W275-W286. doi:10.1093/nar/gkaa394

#### Contributing author

1. Yang Li, Yizhong Wang, **Cankun Wang**, Anne Fennell, Anjun Ma, Jing Jiang, Zhaoqian Liu, Qin Ma, & Bingqiang Liu. (2023). A Weighted Two-stage Sequence Alignment Framework to Identify DNA Motifs from ChIP-exo Data. *bioRxiv*, 2023.2004.2006.535915. doi:10.1101/2023.04.06.535915
2. Anjun Ma, Xiaoying Wang, Jingxian Li, **Cankun Wang**, Tong Xiao, Yuntao Liu, Hao Cheng, Juexin Wang, Yang Li, Yuzhou Chang, Jinpu Li, Duolin Wang, Yuexu Jiang, Li Su, Gang Xin, Shaopeng Gu, Zihai Li, Bingqiang Liu, Dong Xu, & Qin Ma. (2023). Single-cell biological network inference using a heterogeneous graph transformer. *Nature Communications*, 14(1), 964. doi:10.1038/s41467-023-36559-0
3. Yizhong Wang, Yang Li, **Cankun Wang**, Qin Ma, & Bingqiang Liu. (2023). CEMIG: Prediction of the cis-regulatory motif using the De Bruijn graph from ATAC-seq. *bioRxiv*, 2023.2005.2026.542440. doi:10.1101/2023.05.26.542440
4. Jeffrey R. Atkinson, Andrew D. Jerome, Andrew R. Sas, Ashley Munie, **Cankun Wang**, Anjun Ma, William D. Arnold, & Benjamin M. Segal. (2022). Biological aging of CNS-resident cells alters the clinical course and immunopathology of autoimmune demyelinating disease. *JCI Insight*, 7(12). doi:10.1172/jci.insight.158153
5. Faith H. Brennan, Yang Li, **Cankun Wang**, Anjun Ma, Qi Guo, Yi Li, Nicole Pukos, Warren A. Campbell, Kristina G. Witcher, Zhen Guan, Kristina A. Kigerl, Jodie C. E. Hall, Jonathan P. Godbout, Andy J. Fischer, Dana M. Mctigue, Zhigang He, Qin Ma, & Phillip G. Popovich. (2022). Microglia coordinate cellular interactions during spinal cord repair in mice. *Nature Communications*, 13(1), 4096. doi:10.1038/s41467-022-31797-0
6. Shuo Chen, Diana Acosta, Liangping Li, Jiawen Liang, Yuzhou Chang, **Cankun Wang**, et al. (2022). Wolframin is a novel regulator of tau pathology and neurodegeneration. *Acta Neuropathologica*. doi:10.1007/s00401-022-02417-4
7. Shuo Chen, Yuzhou Chang, Liangping Li, Diana Acosta, Yang Li, Qi Guo, **Cankun Wang**, Emir Turkes, Cody Morrison, Dominic Julian, Mark E. Hester, Douglas W. Scharre, Chintda Santiskulvong, Sarah Xueying Song, Jasmine T. Plummer, Geidy E. Serrano, Thomas G. Beach,

