

# 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

Associate 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, 09/2024-present

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, 01/2019-08/2024

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

## Peer-reviewed Publications (45)

### *Computational Genomics, Bioinformatics and Machine Learning Applications*

1. IGVF Consortium. Deciphering the impact of genomic variation on function. *Nature*, 2024.
2. Yicheng Tao, Fan Feng, Xin Luo, Conrad V. Reihsmann, Alexander L. Hopkirk, Jean-Philippe Cartiailler, Marcela Brissova, Stephen C. J. Parker, Diane C. Saunders, and **Jie Liu**. CNTools: A computational toolbox for cellular neighborhood analysis from multiplexed images. *PLOS Computational Biology*, 2024.
3. Shuze Wang, Saikat Chakraborty, Yujuan Fu, Mary P. Lee, **Jie Liu** and Joerg Waldhaus. 3D reconstruction of the mouse cochlea from scRNA-seq data suggests morphogen-based principles in apex-to-base specification. *Developmental Cell*, 2024.
4. Joerg Waldhaus\*, Linghua Jiang\*, Liqian Liu, **Jie Liu**, Robert Keith Duncan. Mapping the developmental potential of mouse inner ear organoids at single-cell resolution. *iScience*, 2024. (\* indicates equal contribution)

5. John T. Walker, Diane C. Saunders, Vivek Rai, Hung-Hsin Chen, Peter Orchard, Chunhua Dai, Yasmine D. Pettway, Alexander L. Hopkirk, Conrad V. Reihsmann, Yicheng Tao, Simin Fan, Shristi Shrestha, Arushi Varshney, Lauren E. Petty, Jordan J. Wright, Christa Ventresca, Samir Agarwala, Radhika Aramandla, Greg Poffenberger, Regina Jenkins, Shaojun Mei, Nathaniel J. Hart, Sharon Phillips, Hakmook Kang, Dale L. Greiner, Leonard D. Shultz, Rita Bottino, **Jie Liu**, Jennifer E. Below, The HPAP Consortium, Stephen C. J. Parker, Alvin C. Powers, and Marcela Brissova. Genetic risk converges on regulatory networks mediating early type 2 diabetes. *Nature*, 2023.
6. Rachana Haliyur, David H Parkinson, Feiyang Ma, Jing Xu, Qiang Li, Yuanhao Huang, Lam C Tsoi, Rachael Bogle, **Jie Liu**, Johann E Gudjonsson, Rajesh C Rao. Liquid biopsy for proliferative diabetic retinopathy: single-cell transcriptomics of human vitreous reveals inflammatory T cell signature. *Ophthalmology Science*, 2024
7. Zhenhao Zhang, Yiyang Qiu, Fan Feng, **Jie Liu**. A generalizable framework to comprehensively predict epigenome, chromatin organization, and transcriptome. *Nucleic Acids Research*, 2023.
8. Fan Feng, Feitong Tang, Yijia Gao, Dongyu Zhu, Tianjun Li, Shuyuan Yang, Yuan Yao, Yuanhao Huang, **Jie Liu**. GenomicKB: a knowledge graph for the human genome. *Nucleic Acids Research*, 2023.
9. Yuanhao Huang, Bingjiang Wang, **Jie Liu**. NucleoMap: a computational tool for identifying nucleosomes in ultra-high resolution contact maps. *PLOS Computational Biology*, 2022.
10. Zhenhao Zhang, Fan Feng, **Jie Liu**. Characterizing collaborative transcription regulation with a graph-based deep learning approach. *PLOS Computational Biology*, 2022.
11. Fan Feng, Yuan Yao, Xue Qing David Wang, Xiaotian Zhang, and **Jie Liu**. Connecting high-resolution 3D chromatin organization with epigenomics. *Nature Communications*, 2022.
12. 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  $\beta$ -globin locus regulates fetal hemoglobin expression. *eLife*, 2021. (\* indicates co-first authors, † indicates co-corresponding authors)
13. 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.
14. 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.
15. 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.
16. Hyeon-Jin Kim, Galip Gurkan Yardimci, 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.
17. 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
18. **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.
  19. 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.
  20. **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.
  21. 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.
  22. **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.
  23. 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.
  24. 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.
  25. 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.
  26. 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.
  27. **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. *AMLA Joint Summits on Translational Science* (regular paper, podium presentation), 2015.
  28. 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.

29. 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.
30. **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.
31. **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.
32. **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.
33. **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.
34. **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.
35. **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)
36. 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.
37. **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***

38. 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)
39. **Jie Liu**, Chunming Zhang, and David Page. Multiple Testing under Dependence via Graphical Models. *Annals of Applied Statistics*, 2016.
40. 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.

41. **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.
42. **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.
43. **Jie Liu** and David Page. Bayesian Estimation of Latently-grouped Parameters in Undirected Graphical Models. *Neural Information Processing Systems (NIPS)*, 2013.
44. **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.
45. **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.

