Qin Ma, Ph.D.

CONTACT INFORMATION

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Lab Website: https://u.osu.edu/bmbl/
Twitter: @QinMaBMBL

PROFESSIONAL EXPERIENCE

2023-	Professor Department of Biomedical Informatics, College of Medicine, The Ohio State University
2022-	Section Chief of Bioinformatics and Computational Biology Department of Biomedical Informatics, College of Medicine, The Ohio State University
2022-	Leader of the Immuno-Oncology Informatics Group (IOIG) Pelotonia Institute for Immuno-Oncology (PIIO) The Ohio State University
2019-	Associate Professor (with tenure) Department of Biomedical Informatics, College of Medicine, The Ohio State University
2015-2018	Assistant Professor (tenure-track faculty) Department of Mathematics and Statistics and Department of Agronomy, Horticulture & Plant Science, South Dakota State University
2014-2015	Research Scientist (non-tenure-track faculty) Department of Biochemistry & Molecular Biology University of Georgia

EDUCATION

2011-2014	Postdoc	Computational Systems Biology University of Georgia
2005-2010	Ph.D.	Operational Research and Bioinformatics University of Georgia (Supervisor: Prof. Ying Xu, 2008-2010) Shandong University (Supervisor: Prof. Guojun Li, 2005-2008)
2001-2005	B.S.	Applied Mathematics and Algorithm Design Shandong University, Awarded with first-class honors

RESEARCH INTERESTS

- Deep learning and single-cell studies have been making waves in the science and technology communities. My lab focuses on the research of single-cell multi-omics (https://bmblx.bmi.osumc.edu/) and spatially resolved transcriptomics data (https://bmblx.bmi.osumc.edu/spatial/), aiming to develop novel DL methods and enabling tools to discover underlying regulatory programs in diverse biological systems (https://bmblx.bmi.osumc.edu/iris/).

- scMulti-omics brought transformative insights into immuno-oncology, demonstrating success in describing novel immune subsets and defining important regulators of antitumor immunity. One significant challenge in immuno-oncology is identifying the heterogeneity of immune cells in tumors and their differentiation process. To overcome these limitations, a scMulti-omics study can offer detailed identification of diverse immune subsets at a higher resolution and provide an opportunity to understand the contribution of immune cells to tumor progression. Our lab endeavors single-cell applications in immuno-oncological areas (https://bmblx.bmi.osumc.edu/sc-io).
- We are developing computational tools and databases to elucidate the composition and function of microbial communities and their interactions with human diseases, including immuno-oncology-microbiome data mining, computational analysis of human-microbiome interaction, and network analyses in microbiome using metagenome & metatranscriptome data (https://bmblx.bmi.osumc.edu/magical/).

LEADERSHIP DEVELOPMENT

- Section Chief of Bioinformatics and Computational Biology of BMI   2022-
- Leader of the Immuno-Oncology Informatics Group (IOIG) of PIIO   2022-
- Leader of training program development in AI/ML and Health in the Department of Biomedical Informatics at the Ohio State University   2020-
- Co-chair of Student engagement committee in the Department of Biomedical Informatics at the Ohio State University   2020-
- Member of the Leadership Council Committee in the Department of Biomedical Informatics at the Ohio State University   2020-
- Leader of Cancer systems biology research group in the Department of Biomedical Informatics at the Ohio State University   2019-
- Director of the Bioinformatics and Mathematical Biosciences Lab: Supervised multiple postdocs, graduate students, and undergraduate students   2015-
- Group Leader of Systems Biology for Biofuel Study in Computational Systems Biology laboratory (CSBL), University of Georgia   2014-2015

PROFESSIONAL ORGANIZATION MEMBERSHIPS

Editorship
- Associate Editor,   Computational and Structural Biotechnology Journal   2023
- Associate Editor,   Computational Biology and Chemistry   2019-
- Associate Editor,   BMC Genomics   2015-

Membership
- Member,   International Society for Computational Biology (ISCB),   2014-

