Jie Liu

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Education and Training

Education

07/2004	Bachelor in Info. Management & Info. Systems, Beijing University of Posts and Telecom, Beijing, China
07/2007	Master in Signal and Information Processing, Peking University, Beijing, China
05/2009	Master in Computer Science, University of Wisconsin, Madison
05/2011	Master in Statistics, University of Wisconsin, Madison
07/2014	PhD in Computer Science, University of Wisconsin, Madison

Postdoctoral Training

09/2014-12/2018	Senior Fellow in the Department of Genome Sciences, University of Washington

Work Experience

Academic Appointment

01/2019-Present	Assistant Professor in the Department of Computational Medicine and Bioinformatics, University of Michigan - Ann Arbor (4.7-year in rank as of 09/2023)
09/2019-Present	Assistant Professor in Electrical Engineering and Computer Science - Computer Science and Engineering, University of Michigan - Ann Arbor

Research Interests

- Bioinformatics
- Machine learning

Honors and Awards

National

2014	AMIA Marco Ramoni Distinguished Paper Award, AMIA
2020	NHGRI Genomic Innovator Award, NHGRI

Regional

2004	Merit Student of Beijing City (top 1%)

Institutional

2001 - 2003	BUPT student fellowship (top 1%)
2004 - 2007	PKU graduate student fellowship
2014 - 2016	Moore/Sloan Data Science Postdoctoral Fellowship
2015 - 2017	Washington Research Foundation Innovation Postdoctoral Fellowship

Study Sections, Editorial Boards, Journal & Abstract Review

Study Sections

<u>National</u>

2023	ZRG1 CTH-M (70), NIH Study Section

<u>Institutional</u>

2023	U-M MIDAS PODS pilot grant program

Editorial Boards / Journal & Abstract Reviews

<u>Editorial Boards</u>

2021 - 2022	Guest editor, PLOS Computational Biology
2022 - present	Associate editor, PLOS Computational Biology

<u>Journal Review</u>

2014 - present	Journal Reviewer for Nature, Nature Methods, Nature Communications, Genome Research, Cell Genomics, PLOS Computational Biology, Journal of the American Statistical Association, Data Mining and Knowledge Discovery, Machine Learning, Pattern Recognition Letters, Cell Systems, Bioinformatics, Journal of Bioinformatics and Computational Biology, Journal of Digital Imaging, Economic Modelling, Genomics Proteomics & Bioinformatics, BMC Bioinformatics, Computational and Structural Biotechnology Journal

<u>Conference Review</u>

2012 - present	Conference Program Committee and review a total number of 141 papers for the following conferences: RECOMB 2022, NeurIPS 2022, ICML2022, ICLR2022, NeurIPS 2021, ICLR 2021, AAAI 2021, NeurIPS 2020, RECOMB 2020, AAAI 2020, ICLR 2020, NeurIPS 2019, RECOMB 2019, ICML 2019, ICLR 2019, AMIA Informatics Summit 2019, NeurIPS 2018, ISMB 2018, AMIA 2018, ICML 2018, RECOMB 2018, ICLR 2018, AMIA Informatics Summit 2018, NIPS-MLCB 2017, NIPS 2017, AMIA 2017, AMIA-TBI/CRI 2017, AAAI 2017, NIPS 2016, AMIA 2016, AAAI 2016, AMIA-TBI/CRI 2016, ACMBCB 2016, MLSB 2016, NIPS 2015, IJCAI 2015, AMIA 2015, AMIA-TBI/CRI 2015, AISTATS 2015, WABI2015, NIPS 2014, UAI 2014, AAAI 2014, AMIA 2014, IJCAI 2013, AMIA 2013, GENSIPS 2012

<u>Workshop Organizer</u>

2021	Workshop on machine learning methods for single-cell analysis, ACM-BCB, Co-Chair

<u>Journal Advisor</u>

2022-2023	Guest advisor for the F1000Research collection: Machine Learning in Genomics