## **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, Nature Methods, Nature Communications, Genome Research, Cell Genomics, Nucleic Acids Research, 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:** RSGDREAM 2023, 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

**Conference Area Chair:** ACM-BCB 2023, MLCB 2023

**Working Group and Focus Group leadership at NIH Consortia:** NIH/IGVF Machine Learning Focus Group (co-lead, 2024-present), NIH/PanKbase Data and Metadata Working Group (co-lead, 2024-present)

## **Honors and Awards**

2024 Endowment for the Basic Sciences Teaching Award (U-M/DCMB)  
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, 2022 Fall, 2023 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** (11 PhDs, 6 masters, 3 undergrads)

Yuanhao Huang, PhD candidate, Bioinformatics, U Michigan  
Zhenhao Zhang, PhD candidate, Bioinformatics, U Michigan  
Sean Moran, PhD candidate, Bioinformatics, U Michigan  
Linghua Jiang, PhD candidate, Bioinformatics, U Michigan  
Yicheng Tao, PhD student, EECS, U Michigan  
Xin Luo, PhD student, Bioinformatics, U Michigan  
Zheyu Zhang, PhD student, EECS, U Michigan  
Yiqun Wang, PhD student, Bioinformatics, U Michigan  
Zhaowei Han, PhD student, Bioinformatics, U Michigan  
Lingxiao Guan, PhD student, EECS, U Michigan  
Xinyu Bao, PhD student, EECS, U Michigan  
Haohong Shang, master student, EECS, U Michigan  
Xuteng Luo, master student, EECS, U Michigan  
Meiqi Zhao, master student, School of Information, U Michigan  
Runbo Mao, master student, Bioinformatics, U Michigan  
Tiancheng Jiao, undergraduate student, EECS, U Michigan  
Yingjie Zuo, undergraduate student, EECS, U Michigan  
Yijun Pan, undergraduate student, EECS, U Michigan

### **Past Mentees** (2 PhDs, 6 masters, 23 undergrads, 1 research volunteer)

Fan Feng, PhD candidate, Bioinformatics, U Michigan. First position: research fellow at Vanderbilt University Medical Center

Shuze Wang, PhD candidate, Bioinformatics, U Michigan. First position: Staff Scientist at Massachusetts General Hospital

Shuyuan Yang, master student, EECS, U Michigan. First position: graduate program at U-M

Yijia Gao, master student, EECS, U Michigan. First position: graduate program at U-M

Tianshu Huang, undergraduate student, EECS, U Michigan. First position: graduate program at UCSD

Dongyu, Zhu, master student, School of Information, U Michigan. First position: industry

Feiyang Deng, master student, Biostatistics, U Michigan. First position: PhD program at Biostatistics at U-M

Feitong Tang, undergraduate student, EECS, U Michigan. First position: graduate program at U-M

Shaochun Zheng, undergraduate student, EECS, U Michigan. First position: graduate program at UCSD

Jiyue Zhu, undergraduate student, EECS, U Michigan. First position: graduate program at UCSD

Jiyu Chen, undergraduate student, EECS, U Michigan. First position: graduate program at U-M

Chengfan Li, undergraduate student, EECS, U Michigan. First position: graduate program at Brown

Zexuan Yang, undergraduate student, EECS, U Michigan. First position: industry

Jiahao Qiu, undergraduate student, EECS, U-M. First position: CSE grad program at Princeton U

Hongxi Pu, undergraduate student, CS (LSA), U-M. First position: industry

Xinyu Lu, undergraduate student, EECS, U-M. First position: CSE grad program at CMU

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

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

## **Prelim/Thesis Committee**

Katarina Pavlovic, PhD student (advisor: Dr. Boyle), DCMB, 09/24  
Boran Gao, PhD student (advisor: Dr. Zhou), Biostatistics, 04/24, 06/24  
Keagan Moo, PhD student (advisor: Dr. Parker), DCMB, 01/24  
Alice Wang, PhD student (advisor: Dr. Parker), DCMB, 01/24  
Kinsey Van Deynze, PhD student (advisor: Dr. Boyle), DCMB, 08/22  
Avery Maddox, PhD student (advisor: Dr. Rao), DCMB, 08/22, 05/23, 04/24  
Kaiwen Deng, PhD student (advisor: Dr. Guan), DCMB, 06/22  
Hengshi Yu, PhD student (advisor: Dr. Welch), DCMB, 09/21, 06/22  
Ryan Rebernick, MD/PhD (advisor: Dr. Cieslik) student in DCMB, 06/22  
Yuheng Du, PhD student (advisor: Dr. Garmire), DCMB, 07/22, 04/23, 06/24  
Yufeng Zhang, PhD student (advisor: Dr. Najarian), DCMB, 04/22  
Zijun Gao, PhD student (advisor: Dr. 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, 06/22  
Ying Yang, PhD student (advisor: Dr. Klionsky), MCDB, 12/20  
Hanrui Zhang, PhD student (advisor: Dr. Guan), DCMB, 01/21, 07/22, 01/23, 10/23  
Wenjin Gu, PhD student (advisor: Dr. Mills), DCMB, 12/20  
Chao Gao, PhD student (advisor: Dr. Welch), DCMB, 08/20, 12/21, 03/23, 11/23  
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, 09/21, 04/22  
Chen Sun, PhD student (advisor: Dr. Mills), DCMB, 06/19

## **Invited Talks**

“Computational infrastructures for consolidating our knowledge regarding the human genome”

University of Texas, Health Science Center at Houston, May 2023

Brown University, March 2024

University of Wisconsin-Madison, May 2024

“GenomicKB: a knowledge graph for the human genome”

IGVF Catalog WG, December 2022

“A generalizable framework to comprehensively predict epigenome, chromatin organization, and transcriptome”

GSK, September 2022

“A database for high-resolution chromatin contact maps and human genetic variants”

NIH Common Fund Data Ecosystem, Jan 2022

“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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