Conference program committee
- Computational systems biology area chair, IEEE   International   Conference   on Medical Artificial Intelligence (IEEE MedAI)   2023
- Program Committee and Award Committee Member, International Conference on Intelligent Biology and Medicine (ICIBM),   2019-2020
- Program Committee Member, The IEEE International Conference on Bioinformatics and Biomedicine (BIBM),   2016-2020

MEDIA APPEARANCES

- [August 4th, 2021] Interviewed by Stephanie DeMarco, Assistant Editor of Drug Discovery News, regarding "single-cell sequencing and machine learning to study how cell behavior changes when cells shift from healthy to diseased states".
- [April 23rd, 2021] Interviewed by the Technology editor (Jeffery Perkel) at Nature regarding the advances and challenges in single-cell multi-omics bioinformatics.
- [November 18, 2018] DD news. It is just an expression. A trio of institutions is looking to explore not just linking genes with diseases, but how they are expressed, in hopes of determining more about how diseases advance. A four-year, $1.04 million National Institutes of Health Research Project grant (R01).   (Link)
- [Jan 24, 2018] Dr. Qin Ma and the BMBL are highlighted on the January edition of the SD EPSCoR Newsletter. The issue looks at Ma lab and profiles a software program (QUBIC-R) that helps model and visualize gene expression networks.   (Link)

INVITED PRESENTATIONS

1. (2023) Graph representation learning of single-cell biological network inference. The **keynote speaker** for APBC 2023, The 21st Asia Pacific Bioinformatics Conference. April 14-16, 2023. Changsha, Hunan, China
2. (2021) **Keynote speaker** for a webcast of Single cell multi-omics methods. Nature Reviews Molecular Cell Biology and Nature Communications and sponsored by Illumina. September 22, 2021.
3. (2019) Towards heterogeneous regulatory landscapes across complex diseases based on single-cell multi-omics data. **Keynote Speaker** for International Conference on Mathematics and Bioinformatics interdisciplinary Research. Nov 21-23, 2019, Qingdao, China.

RESEARCH GRANTS

1. NIAID (P01AI177687)   PI of Data Science Core   2023-2028
   Title: Multi-Omics Analysis of Broadly Neutralizing Antibodies and Therapeutic Vaccination.
2. NCI (P01CA267108)   PI of Data Core   2023-2028
   Title: Sex, Chromosomes, and Immunity in Bladder Cancer
3. NIDDK (R01DK138504)   MPI (Wang, Ma, Eadon)   2023-2028
   Title: SCH: Graph-based Spatial Transcriptomics Computational Methods in Kidney Diseases
4. NIAID (R01AI171027)   site PI (PI: Mitchell Grayson)   2023-2028
   Title: Pre-Existing Atopy and Respiratory Viral Infections
5. NIGMS (R01GM152585)   MPI (Chung, Ma)   2023-2028
   Title: Statistical power analysis framework for multi-sample and cross-platform spatial omics experiments. (16% percentile)
6. NIA (U54AG075931)   PI of Data Analysis Core   2021-2026
   Title: Tri-State SenNET Lung and Heart Tissue Mapping Consortium.
   TriState-SenNet: https://tristatesennet.pitt.edu/data-analysis-core/
7. NCI (U24CA252977)   MPI (Bridges, Paskett, Ma)   2020-2025
   Title: Participant Engagement and Cancer Genome Sequencing: Coordinating Center.
   PECGS-portal: https://pecgs.org/pecgs/network-members/8.
8. NSF (1945971)   PI   2021-2024

Title: A reinforced imputation framework for accurate gene expression recovery from single-cell RNA-seq data
9. NHGRI (R21HG012482)   MPI (Chung, Ma)   2022-2024
   Title: Statistical Power Calculation Framework for Spatially Resolved Transcriptomics Experiments
10. NIGMS (R01GM131399)   PI   2018-2023
    Title: Construction of cell type specific gene co-regulation signatures based on single cell transcriptomics data.
    Project website: https://u.osu.edu/bmbl/highlights/r01/.

