LIANG (ADAM) DING

511 Live Oak Ave Unit 4, Arcadia, CA 91006

(956) *·* 802 *·* 8972 *⋄* [adamdingliang@gmail.com](mailto:adamdingliang@gmail.com)

# EXPERIENCE

**Spatial Genomics, Inc.** March 2024 - Present

*Senior Bioinformatics Scientist Pasadena, CA*

* Collaborated with assay development scientists to leverage spatial information to improve cell type iden- tification 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 mi- croenvironment.
* Led the development of a novel algorithm to optimize barcode gene selection and distribution using

reference scRNA-seq data to avoid 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](https://tutorials.spatialgenomics.com/intro.html) for clustering, annotation, integration, and imputa-

tion of [GenePS](https://spatialgenomics.com/product/) data from customers.

* Created business brochures and posters to showcase the applications of GenePS data.

**Spatial Genomics, Inc.** September 2022 - February 2024

*Bioinformatics Scientist Pasadena, CA*

* Spatial data analysis and visualization, such as the [mouse kidney Minerva story](http://kidneyviewer.spatialgenomics.com/), serve 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** December 2018 - September 2022

*Bioinformatics Research Scientist 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](https://www.nature.com/articles/s41467-025-59620-6) is a python/R package designed for preprocessing, QC, clustering, network inference, hidden driver analysis, visualization of scRNA-seq analysis.

[NetBID2](https://www.nature.com/articles/s41467-023-38335-6) is an R package for data-driven network-based Bayesian inference of drivers. [SJARACNe](https://github.com/jyyulab/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 grant proposal drafting.

**St. Jude Children’s Research Hospital** July 2016 - December 2018

*Senior Software Engineer 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 softwares for analyzing multi-omics data.

**University of Georgia, Athens, Georgia** September 2011 - June 2016

*Graduate Instructor Athens, Georgia*

* Lectured, oversaw in-class activities, and created all tests, quizzes, labs, projects for a fast-paced system programming course which 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 *July 2016*

Ph.D., Computer Science

## University of Texas - Pan America, Edinburg, Texas *August 2011*

M.S., Computer Science

**Zhengzhou University, Henan, China** *December 2008*

M.S., Applied Mathematics B.S., Applied Mathematics

# TECHNICAL STRENGTHS

**Operating Systems** Mac OS X, Linux, Windows

**Computer Languages** Python, Rust, R, Bash, C++/C, SQL, Latex, Javascript

**Databases** PostgreSQL, MySQL, SQLite

**Tools** Nvidia RAPIDS, PyTorch, 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. Sorted by year.

## Peer Reviewed Journals

1. Pan Q.\*, **Ding L.**\*, Hladyshau S., Yao X., et al., Chi H., Yu J.*#* [scMINER](https://github.com/jyyulab/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](https://github.com/jyyulab/NetBID) 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](https://www.sciencedirect.com/science/article/pii/S277241582200013X). 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](https://github.com/stjude/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 (IS- BRA 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*((*logn*)*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, iConcep 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