

CURRICULUM VITAE

Anjun Ma, Ph.D.

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EDUCATION

- Ph.D.** 2017-2020 **Biomedical Sciences**
The Ohio State University, Columbus, OH, USA
Advisor: Prof. Qin Ma,
Dissertation: Elucidation of Transcriptional Regulatory Mechanisms from Single-cell RNA-Sequencing Data
Training: *Statistic Modeling, Bioinformatics, and Computational System Biology.*
- M.S.** 2014-2017 **Biological Science**
South Dakota State University, Brookings, SD, USA
Advisor: Prof. Yang Yen
Thesis: Investigation of Candidate Loci Associated with Maize Perennialism.
Training: *Plant Science, Breeding, and Molecular & Genetic Biology*
- 2012-2014 **Molecular Biology**
Illinois Institute of Tech, Chicago, IL, USA
- B.E.** 2008-2012 **Bioengineering**
Nanjing Tech University, Nanjing, Jiangsu, China

RESEARCH INTERESTS

- Developing enabling tools and benchmarking pipelines for single-cell RNA-Seq data.
- Developing deep learning-based methods for single-cell multi-omics integration.
- Gene regulatory network inference, motif finding and comparison.
- Single-cell drug resistance analysis via deep transfer learning.
- Metagenomics and Metatranscriptomics analysis for the discovery of human-microbiome interaction.

POSITIONS AND EMPLOYMENTS

- 2019-2020 Graduate Assistant, The Ohio State University
2017-2018 Graduate Assistant, South Dakota State University
2014-2017 Graduate Teaching Assistant, South Dakota State University

PROFESSIONAL MEMBERSHIPS AND HONORS

- 2019-present Reviewer, Int. J. of Bioinformatics Research and Applications
 2019-present Reviewer, Bioinformatics
 2019-present Reviewer, Computational Biology and Chemistry
 2019 - 2020 Member, American Association for the Advancement of Science
 2019/11 Travel Fellowship, RSGDREAM 2019

JOURNAL PUBLICATIONS (*co-first author, ★ Highlight paper)**2020**

- ★1. **Anjun Ma***, Cankun Wang*, *et al.* IRIS3: Integrated Cell-type-specific Regulon Inference Server from Single-cell RNA-Seq data. *Nucleic Acids Research*. 2020. gkaa394, <https://doi.org/10.1093/nar/gkaa394>.
- ★2. Juexin Wang*, **Anjun Ma***, *et al.* scGNN: a novel graph neural network framework for single-cell RNA-Seq analyses. *BioRxiv*. doi.org/10.1101/2020.08.02.233569.
- ★3. **Anjun Ma***, Adam McDermaid*, *et al.* Integrative Methods and Practical Challenges for Single-cell Multi-omics. *Trends in Biotechnology*. 2020. doi.org/10.1016/j.tibtech.2020.02.013.
- ★4. Yang Li, **Anjun Ma**, *et al.* Towards heterogeneous regulatory landscapes across complex diseases using single-Cell omics. *Trends in Genetics*. <https://doi.org/10.1016/j.tig.2020.08.004>.
5. Zhenyu Wu, Patrick Lawrence, **Anjun Ma**, *et al.* Single-cell Techniques and Deep Learning in Predicting Drug Response. *Trends in Pharmacological Sciences*. 2020. 41, 12:1050-1065.
6. Juexin Wang, **Anjun Ma**, *et al.* Inductive Inference of Gene Regulatory Network Using Supervised and Semi-supervised Graph Neural Networks. *Computational and Structural Biotechnology Journal*. 2020. 18:3335-3343.
7. Minghui Wang, Xiaowen Cui, Shan Li, Xinhua Yang, **Anjun Ma**, *et al.* DeepMal: Accurate prediction of protein malonylation sites by deep neural networks. *Chemometrics and Intelligent Laboratory Systems*. 2020. <https://doi.org/10.1016/j.chemolab.2020.104175>.
8. Zhaoqian Liu*, **Anjun Ma***, *et al.* Network analyses in microbiome and host-microbiome relationships based on high-throughput multi-omics data. *Briefings in Bioinformatics*. 2020. bbaa005. doi.org/10.1093/bib/bbaa005.
9. Zhaomin Yu, Cheng Chen, **Anjun Ma**, *et al.* DNNAce: prediction of prokaryote lysine acetylation sites through deep neural networks with multi-information fusion. *Chemom. Intell. Lab. Syst.* 2020. 200, 103999.
10. Bimal Paudel, Yongbin Zhuang, Aravind Galla, Subha Dahal, Yinjie Qiu, **Anjun Ma**, Tajbir Raihan & Yang Yen. WFhb1-1 plays an important role in resistance against Fusarium head blight in wheat. *Scientific Reports*. 2020. 10, 7794.