MENTORING

Junior faculty
Anjun Ma (Biomedical Informatics at OSU)	Faculty mentor committee chair	2023-
Lijun Cheng (Biomedical Informatics at OSU)	Faculty mentor committee	2021-
Maciej Pietrzak (Biomedical Informatics at OSU)	Faculty mentor committee	2021-

Research Scientists
Anjun Ma (Biomedical Informatics at OSU)	Mentor	2021-2023
Cankun Wang (BISR at OSU)	Project Mentor	2019-
Megan McNutt	Neuroscience at OSU	2021-

Post-Docs
Xiaoying Wang (Deep learning at PIIO)	Mentor	2023-
Jordan Krull (Immunology at PIIO)	Mentor	2022-
Yang Li (Biomedical Informatics at OSU)	Mentor	2019-2023
Adam McDermaid (Statistics at SDSU)	Mentor	2018-2019
Anjun Ma (Biomedical Informatics at OSU)	Mentor	2020-2021

Ph.D. Students
Yi Jiang (BSGP at OSU)	Thesis Committee, Chair	2023-
Jia Qu (BSGP at OSU)	Thesis Committee, Chair	2023-
Mirage Modi (MSTP at OSU)	Thesis Committee, Chair	2023-
Yuzhou Chang (BSGP at OSU)	Thesis Committee, Chair	2019-
Hao Cheng (BSGP at OSU)	Thesis Committee, Chair	2022-
Qi Guo (BSGP at OSU)	Thesis Committee, Chair	2022-
Yingjie Li (BSGP at OSU)	Thesis Committee, Chair	2022-
Paul Toth (MCDB at OSU)	Mentor (rotating PhD)	2021
Patrick J. Lawrence (BSGP at OSU)	Mentor (rotating PhD)	2020
Anjun Ma (BSGP at OSU)	Thesis Committee, Chair	2017-2020
Marlena Merling (BSGP at OSU)	Mentor (rotating PhD)	2019-2020
Adam McDermaid (Statistics at SDSU)	Thesis Committee, Chair	2015-2018
Brandon Monier (Biology at SDSU)	Project Advisor	2016-2018

Visiting Scholars
Jichang Wu (Professor)	Shandong University	2016-2021
Jing Jiang (Ph.D. candidate)	Xiamen University	2019-2020
Zhaoqian Liu (Ph.D. candidate)	Shandong University	2019-2020
Ren Qi (Ph.D. candidate)	Tianjin University	2020
Junyi Chen (Ph.D. candidate)	City University of Hong Kong	2019

Master Students

Yuzhou Chang (BSGP at OSU)	Project Advisor	2019-2020
Shaopeng Gu (Statistics at SDSU)	Thesis Committee, Chair	2018-2019
Cankun Wang (Software Engineering at SDSU)	Thesis Committee, Chair	2018-2019
Jinyu Yang (Statistics at SDSU)	Thesis Committee, Chair	2016-2018
Juan Xie (Statistics at SDSU)	Thesis Committee, Chair	2016-2018

Undergraduate Students

Ana Xiong	Data Science at OSU	2021
Edison Gu	Data Science at OSU	2021-2022
Jiaxin Yang	Data science at OSU	2021
Sheen Brown	Mathematics at OSU	2022
Shicong Wang	Computer Science at OSU	2021
Yingyi Zhu	Biological Engineering at OSU	2021
Zichun Zhang	Mathematics Department at OSU (Volunteer)	2019-2020
Weiliang Liu	Mathematics Department at OSU (Volunteer)	2019
Jennifer Xu	Biostatistics at University of North Carolina, Chapel Hill	2019
Minxuan Sun	Computer Science Department at SDSU	2017-2019
Paige Hinton	Mathematics and Statistics Department at SDSU	2018-2019
Yiran Zhang	Computer Science Department at SDSU	2015-2016
Xiaozhu Jin	Computer Science Department at SDSU	2016-2017
Shuai Li	Computer Science Department at SDSU	2017
Yirong Wang	Computer Science Department at SDSU	2018
Zoey Glenn	REU student from Drake University	2016
Jason Kiehne	REU student from Simpson College	2016