- Karen E. Duff, Qin Ma, & Hongjun Fu. (2022). Spatially resolved transcriptomics reveals genes associated with the vulnerability of middle temporal gyrus in Alzheimer's disease. *Acta Neuropathologica Communications*, 10(1), 188. doi:10.1186/s40478-022-01494-6
8. SenNet Consortium. (2022). NIH SenNet Consortium to map senescent cells throughout the human lifespan to understand physiological health. *Nature Aging*, 2(12), 1090-1100. doi:10.1038/s43587-022-00326-5
9. Yang Li, Anjun Ma, Yizhong Wang, **Cankun Wang**, Shuo Chen, Hongjun Fu, Bingqiang Liu, & Qin Ma. (2022). Enhancer-driven gene regulatory networks inference from single-cell RNA-seq and ATAC-seq data. *bioRxiv*, 2022.2012.2015.520582. doi:10.1101/2022.12.15.520582
10. Ying Li, Jianing Zhao, Zhaoqian Liu, **Cankun Wang**, Lizheng Wei, Siyu Han, & Wei Du. (2021). De novo Prediction of Moonlighting Proteins Using Multimodal Deep Ensemble Learning. *Frontiers in Genetics*, 12.
11. Juexin Wang, Anjun Ma, Yuzhou Chang, Jianting Gong, Yuexu Jiang, Ren Qi, **Cankun Wang**, Hongjun Fu, Qin Ma, & Dong Xu. (2021). scGNN is a novel graph neural network framework for single-cell RNA-Seq analyses. *Nature Communications*, 12(1), 1882. doi:10.1038/s41467-021-22197-x
12. Ying Li, Qi Zhang, Zhaoqian Liu, **Cankun Wang**, Siyu Han, Qin Ma, & Wei Du. (2020). Deep forest ensemble learning for classification of alignments of non-coding RNA sequences based on multi-view structure representations. *Briefings in Bioinformatics*(bbaa354). doi:10.1093/bib/bbaa354
13. Mengting Niu, Jun Zhang, Yanjuan Li, **Cankun Wang**, Zhaoqian Liu, Hui Ding, Quan Zou, & Qin Ma. (2020). CirRNAPL: A web server for the identification of circRNA based on extreme learning machine. *Computational and Structural Biotechnology Journal*, 18, 834-842. doi:10.1016/j.csbj.2020.03.028
14. Padmapriya Swaminathan, Michelle Ohrtman, Abigail Carinder, Anup Deuja, **Cankun Wang**, John Gaskin, Anne Fennell, & Sharon Clay. (2020). Water Deficit Transcriptomic Responses Differ in the Invasive *Tamarix chinensis* and *T. ramosissima* Established in the Southern and Northern United States. *Plants*, 9(1), 86. doi:10.3390/plants9010086
15. Juan Xie, Anjun Ma, Yu Zhang, Bingqiang Liu, Sha Cao, **Cankun Wang**, Jennifer Xu, Chi Zhang, & Qin Ma. (2020). QUBIC2: a novel and robust biclustering algorithm for analyses and interpretation of large-scale RNA-Seq data. *Bioinformatics*, 36(4), 1143-1149. doi:10.1093/bioinformatics/btz692
16. Brandon Monier, Adam Mcdermaid, **Cankun Wang**, Jing Zhao, Allison Miller, Anne Fennell, & Qin Ma. (2019). IRIS-EDA: An integrated RNA-Seq interpretation system for gene expression data analysis. *PLOS Computational Biology*, 15(2), e1006792. doi:10.1371/journal.pcbi.1006792
17. Yan Wang, Sen Yang, Jing Zhao, Wei Du, Yanchun Liang, **Cankun Wang**, Fengfeng Zhou, Yuan Tian, & Qin Ma. (2019). Using Machine Learning to Measure Relatedness Between Genes: A Multi-Features Model. *Scientific Reports*, 9(1). doi:10.1038/s41598-019-40780-7
18. Ye Xia, Seth Debolt, Qin Ma, Adam Mcdermaid, **Cankun Wang**, Nicole Shapiro, Tanja Woyke, & Nikos C. Kyrpides. (2019). Improved Draft Genome Sequence of *Bacillus* sp. Strain YF23, Which

