LIANG (ADAM) DING

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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 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 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 for clustering, annotation, integration, and imputation of GenePS data from customers.

· Created business brochures and posters to showcase the applications of GenePS platform.

Spatial Genomics, Inc.   September 2022 - February 2024
Bioinformatics Scientist   *Pasadena, CA*

· Spatial data analysis and visualization, such as the mouse kidney Minerva story, 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 misassigned 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 is a python/R package designed for preprocessing, QC, clustering, network inference, hidden driver analysis, 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 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, C++/C, SQL, Bash, 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

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 (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