High-school Students

Katherine Xu	Dublin Jerome High School	2023

- Admitted by Stanford University (Computer Science major)

Grace Xu	Dublin Jerome High School	2023
Amani Karoub	Millburn High School in NJ	2023
Nicole Karoub	Millburn High School in NJ	2023
Kevin Wang	Columbus Academy	2023
Mohnish Karthikeyan	William Mason High School	2022
Cindy Tong	Watkins Memorial High School	2021

- Admitted by Princeton University (Computer Science major)

ACADEMIC SERVICES

International

• European Commission	Panel Reviewer,	2023-
• UK Research and Innovation (UKRI)	External Reviewer,	2022-
• KU Leuven (University of Leuven, Belgium)	External Reviewer,	2022-
• Neurosciences and Mental Health Board of Medical Research Council at UK research and innovation	External Reviewer,	2022-
• Dutch Cancer Society, Netherlands	External Reviewer,	2021-
• Austrian Science Fund	External Reviewer,	2021-
• Luxembourg National Research Fund	External Reviewer,	2021-
• German Research Foundation,	External Reviewer,	2020-

- Research Grants Council of Hong Kong,   External Reviewer,   2016-
- Food and Health Bureau of The Government of the HKSAR, External Reviewer 2019
- Israel Science Foundation (ISF)   External Reviewer,   2020
- Swiss National Science Foundation (SNSF) External Reviewer   2020
- NSERC, Canada,   External Reviewer,   2018

National

- NSF Informatics 3 panel,   Panel Reviewer,   2022
- NIH BDMA study section   Panel Reviewer   2022
- USDA NIFA FACT program   Panel Reviewer,   2019-2020
- NSF GRFP review panel   Reviewer   2020
- NSF PBI review panel,   Panel Reviewer,   2016
- Peer-reviewed journals (>150 manuscripts)   Reviewer,   2013-
  (1) Nature, (2) Nature Biotechnology, (3) Nature Communications, (4) Genome Research, (5) Genome Biology, (6) Nucleic Acids Research, (7) Science Advances, (8) PLoS Computational Biology, (9) Briefings in Bioinformatics, (10) Bioinformatics.

SELECTED PUBLICATIONS (H-index: 40; 10-index: 97)

1. 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 Feb 23;S0966-842X(23)00030-6. PMID: 36841736
   DOI: 10.1016/j.tim.2023.01.011
2. Anjun Ma, Xiaoying Wang, Cankun Wang, Jingxian Li, Tong Xiao, Juexing Wang, Yuzhou Chang, Yang Li, Yuntao Liu, Shaopeng Gu, Duolin Wang, Yuexu Jiang, Jinpu Li, Li Su, Zihai Li, Bingqiang Liu$^\$$, Dong Xu$^\$$, Qin Ma$^\$$, Single-cell biological network inference using a heterogeneous graph transformer.
   Nature Communications. 14, Article number: 964 (2023). PMID: 36810839
   DOI: 10.1038/s41467-023-36559-0
3. Yi Jiang, Ruheng Wang, Jiuxin Feng, Junru Jin, Sirui Liang, Zhongshen Li, Yingying Yu, Qin Ma$^\$$, and Leyi Wei$^\$$, Explainable deep hypergraph learning modeling the peptide secondary structure prediction.
   Advanced Science. 2023 Feb 15;e2206151. doi: 10.1002/advs.202206151.
   PMID: 36794291
4. Shiqiao Ye*, Cankun Wang*, Zhaohui Xu, Hui Lin, Xiaoping Wan, Yang Yu, Joe Z. Zhang, Yang Zhou, Chun Liu, Matthew Alonzo, Jianli Bi, Angelina Ramirez-Navarro, Isabelle Deschenes, Qin Ma, Vidu Garg, Joseph C. Wu, Ming-Tao Zhao. Single-cell transcriptomics reveals impaired human cardiac cell lineage determination and cardiomyocyte proliferation due to NOTCH1 deficiency.
   Circulation Research. 2022 Dec 30. doi: 10.1161/CIRCRESAHA.122.321398.
   PMID: 36583388
5. Patty Lee, Philip Blood, Katy Börner, Judith Campisi, Feng Chen, Heike Daldrup-Link, Phil De Jager, Li Ding, Francesca Duncan, Oliver Eickelberg, Rong Fan, Toren Finkel, Vesna Garovic, Nils Gehlenborg, Carolyn Glass, Ziv Bar-Joseph, Pragati Katiyar, So-Jin Kim, Melanie Königshoff, George Kuchel, Haesung Lee, Jun H Lee, Jian Ma, Qin Ma, Simon Melov, Kay Metis, Ana L Mora, Nicolas Musi, Nicola Neretti, João F. Passos, Irfan Rahman, Juan Carlos Rivera-Mulia, Paul Robson, Mauricio Rojas, Ananda L Roy, Birgit Schilling, Pixu Shi, Jonathan Silverstein, Vidyani Suryadevera, Jichun Xie, Jinhua Wang, A Ian Wong, Laura Niedernhofer, NIH SenNet Consortium

