

LIANG (ADAM) DING

511 Live Oak Ave Unit 4, Arcadia, CA 91006
(956) · 802 · 8972 ◇ adamdingliang@gmail.com

EXPERIENCE

Spatial Genomics, Inc.

Senior Bioinformatics Scientist

March 2024 - Present

Pasadena, CA

- Collaborated with assay development scientists to leverage spatial information to improve cell type identification for human solid tumors and mouse liver MASH. Identified disease-associated spatial niches and cell-cell communications between immune cell subpopulations and tumor cells in the tumor microenvironment.
- Led the development of a novel algorithm to optimize barcode gene selection and distribution using reference bulk and/or scRNA-seq data to avoid the optical crowding issue in decoding the barcode genes from raw images. Provided detailed steps and guidance for software engineers to implement the algorithm.
- Led the development of [Spatial Genomics tutorials](#) for clustering, annotation, integration, and imputation of [GenePS](#) data from customers.
- Created business brochures and posters to showcase the applications of GenePS data.

Spatial Genomics, Inc.

Bioinformatics Scientist

September 2022 - February 2024

Pasadena, CA

- Spatial data analysis and visualization, such as the [mouse kidney Minerva story](#), served as a showcase for the launch of the GenePS platform.
- Designed a novel deep degenerative algorithm for spatial niche alignment across ROIs by integrating spatial, image, and expression information from cells' spatial neighborhoods. Developed tools for mis-assigned transcript correction due to imperfect cell or nuclei segmentation.
- Standard and customized gene panel designs, as well as probe designs for both internal and external use.
- Comparative analysis of data from commercial in-situ platforms to guide the assay and 2nd generation instrument developments.

St. Jude Children's Research Hospital

Bioinformatics Research Scientist

December 2018 - September 2022

Memphis, TN

- Oversaw and led the development of systems biology algorithms and software for scRNA-seq analysis, spatial and single-cell transcriptomics integration, and gene network reconstruction.

Systems biology tools and algorithms:

[scMINER](#) is a python/R package designed for preprocessing, QC, clustering, network inference, hidden driver analysis, and visualization of scRNA-seq analysis.

[NetBID2](#) is an R package for data-driven network-based Bayesian inference of drivers.

[SJARACNe](#) is a scalable software tool for reverse engineering gene networks.

- Applied systems biology approaches to identify biomarkers and therapeutic targets for cancer treatment.
- Manuscript writing and assisting with grant proposal drafting.

St. Jude Children's Research Hospital

Senior Software Engineer

July 2016 - December 2018

Memphis, TN

- Development of bioinformatics workflow infrastructure for both research and clinical applications.
- Analyzed genomics sequencing data from the clinical labs and ultimately provided feedback to impact patient care.

- Collaborated with scientists to develop algorithms and software for analyzing multi-omics data.

University of Georgia, Athens, Georgia

Graduate Instructor

September 2011 - June 2016

Athens, Georgia

- Lectured, oversaw in-class activities, and created all tests, quizzes, labs, and projects for a fast-paced system programming course that held approximately 30 students.

Lab Instructor and Teaching Assistant

- Taught Java programming and Eclipse.
- Designed and graded lab assignments and projects.
- Explained complex concepts in small groups and held office hours for individual student discussion.

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

Operating Systems

Mac OS X, Windows, Linux

Computer Languages

Python, Rust, R, Bash, C++/C, SQL, Latex, Javascript

Databases

PostgreSQL, SQLite

Tools

PyTorch, Nvidia RAPIDS, Nextflow, Snakemake, Git, Docker

Single-cell/Spatial analysis

Scanpy, Seurat, scvi-tools, Squidpy, SpatialData, Minerva

Image analysis

ImageJ/Fiji, OpenCV, Baysor, Cellpose

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. 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. Silveira A.B.*, Kasper L.H., Fan Y., Jin H., Wu G., Shaw T., Zhu X., Larson J.D., Easton J., Shao Y., Yergeau D.A., Rosencrance C., Boggs K., Rusch M.C., **Ding L.**, Zhang J., et al., Zhang J., Baker S.J.# H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. *Acta Neuropathologica.* 137(4):637-655, 2019.
12. 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.
13. 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.
14. 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.
15. **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, 2017
- 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