Teaching

Mentorship

<u>Graduate Student (PhD, 11 in total, 1 graduated)</u>

01/2019-04/2023	Shuze Wang, DCMB, U-M. First position: Staff Scientist at Massachusetts General Hospital. Thesis title: Deciphering the Molecular Mechanisms Underlying Cochlea Development in Mice using Next-Generation Sequencing Technologies and Comprehensive Computational Approach (co-mentored by Dr. Joerg Waldhaus)
01/2019-Present	Fan Feng, DCMB, U-M, Ongoing, expected PhD graduation in Aug 2023
01/2020-Present	Yuanhao Huang, DCMB, U-M, Ongoing, expected PhD graduation in Aug 2024
05/2020-Present	Zhenhao Zhang, DCMB, U-M, Ongoing, expected PhD graduation in Dec 2024
01/2021-Present	Sean Moran, DCMB, U-M, Ongoing, expected PhD graduation in Apr 2025
01/2021-Present	Linghua Jiang, DCMB, U-M, Ongoing, expected PhD graduation in Dec 2025

09/2021-Present	Zheyu Zhang, CSE, U-M, Ongoing, expected PhD graduation in Apr 2027
01/2022-Present	Xin Luo, DCMB, U-M, Ongoing, expected PhD graduation in April 2027
09/2022-Present	Yicheng Tao, CSE, U-M, Ongoing, expected PhD graduation in Apr 2026
09/2022-Present	Yiqun Wang, DCMB, U-M, Ongoing, expected PhD graduation in Apr 2027
12/2022-Present	Lingxiao Guan, CSE, U-M, Ongoing, expected PhD graduation in Apr 2027

Graduate Student (Master, 8 in total, 4 graduated)

01/2019-05/2020	Mingyu Du, Biostat, U-M, First position: PhD program at UCI
01/2019-08/2020	Yufeng Zhang, Biostat, U-M, First position: PhD program in Bioinformatics at U-M
11/2019-04/2021	Xinjun Li, Statistics, U-M, First position: Industry
05/2020-12/2020	Peiyao Zhao, Biostat, U-M, First position: PhD program in Biostatistics at U-M
09/2022-Present	Dongyu Zhu, School of Information, U-M, Ongoing
12/2022-Present	Feiyang Deng, Biostat, U-M, Ongoing
12/2022-Present	Zhaowei Han, DCMB, U-M, Ongoing
01/2023-Present	Feitong Tang, CSE, U-M, Ongoing

Undergraduate Student (27 in total, 20 graduated)

06/2018-08/2018	Kaishu Mason, Harvard University, First position: PhD program at U Penn
04/2019-06/2020	Yujuan Fu, CSE, U-M, First position: PhD program at the University of Washington
09/2019-05/2020	Yijiao Qin, CSE, U-M, First position: master program at CMU
01/2020-08/2020	Yue Kuang, CSE, U-M, First position: master program in CS at Columbia U
01/2020-08/2020	Samual Yuan, CSE, U-M, Independent Study
01/2020-04/2021	Yuan Yao, CSE, U-M, First position: PhD program at U-M
01/2020-04/2021	Ziqiao Ma, CSE, U-M, First position: PhD program at U-M
02/2020-07/2020	Chenghao Xu, CUHK-SZ, Visiting student. First position: master program at NYU
04/2020-04/2021	Bingjiang Wang, CSE, U-M, First position: master program at UCSD
06/2020-04/2021	Benjamin Wurman, CSE, U-M, First position: Industry
07/2020-12/2020	Wenfei Tang, CSE, U-M, First position: master program at U-M
08/2020-12/2020	Zhuowen Shen, CSE, U-M, First position: master program in CSE at U-M
09/2020-06/2022	Hongxi Pu, LSA, U-M, First position: master program at U-M
01/2021-05/2021	Wai Yan Leung, Volunteer, U-M, First position: master program at Georgia Tech
02/2021-08/2022	Tianjun Li, CSE, U-M, First position: master program at CMU
03/2021-06/2022	Yiyang Qiu, CSE, U-M, First position: master program in CMU
04/2021-06/2022	Simin Fan, CSE, U-M, First position: PhD Program at EPFL
04/2021-08/2022	Jiahao Qiu, CSE, U-M, First position: PhD program at Princeton University
04/2021-08/2022	Xinyu Lu, CSE, U-M, First position: master program at CMU
01/2022-08/2022	Hao Pan, CSE, U-M, First position: master program at Columbia University
04/2022-Present	Shuyuan Yang, Data Science, U-M, Ongoing
04/2022-Present	Yijia Gao, CSE, U-M, Ongoing
04/2022-Present	Shaochun Zheng, CSE, U-M, Ongoing
04/2022-Present	Jiyue Zhu, CSE, U-M, Ongoing