2019

- ★11. Jinyu Yang, **Anjun Ma**, *et al.* 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>.
- ★12. Juan Xie, **Anjun Ma**, *et al.* QUBIC2: A novel and robust biclustering algorithm for analyses and interpretation of large-scale RNA-Seq data. *Bioinformatics*. 2019. doi.org/10.1093/bioinformatics/btz692.
- 13. Ren Qi*, **Anjun Ma***, Quan Zou, Qin Ma. Clustering and Classification Methods for Single-cell RNA-sequencing Data. *Briefings in Bioinformatics*. 2019. Bbz062. doi.org/10.1093/bib/bbz062.
- 14. **Anjun Ma***, Yinjie Qiu*, *et al.* The genetics and genome-wide screening of regrowth loci, a key component of perennialism in *Zea diploperennis*. *G3: GENES, GENOMES, GENETICS*. 2019. vol. 9 no. 5 1393-1403; doi.org/10.1534/g3.118.200977
- 15. **Anjun Ma***, Minxuan Sun*, *et al.* MetaQUBIC: a computational pipeline for gene-level functional profiling of metagenome and metatranscriptome. *Bioinformatics*. 2019. btz414. doi.org/10.1093/bioinformatics/btz414
- 16. Bin Yu, Wenying Qiu, Cheng Chen, **Anjun Ma**, *et al.* SubMito-XGBoost: predicting protein submitochondrial localization by fusing multiple feature information and eXtreme gradient boosting. *Bioinformatics*. 2019. Btz734. [doi: 10.1093/bioinformatics/btz734](https://doi.org/10.1093/bioinformatics/btz734).

2018 (in SDSU)

- 17. Fang Zhang*, **Anjun Ma***, *et al.* A Central Edge Selection Based Overlapping Community Detection Algorithm for the Detection of Overlapping Structures in Protein-Protein Interaction Networks. *Molecules*. 2018, 23(10), 2633. [doi: 10.3390/molecules23102633](https://doi.org/10.3390/molecules23102633).
- 18. Xiaoying Wang, Bin Yu, **Anjun Ma**, *et al.* Protein–protein interaction sites prediction by ensemble random forests with synthetic minority oversampling technique. *Bioinformatics*. 2018, 1–8. [doi: 10.1093/bioinformatics/bty995](https://doi.org/10.1093/bioinformatics/bty995).
- 19. Xin Chen*, **Anjun Ma***, *et al.* RECTA: Regulon Identification Based on Comparative Genomics and Transcriptomics analysis. *Genes*, 2018, 9(6), 278. [doi:10.3390/genes9060278](https://doi.org/10.3390/genes9060278).
- 20. Sen Liang, **Anjun Ma**, *et al.* A Review of Matched-pairs Feature Selection Methods for Gene Expression Data Analysis. *Computational and Structural Biotechnology Journal*, 2018, 16: 88-97.
- 21. Juan Xie, **Anjun Ma**, *et al.* It is time to apply biclustering: a comprehensive review of biclustering applications in biological and biomedical data. *Briefings in Bioinformatics*. 2018, 1: 16. [doi: 10.1093/bib/bby014](https://doi.org/10.1093/bib/bby014).

