CURRICULUM VITAE

Anjun Ma, Ph.D.

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PROFESSIONAL EXPERIENCE

05/2023 – Present   **Clinical Research Professor**
                           Department of Biomedical Informatics, OSU, OH, USA
11/2021 – 05/2023   **Research Scientist**
                           Biomedical Informatics Shared Resources
                           Department of Biomedical Informatics, OSU, OH, USA

EDUCATION

Postdoc 2021   **Computational Biology**
                           The Ohio State University, Columbus, OH, USA
Ph.D.   2017 – 2020   **Biomedical Sciences**
                           The Ohio State University, Columbus, OH, USA
                           "Elucidation of Transcriptional Regulatory Mechanisms from
                           Single-cell RNA-Sequencing Data." (**Advisor**: Prof. Qin Ma)
M.S.   2014 – 2017   **Biological Science (plant science direction)**
                           South Dakota State University, Brookings, SD, USA
                           "Investigation of Candidate Loci Associated with Maize
                           Perennialism." (**Advisor**: Prof. Yang Yen)
            2012 – 2014   **Molecular Biology**
                           Illinois Institute of Tech, Chicago, IL, USA
B.E.   2008 – 2012   **Bioengineering**
                           Nanjing Tech University, Nanjing, Jiangsu, China

RESEARCH INTERESTS

- Develop enabling tools and benchmarking pipelines for single-cell data analysis.
- Develop computational methods for single-cell and spatial multi-omics analysis.
- 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.

TEACHING EXPERIENCES

- **Lecturer**, Analysis and Applications of Genome-Scale Data (BMI 8130), Spring 2023, Department of Biomedical Informatics, The Ohio State University.
- **Lecturer**, Analysis and Applications of Genome-Scale Data (BMI 8130), Autumn 2021, Department of Biomedical Informatics, The Ohio State University.
- **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 workshop, 09/2019, Department of Biomedical Informatics, The Ohio State University.
- **Guest lecturer**, Construction of cell-type-specific gene co-regulations signatures based on single-cell transcriptomics analysis and application in Cancer research. Department of Computer Science, Jilin University. 06/17/2019. (Three-day workshop, Invited by Prof. Yan Wang)
- **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.

PROFESSIONAL ORGANIZATION MEMBERSHIP

Editorship
2022- Present   Guest Editor
                Single-cell special issue on *Biomolecules* (IF 6.064)
                https://www.mdpi.com/journal/biomolecules/special_issues/L55QV16FUD

Reviewer
2020 – Present Nucleic Acids Research
2019 – Present Computational Biology and Chemistry
2019 – 2020   Bioinformatics
2019 – present Int. J. of Bioinformatics Research and Applications
2021   Frontiers in Medicine
2021   Scientific Reports
2021   Frontiers in Physiology
2021 – present NAR Genetics

Honors
2019/11   Travel Fellowship, RSGDREAM 2019

Others

2019 – 2021   Member, American Association for the Advancement of Science
2019 – 2020   Graduate Assistant, The Ohio State University, Columbus, OH
2017 – 2018   Graduate Assistant, South Dakota State University, SD
2014 – 2017   Graduate Teaching Assistant, South Dakota State University, SD

Funding information

Pending

1. **NIH R01** (Role: **co-I, 25%**; PI: Qin Ma) 2023
   Title: Construction of cell-specific gene co-regulation signatures based on single-cell transcriptomics analysis.
2. **NIH-NCI P01** (Role: **co-I, 20%**; PI: Dan Barouch) 2023
   Title: OSU-Harvard Center for Human Immunology, Mechanisms and Efficacy of Sex-bias to Vaccines.
3. **NIH-NCI R01** (Role: **co-I, 10%**; PI: Haitao Wen) 2023
   Title: Modulation of ferroptotic cell death by mitochondrial calcium signaling.
4. **NIH-NCI R01** (Role: **co-I, 10%**; PI: Zihai Li) 2023
   Title: GRP94 in Treg Biology and Immunotherapy.