to map senescent cells throughout the human lifespan to understand physiological health.
Nature Aging. 2, pages1090–1100 (2022).

6. Junyi Chen, Xiaoying Wang, Anjun Ma$^{\$}$, Bingqiang Liu, Dong Xu, Lang Li, Qin Ma$^{\$}$, Deep transfer learning of cancer drug responses by integrating bulk and single-cell RNA-seq data.
Nature Communications. 2022. DOI : 10.1038/s41467-022-34277-7
PMID: 36310235.

7. Bao Zhao, Weipeng Gong, Anjun Ma, Jianwen Chen, Hong Dong, Zihao Liu, Lingling Wang, Tamio Okimoto, Devin M. Jones, Yu L. Lei, Meixiao Long, Kenneth J. Oestreich, Qin Ma, Gang Xin, David P. Carbone, Kai He, Zihai Li and Haitao Wen*. SUSD2 suppresses CD8+ T cell antitumor immunity by targeting IL-2 receptor signaling.
Nature Immunology. 2022. DOI: 10.1038/s41590-022-01326-8
PMID: 36266363

8. Panke Qu, Julia N. Faraone, John P. Evans, Yi-Min Zheng, M.D., Lianbo Yu, Qin Ma, Claire Carlin, Gerard Lozanski, Linda J. Saif, Eugene M. Oltz, Richard J. Gumina, Shan-Lu Liu. Durability of Booster mRNA Vaccine Against SARS-CoV-2 BA.2.12.1 and BA.4/5 Subvariants.
New England Journal of Medicine. 2022. DOI: 10.1056/NEJMc2210546.
PMID: 36069925

9. Faith H. Brennan, Yang Li, Cankun Wang, Anjun Ma, Qi Guo, Yi Li, Nicole Pukos, Warren A. Campbell, Kristina G. Witcher, Zhen Guan, Kristina A. Kigerl, Jodie C.E. Hall, Jonathon P. Godbout, Andy J. Fischer, Dana M. McTigue, Zhigang He, Qin Ma, and Phillip G. Popovich. Microglia coordinate cellular interactions during spinal cord repair in mice.
Nature Communications. 2022 Jul 14;13(1):4096. doi: 10.1038/s41467-022-31797-0.
PMID: 35835751.

10. Mor Kenigsbuch, Pierre Bost, Shahar Halevi, Yuzhou Chang, Shuo Chen, Qin Ma, Renana Hajbi, Benno Schwikowski, Bernd Bodenmiller, Elior Peles, Hongjun Fu, Michal Schwartz, Ido Amit, A shared disease-associated oligodendrocyte signature among multiple CNS pathologies.
Nature Neuroscience. 2022 Jul;25(7):876-886. doi: 10.1038/s41593-022-01104-7.
PMID: 35760863.

11. Anjun Ma, Gang Xin, Qin Ma$^{\$}$. The use of single-cell multi-omics in immuno-oncology.
Nature communications.
2022 Jul;25(7):876-886. doi: 10.1038/s41593-022-01104-7. PMID: 35585090
https://doi.org/10.1038/s41467-022-30549-4.