04/2022-Present	Jiyu Chen, CSE, U-M, Ongoing
04/2022-Present	Chengfan Li, CSE, U-M, Ongoing
04/2022-Present	Zexuan Yang, CSE, U-M, Ongoing

Teaching Activity
Institutional

11/2020	Guest Instructor, BIOINF-590 Image Processing and Advanced Machine Learning for Cancer Bioinformatics, 2020 Fall
04/2021	Facilitator, PIBS 503 Data Storage, Ownership & Peer Review, U-M, 2021 Winter
09/2021-Present	Co-developer and co-director, BIOINF 593/EECS 598 Machine Learning in Computational Biology (a new course co-developed by me and Dr. Joshua Welch), U-M, 2021 Fall, 2022 Fall, 2023 Fall

Dissertation Committees (9 in total, 4 graduated)

01/2019-03/2021	Shengcheng Dong, University of Michigan, DCMB, Committee Member. Thesis title: Computational Methods to Identify Regulatory Variants in the Non-coding Regions of the Human Genome
05/2019-04/2022	Vivek Rai, University of Michigan, DCMB, Committee Member. Thesis title: Using integrative multiomics approaches to dissect type 2 diabetes genetic risk in pancreatic islets
08/2020-Present	Chao Gao, University of Michigan, DCMB, Committee Member
01/2021-Present	Hanrui Zhang, University of Michigan, DCMB, Committee Member
03/2021-06/2022	Jingcheng Xiao, University of Michigan, Pharmacy, Committee Member. Thesis title: Pharmacometric Modeling and Simulation in Special Populations
09/2021-06/2022	Hengshi Yu, University of Michigan, DCMB, Committee Member. Thesis title: Deep Generative Models for Single-Cell Perturbation Experiments
02/2022-Present	Zijun Gao, University of Michigan, DCMB, Committee Member
04/2023-Present	Yuheng Du, University of Michigan, DCMB, Committee Member
05/2023-Present	Avery Maddox, University of Michigan, DCMB, Committee Member

Prelim Exam Committees (18 in total)

05/2019	Stephen Lindsly, Prelim Exam, DCMB, Committee Member
06/2019	Chen Sun, Prelim Exam, DCMB, Committee Member
12/2020	Ying Yang, Prelim Exam, MCDB, Committee Member
12/2020	Wenjin Gu, Prelim Exam, DCMB, Committee Member
07/2021	April Kriebel, Prelim Exam, DCMB, Committee chair
07/2021	Chen Li, Prelim Exam, DCMB, Committee Member
07/2021	Jialin Liu, Prelim Exam, DCMB, Committee Member
08/2021	Alec Chu, Prelim Exam, Cellular and Molecular Pathology, Committee Member
08/2021	Kevin Yang, Prelim exam, DCMB, Committee Member
08/2021	Qianhui Huang, Prelim exam, DCMB, Committee Member
04/2022	Yufeng Zhang, Prelim Exam, DCMB, Committee Member
06/2022	Kaiwen Deng, Prelim Exam, DCMB, Committee Member
06/2022	Ryan Rebernick, MD/PhD Prelim Exam, DCMB, Committee Member
07/2022	Yuheng Du, Prelim Exam, DCMB, Committee Member
08/2022	Kinsey Van Deynze, Prelim Exam, DCMB, Committee Member