JOURNAL PUBLICATIONS (*co-first author, $ corresponding author)

Full list: https://scholar.google.com/citations?user=YmUcOjoAAAAJ&hl=en

1. **Ma, A.***, Wang, X.*, Li, J. *et al.* Single-cell biological network inference using a heterogeneous graph transformer. *Nat Commun* **14**, 964 (2023).
2. Qi Wang, Zhaoqian Liu, **Anjun Ma**, Zihai Li, Bingqiang Liu, Qin Ma. "Computational methods and challenges in analyzing intratumoral microbiome data." *Trends in Microbiology (2023)*
3. Jiang, Yi, Ruheng Wang, Jiuxin Feng, Junru Jin, Sirui Liang, Zhongshen Li, Yingying Yu, **Anjun Ma** et al. "Explainable Deep Hypergraph Learning Modeling the Peptide Secondary Structure Prediction." *Advanced Science (Weinheim, Baden-wurttemberg, Germany)* (2023): e2206151-e2206151.
4. **Ma, Anjun**, Gang Xin, and Qin Ma. "The use of single-cell multi-omics in immuno-oncology." *Nature Communications* 13, no. 1 (2022): 2728.
5. **Ma, Anjun**, Juexin Wang, Dong Xu, and Qin Ma. "Deep learning analysis of single-cell data in empowering clinical implementation." *Clinical and Translational Medicine* 12, no. 7 (2022).
6. Chen, Junyi, Xiaoying Wang, **Anjun Ma$**, Qi-En Wang, Bingqiang Liu, Lang Li, Dong Xu, and Qin Ma. "Deep transfer learning of cancer drug responses by integrating bulk and single-cell RNA-seq data." *Nature Communications* 13, no. 1 (2022): 6494.

7. Wang, Xiaoying, Cankun Wang, Lang Li, Qin Ma, **Anjun Ma$**, and Bingqiang Liu$. "DESSO-DB: A web database for sequence and shape motif analyses and identification." *Computational and Structural Biotechnology Journal* 20 (2022): 3053-3058.

8. Zhang, Shuangquan*, **Anjun Ma***, Jing Zhao, Dong Xu, Qin Ma, and Yan Wang. "Assessing deep learning methods in cis-regulatory motif finding based on genomic sequencing data." *Briefings in Bioinformatics* 23, no. 1 (2022): bbab374.

9. Lee, Patty J., Philip Blood, Katy Börner, Judith Campisi, Feng Chen, Heike Daldrup-Link, Phil De Jager et al. "NIH SenNet Consortium: Mapping senescent cells in the human body to understand health and disease." (2022).

10. Zhang, Shuangquan, Lili Yang, Xiaotian Wu, Nan Sheng, Yuan Fu, **Anjun Ma**, and Yan Wang. "MMGraph: a multiple motif predictor based on graph neural network and coexisting probability for ATAC-seq data." *Bioinformatics* 38, no. 19 (2022): 4636-4638.

11. Brennan, Faith H., Yang Li, Cankun Wang, **Anjun Ma**, Qi Guo, Yi Li, Nicole Pukos et al. "Microglia coordinate cellular interactions during spinal cord repair in mice." *Nature Communications* 13, no. 1 (2022): 4096.

12. Atkinson, Jeffrey R., Andrew D. Jerome, Andrew R. Sas, Ashley Munie, Cankun Wang, **Anjun Ma**, William D. Arnold, and Benjamin M. Segal. "Biological aging of CNS-resident cells alters the clinical course and immunopathology of autoimmune demyelinating disease." *JCI insight* 7, no. 12 (2022).

13. Gu, Haocheng, Hao Cheng, **Anjun Ma**, Yang Li, Juexin Wang, Dong Xu, and Qin Ma. "scGNN 2.0: a graph neural network tool for imputation and clustering of single-cell RNA-Seq data." *Bioinformatics* 38, no. 23 (2022): 5322-5325.

14. Kwon, Hyunwoo, Johanna M. Schafer, No-Joon Song, Satoshi Kaneko, Anqi Li, Tong Xiao, **Anjun Ma** et al. "Androgen conspires with the CD8+ T cell exhaustion program and contributes to sex bias in cancer." *Science immunology* 7, no. 73 (2022): eabq2630.

15. Song, No-Joon, Carter Allen, Anna E. Vilgelm, Brian P. Riesenberg, Kevin P. Weller, Kelsi Reynolds, Karthik B. Chakravarthy, Amrendra Kumar, Aastha Khatiwada, Zequn Sun, **Anjun Ma** et al. "Treatment with soluble CD24 attenuates COVID-19-associated systemic immunopathology." *Journal of Hematology & Oncology* 15 (2022): 1-18.

