

Qin Ma, Ph.D.

Associate Professor

Bioinformatics and Mathematical Biosciences Lab

**CONTACT INFORMATION**

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PROFESSIONAL EXPERIENCE

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

- Single-cell multi-omics data modeling and analyses
- Regulatory DNA motif prediction
- Microbial systems biology

LEADERSHIP DEVELOPMENT

- 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 Biology and Chemistry 2019-
- Associate Editor, BMC Genomics 2015-
- Editor board member, Briefings in Bioinformatics 2019-
- Editor board member, Scientific Reports, 2018-

Membership

- Member, International Society for Computational Biology (ISCB), 2014-
- Member, American Society for Microbiology (ASM), 2013-2015
- Member, Bioenergy Research Center of Department of Energy 2011-2016

Conference program committee

- 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

PROFESSIONAL HONORS AND AWARDS

- Recognized Reviewer, Computational and Structural Biotechnology Journal, 2019
- Significant achievement in research, South Dakota State University, 2018
- Excellent Reviewers, Mathematical Biosciences, 2013-2015

MEDIA APPEARANCES

- [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. (2021) CTSA Community Reviewer Training Program: Increasing Diverse Perspectives in Pilot Grant Reviews by Integrating Community Input. Wednesday, March 31. Washington Marriott Wardman Park. Faculty representative at OSU.

Speaker page: <https://ts21.actscience.org/people/YJ2bhKprzBQWBsqB4>

2. (2020) Development of Enabling Computational Techniques for Single-cell Multi-Omics Data. September 11th. Nationwide Children's Hospital. (Invited by Dr. Kloczkowski). Columbus, OH 43210
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.
4. (2019) Co-regulation Gene Signatures from Single-cell RNA-Sequencing Data Analysis, International Conference on Mathematical Multiscale Modeling in Biology - Guanacaste, Costa Rica, October 22-24, 2019.
5. (2017) Computational modeling and bioinformatic applications in big biological data. May 23rd. Nankai University, Tianjin, China. (Invited by Drs. Han Zhang and Quan Zou)
6. (2015) Metabolic and Regulatory Network Analysis in Systems Biology, Dec. 21th, Biological Department, Nanjing Medical University, Nanjing, China.
7. (2015) Development and application of bioinformatic tools driven by genomic and transcriptomic data, Institute of Applied Mathematics, Academy of Mathematics & System Science, Chinese Academy of Sciences, May 18th, 2015, Beijing, China
8. (2015) Development and application of bioinformatic tools driven by genomic and transcriptomic data, Institute for Interdisciplinary Information Sciences, Tsinghua University, May 21st, 2015, Beijing, China.
9. (2015) Computational Methods in Bioinformatics: Omics data mining and modeling, January 6, 2015, Model Animal Research Center of Nanjing University, Nanjing, China.
10. (2019) Develop computational methods driven by addressing fundamental microbial genomic and transcriptomic questions. 08/12, Indiana University, Indianapolis, IN.
11. (2019) Construction of cell specific gene co-regulations signatures based on single cell multi-omics data analysis, August 15, 2019, Department of Computer Science, University of Missouri Columbia, MO. (Invited by Dr. Dong Xu)
12. (2018) Development of computational techniques in elucidating gene regulation. October 1st, 2018. Ohio State University, Columbus, OH 43210
13. (2018) Development and application of computational methods driven by addressing genomic and transcriptomic questions. 09/10. Indiana University, Indianapolis, IN.
14. (2018) Hypothesis-driven and discovery-driven analysis of Grapevine expression data. January 16th. Plant & Animal Genome Conference, Jan. 14-18, San Diego, CA, USA
15. (2017) RNA Sequencing Analyses & Mapping Uncertainty, August 25th, 2017, The Y1 meeting for the NSF Plant Genome Research Program, the University of California, Davis campus in Davis, California.
16. (2017) Regulatory DNA motif identification by integrating DNA shape in a deep learning framework. Great Lakes Bioinformatics Conference, May 15 – 17. Chicago.
17. (2017) Computational modeling and bioinformatic applications in big biological data, May 11th, Department of Cell Systems and Anatomy, UT Health at San Antonio.
18. (2017) Development and application of computational methods driven by addressing bacterial genomic and transcriptomic questions, 03/02, University of Nebraska, Lincoln.
19. (2016) DMINDA² web server: regulatory DNA motif identification and analyses. July 11. Orlando, Florida. Intelligent Systems for Molecular Biology (ISMB). Technology Track Presentation.
20. (2015) Development and application of computational tools driven by addressing bacterial genomic and transcriptomic questions, June 05, 2015, Department of Biostatistics and Bioinformatics, Emory University, GA.