12. Qin Ma$^{\$}$, Dong Xu, Deep learning shapes single-cell data analysis.
Nature Reviews Molecular Cell Biology (2022). PMID: 35197610
https://doi.org/10.1038/s41580-022-00466-x

13. Hyunwoo Kwon, Johanna M Schafer, No-Joon Song, Kaneko Satoshi, Anqi Li, Tong Xiao, Anjun Ma, Carter Allen, Komal Das, Lei Zhou, Brian Riesenberg, Yuzhou Chang, Payton Weltge, Maria Velegraki, David Oh, Lawrence Fong, Qin Ma, Debasish Sundi, Dongjun Chung, Xue Li, Zihai Li. Androgen conspires with the CD8+ T cell exhaustion program and contributes to sex bias in cancer.
Science Immunology. 2022 Jul;7(73):eabq2630. doi: 10.1126/sciimmunol.abq2630.
PMID: 35420889.

14. Norah Alghamdi, Wennan Chang, Pengtao Dang, Xiaoyu Lu, Changlin Wan, Silpa Gampala, Zhi Huang, Jiashi Wang, Qin Ma, Yong Zang, Melissa Fishel, Sha Cao, Chi

Zhang. A graph neural network model to estimate cell-wise metabolic flux using single cell RNA-seq data.
Genome Research. 2021 Jul 22;gr.271205.120. doi: 10.1101/gr.271205.120.
PMID: 34301623

15. Juexin Wang, Anjun Ma, Jianting Gong, Yuexu Jiang, Yuzhou Chang, Ren Qi, Qin Ma[$], Dong Xu[$], scGNN is a novel graph neural networks model for single-cell transcriptome analysis.
Nature Communications. 12:1882. https://rdcu.be/chszu.
https://doi.org/10.1038/s41467-021-22197-x.

16. Tianliang Li, Ligang Kong, Xinghui Li, Sijin Wu, Kuldeep Attri, Yan Li, Weipeng Gong, Bao Zhao, Lupeng Li, Laura Herring, John Asara, Lei Xu, Xiaobo Luo, Yu Lei, Qin Ma, Stephanie Seveau, John Gunn, Xiaolin Cheng, Pankaj Singh, Douglas Green, Haibo Wang, Haitao Wen. Listeria monocytogenes upregulates mitochondrial calcium signaling to inhibit LC3-associated phagocytosis as a survival strategy.
Nature Microbiology. 2021. https://doi.org/10.1038/s41564-020-00843-2.

17. Anjun Ma, Cankun Wang, Faith Brennan, Adam McDermaid, Yuzhou Chang, Chi Zhang, Bingqiang Liu, and Phillip Popovich, Qin Ma[$], IRIS3: Integrated Cell-type-specific Regulon Inference from Single-cell RNA-Seq.
Nucleic Acids Research (WSI 2020). DOI: 10.1093/nar/gkaa394. 2020.
PMID: 32421805. News.

18. Changlin Wan, Wennan Chang, Yu Zhang, Fenil Shah, Sha Cao, Xin Chen, Melissa Fishel, Qin Ma[$], Chi Zhang[$], LTMG: A statistical model of transcriptional regulatory states in single cell RNA-Seq data.
Nucleic Acids Research, Volume 47, Issue 18, 10 October 2019, Page e111, https://doi.org/10.1093/nar/gkz655. PMID: 31372654.

19. Jinyu Yang, Anjun Ma, Cankun Wang, Adam Hoppe, Chi Zhang, Yan Wang, Bingqiang Liu, Qin Ma[$]. Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework.
Nucleic Acids Research, Volume 47, Issue 15, 05 September 2019, Pages 7809–7824, gkz672. doi: 10.1093/nar/gkz672. PMID: 31372637.

