

LIANG (ADAM) DING

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EXPERIENCE

Spatial Genomics, Inc.

Senior Bioinformatics Scientist

March 2024 - Present

Pasadena, CA

- Spearheaded collaboration with assay scientists to leverage spatial transcriptomics for improving cell-type identification accuracy in human solid tumors and mouse MASH liver, identifying disease-associated spatial niches and immune-tumor cell communications.
- Led development of a novel barcode optimization algorithm using bulk and/or scRNA-seq references to resolve optical crowding in raw image decoding; documented implementation protocols for software engineers, enhancing decoding efficiency.
- Designed and delivered customer-facing [tutorials and analysis workflows](#) (e.g., clustering, annotation, integration, imputation) to support adoption of [GenePS](#), Spatial Genomics' imaging platform.
- Translated technical insights into business collateral (brochures, posters) showcasing GenePS applications for key stakeholders.

Spatial Genomics, Inc.

Bioinformatics Scientist

September 2022 - February 2024

Pasadena, CA

- Pioneered a deep generative model-based algorithm (autoencoders and Bayesian inference) for spatial niche alignment, correcting transcript misassignments by integrating imaging, spatial coordinates, and expression data.
- Developed spatial data showcases (e.g., [mouse kidney Minerva story](#)) to demonstrate GenePS capabilities at launch.
- Conducted comparative benchmarking of commercial in situ platforms to inform second-generation platform and assay development.
- Designed standardized/custom gene panels and probes for internal/external use.

St. Jude Children's Research Hospital

Bioinformatics Research Scientist

December 2018 - September 2022

Memphis, TN

- Directed development of systems biology tools for multiomics analysis (scRNA-seq, spatial transcriptomics, gene networks), including:
[scMINER](#) (Python/R): Preprocessing, QC, clustering, gene network reconstruction, hidden driver inference, and visualization [1].
[NetBID2](#) (R): Data-driven network-based Bayesian inference of drivers [6].
[SJARACNe](#) (Python/C++): Scalable gene network reverse engineering.
- Applied computational approaches to identify biomarkers/therapeutic targets with clinical relevance in leukemia [2, 3].
- Contributed to research funding through co-authorship of peer-reviewed publications and successful grant proposals, demonstrating translational impact.

St. Jude Children's Research Hospital

Senior Software Engineer

July 2016 - December 2018

Memphis, TN

- Developed bioinformatics workflows for clinical/research genomics (WES, WGS), improving patient data analysis pipelines.
- Collaborated with scientists to develop algorithms for multiomics data analysis (e.g., [RNAIndel](#) [10], [Episomizer](#) [11]).

- Analyzed clinical sequencing data to inform treatment decisions and enhance patient care.

University of Georgia, Athens, Georgia

Graduate Instructor/Lab Instructor

September 2011 - June 2016

Athens, Georgia

- Designed/lectured system programming courses (C, Java); developed labs, projects, and assessments for 30+ students.

EDUCATION

University of Georgia, Athens, Georgia

Ph.D., Computer Science

July 2016

University of Texas - Pan America, Edinburg, Texas

M.S., Computer Science

August 2011

Zhengzhou University, Henan, China

M.S., Applied Mathematics

B.S., Applied Mathematics

December 2008

TECHNICAL STRENGTHS

Computer Languages	Python, Rust, R, Bash, C++/C, SQL, Latex, Javascript
Databases	PostgreSQL, SQLite
Tools	PyTorch, PyG, Git, Nvidia RAPIDS, Nextflow, Snakemake, Docker
Single-cell/Spatial analysis	Scanpy, Seurat, scvi-tools, Squidpy, SpatialData, Minerva
Image analysis	ImageJ/Fiji, OpenCV, Baysor, Cellpose
Cloud computing	AWS, Microsoft Azure

PUBLICATIONS

* First authors contributed equally. # Corresponding authors. Sort by year in descending order.

Peer Reviewed Journals

1. Pan Q.*, **Ding L.***, Hladyshau S., Yao X., et al., Chi H., Yu J.# [scMINER](#): a mutual information-based framework for clustering and hidden driver inference from single-cell transcriptomics data. *Nature Communications* 16, 4305, 2025.
2. McCastlain K.*, Welsh C.*, Ni Y.*, **Ding L.***, et al., Yu J., Pounds S., Kundu M.# Somatic mitochondrial DNA mutations are a source of heterogeneity among primary leukemic cells. *Science Advanced*, 2025.
3. Huang X.*, Li Y.*, Zhang J.*, Yan L., Zhao H., **Ding L.**, et al., Yu J.#, Yang J.# Single-cell systems pharmacology identifies development-driven drug response and combination therapy in B cell acute lymphoblastic leukemia. *Cancer cell*, 42(4), 2024.
4. Yan K.*, Condori J., Ma Z., **Ding L.**, Dhungana Y., et al., Gottschalk S.#, Yu J.# Integrome signatures of lentiviral gene therapy for SCID-X1 patients. *Science Advances*, 9(40), 2023.
5. Zhang Y.*, Pool A.H., Wang T., Liu L., Kang E., Zhang B., **Ding L.**, Frieda K., Palmiter R., Oka Y.# Parallel neural pathways control sodium consumption and taste valence. *Cell*, 186(26), 2023.
6. Dong X.*, **Ding L.**, et al., Chi H., Zhang J., Yu J.# [NetBID2](#) provides comprehensive hidden driver analysis. *Cell*, 14(1), 2023.