21. (2015) Development and application of bioinformatic tools driven by genomic and transcriptomic data, July 28, 2015, Department of Computer Science, University of Missouri Columbia, MO. (Invited by Dr. Dong Xu)
22. (2015) Omics data mining & modeling and biological systems inference in Bioinformatics, January 22, 2015, MD Anderson Cancer Center, Houston, TX.
23. (2014) Inference of reliable genome-scale bacterial metabolic network based on transcriptomic data in support of genetic engineering, (BioEnergy Science Center) BESC retreat, June 9-11, 2014, Chattanooga, TN.
24. (2012) Elucidation of the Dynamic Supercoil Structures of folded E. coli Chromosome, Department of Biostatistics and Bioinformatics, Emory University, USA.
25. (2009) QUBIC: A Qualitative Biclustering Algorithm for Analyses of Gene Expression Data, the 8th Annual International Conference on Computational Systems Bioinformatics, Stanford University, USA.

RESEARCH GRANTS

1. NIH-NIGMS (R01) 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/bmb1/highlights/r01/>.
2. NIH-NIGMS (Administrative Supplements Equipment) PI 2020-2021
Title: Construction of cell type specific gene co-regulation signatures based on single cell transcriptomics data.
3. NIH (NCI-U24) MPI 2020-2025
Title: Participant Engagement and Cancer Genome Sequencing: Coordinating Center.
4. NSF (EAGER) PI 2021-2023
Title: A reinforced imputation framework for accurate gene expression recovery from single-cell RNA-seq data
5. OSU (CCTS) PI 2020-2021
Title: Deep Transfer Learning of Drug Sensitivity by Integrating Bulk and Single-cell RNA-Seq data
6. NSF-PGRP co-PI 2016-2022
Title: Adapting perennial crops for climate change: Graft transmissible effects of rootstocks on grapevine shoots.
7. NIH (R25 R25MD011712) co-I (MPI Coombes, Huang, Bai) 2017-2021
Title: Training informaticians in big data (TIBD).
8. NIH (R01 R01HL131665) co-I (PI Zhao) 2019-2021
Title: Regulation of proteolysis by deubiquiting enzyme in lung inflammatory disease.
9. NIH (R01) co-I (PI: Dana McTigue) 2021-2026
Title: Identify mechanisms driving neurogenic NASH.
10. NIH (R01) co-I (PI: Jason Wester) 2021-2026
Title: Development of neuronal subtypes and local circuits in the hippocampus.
11. NIH (R01) co-I (PI: Haitao Wen) 2021-2026
Title: Targeting immune inhibitory molecule SUSD2 to reverse immunosuppression
12. NIH (R01) co-I (PI: Xuefeng Liu) 2019-2023
Title: conditionally reprogrammed cell model for castration-resistant prostate cancer.
13. BMI pilot PI (Ma) 2021-2022
Title: Gene regulatory network inference based on single-cell multi-omics data.

MENTORINGPost-Docs

Anjun Ma (Biomedical Informatics at OSU)	Mentor	2021-
Yang Li (Biomedical Informatics at OSU)	Mentor	2019-
Cankun Wang (BISR at OSU)	Project Mentor	2019-
Adam McDermaid (Statistics at SDSU)	Mentor	2018-2019

Ph.D. Students

Yuzhou Chang (BSGP at OSU)	Thesis Committee, Chair	2019-
Zhenyu Wu (MCDB at OSU)	Thesis Committee, Chair	2020-
Wantong Li (MCDB at OSU)	Thesis Committee, Chair	2021-
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-
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

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

Cindy Tong	Watkins Memorial High School	2021-
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ACADEMIC SERVICES

International

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

National

- USDA NIFA FACT program Panel Reviewer, 2019-2020
- NSF GRFP review panel Reviewer 2020
- NSF PBI review panel, Panel Reviewer, 2016
Reviewed Integrative Organismal Systems proposals submitted to the Plant-Biotic Interactions (PBI) Program within the Physiological and Structural Systems Cluster.
- 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: 26; 10-index: 56)

1. 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>.
2. 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>.
3. 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](#).
4. 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.
5. 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.

