

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

Biomedical Informatics Specialist

09/2019 – Now

The Ohio State University Wexner Medical Center

- Perform the state-of-art analysis of Single-cell multi-omics data and Next-generation sequencing data
- Design and implement integrated bioinformatics web application, software and databases via working with the Biomedical Informatics faculty
- Interact with biomedical researchers, providing technical expertise and developing successful solutions to meet their requirements

Student Intern

05/2019 – 07/2019

The Ohio State University Wexner Medical Center

- Research in 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

- Research in identification of DNA transcription factors motif
- Research in development of 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

- Establishes of a test for motif finding efficiency between our algorithm and other popular tools and explored the optimization as well as the feasibility of further iterations.
- Research in correlations between DNA mapped sequencing data and statistical analysis

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

1. 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, btz692. <https://doi.org/10.1093/bioinformatics/btz692>.
2. 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>.
3. 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>.
4. 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>.
5. 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>.
6. 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>.
7. 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>.
8. 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

1. Identification of Regulatory DNA Motifs Using ChIP-exo data. Jul 26, 2019, BMI Internship Poster Session. Columbus, OH. (Poster presentation)
2. Development of Regulatory Motif Identification program. Apr 23, 2019, BioSNTR Plant Science Research Day. Brookings, SD. (Oral Presentation)
3. Combining Computational Methods and Experimental Data for Motif Prediction. Apr 26, 2018, BioSNTR Plant Science Research Day. Brookings, SD. (Poster Presentation)

Skills

- Next-generation sequence data analyses
- R, C, Python programming
- Web development
- Linux server maintenance
- Database management
- Data visualization
- Mathematical & Statistical modelling