7. Chang D.*, **Ding L.***, Malmberg R., Robinson D, Wicker M., Yan H., Martinez A., Cai L.# [Optimal learning of Markov \$k\$ -tree topology](#). Journal of Computational Mathematics and Data Science, 4(100046), 2022.
8. Shi H.*, Yan K.*, **Ding L.**, Qian C., Chi H., Yu J.# Network Approaches for Dissecting the Immune System. iScience 23(8), 2020.
9. Silveira A.B., Kasper L.H., Fan Y., et al., **Ding L.**, Zhang J., Finkelstein D., et al., Baker S.J.# H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. Acta Neuropathol. 137(4): 637-655, 2019.
10. Kohei K.*, **Ding L.**, Michael N.E., Stephen V.R., Scott N., John E., Juncheng D., Soheil M., Rhonda E.R., Michael R., Zhang, J.# [RNAIndel](#): discovering somatic coding indels from tumor RNA-Seq data. Bioinformatics, btz753, 2019.
11. Xu K.*, **Ding L.**, Chang T.C., et al., Baker S.J., Wu G.# Structure and evolution of [double minutes](#) in diagnosis and relapse brain tumors. Acta Neuropathologica. 137(1):123-137, 2019.
12. Alexander T.B.*, Gu Z.*, Iacobucci I.*, Dickerson K., Choi J.K., Xu B., et al., **Ding L.**, Liu Y., Zhang J., et al., Inaba H.#, Mullighan C.G.# The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 562(7727):373-379, 2018.
13. Mohebbi M.*, **Ding L.**, Malmberg R.L., Momany C., Rasheed K., Cai L.# Accurate prediction of human miRNA targets via graph modeling of miRNA-target duplex. Journal of Bioinformatics and Computational Biology, 7:1850013, 2018.
14. **Ding L.***, Xue X., LaMarca S., Mohebbi M., Samad A., Malmberg R.L.#, Cai L.# Accurate Prediction of [RNA Nucleotide Interactions](#) with Backbone k -Tree Model. Bioinformatics, 31(16): 2660-2667, 2015.

Conference Proceedings

1. **Ding L.***, Xue X., LaMarca S., Mohebbi M., Samad A., Malmberg R.#, and Cai L.# (2014) Abinitio prediction of RNA nucleotide interactions with backbone k -tree model, Proceedings of ECCB'14 Workshop on Computational Methods for Structural RNAs, Strasbourg France, 25-42.
2. **Ding L.***, Samad A., Xue X., Huang X., Malmberg R.#, and Cai L.# (2014) Stochastic k -tree grammar and its application in bimolecular structure modeling, International Conference on Language and Automata Theory and Applications (LATA 2014) Vol 8370, 308-322.
3. **Ding L.***, Robertson J., Malmberg R.#, and Cai L.# (2013) Protein closed loop prediction from contact probabilities, International Symposium on Bioinformatics Research and Applications (ISBRA 2013), 199-210.
4. **Ding L.**, Fu B., and Zhu B. (2011) Minimum Interval Cover and Its Application to Genome Sequencing. International Conference on Combinatorial Optimization and Applications (COCOA 2011), 287- 298.
5. **Ding L.**, Fu B., and Fu Y. (2010) Improved Sublinear Time Algorithm for Width- bounded Separators. International Workshop on Frontiers in Algorithmics, 101-112.
6. **Ding L.**, Fu B., Fu Y., Lu Z., and Zhao Z. (2010) $O((\log n)^2)$ Time Online Approximation Schemes for Bin Packing and Subset Sum Problem. International Workshop on Frontiers in Algorithmics, 250-261.

Book Chapters

1. Cai L., **Ding L.**, Huang X., Malmberg R.L., and Xue X. (2014) Stochastic grammar systems for biomolecular structure modeling, Integrative Bioinformatics for Biomedical Research: A No Boundary Thinking Approach, Huang and Moore ed. Cambridge Press, to appear.

2. **Ding L.**, Fu B. (2013) Algebrization and Randomization Methods. Handbook of Combinatorial Optimization, Springer, pp 171-220.
3. **Ding L.**, Fu B., Fu Y., Wan Y. (2012) Application of Width-Bounded Separators to Protein Side-Chain Packing Problem, Sequence and Genome Analysis: Methods and Applications, iConcept Press.

Preprints

1. Michael R., **Ding L.**, Sasi A., Andrew T., Hongjian J., Michael M., Lawryn K., Andre S., Michael A.D., Suzanne J.B., Zhang J.. XenoCP: Cloud-based BAM cleansing tool for RNA and DNA from Xenograft. bioRxiv 843250.
2. **Ding L.**, Samad, A., Xue, X., Huang, X., Cai, L. (2013) Polynomial kernels collapse the W-hierarchy. arXiv preprint arXiv:1308.3613.

HONORS AND AWARDS

- Ovation Silver Award, St. Jude Children's Research Hospital, 2018
- Dissertation Completion Award, Graduate School, University of Georgia, Athens, Georgia, 2015
- Outstanding Graduate Teaching Assistant Award, Graduate School, University of Georgia, Athens, Georgia, 2015
- CUDA and GPU Programming Certificate CUDA, Department of Computer Science, University of Georgia, 2013
- Outstanding Student Scholarship, Zhengzhou University, Henan, China, 2005