08/2022	Avery Maddox, Prelim Exam, DCMB, Committee Member
04/2023	Alice Wang, Prelim Exam, DCMB, Committee Member
05/2023	Keagan Moo, Prelim Exam, DCMB, Committee Member

Memberships in Professional Societies

| 2018 - Present | International Society for Computational Biology |

Committee/Service

Institutional

2019 - 2020	MIDAS evaluation committee, U-M, Member
2019 - 2022	Bioinformatics PhD Admissions Committee, U-M, Member
2020 - 2022	DCMB/CCMB Seminar Committee, U-M, Co-Lead
2021 - 2022	BIOINFO master admissions committee, U-M, Member
2022 - present	Bioinformatics PhD Admissions Committee, U-M, Co-Chair

Volunteer Service

Volunteer

| 2020 - present | Judge, MIRCORE high school research program, provide feedback, evaluation, and direct interaction with high school students |

Scholarly Activities

Presentations

Extramural Invited Presentation

Speaker

1. Graphical-model Based Multiple Testing under Dependence, with Applications to Genome-wide Association Studies, **Liu J**, Uncertainty in Artificial Intelligence (UAI), 08/2012, Catalina Island, CA

2. Multiple Testing under Dependence with Applications to Genome-wide Association Studies, **Liu J**, Department of Computer Science, Colorado State University, 03/2013, Fort Collins, CO

3. Genetic Variants Improve Breast Cancer Risk Prediction on Mammograms, **Liu J**, American Medical Informatics Association Symposium, 11/2013, Washington, DC

4. The Promise and Computational Challenges of Personalized Medicine, **Liu J**, Lane Center for Computational Biology, Carnegie Mellon University, 03/2014, Pittsburgh, PA

5. The Promise and Computational Challenges of Personalized Medicine, **Liu J**, IBM T. J. Watson Research Center, 03/2014, Yorktown Heights, NY

6. The Promise and Computational Challenges of Personalized Medicine, **Liu J**, University of Chicago, 04/2014, Chicago, IL

7. New Genetic Variants Improve Personalized Breast Cancer Diagnosis, **Liu J**, AMIA Joint Summits on Translational Science, 04/2014, San Francisco, CA

8. Leveraging Interaction between Genetic Variants and Mammographic Findings for Personalized Breast Cancer Diagnosis, **Liu J**, AMIA Joint Summits on Translational Science, 03/2015, San Francisco, CA

9. Machine Learning for Understanding the Dynamics of Cell Populations, **Liu J**, Duke University, 01/2018, Durham, NC

10. Machine Learning for Understanding the Dynamics of Cell Populations, **Liu J**, University of Arizona, 02/2018, Tucson, AZ

11. Machine Learning for Understanding the Dynamics of Cell Populations, **Liu J**, Brandeis University, 02/2018, Waltham, MA

12. Machine Learning for Understanding the Dynamics of Cell Populations, **Liu J**, Rice University,

03/2018, Houston, TX

13.   Unsupervised embedding of single-cell Hi-C data, **Liu J**, Annual Conference on Intelligent Systems for Molecular Biology, 07/2018, Chicago, IL

14.   An accurate and interpretable model for predicting high resolution 3D chromatin organization, **Liu J**, 4DN JAWG, 09/2019, Virtual

15.   Computational methods for single cell chromatin organization analysis, **Liu J**, JSM 2020, 08/2020, Virtual

16.   A database for high-resolution chromatin contact maps and human genetic variants, **Liu J**, NIH Common Fund Data Ecosystem, 03/2021, Virtual

17.   Connecting High-resolution 3D Chromatin Organization with Epigenomics, **Liu J**, Feng F, ISMB, 07/2022, Madison, WI

