

Jie Liu

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Research Interests

bioinformatics, machine learning, and medical informatics

Education

PhD in Computer Science, University of Wisconsin-Madison, 07/2014
Thesis: Statistical Methods for Genome-wide Association Studies and Personalized Medicine
Master in Statistics, University of Wisconsin-Madison, 05/2011
Master in Computer Science, University of Wisconsin-Madison, 05/2009
Master in Signal and Information Processing, Peking University, 07/2007
Bachelor in Info. Management & Info. Systems, Beijing Univ. of Posts and Telecom, 07/2004

Employment

Assistant Professor, Department of Computational Medicine and Bioinformatics, Department of Computer Science and Engineering, UM Comprehensive Cancer Center, Michigan Institute for Data Science, University of Michigan, 01/2019-present

Research Associate, Department of Genome Sciences, University of Washington, 09/2014-12/2018

Peer-reviewed Publications (36)

Bioinformatics and Other Machine Learning Applications

1. Yuanhao Huang, Bingjiang Wang, Jie Liu. NucleoMap: a computational tool for identifying nucleosomes in ultra-high resolution contact maps. *PLOS Computational Biology*, 2022.
2. Zhenhao Zhang, Fan Feng, **Jie Liu**. Characterizing collaborative transcription regulation with a graph-based deep learning approach. *PLOS Computational Biology*, 2022.
3. Fan Feng, Yuan Yao, Xue Qing David Wang, Xiaotian Zhang, and **Jie Liu**. Connecting high-resolution 3D chromatin organization with epigenomics. *Nature Communications*, 2022.
4. Pamela Himadewi*, Xue Qing David Wang*, Fan Feng*, Haley Gore, Yushuai Liu, Lei Yu, Ryo Kurita, Yukio Nakamura, Gerd P Pfeifer, **Jie Liu**[†], Xiaotian Zhang[†]. 3' HS1 CTCF binding site in human β -globin locus regulates fetal hemoglobin expression. *eLife*, 2021. (* indicates co-first authors, [†] indicates co-corresponding authors)
5. Qiang Li, Fengbiao Mao, Yuanhao Huang, Bo Zhou, Brian W. Basinski, Michael Aksu, **Jie Liu**, Yali Dou and Rajesh C. Rao. p53 inactivation unmasks histone methylation-independent and cytoplasmic-dependent WDR5 functions that drive self-renewal and differentiation of pluripotent stem cells. *Stem Cell Reports*, 2021.

