

# Cankun Wang

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

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01/2018 – 08/2019 M.S. in Plant Science  
South Dakota State University, Brookings, SD, USA  
09/2013 – 06/2017 B.S. in Software Engineering  
Beijing Jiaotong University, Beijing, China

## Employment

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### Biomedical Informatics Specialist

09/2019 – Now

The Ohio State University Wexner Medical Center

- Performed the state-of-art analysis of single-cell multi-omics data and next-generation sequencing data
- Designed and implemented integrated bioinformatics web application, packages, and databases
- 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

### Student Intern

05/2019 – 07/2019

The Ohio State University Wexner Medical Center

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

### Graduate Research Assistant

01/2018 – 05/2019

Department of Plant Science, South Dakota State University, USA

- 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

### Research Assistant

09/2017 – 12/2017

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

### Data Analyst Intern

02/2014 – 07/2014

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

## Publications

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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*. Accessed May 18, 2020. <https://doi.org/10.1093/nar/gkaa394>.
4. 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 (December 2021): 1882. <https://doi.org/10.1038/s41467-021-22197-x>.
5. 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>.
6. 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>.
7. 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>.
8. 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>.
9. 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>.
10. 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, btz69rma. <https://doi.org/10.1093/bioinformatics/btz692>.
11. 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>.
12. 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>.
13. 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>.
14. 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>.

15. 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>.
16. 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>.
17. 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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1. Analyze RNA-seq data using IRIS-EDA web server. Mar 1<sup>st</sup>, 2021. Vitismeeet: grapes at UC Davis & SLU. Columbus, OH. (Oral Presentation)
2. Computational tool and pipeline for RNA-seq data analysis. Jun 3<sup>rd</sup>, 2020, NSF PGRP Grape Grafting Annual Meeting. Columbus, OH. (Oral Presentation)
3. Identification of Regulatory DNA Motifs Using ChIP-exo data. Jul 26<sup>th</sup>, 2019, BMI Internship Poster Session. Columbus, OH. (Poster presentation)
4. Development of Regulatory Motif Identification program. Apr 23<sup>rd</sup>, 2019, BioSNTR Plant Science Research Day. Brookings, SD. (Oral Presentation)
5. Combining Computational Methods and Experimental Data for Motif Prediction. Apr 26<sup>th</sup>, 2018, BioSNTR Plant Science Research Day. Brookings, SD. (Poster Presentation)

## Teaching experiences

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1. Lecturer, BISR RNA-Seq workshop, Spring 2021, Department of Biomedical Informatics, OSU
2. Guest lecturer, Applications of Machine Learning and Artificial Intelligence (BMI-8050), Autumn 2020, Department of Biomedical Informatics, OSU
3. Guest lecturer, Single-cell sequencing data analysis workshop, Summer 2020, ILU
4. Teaching assistant, Applied Bioinformatics (STAT-735), Spring 2019, Department of Mathematics & Statistics, SDSU

## Skills

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- 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)