

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

- Spearheaded Azure Cloud computing platform development for the Department of Biomedical Informatics, ensuring reliable and efficient cloud-based solutions for critical research projects.
- 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**

The Department of Internal Medicine at University of South Dakota Sanford School of Medicine

- 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. Ye, Shiqiao*, **Cankun Wang***, Zhaohui Xu, Hui Lin, Xiaoping Wan, Yang Yu, Subhodip Adhichary, et al. n.d. "Impaired Human Cardiac Cell Development Due to NOTCH1 Deficiency." *Circulation Research*, 2023. <https://doi.org/10.1161/CIRCRESAHA.122.321398>.
2. Wang, Xiaoying*, **Cankun Wang***, Lang Li, Qin Ma, Anjun Ma, and Bingqiang Liu. "DESSO-DB: A Web Database for Sequence and Shape Motif Analyses and Identification." *Computational and Structural Biotechnology*, 2022, <https://doi.org/10.1016/j.csbj.2022.06.031>.
3. **Wang, Cankun**, Yujia Xiang, Hongjun Fu, and Qin Ma. "Use of ScREAD to Explore and Analyze Single-Cell and Single-Nucleus RNA-Seq Data for Alzheimer's Disease." *STAR Protocols*, 2021, <https://doi.org/10.1016/j.xpro.2021.100513>.
4. Jiang, Jing*, **Cankun Wang***, Ren Qi, Hongjun Fu, and Qin Ma. "ScREAD: A Single-Cell RNA-Seq Database for Alzheimer's Disease." *iScience*, 2020, <https://doi.org/10.1016/j.isci.2020.101769>.

5. Ma, Anjun*, **Cankun Wang***, Yuzhou Chang, Faith H Brennan, Adam McDermaid, Bingqiang Liu, Chi Zhang, Phillip G Popovich, and Qin Ma. “IRIS3: Integrated Cell-Type-Specific Regulon Inference Server from Single-Cell RNA-Seq.”
Nucleic Acids Research, 2020, <https://doi.org/10.1093/nar/gkaa394>.

Contributing author

1. Ma, Anjun, Xiaoying Wang, Jingxian Li, **Cankun Wang**, Tong Xiao, Yuntao Liu, Hao Cheng, et al. “Single-Cell Biological Network Inference Using a Heterogeneous Graph Transformer.”
Nature Communications, 2023, <https://doi.org/10.1038/s41467-023-36559-0>.
2. SenNet Consortium, “NIH SenNet Consortium to Map Senescent Cells throughout the Human Lifespan to Understand Physiological Health,”
Nature Aging, 2022, <https://doi.org/10.1038/s43587-022-00326-5>.
3. Chen, Shuo, Yuzhou Chang, Liangping Li, Diana Acosta, Yang Li, Qi Guo, **Cankun Wang**, et al. “Spatially Resolved Transcriptomics Reveals Genes Associated with the Vulnerability of Middle Temporal Gyrus in Alzheimer’s Disease.”
Acta Neuropathologica Communications, 2022, <https://doi.org/10.1186/s40478-022-01494-6>.
4. Brennan, Faith H., Yang Li, **Cankun Wang**, Anjun Ma, Qi Guo, Yi Li, Nicole Pukos, et al. “Microglia Coordinate Cellular Interactions during Spinal Cord Repair in Mice.”
Nature Communications, 2022, <https://doi.org/10.1038/s41467-022-31797-0>.
5. Atkinson, Jeffrey R., Andrew D. Jerome, Andrew R. Sas, Ashley Munie, **Cankun Wang**, Anjun Ma, William D. Arnold, and Benjamin M. Segal. “Biological Aging of CNS-Resident Cells Alters the Clinical Course and Immunopathology of Autoimmune Demyelinating Disease.”
JCI Insight, 2022, <https://doi.org/10.1172/jci.insight.158153>.
6. Chen, Shuo, Diana Acosta, Liangping Li, Jiawen Liang, Yuzhou Chang, **Cankun Wang**, Julie Fitzgerald, et al. “Wolframin Is a Novel Regulator of Tau Pathology and Neurodegeneration.”
Acta Neuropathologica, 2022, <https://doi.org/10.1007/s00401-022-02417-4>.
7. Wang, Juexin, Anjun Ma, Yuzhou Chang, Jianting Gong, Yuexu Jiang, Ren Qi, **Cankun Wang**, Hongjun Fu, Qin Ma, and Dong Xu. “ScGNN Is a Novel Graph Neural Network Framework for Single-Cell RNA-Seq Analyses.”
Nature Communications, 2021, <https://doi.org/10.1038/s41467-021-22197-x>.
8. Li, Ying, Jianing Zhao, Zhaoqian Liu, **Cankun Wang**, Lizheng Wei, Siyu Han, and Wei Du. “De Novo Prediction of Moonlighting Proteins Using Multimodal Deep Ensemble Learning.”
Frontiers in Genetics, 2021, <https://www.frontiersin.org/articles/10.3389/fgene.2021.630379>.
9. Li, Ying, Qi Zhang, Zhaoqian Liu, **Cankun Wang**, Siyu Han, Qin Ma, and Wei Du. “Deep Forest Ensemble Learning for Classification of Alignments of Non-Coding RNA Sequences Based on Multi-View Structure Representations.”
Briefings in Bioinformatics, 2020, <https://doi.org/10.1093/bib/bbaa354>.