18.   A generalizable framework to comprehensively predict epigenome, chromatin organization, and transcriptome, **Liu J**, GSK, 09/2022, Virtual

19.   GenomicKB: a knowledge graph for the human genome, **Liu J**, IGVF Catalog WG, 12/2022, Virtual

20.   A generalizable framework to comprehensively predict epigenome, chromatin organization, and transcriptome, **Liu J**, 4DN Predictive Modeling Working Group, 05/2023, Virtual

21.   A generalizable framework to comprehensively predict epigenome, chromatin organization, and transcriptome, **Liu J**, IGVF Seminar Series, 05/2023, Virtual

22.   A generalizable framework to comprehensively predict epigenome, chromatin organization, and transcriptome, **Liu J**, Feng F, GLBIO 2023, 05/2023, Montreal, Quebec, Canada

23.   Computational infrastructures for consolidating our knowledge regarding the human genome, **Liu J**, University of Texas Health Science Center, 05/2023, Houston, TX

24.   Allele-specific analysis of human epigenome, transcriptome and high-resolution chromatin organization, NIH Common Fund Data Ecosystem, 06/2023, Virtual

Publications/Scholarship
(Co-First Author *; Corresponding author **; Co-Last author ***)

Peer-Reviewed

Journal Article

1.   **Liu J**, Kang S, Tang C, Ellis LB, Li T: Meta-prediction of protein subcellular localization with reduced voting. *Nucleic Acids Research*.35(15)01/2007

2.   Wan J, Kang S, Tang C, Yan J, Ren Y, **Liu J**, Gao X, Banerjee A, Ellis LB M, Li T: Meta-prediction of phosphorylation sites with weighted voting and restricted grid search parameter selection. *Nucleic Acids Research*.36(4): e22-e22, 03/2008. PM18234718

3.   **Liu J**, Hu Z, Tan S: Cross-sectional stock return analysis using support vector regression. *Applied Economics Letters*.17(1): 71-74, 01/2009

4.   Wu Y, Abbey CK, Chen X, **Liu J**, Page DC, Alagoz O, Peissig P, Onitilo AA, Burnside ES: Developing a utility decision framework to evaluate predictive models in breast cancer risk estimation. *J Med Imaging (Bellingham)*.2(4): 041005, 10/2015. PM26835489

5.   Burnside ES, **Liu J**, Wu Y, Onitilo AA, McCarty CA, Page CD, Peissig PL, Trentham-Dietz A, Kitchner T, Fan J, Yuan M: Comparing Mammography Abnormality Features to Genetic Variants in the Prediction of Breast Cancer in Women Recommended for Breast Biopsy. *Acad Radiol*.23(1): 62-69, 01/2016. PM26514439

6.   Fan J, Wu Y, Yuan M, Page D, **Liu J**, Ong IM, Peissig P, Burnside E: Structure-leveraged methods in breast cancer risk prediction. *Journal of Machine Learning Research*.1705/2016

7.   **Liu J**, Zhang C, Page D: Multiple Testing under Dependence via Graphical Models. *Annals of Applied Statistics*.10(3): 1699-1724, 08/2016

8.   **Liu J**, Halloran JT, Bilmes JA, Daza RM, Lee C, Mahen EM, Prunkard D, Song C, Blau S, Dorschner MO, Gadi VK, Shendure J, Blau CA, Noble WS: Comprehensive statistical inference of the clonal structure

of cancer from multiple biopsies. *Sci Rep*.7(1): 16943, 12/2017. PM29208983

9. Kim J-S, He X, **Liu J**, Duan Z, Kim T, Gerard J, Kim B, Pillai MM, Lane WS, Noble WS, Budnik B, Waldman T: Systematic proteomics of endogenous human cohesin reveals an interaction with diverse splicing factors and RNA-binding proteins required for mitotic progression. *J Biol Chem*.294(22): 8760-8772, 05/2019. PM31010829