6. Xinjun Li, Fan Feng, Hongxi Pu, Wai Yan Leung, **Jie Liu**. scHiCTools: a computational toolbox for analyzing single-cell Hi-C data. *PLOS Computational Biology*, 2021.
7. Shuze Wang, Mary P. Lee, Scott Jones, **Jie Liu** and Joerg Waldhaus. Mapping the regulatory landscape of auditory hair cells from single-cell multi-omics data. *Genome Research*, 2021.
8. Hyeon-Jin Kim, Galip Gurkan Yardimici, Giancarlo Bonora, Vijay Ramani, **Jie Liu**, Ruolan Qiu, Choli Lee, Jennifer Hesson, Carol B Ware, Jay Shendure, Zhijun Duan, William Stafford Noble. Capturing cell type-specific chromatin structural patterns by applying topic modeling to single-cell Hi-C data. *PLOS Computational Biology*, 2020.
9. Qiang Li, Fengbiao Mao, Bo Zhou, Yuanhao Huang, Zhenhua Zou, Aaron D. denDekker, Jing Xu, Sean Hou, **Jie Liu**, Yali Dou, and Rajesh C. Rao. p53 Integrates Temporal WDR5 Inputs during Neuroectoderm and Mesoderm Differentiation of Mouse Embryonic Stem Cells. *Cell Reports*, 2020
10. **Jie Liu**, Yuanhao Huang, Ritambhara Singh, Jean-Philippe Vert and William Stafford Noble. Jointly embedding multiple single-cell omics measurements. *The Workshop on Algorithms in Bioinformatics (WABI)*, 2019.
11. Jung-Sik Kim, Xiaoyuan He, **Jie Liu**, Zhijun Duan, Taeyeon Kim, Julia Gerard, Brian Kim, Manoj M. Pillai, William S. Lane, William S. Noble, Bogdan Budnik, Todd Waldman. Systematic proteomics of endogenous human cohesin reveals an interaction with diverse splicing factors and RNA binding proteins required for mitotic progression. *Journal of Biological Chemistry*, 2019.
12. **Jie Liu**, Dejun Lin, Gurkan Yardimci, and William S. Noble. Unsupervised embedding of single-cell Hi-C data. *The 26th Annual Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2018.
13. Shara I. Feld, Kaitlin M. Woo, Roxana Alexandridis, Yirong Wu, **Jie Liu**, Peggy Peissig, Adedayo A. Onitilo, Jennifer Cox, C. David Page, Elizabeth S. Burnside. Improving breast cancer risk prediction by using demographic risk factors, abnormality features on mammograms and genetic variants. *AMLA Annual Symposium*, 2018.
14. **Jie Liu**, John T. Halloran, Jeffrey A. Bilmes, Riza M. Daza, Choli Lee, Elisabeth M. Mahen, Donna Prunkard, Chaozhong Song, Sibel Blau, Michael O. Dorschner, Vijayakrishna K. Gadi, Jay Shendure, C. Anthony Blau, and William S. Noble. Comprehensive statistical inference of the clonal structure of cancer from multiple biopsies. *Scientific Reports*, 2017.
15. Yirong Wu, Craig K. Abbey, **Jie Liu**, Irene Ong, Peggy Peissig, Adedayo A. Onitilo, Jun Fan, Ming Yuan and Elizabeth S. Burnside. Discriminatory Power of Common Genetic Variants in Personalized Breast Cancer Diagnosis. *SPIE Medical Imaging conference* (oral presentation), 2016.
16. Elizabeth S. Burnside, **Jie Liu**, Yirong Wu, Adedayo A. Onitilo, Catherine A. McCarty, C. David Page, Peggy L. Peissig, Amy Trentham-Dietz, Terrie Kitchner, Jun Fan and Ming Yuan. Comparing Mammography Abnormality Features and Genetic Variants in the Prediction of Breast Cancer in Women Recommended for Breast Biopsy. *Academic Radiology* 23(1), 2016.
17. Yirong Wu, Craig K. Abbey, Xianqiao Chen, **Jie Liu**, David C. Page, Oguzhan Alagoz, Peggy Peissig, Adedayo A. Onitilo, Elizabeth S. Burnside. Developing a Utility Decision Framework to Evaluate Predictive Models in Breast Cancer Risk Estimation. *Journal of Medical Imaging*, 2015.