TOOL DEVELOPMENT

- **scGNN**: single-cell **G**raph **N**eural **N**etwork (<https://github.com/juexinwang/scGNN>)
- **GRGNN**: **G**ene **R**egulatory **G**raph **N**eural **N**etwork (<https://github.com/juexinwang/GRGNN>)
- **IRIS3**: Integrated cell-type-specific **R**egulon **I**nference **S**erver from **S**ingle-cell **R**NA-**S**eq. (<https://bmbi.bmi.osumc.edu/iris3/>)
- **DESSO**: Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. (<https://bmbi.bmi.osumc.edu/DESSO/>; <https://github.com/viyjy/DESSO>)
- **MetaQUBIC**: a computational pipeline for gene-level functional profiling of metagenome and metatranscriptome. (<https://github.com/OSU-BMBL/metaqubic>)
- **QUBIC2**: A novel and robust biclustering algorithm for analyses and interpretation of large-scale RNA-Seq data. (<https://github.com/OSU-BMBL/QUBIC2>)

TEACHING EXPERIENCES

- **Guest lecturer**, Applications of Machine Learning and Artificial Intelligence in Biomedical Informatics (BMI 8050), Autumn 2020, Department of Biomedical Informatics, The Ohio State University.
- **Guest lecturer**, Analysis and Applications of Genome-Scale Data (BMI 8130), autumn 2019, Department of Biomedical Informatics, The Ohio State University.
- **Guest lecturer**, Next Generation Sequencing Data Analysis (PS-735), 2018, Department of Mathematics and Statistics, and Agronomy, Horticulture, and Plant Science Department, SDSU.
- **Lecturer**, General Biology Lab (BIOL 101 & BIOL 103), 2014-2016, Department of Biology and Microbiology, SDSU.

INVITED PRESENTATIONS

- Cell-type-specific gene regulation inference using single-cell RNA-seq data. PIIO at OSU. Oct 8th, 2020. (Invited by Dr. Zihai Li)
- Cell-type-specific gene regulation inference using single-cell RNA-seq data. Emory University. June 19th, 2020. (Invited by Dr. Steve Qin)
- Single-cell RNA-Seq analysis introduction. Department of Biomedical Informatics, OSU. Sep 4th, 2019. (Department workshop)
- Construction of cell specific gene co-regulations signatures based on single cell transcriptomics analysis and application in Cancer research. Department of Computer Science, Jilin University. June 17th, 2019. (Invited by Prof. Yan Wang)

CONFERENCE POSTERS

- **Anjun Ma**, Cankun Wang, Yuzhou Chang, Adam McDermaid, Bingqiang Liu, Chi Zhang, and Qin Ma. Towards cell-type-specific gene regulation in heterogeneous cancer cells. #4409. American Association for Cancer Research. June 2020. Online.
- **Anjun Ma**, Cankun Wang, Yuzhou Chang, Qin Ma, CeRIS: Cell-type-specific

Regulon Inference from Single-cell RNA-Seq. 2019 PQG Conference: Quantitative Challenges in Cancer Immunology & Immunotherapy. Nov 4-5, 2019. Boston, MA

- **Anjun Ma**, Qin Ma, IRIS3: Interpretation of cell-type-specific regulons identification from single-cell RNA-Sequencing data. OSU Trainee Research Day. April 1st, 2019. The Ohio State University.
- **Anjun Ma**, Qin Ma, Bioinformatics and Mathematical Biosciences Lab, Faculty Excellence Showcase on Celebration of Faculty Excellence. Brookings, SD, February 21, 2018
- **Anjun Ma**, et al, Molecular mapping of perennial genes in Zea L., 58th Annual Maize Genetics Conference, Jacksonville, Florida, 2016; Biochemical and Molecular Genetics 119.