10. Li Q, Mao F, Zhou B, Huang Y, Zou Z, denDekker AD, Xu J, Hou S, **Liu J**, Dou Y, Rao RC: p53 Integrates Temporal WDR5 Inputs during Neuroectoderm and Mesoderm Differentiation of Mouse Embryonic Stem Cells. *Cell Reports*.30(2): 465-480.e6, 01/2020. PM31940490

11. Kim H-J, Yardımcı GG, Bonora G, Ramani V, **Liu J**, Qiu R, Lee C, Hesson J, Ware CB, Shendure J, Duan Z, Noble WS: Capturing cell type-specific chromatin compartment patterns by applying topic modeling to single-cell Hi-C data. *PLoS Comput Biol*.16(9): e1008173, 09/2020. PM32946435

12. Li X, Feng F, Pu H, Leung WY, **Liu J****: scHiCTools: A computational toolbox for analyzing single-cell Hi-C data. *PLoS Computational Biology*.17(5)05/2021. PM34003823

13. Himadewi P, David Wang XQ, Feng F, Gore H, Liu Y, Yu L, Kurita R, Nakamura Y, Pfeifer GP, **Liu J****, Zhang X**: 3'HS1 CTCF binding site in human β-globin locus regulates fetal hemoglobin expression. *eLife*.1009/2021. PM34585664

14. Wang S, Lee MP, Jones S, **Liu J**, Waldhaus J: Mapping the regulatory landscape of auditory hair cells from single-cell multi-omics data. *Genome Res*.31(10): 1885-1899, 10/2021. PM33837132

15. Li Q, Huang Y, Xu J, Mao F, Zhou B, Sun L, Basinski BW, Aksu M, Liu J, Dou Y, Rao RC: p53 inactivation unmasks histone methylation-independent WDR5 functions that drive self-renewal and differentiation of pluripotent stem cells. *Stem Cell Reports*.16(11): 2642-2658, 11/2021. PM34715053

16. Zhang Z, Feng F, **Liu J****: Characterizing collaborative transcription regulation with a graph-based deep learning approach. *PLoS Computational Biology*.18(6)06/2022. PM35666736

17. Huang Y, Wang B, **Liu J****: NucleoMap: A computational tool for identifying nucleosomes in ultra-high resolution contact maps. *PLoS Computational Biology*.18(7)07/2022. PM35834552

18. Feng F, Yao Y, Wang XQ D, Zhang X, **Liu J****: Connecting high-resolution 3D chromatin organization with epigenomics. *Nature Communications*.13(1)12/2022. PM35440119

19. Feng F, Tang F, Gao Y, Zhu D, Li T, Yang S, Yao Y, Huang Y, **Liu J****: GenomicKB: a knowledge graph for the human genome. *Nucleic Acids Research*.51(D1): D950-D956, 01/2023. PM36318240

20. Zhang Z, Feng F, Qiu Y, **Liu J****: A generalizable framework to comprehensively predict epigenome, chromatin organization, and transcriptome. *Nucleic Acids Research*. 2023 (In Press)

Conference Proceedings (full-length articles, peer-reviewed)

21. **Liu J**, Peissig P, Zhang C, Burnside E, McCarty C, Page D: High-Dimensional Structured Feature Screening Using Binary Markov Random Fields, Conference Proceeding, The 15th International Conference on Artificial Intelligence and Statistics (AISTATS), La Palma, Canary Islands, 2012

22. **Liu J**, Peissig P, Zhang C, Burnside E, McCarty C, Page D: Graphical-model Based Multiple Testing under Dependence, with Applications to Genome-wide Association Studies, Conference Proceeding, The Conference on Uncertainty in Artificial Intelligence (UAI), United States, 2012

23. **Liu J**, Vidaillet H, Burnside E, Page D: A Collective Ranking Method for Genome-wide Association Studies, United States, *ACM-BCB*, 2012