18. Jeremy Weiss, Finn Kuusisto, Kendrick Boyd, **Jie Liu**, David Page. Machine Learning for Treatment Assignment: Improving Individualized Risk Attribution. *American Medical Informatics Association Symposium (AMIA)*, 2015.
19. **Jie Liu**, Yirong Wu, Irene Ong, David Page, Peggy Peissig, Catherine McCarty, Adedayo A. Onitilo and Elizabeth Burnside. Leveraging Interaction between Genetic Variants and Mammographic Findings for Personalized Breast Cancer Diagnosis. *AMIA Joint Summits on Translational Science* (regular paper, podium presentation), 2015.
20. Yirong Wu, **Jie Liu**, Alejandro Munoz del Rio, David C. Page, Oguzhan Alagoz, Peggy Peissig, Adedayo A. Onitilo and Elizabeth S. Burnside. Developing a Clinical Utility Framework to Evaluate Prediction Models in Radiogenomics. *SPIE Medical Imaging conference* (oral presentation), 2015.
21. Yirong Wu, **Jie Liu**, David Page, Peggy Peissig, Catherine McCarty, Adedayo A. Onitilo and Elizabeth S. Burnside. Comparing the Value of Mammographic Features and Genetic Variants in Breast Cancer Risk Prediction. *American Medical Informatics Association Symposium (AMIA)* (regular paper, podium presentation), 2014.
22. **Jie Liu**, David Page, Peggy Peissig, Catherine McCarty, Adedayo A. Onitilo, Amy Trentham-Dietz and Elizabeth Burnside. New Genetic Variants Improve Personalized Breast Cancer Diagnosis. *AMIA Joint Summits on Translational Science* (regular paper, podium presentation, **Marco Ramoni Distinguished Paper Award**), 2014.
23. **Jie Liu**, David Page, Houssam Nassif, Jude Shavlik, Peggy Peissig, Catherine McCarty, Adedayo A. Onitilo and Elizabeth Burnside. Genetic Variants Improve Breast Cancer Risk Prediction on Mammograms. *American Medical Informatics Association Symposium (AMIA)* (regular paper, podium presentation), 2013.
24. **Jie Liu**, Elizabeth Burnside and David Page. Predicting Breast Cancer and Prostate Cancer Susceptibility from Single Nucleotide Polymorphisms. *ICML 2013 Workshop on Role of Machine Learning in Transforming Healthcare*, 2013.
25. **Jie Liu** and David Page. Structure Learning of Undirected Graphical Models with Contrastive Divergence. *ICML 2013 Workshop on Structured Learning: Inferring Graphs from Structured and Unstructured Inputs*, 2013.
26. **Jie Liu**, Humberto Vidaillet, Elizabeth Burnside and David Page. A Collective Ranking Method for Genome-wide Association Studies. *ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM BCB)*, 2012.
27. **Jie Liu***, Zaixia Hu* and Shaohua Tan. Cross-Sectional Stock Return Analysis Using Support Vector Regression. *Applied Economics Letters* 17(1), 2009. (* indicates equal contribution)
28. Ji Wan, Shuli Kang, Chuanning Tang, Jianhua Yan, Yongliang Ren, **Jie Liu**, Xiaolian Gao, Arindam Banerjee, Lynda B.M.Ellis and Tongbin Li. Meta-prediction of Phosphorylation Sites with Weighted Voting and Restricted Grid Search Parameter Selection. *Nucleic Acids Research* 36(4), 2008.
29. **Jie Liu**, Shuli Kang, Chuanning Tang, Lynda B.M. Ellis and Tongbin Li. Meta-prediction of Protein Subcellular Localization with Reduced Voting. *Nucleic Acids Research* 35(15), 2007.

Machine Learning and Statistics

30. Sinong Geng*, Zhaobin Kuang*, **Jie Liu**, Stephen Wright, and David Page. Stochastic Learning for Sparse Discrete Markov Random Fields with Controlled Gradient Approximation Error. *Uncertainty in Artificial Intelligence (UAI)*, 2018. (* indicates co-first authors)
31. **Jie Liu**, Chunming Zhang, and David Page. Multiple Testing under Dependence via Graphical Models. *Annals of Applied Statistics*, 2016.
32. Jun Fan, Yirong Wu, Ming Yuan, David Page, **Jie Liu**, Irene Ong, Peggy Peissig and Elizabeth Burnside. Structure-leveraged Methods in Breast Cancer Risk Prediction. *Journal of Machine Learning Research*, 17, 1-15, 2016.
33. **Jie Liu**, Chunming Zhang, Elizabeth Burnside and David Page. Learning a Semiparametric Graphical Model for Multiple Testing under Dependence. The *31st International Conference on Machine Learning (ICML)*, 2014.
34. **Jie Liu**, Chunming Zhang, Elizabeth Burnside and David Page. Learning Heterogeneous Hidden Markov Random Fields. The *17th International Conference on Artificial Intelligence and Statistics (AISTATS)*, 2014.
35. **Jie Liu** and David Page. Bayesian Estimation of Latently-grouped Parameters in Undirected Graphical Models. *Neural Information Processing Systems (NIPS)*, 2013.
36. **Jie Liu**, Chunming Zhang, Catherine McCarty, Peggy Peissig, Elizabeth Burnside and David Page. Graphical-model Based Multiple Testing under Dependence, with Applications to Genome-wide Association Studies. *Uncertainty in Artificial Intelligence (UAI)* (oral presentation), 2012.
37. **Jie Liu**, Chunming Zhang, Catherine McCarty, Peggy Peissig, Elizabeth Burnside and David Page. High-Dimensional Structured Feature Screening Using Binary Markov Random Fields. The *15th International Conference on Artificial Intelligence and Statistics (AISTATS)*, 2012.