16. Zhao, Bao, Weipeng Gong, **Anjun Ma**, Jianwen Chen, Maria Velegraki, Hong Dong, Zihao Liu et al. "SUSD2 suppresses CD8+ T cell antitumor immunity by targeting IL-2 receptor signaling." *Nature Immunology* (2022): 1-12.

17. Chang, Yuzhou, Fei He, Juexin Wang, Shuo Chen, Jingyi Li, Jixin Liu, Yang Yu, Li Su, **Anjun Ma** et al. "Define and visualize pathological architectures of human tissues from spatially resolved transcriptomics using deep learning." *Computational and Structural Biotechnology Journal* 20 (2022): 4600-4617.

18. Jiang, Lei, Yuexu Jiang, Cankun Wang, Clement Essien, Juexin Wang, **Anjun Ma**, Qin Ma, and Dong Xu. "Machine learning development environment for single-cell sequencing data analyses." In *2022 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pp. 3824-3826. IEEE, 2022.

19. 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 (2021): 1882.

20. Liu, Zhaoqian*, **Anjun Ma***, Ewy Mathé, Marlena Merling, Qin Ma, and Bingqiang Liu. "Network analyses in microbiome based on high-throughput multi-omics data." *Briefings in bioinformatics* 22, no. 2 (2021): 1639-1655.

21. Yu, Bin, Cheng Chen, Xiaolin Wang, Zhaomin Yu, **Anjun Ma**, and Bingqiang Liu. "Prediction of protein–protein interactions based on elastic net and deep forest." *Expert Systems with Applications* 176 (2021): 114876.

22. **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 (2020): W275-W286.

23. **Ma, Anjun***, Adam McDermaid*, Jennifer Xu, Yuzhou Chang, and Qin Ma. "Integrative methods and practical challenges for single-cell multi-omics." *Trends in biotechnology* 38, no. 9 (2020): 1007-1022.

24. Li, Yang*, **Anjun Ma***, Ewy A. Mathé, Lang Li, Bingqiang Liu, and Qin Ma. "Elucidation of biological networks across complex diseases using single-cell omics." *Trends in Genetics* 36, no. 12 (2020): 951-966.

25. Qi, Ren*, **Anjun Ma***, Qin Ma, and Quan Zou. "Clustering and classification methods for single-cell RNA-sequencing data." *Briefings in bioinformatics* 21, no. 4 (2020): 1196-1208.

26. Wu, Zhenyu, Patrick J. Lawrence, **Anjun Ma,** Jian Zhu, Dong Xu, and Qin Ma. "Single-cell techniques and deep learning in predicting drug response." *Trends in pharmacological sciences* 41, no. 12 (2020): 1050-1065.

27. Wang, Juexin, **Anjun Ma**, Qin Ma, Dong Xu, and Trupti Joshi. "Inductive inference of gene regulatory network using supervised and semi-supervised graph neural networks." *Computational and structural biotechnology journal* 18 (2020): 3335-3343.

28. Wang, Minghui, Xiaowen Cui, Shan Li, Xinhua Yang, **Anjun Ma**, Yusen Zhang, and Bin Yu. "DeepMal: Accurate prediction of protein malonylation sites by deep neural networks." *Chemometrics and Intelligent Laboratory Systems* 207 (2020): 104175.

29. Yu, Bin, Zhaomin Yu, Cheng Chen, **Anjun Ma**, Bingqiang Liu, Baoguang Tian, and Qin Ma. "DNNAce: prediction of prokaryote lysine acetylation sites through deep

neural networks with multi-information fusion." *Chemometrics and intelligent laboratory systems* 200 (2020): 103999.

30. Paudel, Bimal, Yongbin Zhuang, Aravind Galla, Subha Dahal, Yinjie Qiu, **Anjun Ma**, Tajbir Raihan, and Yang Yen. "WFhb1-1 plays an important role in resistance against Fusarium head blight in wheat." *Scientific reports* 10, no. 1 (2020): 7794.

31. Yu, Bin, Chen Chen, Ren Qi, Ruiqing Zheng, Patrick J. Skillman-Lawrence, Xiaolin Wang, **Anjun Ma**, and Haiming Gu. "scGMAI: a Gaussian mixture model for clustering single-cell RNA-Seq data based on deep autoencoder." *Briefings in bioinformatics* 22, no. 4 (2021): bbaa316.