6. 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
7. 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>
8. 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>.
9. 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.
10. Xizeng Mao, Qin Ma, Chuan Zhou, Xin Chen, Hanyuan Zhang, Jincal 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.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.](#)

17. 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.](#)
18. 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.
19. 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.](#)
20. 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](#).
21. 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.
22. 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.
23. 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.
24. 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.
25. 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.
26. 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, OSU-ISU Big Data training program, Summer 2020, Single-cell RNA-Sequencing data analysis and application.
- Lecture, Analysis and Applications of Genome-Scale Data (BMI 8130), Autumn 2019, TR 9:35-10:55pm. 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.
- 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, Ind Stud Biom Sci (BSGP 7930), Fall 2019, The Ohio State University.
- Lecture, Next Generation Sequencing Data Analysis (PS-735), 2016-2018 Department of Mathematics and Statistics, and Agronomy, Horticulture, and Plant Science Department, SDSU (57 graduate students).

DEVELOPED WEB SERVERS & DATABASES

1. scREAD: A Single-cell RNA-Seq Database for Alzheimer's Disease. Link: <https://bmbls.bmi.osumc.edu/scread>.
2. IWOD: An integrative webserver for optimized tissue data deconvolution. Link: <https://shiny.ph.iu.edu/iwod/>.
3. IRIS3: Integrated Cell-type-specific Regulon Inference from Single-cell RNA-Seq. Link: <https://bmbl.bmi.osumc.edu/iris3/>.
4. DESSO: A web server for DNA and Shape motif identification based on a Deep Learning framework. Link: <https://bmbl.bmi.osumc.edu/DESSO/>. GitHub source code: <https://github.com/vijjy/DESSO>.
5. DMINDA: An integrated web server for DNA Motif prediction and analyses. Link: <http://bmbl.sdstate.edu/DMINDA2/>.
6. IRIS-EDA: A Shiny package for differentially expressed gene analysis. Link: <http://bmbl.sdstate.edu/IRIS/>. GitHub: <https://github.com/btmonier/iris>.
7. LncFinder: Identifying and discovering new lncRNA transcripts have been the fundamental process in lncRNA-related research. Link: <https://bmbl.bmi.osumc.edu/lncfinder/>.
8. DOOR2: Database of prokaryotic Operons. Link: <http://csbl.bmb.uga.edu/DOOR/index.php>
9. DMINDA2.0, DNA motif prediction and analysis web server, Jinyu Yang. Link: <https://bmbl.bmi.osumc.edu/DMINDA2/index.php>.

DEVELOPED SOFTWARE PACKAGES

1. CeRIS: Cell-type-specific regulon inference from single-cell RNA-Sequencing data. Link: <https://github.com/OSU-BMML/CeRIS>.
2. LTMG: An R package for Single Cell RNA-seq data analysis within the Left Truncated Mixture Gaussian scheme. Link: <https://github.com/zy26/LTMGSCA>.
3. MetaQUBIC: A biclustering-based package for metagenomic and metatranscriptomic data. Link: <https://github.com/OSU-BMML/metaqubic>.
4. BRIC: A novel biclustering method for the detection of the repertoire of active gene regulatory signals and cell type prediction from single cell RNA-Seq datasets. Link: <https://github.com/maqin2001/BRIC>.

5. ViDGER: interpretation of differential gene expression results of RNA-seq data. <https://github.com/btmonier/vidger>.
6. Cancer-evolution: A phylogenetic model for understanding the effect of gene duplication on cancer progression. Link: <http://code.google.com/p/cancer-evolution/>.
7. QUBIC2.0: A novel biclustering algorithm for large-scale bulk RNA-sequencing and single-cell RNA-sequencing data analysis. Link: <https://github.com/maqin2001/qubic2>.
8. QUBIC R package, Bioconductor, Yu Zhang and Juan Xie. Link: <http://bioconductor.org/packages/devel/bioc/html/QUBIC.html>.
9. Supercoil: Bacterial chromosome folding structure under different conditions
Link: <https://code.google.com/p/supercoil/>.
10. BoBro: an integrated toolkit for prediction and analysis of *cis*-regulatory motifs
Link: <https://code.google.com/p/bobro/>.
11. GOST: an orthology mapping tool for prokaryotes.
Link: <https://code.google.com/p/gost-an-orthology-mapping-tool/>.
12. QUBIC: A QUalitative BIClustering tool for analysis of transcriptomic data.
Link: <https://code.google.com/p/qubic-biclustering/>.