20. Zhenyu Wu, Patrick J. Lawrence, Anjun Ma, Jian Zhu, Dong Xu, Qin Ma[$], Single-cell Techniques and Deep Learning in Predicting Drug Response.
Trends in Pharmacological Sciences. 2020. PMID: 33153777.
DOI: 10.1016/j.tips.2020.10.004

21. Yang Li, Anjun Ma, Ewy Mathe, Bingqiang Liu, Lang Li, Qin Ma[$], Elucidation of Biological Networks Across Complex Diseases Using Single-Cell Omics.
Trends in Genetics. 2020. PMID: 32868128.
DOI: https://doi.org/10.1016/j.tig.2020.08.004

22. Anjun Ma, Adam McDermaid, Jennifer Xu, Yuzhou Chang, Qin Ma[$], Integrative methods and practical challenges for single-cell multi-omics.
Trends in Biotechnology. March 26, 2020. PMID: 32818441.
DOI: https://doi.org/10.1016/j.tibtech.2020.02.013.

23. Wen-Chi Chou, Qin Ma, Shihui Yang, Sha Cao, Steven D. Brown, Ying Xu, Analysis of strand-specific RNA-Seq data using machine learning reveals the structures of transcription units in *Clostridium thermocellum*.
Nucleic Acids Research. 2015 May 26;43(10):e67. doi: 10.1093/nar/gkv177.
PMID: 25765651.

24. Xizeng Mao, Qin Ma, Chuan Zhou, Xin Chen, Hanyuan Zhang, Jincai Yang, Fenglou Mao, Wei Lai, Ying Xu. DOOR 2.0: presenting operons and their functions through dynamic and integrated views.

Nucleic Acids Research. 2014 Jan;42(Database issue):D654-9.
doi: 10.1093/nar/gkt1048. PMID: 24214966.

25. Qin Ma, Hanyuan Zhang, Xizeng Mao, Chuan Zhou, Bingqiang Liu, Xin Chen, and Ying Xu, DMINDA: An integrated high-performance web server for DNA Motif analyses.
Nucleic Acids Research. 2014 Jul;42(Web Server issue):W12-9.
doi: 10.1093/nar/gku315. PMID: 24753419.

26. Qin Ma, Jaxk Reeves, David A. Liberles, Lili Yu, Zheng Chang, Jing Zhao, Ying Xu, Liang Liu, A Phylogenetic Model for Understanding the Effect of Gene Duplication on Cancer Progression.
Nucleic Acids Research. 2014 Mar;42(5):2870-8. doi: 10.1093/nar/gkt1320.
PMID: 24371277.

27. Qin Ma, Yanbin Yin, Mark A. Shell, Han Zhang, Guojun Li, Ying Xu, Computational analyses of transcriptomic data reveal the dynamic organization of the E. coli chromosome under different conditions.
Nucleic Acids Research. 2013 Jun;41(11):5594-603. doi: 10.1093/nar/gkt261.
PMID: 23599001.

28. Guojun Li, Qin Ma, Xizeng Mao, Yanbin Yin, Xiaoran Zhu, Ying Xu. Integration of sequence-similarity and functional association information can overcome intrinsic problems in orthology mapping across bacterial genomes.
Nucleic Acids Research. 2011 Dec;39(22):e150. doi: 10.1093/nar/gkr766.
PMID: 21965536.

29. Guojun Li, Bingqiang Liu, Qin Ma, Ying Xu, A new framework for identifying cis-regulatory motifs in prokaryotes.
Nucleic Acids Research. 2011 Apr;39(7):e42. doi: 10.1093/nar/gkq948.
PMID: 21149261.

30. Guojun Li, Qin Ma, Haibao Tang, Andrew H. Paterson, Ying Xu, QUBIC: A Qualitative Biclustering Algorithm for Analyses of Gene Expression Data.
Nucleic Acids Research. 2009 Aug;37(15):e101. doi: 10.1093/nar/gkp491.
PMID: 19509312.
Highlights from independent review.