32. Yu, Bin, Wenying Qiu, Cheng Chen, **Anjun Ma**, Jing Jiang, Hongyan Zhou, and Qin Ma. "SubMito-XGBoost: predicting protein submitochondrial localization by fusing multiple feature information and eXtreme gradient boosting." *Bioinformatics* 36, no. 4 (2020): 1074-1081.

33. **Ma, Anjun***, Minxuan Sun*, Adam McDermaid, Bingqiang Liu, and Qin Ma. "MetaQUBIC: a computational pipeline for gene-level functional profiling of metagenome and metatranscriptome." *Bioinformatics* 35, no. 21 (2019): 4474-4477.

34. **Ma, Anjun***, Yinjie Qiu*, Tajbir Raihan, Bimal Paudel, Subha Dahal, Yongbin Zhuang, Aravind Galla, Donald Auger, and Yang Yen. "The genetics and genome-wide screening of regrowth loci, a key component of perennialism in Zea diploperennis." *G3: Genes, Genomes, Genetics* 9, no. 5 (2019): 1393-1403.

35. 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* 47, no. 15 (2019): 7809-7824.

36. 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." *Bioinformatics* 36, no. 4 (2020): 1143-1149.

37. Xie, Juan, **Anjun Ma**, Anne Fennell, Qin Ma, and Jing Zhao. "It is time to apply biclustering: a comprehensive review of biclustering applications in biological and biomedical data." *Briefings in bioinformatics* 20, no. 4 (2019): 1450-1465.

38. Wang, Xiaoying, Bin Yu, **Anjun Ma**, Cheng Chen, Bingqiang Liu, and Qin Ma. "Protein–protein interaction sites prediction by ensemble random forests with synthetic minority oversampling technique." *Bioinformatics* 35, no. 14 (2019): 2395-2402.

39. Zhang, Fang*, **Anjun Ma***, Zhao Wang, Qin Ma, Bingqiang Liu, Lan Huang, and Yan Wang. "A central edge selection based overlapping community detection algorithm for the detection of overlapping structures in protein–protein interaction networks." *Molecules* 23, no. 10 (2018): 2633.

40. Chen, Xin*, **Anjun Ma***, Adam McDermaid, Hanyuan Zhang, Chao Liu, Huansheng Cao, and Qin Ma. "RECTA: Regulon identification based on comparative genomics and transcriptomics analysis." *Genes* 9, no. 6 (2018): 278.

41. Liang, Sen, **Anjun Ma**, Sen Yang, Yan Wang, and Qin Ma. "A review of matched-pairs feature selection methods for gene expression data analysis." *Computational and structural biotechnology journal* 16 (2018): 88-97.

TOOL DEVELOPMENT

- **DeepMAPS**: a deep learning based multi-omics analysis platform for single cells (https://bmbls.bmi.osumc.edu/deepmaps/)
- **scDEAL**: Deep Transfer Learning of Drug Sensitivity by Integrating Bulk and Single-cell RNA-seq data (https://github.com/OSU-BMBL/scDEAL)
- **scGNN**: **s**ingle-**c**ell **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**: **I**ntegrated cell-type-specific **R**egulon **I**nference **S**erver from **S**ingle-cell RNA-**S**eq. (https://bmbl.bmi.osumc.edu/iris3/)
- **DESSO**: Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. (https://bmbl.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)

INVITED PRESENTATIONS

- Graph representation and deep learning for single-cell multi-omics analysis. SenNet TriState monthly meeting. Online webinar. May 3, 2023
- Graph representation and deep learning for single-cell multi-omics analysis. SenNet TriState Annual meeting. Ohio State University, USA. Apr 11, 2023
- Computational tool development for single-cell sequencing data. Department of Biomedical Informatics. Ohio State University, USA. Jan 18, 2023
- Deep transfer learning for single-cell drug response prediction. Jilin University, China. Online webinar. Dec 16, 2022
- Graph neural network applications in single-cell Multi-omics analysis. Frontline Genomics. Online webinar. Dec 9, 2021
- Cell-type-specific gene regulation inference using single-cell RNA-seq data. PIIO at OSU. July 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. (Invited by Dr. Yue Zhao)

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.