- Has Plant Growth-Promoting Activity. *Microbiology Resource Announcements*, 8(15). doi:10.1128/MRA.00099-19
19. Ye Xia, Seth Debolt, Qin Ma, Adam Mcdermaid, **Cankun Wang**, Nicole Shapiro, Tanja Woyke, & Nikos C. Kyrpides. (2019). Improved Draft Genome Sequence of *Pseudomonas poae* A2-S9, a Strain with Plant Growth-Promoting Activity. *Microbiology Resource Announcements*, 8(15). doi:10.1128/MRA.00275-19
  20. Jinyu Yang, Anjun Ma, Adam D Hoppe, **Cankun Wang**, Yang Li, Chi Zhang, Yan Wang, Bingqiang Liu, & Qin Ma. (2019). Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. *Nucleic Acids Research*, 47(15), 7809-7824. doi:10.1093/nar/gkz672
  21. Adam Mcdermaid, Xin Chen, Yiran Zhang, **Cankun Wang**, Shaopeng Gu, Juan Xie, & Qin Ma. (2018). A New Machine Learning-Based Framework for Mapping Uncertainty Analysis in RNA-Seq Read Alignment and Gene Expression Estimation. *Frontiers in Genetics*, 9. doi:10.3389/fgene.2018.00313
  22. Siyu Han, Yanchun Liang, Qin Ma, Yangyi Xu, Yu Zhang, Wei Du, **Cankun Wang**, & Ying Li. LncFinder: an integrated platform for long non-coding RNA identification utilizing sequence intrinsic composition, structural information and physicochemical property. *Briefings in Bioinformatics*. doi:10.1093/bib/bby065

## PRESENTATIONS

- |       |  |
|-------|--|
| 2023, | <b>A Weighted Two-stage Sequence Alignment Framework to Identify DNA Motifs from ChIP-exo Data</b><br>International Conference on Intelligent Biology and Medicine (ICIBM 2023). Tampa, FL.<br>(Oral Presentation) |
| 2021, | <b>Analyze RNA-seq data using IRIS-EDA web server</b><br>Vitismet: grapes at UC Davis & SLU. Columbus, OH. (Oral Presentation)   |
| 2020, | <b>Computational tool and pipeline for RNA-seq data analysis</b><br>NSF PGRP Grape Grafting Annual Meeting. Columbus, OH. (Oral Presentation)  |
| 2019, | <b>Identification of Regulatory DNA Motifs Using ChIP-exo data</b><br>BMI Internship Poster Session. Columbus, OH. (Poster presentation)   |
| 2019, | <b>Development of Regulatory Motif Identification program</b><br>BioSNTR Plant Science Research Day. Brookings, SD.  |
| 2018, | <b>Combining Computational Methods and Experimental Data for Motif Prediction</b><br>BioSNTR Plant Science Research Day. Brookings, SD. (Poster Presentation)  |

## TEACHING

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| 2021, | <b>BISR CRISPR screening workshop</b> , Lecturer<br>Department of Biomedical Informatics, OSU |
| 2021, | <b>BISR RNA-Seq workshop</b> , Lecturer<br>Department of Biomedical Informatics, OSU          |

- 2020, **Applications of Machine Learning and Artificial Intelligence**, Guest Lecturer  
Department of Biomedical Informatics, OSU
- 2020, **Single-cell sequencing data analysis workshop**, Guest Lecturer  
Iowa State University
- 2019, **Applied Bioinformatics**, Teaching assistant (Dr. Xijin Ge)  
Department of Mathematics and Statistics, South Dakota State University

## MENTORING

- 2022-, Megan McNutt (Senior Research Technician at OSU)
- 2023-, Grace Xu (High school intern at Dublin, OH)
- 2023, Kevin Wang (High school intern at Columbus, OH)
- 2022, Jiaxin Yang (Undergraduate at OSU)
- 2022, Mohnish Karthikeyan (High school intern at Mason, OH)

## AWARDS

- 2022, Excellence in Team Science (staff) in the Department of Biomedical Informatics, OSU

## SKILLS

- Next-generation sequencing and single-cell multi-omics data analyses (R, Python, HPC system)
- Cloud infrastructure development and management (AWS, Azure)
- Full stack web development (Vue.js, NestJS, TypeScript, MySQL)
- DevOps (GitHub Actions, Azure DevOps, Docker)
- Deep learning model development & deployment (ConvNet, Graph Transformer, AWS Sagemaker)
- Data visualization (Adobe Illustrator, ggplot2, Circos)