31. Juan Xie, Anjun Ma, Yu Zhang, Bingqiang Liu, Sha Cao, Cankun Wang, Jennifer Xu, Chi Zhang, Qin Ma[$], QUBIC2: A Novel and Robust Biclustering Algorithm for Analyses and Interpretation of Large-Scale RNA-Seq Data.
Bioinformatics. 2019 Sep 10. pii: btz692. doi: 10.1093/bioinformatics/btz692.
PMID: 31503285.
Highlights from independent review.

32. Brandon Monier, 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. 2019 Feb 14;15(2):e1006792.
doi: 10.1371/journal.pcbi.1006792. PMID: 30763315.

33. Siyu Han, Yanchun Liang, Qin Ma, Cankun Wang, Yangyi Xu, Yu Zhang, Wei Du and Ying Li, LncFinder: an integrated package for long non-coding RNA identification utilizing sequence intrinsic composition, structural information and physicochemical property.
Briefings in Bioinformatics. 2019 Nov 27;20(6):2009-2027. doi: 10.1093/bib/bby065.
PMID: 30084867.
Highlights from independent review.

34. Jing Jiang, Cankun Wang, Ren Qi, Hongjun Fu, Qin Ma[$], scREAD: A benchmarking database for single-cell sequencing data analysis in Alzheimer's Disease. iScience. 2020. DOI: https://doi.org/10.1016/j.isci.2020.101769. News.

35. Anjun Ma, Minxuan Sun, Adam McDermaid, Bingqiang Liu, Qin Ma[$], MetaQUBIC: a computational pipeline for gene-level functional profiling of metagenome and metatranscriptome.
Bioinformatics, Volume 35, Issue 21, 1 November 2019, Pages 4474–4477, https://doi.org/10.1093/bioinformatics/btz414. PMID: 31116375.

36. Xiaoying Wang, Bin Yu, Anjun Ma, Cheng Chen, Bingqiang Liu, Qin Ma[$], Protein-protein interaction sites prediction by ensembling random forests with synthetic minority oversampling technique.
Bioinformatics. 2019 Jul 15;35(14):2395-2402. doi: 10.1093/bioinformatics/bty995. PMID: 30520961.

37. Bin Yu, Wenying Qiu, Cheng Chen, Anjun Ma, Jing Jiang, Hongyan Zhou, Qin Ma[$], SubMito-XGBoost: Prediction of protein submitochondrial localization by fusing multiple feature information and eXtreme Gradient Boosting.
Bioinformatics. 2019 Oct 11. pii: btz734. doi: 10.1093/bioinformatics/btz734. PMID: 31603468.

38. Yu Zhang, Juan Xie, Jinyu Yang, Anne Fennell and Qin Ma[$], QUBIC: a Bioconductor package for qualitative biclustering analysis of gene co-expression data.
Bioinformatics. 2017 Feb 1;33(3):450-452. doi: 10.1093/bioinformatics/btw635. PMID: 28172469.

39. Jinyu Yang, Adam McDermaid, Xin Chen, and Qin Ma[$], DMINDA 2.0: integrated and systematic views of regulatory DNA motif identification and analyses.
Bioinformatics, Volume 33, Issue 16, 15 August 2017, Pages 2586–2588, https://doi.org/10.1093/bioinformatics/btx223. PMID: 28419194.

40. Qin Ma, Bingqiang Liu, Chuan Zhou, Yanbin Yin, Guojun Li, Ying Xu, An integrated toolkit for accurate prediction and analysis of cis regulatory elements at a genome scale.
Bioinformatics. 2013 Sep 15;29(18):2261-8. doi: 10.1093/bioinformatics/btt397. PMID: 23846744.

TEACHING

- Lecture director, Analysis and Applications of Genome-Scale Data (BMI 8130), Autumn 2019-2023. Department of Biomedical Informatics, The Ohio State University.
- Lecture director, Applications of Machine Learning and AI in Biomedical Informatics (BMI 8050), Fall 2020, Monday 2:15-5:00 pm. Department of Biomedical Informatics, The Ohio State University.
- Lecture, Fundamentals of grant writing (BSGP 7070), Autumn 2019, Monday, 3:00pm-5:30pm. The Ohio State University.