10. Niu, Mengting, Jun Zhang, Yanjuan Li, **Cankun Wang**, Zhaoqian Liu, Hui Ding, Quan Zou, and Qin Ma. "CirRNAPL: A Web Server for the Identification of CircRNA Based on Extreme Learning Machine."
Computational and Structural Biotechnology, 2020, <https://doi.org/10.1016/j.csbj.2020.03.028>.
11. Swaminathan, Padmapriya, Michelle Ohrtman, Abigail Carinder, Anup Deuja, **Cankun Wang**, John Gaskin, Anne Fennell, and Sharon Clay. "Water Deficit Transcriptomic Responses Differ in the Invasive Tamarix Chinensis and T. Ramosissima Established in the Southern and Northern United States."
Plants, 2020, <https://doi.org/10.3390/plants9010086>.
12. Xie, Juan, Anjun Ma, Yu Zhang, Bingqiang Liu, Sha Cao, **Cankun Wang**, Jennifer Xu, Chi Zhang, and Qin Ma. "QUBIC2: A Novel and Robust Biclustering Algorithm for Analyses and Interpretation of Large-Scale RNA-Seq Data." Edited by Inanc Birol.
Bioinformatics, 2019, <https://doi.org/10.1093/bioinformatics/btz692>.
13. Yang, Jinyu, Anjun Ma, Adam D. Hoppe, **Cankun Wang**, Yang Li, Chi Zhang, Yan Wang, Bingqiang Liu, and Qin Ma. "Prediction of Regulatory Motifs from Human Chip-Sequencing Data Using a Deep Learning Framework."
Nucleic Acids Research, 2019, <https://doi.org/10.1093/nar/gkz672>.
14. Xia, Ye, Seth DeBolt, Qin Ma, Adam McDermaid, **Cankun Wang**, Nicole Shapiro, Tanja Woyke, and Nikos C. Kyrpides. "Improved Draft Genome Sequence of Bacillus Sp. Strain YF23, Which Has Plant Growth-Promoting Activity."
Microbiology Resource Announcements, 2019, <https://doi.org/10.1128/MRA.00099-19>.
15. Xia, Ye, Seth DeBolt, Qin Ma, Adam McDermaid, **Cankun Wang**, Nicole Shapiro, Tanja Woyke, and Nikos C. Kyrpides. "Improved Draft Genome Sequence of Pseudomonas Poae A2-S9, a Strain with Plant Growth-Promoting Activity."
Microbiology Resource Announcements, 2019, <https://doi.org/10.1128/MRA.00275-19>.
16. Monier, Brandon, Adam McDermaid, **Cankun Wang**, Jing Zhao, Allison Miller, Anne Fennell, and Qin Ma. "IRIS-EDA: An Integrated RNA-Seq Interpretation System for Gene Expression Data Analysis."
PLOS Computational Biology, 2019, <https://doi.org/10.1371/journal.pcbi.1006792>.
17. Wang, Yan, 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, 2018, <https://doi.org/10.1038/s41598-019-40780-7>.
18. Han, Siyu, Yanchun Liang, Qin Ma, Yangyi Xu, Yu Zhang, Wei Du, **Cankun Wang**, and Ying Li. "LncFinder: An Integrated Platform for Long Non-Coding RNA Identification Utilizing Sequence Intrinsic Composition, Structural Information and Physicochemical Property."

Briefings in Bioinformatics, 2018, <https://doi.org/10.1093/bib/bby065>.

19. McDermaid, Adam, Xin Chen, Yiran Zhang, **Cankun Wang**, Shaopeng Gu, Juan Xie, and Qin Ma. "A New Machine Learning-Based Framework for Mapping Uncertainty Analysis in RNA-Seq Read Alignment and Gene Expression Estimation."

Frontiers in Genetics, 2018, <https://doi.org/10.3389/fgene.2018.00313>.

PRESENTATIONS

- 2021, **Analyze RNA-seq data using IRIS-EDA web server**
Vitismet: grapes at UC Davis & SLU. Columbus, OH. (Oral Presentation)
- 2020, **Computational tool and pipeline for RNA-seq data analysis**
NSF PGRP Grape Grafting Annual Meeting. Columbus, OH. (Oral Presentation)
- 2019, **Identification of Regulatory DNA Motifs Using ChIP-exo data**
BMI Internship Poster Session. Columbus, OH. (Poster presentation)
- 2019, **Development of Regulatory Motif Identification program**
BioSNTR Plant Science Research Day. Brookings, SD.
- 2018, **Combining Computational Methods and Experimental Data for Motif Prediction**
BioSNTR Plant Science Research Day. Brookings, SD. (Poster Presentation)

TEACHING EXPERIENCES

- 2021, **BISR CRISPR screening workshop**, Lecturer
Department of Biomedical Informatics, OSU
- 2021, **BISR RNA-Seq workshop**, Lecturer
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

SKILLS

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