24. **Liu J**, Page D, Nassif H, Shavlik J, Peissig P, McCarty C, Onitilo AA, Burnside E: Genetic variants improve breast cancer risk prediction on mammograms, Conference Proceeding, AMIA Annual Symposium, Washington, DC, 2013

25. **Liu J**, Page D: Bayesian Estimation of Latently-grouped Parameters in Undirected Graphical Models, Advances in Neural Information Processing Systems, 2013

26. **Liu J**, Page D, Peissig P, McCarty C, Onitilo AA, Trentham-Dietz A, Burnside E: New genetic variants improve personalized breast cancer diagnosis, *AMIA Joint Summits on Translational Science*, 2014

27. **Liu J**, Zhang C, Burnside E, Page D: Learning a Semiparametric Graphical Model for Multiple Testing under Dependence, The 31st International Conference on Machine Learning (ICML), Beijing, China, 2014

28. Wu Y, **Liu J**, Page D, Peissig P, McCarty C, Onitilo AA, Burnside ES: Comparing the value of mammographic features and genetic variants in breast cancer risk prediction, Conference Proceeding,

AMIA Annual Symposium, Washington, DC, 2014

29.   **Liu J**, Zhang C, Burnside E, Page D: Learning Heterogeneous Hidden Markov Random Fields, Conference Proceeding, The International Conference on Artificial Intelligence and Statistics (AISTATS), Reykjavic, Iceland, 2014

30.   **Liu J**, Wu Y, Ong I, Page D, Peissig P, McCarty C, Onitilo AA, Burnside E: Leveraging Interaction between Genetic Variants and Mammographic Findings for Personalized Breast Cancer Diagnosis, Conference Proceeding, AMIA Joint Summits on Translational Science, San Francisco, CA, 2015

31.   Weiss J, Kuusisto F, Boyd K, **Liu J**, Page D: Machine Learning for Treatment Assignment: Improving Individualized Risk Attribution, Conference Proceeding, AMIA Annual Symposium, San Francisco, CA, 2015

32.   Wu Y, **Liu J**, Del Rio AM, Page DC, Alagoz O, Peissig P, Onitilo AA, Burnside ES: Developing a clinical utility framework to evaluate prediction models in radiogenomics, Proc SPIE Int Soc Opt Eng, 2015

33.   Wu Y, Abbey CK, **Liu J**, Ong I, Peissig P, Onitilo AA, Fan J, Yuan M, Burnside ES: Discriminatory power of common genetic variants in personalized breast cancer diagnosis, Proc SPIE Int Soc Opt Eng, 2016

34.   Geng S, Kuang Z, **Liu J**, Wright S, Page D: Stochastic Learning for Sparse Discrete Markov Random Fields with Controlled Gradient Approximation Error, Conference Proceeding, The Conference on Uncertainty in Artificial Intelligence (UAI), Monterey, CA, 2018

35.   **Liu J**, Lin D, Yardlmcl GG, Noble WS: Unsupervised embedding of single-cell Hi-C data, Conference Proceeding, The 26th Conference on Intelligent Systems for Molecular Biology (ISMB), Chicago, IL, 2018

36.   Feld SI, Woo KM, Alexandridis R, Wu Y, **Liu J**, Peissig P, Onitilo AA, Cox J, Page CD, Burnside ES: Improving breast cancer risk prediction by using demographic risk factors, abnormality features on mammograms and genetic variants, AMIA Annual Symposium, San Francisco, CA, 2018

37.   **Liu J**, Huang Y, Singh R, Vert JP, Noble WS: Jointly embedding multiple single-cell omics measurements, Conference Proceeding, Workshop on Algorithms in Bioinformatics (WABI), Niagara Falls, NY, 2019

Submitted Peer-Reviewed

Preprint

1.   Tao Y, Feng F, Luo X, **Liu J****: CNTools: A computational toolbox for cellular neighborhood analysis from multiplexed images. *Nature Communications*. (Under review)

