

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

- Performed the state-of-art analysis and visualizations of single-cell multi-omics data and next-generation sequencing data
- Designed and implemented integrated bioinformatics full-stack web applications
- Leveraged clinical variables from electronic medical/health records (EMR/EHR) to study activities from intensive care patients with critical illness
- Provided technical expertise and solutions to meet biomedical researchers' data analysis requirements

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

First or corresponding author (corresponding author)*

1. **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* 2, no. 2 (June 18, 2021): 100513. <https://doi.org/10.1016/j.xpro.2021.100513>.
2. Jiang, Jing*, **Cankun Wang***, Ren Qi, Hongjun Fu, and Qin Ma. "ScREAD: A Single-Cell RNA-Seq Database for Alzheimer's Disease." *IScience* 23, no. 11 (November 20, 2020): 101769. <https://doi.org/10.1016/j.isci.2020.101769>.
3. 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* 48, no. W1 (July 2, 2020): W275–86. <https://doi.org/10.1093/nar/gkaa394>.<https://doi.org/10.1093/nar/gkaa394>.

Contributing author

1. Chen, Shuo, Yuzhou Chang, Liangping Li, Diana Acosta, Cody Morrison, **Cankun Wang**, Dominic Julian, et al. "Spatially Resolved Transcriptomics Reveals Unique Gene Signatures Associated with Human Temporal Cortical Architecture and Alzheimer's Pathology," July 8, 2021. <https://doi.org/10.1101/2021.07.07.451554>.
2. 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* 12, no. 1 (March 25, 2021): 1882. <https://doi.org/10.1038/s41467-021-22197-x>.
3. Wang, Yan, Shuangquan Zhang, Anjun Ma, **Cankun Wang**, Zhenyu Wu, Dong Xu, and Qin Ma. “Assessing Deep Learning Algorithms in Cis-Regulatory Motif Finding Based on Genomic Sequencing Data.” *BioRxiv*, December 1, 2020, 2020.11.30.403261. <https://doi.org/10.1101/2020.11.30.403261>.
 4. 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*, no. bbaa354 (December 23, 2020). <https://doi.org/10.1093/bib/bbaa354>.
 5. 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 Journal* 18 (January 1, 2020): 834–42. <https://doi.org/10.1016/j.csbj.2020.03.028>.
 6. Wang, Juexin, Anjun Ma, Yuzhou Chang, Jianting Gong, Yuexu Jiang, Hongjun Fu, Cankun Wang, Ren Qi, Qin Ma, and Dong Xu. “ScGNN: A Novel Graph Neural Network Framework for Single-Cell RNA-Seq Analyses.” *BioRxiv*, August 3, 2020, 2020.08.02.233569. <https://doi.org/10.1101/2020.08.02.233569>.
 7. 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* 9, no. 1 (January 2020): 86. <https://doi.org/10.3390/plants9010086>.
 8. 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*, September 10, 2019, btz69rrna. <https://doi.org/10.1093/bioinformatics/btz692>.
 9. 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*, August 2, 2019. <https://doi.org/10.1093/nar/gkz672>.
 10. 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.” Edited by David Rasko. *Microbiology Resource Announcements* 8, no. 15 (April 11, 2019). <https://doi.org/10.1128/MRA.00099-19>.
 11. 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.” Edited by Irene L. G. Newton. *Microbiology Resource Announcements* 8, no. 15 (April 11, 2019). <https://doi.org/10.1128/MRA.00275-19>.
 12. 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* 15, no. 2 (February 14, 2019): e1006792.
<https://doi.org/10.1371/journal.pcbi.1006792>.
13. 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* 9, no. 1 (December 2018). <https://doi.org/10.1038/s41598-019-40780-7>.
 14. 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*. Accessed November 24, 2018. <https://doi.org/10.1093/bib/bby065>.
 15. 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* 9 (2018). <https://doi.org/10.3389/fgene.2018.00313>.

PRESENTATIONS

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| 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

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| 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, Single-cell multi-omics data analyses (R, Python, HPC system)
- Full stack web development (Vue.js, GraphQL, NestJS, TypeScript, MySQL)
- DevOps (GitHub Actions, Docker, Kubernetes)
- Ops (GPUs based RHEL systems)
- Deep learning model development & deployment (ConvNet, Graph Neural Nets)
- Data visualization (Adobe AI, R, Circos)