Preprints

- Zhenhao Zhang, Yiyang Qiu, Fan Feng, Jie Liu. A generalizable framework to comprehensively predict epigenome, chromatin organization, and transcriptome. *Submitted*, 2022.

Professional Service

Conference and Workshop Organizer:

ACM-BCB Workshop on Machine-Learning Methods for Single-cell Analysis 2021

Editorial:

PLOS Computational Biology (guest editor, 2021-2022, and associate editor, 2022-present)

Journal Referee: 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

Conference Program Committee: 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

Honors and Awards

2020 NHGRI Genomic Innovator Award
2015 Washington Research Foundation Innovation Postdoctoral Fellowship
2014 AMIA Marco Ramoni Distinguished Paper Award
2014 Moore/Sloan Data Science Postdoctoral Fellowship
2004-2007 PKU graduate student fellowship
2004 Merit Student of Beijing City (top 1%)
2001-2003 BUPT student fellowship (top 1%)

Teaching and Mentoring

Courses

Instructor, BIOINF 593/EECS 598 Machine Learning in Computational Biology, U-M, 2021 Fall
Facilitator, PIBS 503 Data Storage, Ownership and Peer Review, U-M, 2021 Winter
Adjunct instructor, CS 760 Machine Learning, UW-Madison, 2014 Spring.
Guest instructor, STAT 992 Large-scale inference, UW-Madison, 2013 Spring.
Teaching assistant, Introduction to Artificial Intelligence, Peking University, 2005 Spring.

Current Mentees (7 PhDs, 3 masters, 12 undergrads)

Fan Feng, PhD candidate, Bioinformatics, U Michigan
Shuze Wang, PhD candidate, Bioinformatics, U Michigan
Yuanhao Huang, PhD candidate, Bioinformatics, U Michigan
Zhenhao Zhang, PhD student, Bioinformatics, U Michigan
Sean Moran, PhD student, Bioinformatics, U Michigan
Linghua Jiang, PhD student, Bioinformatics, U Michigan
Yicheng Tao, PhD student, EECS, U Michigan
Zheyu Zhang, master student, EECS, U Michigan
Xin Luo, master student, EECS, U Michigan
Jiahao Qiu, undergraduate student, EECS, U Michigan
Hongxi Pu, undergraduate student, CS (LSA), U Michigan
Xinyu Lu, undergraduate student, EECS, U Michigan
Shuyuan Yang, undergraduate student, EECS, U Michigan
Yijia Gao, undergraduate student, EECS, U Michigan

Shaochun Zheng, undergraduate student, EECS, U Michigan
Jiyue Zhu, undergraduate student, EECS, U Michigan
Jiyu Chen, undergraduate student, EECS, U Michigan
Chengfan Li, undergraduate student, EECS, U Michigan
Jiajun Wang, undergraduate student, EECS, U Michigan
Zexuan yang, undergraduate student, EECS, U Michigan
Oliver Li, undergraduate student, EECS, U Michigan

Past Mentees (2 PhDs, 5 masters, 14 undergrads, 1 research volunteer)