2.   Wang S, Chakraborty S, Fu Y, Lee M, **Liu J**, Waldhaus J**: Opposing gradients of retinoic acid and sonic hedgehog specify tonotopic identity in the mouse cochlea. *Developmental Cell*. (Under review)

3.   Walker J, Saunders D, Rai V, Dai C, Orchard P, Hopkirk A, Reihasmann C, Tao Y, Fan S, Shrestha S, Varshney A, Wright J, Pettway Y, Ventresca C, Agarwala S, Aramandla R, Poffenberger G, Jenkins R, Hart N, Greiner D, Shultz L, Bottino R, **Liu J**, Parker S, Powers A, Mei S, Petty L, Chen H-H, Below J, Kang H, Philips S, Brissova M**: Genetic risk converges on regulatory networks mediating early type 2 diabetes. *Nature*. (Under review)

Abstract/Posters

1.   Zhang X, Wang XQ D, Gore H, Himadewi P, Feng F, **Liu J**: 3D Genomics of Acute Meyloid Leukemia Reveals the Imbalance between DNA Methylation Canyon Interactions and Leukemic Specific Enhancer Network Interactions, *Blood*.136, (Supplement 1): 45-45, 2020

2.   Wang S, Lee MP, **Liu J**, Waldhaus J: Single Cell Chromatin Accessibility Delineates Cellular Identities of the Neonatal Organ of Corti, Association for Research in Otolaryngology, San Jose, CA, 2020, *Abstracts of the fourty-third annual midwinter research meeting of the Association for Research in Otolaryngology*.43

3.   Wang S, Lee M, Jones S, **Liu J**, Waldhaus J: Mapping the Regulatory Landscape of Auditory Hair Cells From Single Cell Multi-Omics Data, Association for Research in Otolaryngology, Virtual, 2021, *Abstracts of the fourty-fourth annual midwinter research meeting of the Association for Research in Otolaryngology*

4.   Wang S, Fu Y, Lee M, Jones S, **Liu J**, Waldhaus J: Molecular Mechanism Conferring Spatial Identity during Cochlear Duct Extension, Abstract, the 12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB), Virtual, 2021

5.   Wang S, Fu Y, Lee M, Jones S, **Liu J**, Waldhaus J: Molecular Mechanism Conferring Spatial Identity during Cochlear Duct Extension, Abstract, The 29th conference on Intelligent Systems for Molecular Biology, Virtual, 2021

6.   Zhang H, Zhang Z, Stuart P, Patrick M, **Liu J**, Nair R, Tsoi LC, Elder JT: High resolution chromatin loops associate with gene targets for psoriasis susceptibility regions, Abstract, Journal of Investigative Dermatology, 2022, 142, (8): s81-s81, 2022

7.   Wang S, Chakraborty S, Fu Y, Lee M, Jones S, **Liu J**, Waldhaus J: Opposing gradients of retinoic acid and sonic hedgehog specify tonotopic identity in the mouse cochlea, Abstract, The 30th conference on Intelligent Systems for Molecular Biology, Madison, WI, 2022

8.   Huang Y, Li C, Tang F, Chen J, Zhu J, Zheng S, Luo X, Zhu D, Qiu J, Lu X, **Liu J**: GLKB: a Genomic Literature Knowledge Base, Abstract, The 15th Great Lakes Bioinformatics (GLBIO) conference, Montreal, Quebec, Canada, 2023

9.   Feng F, Tang F, Gao Y, Yang S, Li T, Zhu D, Yao Y, Huang Y, **Liu J**: GenomicKB: a knowledge graph for the human genome, Abstract, The 15th Great Lakes Bioinformatics (GLBIO) conference, Montreal, Quebec, Canada, 2023

10.   Luo X, **Liu J**: Spatial Cell Communication of Single-cell Resolution, Abstract, Human Cell Atlas General Meeting, Toronto, Canada, 2023