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, 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, April 7, 2022. https://doi.org/10.1007/s00401-022-02417-4.
2. Ma, Anjun, Xiaoying Wang, **Cankun Wang**, Jingxian Li, Tong Xiao, Juexing Wang, Yang Li, et al. "DeepMAPS: Single-Cell Biological Network Inference Using Heterogeneous Graph Transformer." bioRxiv, December 11, 2021. https://doi.org/10.1101/2021.10.31.466658.

3. 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.

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 (March 25, 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, btz69rrna. 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

2021,   **Analyze RNA-seq data using IRIS-EDA web server**
            Vitismeet: 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, 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)
● Deep learning model development & deployment (ConvNet, Graph Neural Nets)
● Data visualization (Adobe AI, R, Circos)