Yiyang Qiu, undergraduate student, EECS, U-M. First position: CSE grad program at CMU
Tianjun Li, undergraduate student, EECS, U-M. First position: CSE grad program at CMU
Hao Pan, undergraduate student, EECS, U-M. First position: DS grad program at Columbia U
Feitong Tang, undergraduate student, EECS, U-M. First position: CSE grad program at U-M
Ziqiao Ma, undergraduate student, EECS, U-M. First position: CSE grad program at U-M
Yuan Yao, undergraduate student, EECS, U-M. First position: CSE grad program at U-M
Simin Fan, undergraduate student, EECS, U-M. First position: CSE grad program at EPFL
Xinjun Li, master student, Statistics, U Michigan. First position: Statistics program at U Michigan
Peiyao Zhao, master student, Biostatistics. First position: Biostat PhD program at U Michigan
Bingjiang Wang, undergraduate student, EECS. First position: CSE grad program at UCSD
Zhuowen Shen, undergraduate student, EECS. First position: CSE grad program at U Michigan
Ben Wurman, BS, CS and Mol., Cellular & Dev. Bio., U Michigan. First position: industry
Wai Yan Leung, research volunteer. First position: CS grad program at Georgia Tech
Chenghao Xu, BS in Statistics, CUHK-SZ. First position: master student in Math at NYU
Yufeng Zhang, MS, Biostatistics, U Michigan. First position: PhD student in Bioinfo at U Michigan
Yujuan Fu, BS in EECS, U Michigan. First position: PhD student in Medical Informatics at UW
Yijiao Qin, BS in EECS, U Michigan. First position: master student in Info Networking at CMU
Mingyu Du, MS in Biostatistics, U Michigan. First position: PhD student in Bioinfo at UC-Irvine
Kaishu Mason, BS in Statistics, Harvard. First position: PhD student in Biostat at UPenn
Charles Kwong, PhD in Computer Sciences. UW-Madison. First position: postdoc at Stanford
Sinong Geng, MS in Statistics, UW-Madison. First position: PhD student in CS at Princeton
John T Halloran, PhD in EE, UW. First position: postdoc at UC-Davis

Prelim/Thesis Committee

Yufeng Du, PhD student (advisor: Garmire), DCMB, 06/22
Yufeng Zhang, PhD student (advisor: Najarian), DCMB, 04/22
Zijun Gao, PhD student (advisor: Najarian), DCMB, 04/22
Kevin Yang, PhD student (advisor: Dr. Nesvizhskii), DCMB, 08/21
Qianhui Huang, PhD student (advisor: Dr. Garmire), DCMB, 08/21
April Kriebel, PhD student (advisor: Dr. Welch), DCMB, 07/21
Chen Li, PhD student (advisor: Dr. Welch), DCMB, 07/21
Jialin Liu, PhD student (advisor: Dr. Welch), DCMB, 07/21

Alec Chu, PhD student (advisor: Dr. Marcin Cieslik), Cellular and Molecular Pathology, 08/21
 Jingcheng Xiao, PhD student (advisor: Dr. Haojie Zhu), Pharmacy, 03/21, 12/21
 Ying Yang, PhD student (advisor: Dr. Klionsky), MCDB, 12/20
 Hanrui Zhang, PhD student (advisor: Dr. Guan), DCMB, 01/21, summer 2022
 Wenjin Gu, PhD student (advisor: Dr. Mills), DCMB, 12/20
 Chao Gao, PhD student (advisor: Dr. Welch), DCMB, 08/20
 Shengcheng Dong, PhD student (advisor: Dr. Boyle), DCMB, 01/19, 09/19, 04/20, 09/20, 03/21
 Stephen Lindsly, PhD student (advisor: Dr. Rajapakse), DCMB, 05/19
 Vivek Rai, PhD student (advisor: Dr. Parker), DCMB, 05/19, 06/20
 Chen Sun, PhD student (advisor: Dr. Mills), DCMB, 06/19

Invited Talks

- “A database for high-resolution chromatin contact maps and human genetic variants”
 NIH Common Fund Data Ecosystem, March 2021
- “An accurate and interpretable model for predicting high resolution 3D chromatin organization”
 4DN Consortium, Joint Analysis Working Group, September 2019
- “Computational approaches for understanding chromatin organization and cancer”
 Cancer Center Basic Science Retreat, University of Michigan, June 2019
- “Machine Learning for Understanding the Dynamics of Cell Populations”
 Multiple US universities, Jan-March 2018
- “Tumor heterogeneity analysis via an extensible modeling system”
 eScience Institute, University of Washington, December 2016
- “Genomic Medicine, from the Perspective of Data Science”
 eScience Institute, University of Washington, January 2015
- “The Promise and Computational Challenges of Personalized Medicine”
 Lane Center for Computational Biology, Carnegie Mellon University, March 2014
 Department of Computer Science, University of Michigan, Ann Arbor, March 2014
 IBM T. J. Watson Research Center, March 2014
- “Multiple Testing under Dependence with Applications to Genome-wide Association Studies”
 Department of Computer Science, Colorado State University, March 2013

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