



Lujia Chen

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Google Scholar:

<https://scholar.google.com/citations?user=L7f-43gAAAAJ&hl=en>

EDUCATION

- **Ph.D.** in Biomedical Informatics
University of Pittsburgh, Pittsburgh, Pennsylvania
09/2012 - 11/2016
- **M.S.** in Biomedical Informatics
University of Pittsburgh, Pittsburgh, Pennsylvania
09/2010 - 06/2012
- **M.S. candidate** in Bioinformatics
Medical University of South Carolina, Charleston, South Carolina
09/2009 - 06/2010
- **B.S.** in Biotechnology
University of Science and Technology Beijing, Beijing, China
09/2005 - 05/2009

EMPLOYMENT

Assistant Professor, Department of Biomedical Informatics, University of Pittsburgh
02/2022 - Now

Postdoctoral Fellow, Department of Biomedical Informatics, University of Pittsburgh
11/2016 - 01/2022

ACADEMIC EXPERIENCE

Postdoctoral Fellow, University of Pittsburgh, Pittsburgh
12/2016 - 1/2022

Developing machine learning methods, especially deep learning models, to study cancer cell signaling systems, cancer molecular mechanisms, cancer immunology and cancer pharmacogenomics.

Graduate Student Researcher, University of Pittsburgh, Pittsburgh
09/2010 - 11/2016

Using computational and mathematical methods to analyze transcriptomic data and study cellular signaling pathways in cancers to predict drug response.

RESEARCH SUMMARY

Dr. Chen's research concentrates on developing machine learning methods, especially deep learning models (DLMs) (e.g., Deep Neural Networks, Boltzmann Machine, and topic modeling), to study cancer cell signaling systems, cell-cell communication in tumor microenvironment (TME), heterogeneity in diseases, disease mechanisms and cancer pharmacogenomics. Dr. Chen uses the concise representation learned from the DLM with the causal inference to guide the identification of molecular signatures/biomarkers and predicts the clinical outcomes including drug sensitivity and patient survival. Based on Dr. Chen's strong research background in bioinformatics, biomedical informatics, biology and machine learning, she successfully develops comprehensive AI models that precisely represent the state of signaling systems in cancer cells and use such information to improve the tumor-specific precision medicine (precision oncology).

LEADERSHIP EXPERIENCE

Student Representative, Department of Biomedical Informatics, University of Pittsburgh
2013-2015

Honors/Awards

2014 **SBV Improver** Challenge 4, 1st Place Prize
2013 **DREAM 8 Challenge**, 2nd Place Prize

Funding

NIH **K99/R00** Grant (4R00LM013089) 11/2019-2/2025

Mentoring

Han Zhang, MS (PhD candidate)
Laizhi Zhang (internship)
Adap Sanyukta (internship)
Rameriz Eduardo (internship)
Amanda Zeng (summer student)
Kevin Lu (summer student)
Katherine Hu (summer student)

Teaching

BIOINFO 2032 Journal Club

CONFERENCE TALKS

- scGEM: Unveiling the Nested Tree-Structured Gene Co-Expressing Modules in Single Cell Transcriptome Data, ICIBM2023
- IOhub: a web server that tracks integrative transcriptomic data for immune-oncology, InCoB2023

PUBLICATIONS

Complete List of Papers Published

1. Zhang, H., Lu, X., **Chen, L.** (2023) scGEM: unveiling the nested tree-structured gene co-expressing modules in single cell transcriptome data. *Cancers*, 15 (17), 4277.
2. Sun, R., Zhao, H., Gao, D.S., Ni, A., Li, H., **Chen, L.**, Lu, X., Chen, K. and Lu, B. (2023) Amphiregulin couples IL1RL1+ regulatory T cells and cancer-associated fibroblasts to impede antitumor immunity. *Science Advances*, 9(34), 7399.
3. Young, J., Ren, S., **Chen, L.**, Lu, X. (2023) Revealing the impact of genomic alterations on cancer cell signaling. *Cancers*, 15(15), 3857.
4. **Chen, X.***, **Chen, L.***, et al (2022). An individualized causal framework for learning intercellular communication networks that define microenvironments of individual tumors. *Plos Computational Biology*, 18,12
5. Liu, Z., Cai, C., Ma, X., Liu, J., **Chen, L.**, Lui, V.W.Y., Cooper, G.F. and Lu, X. (2022) A Novel Bayesian Framework Infers Driver Activation States and Reveals Pathway-Oriented Molecular Subtypes in Head and Neck Cancer. *Cancers*, 14(19), p.4825.
6. Ruan, H., Leibowitz, B.J., Peng, Y., Shen, L., **Chen, L.**, Kuang, C., Schoen, R.E., Lu, X., Zhang, L. and Yu, J. (2022) Targeting Myc-driven stress vulnerability in mutant KRAS colorectal cancer. *Molecular biomedicine*, 3(1), pp.1-16.
7. Leibowitz, B.J., Zhao, G., Wei, L., Ruan, H., Epperly, M., **Chen, L.**, Lu, X., Greenberger, J.S., Zhang, L. and Yu, J. (2021) Interferon b drives intestinal regeneration after radiation. *Science Advance*.
8. Chen, X., **Chen, L.**, et al (2021). An individualized causal framework for learning intercellular communication networks that define microenvironments of individual tumors, *bioRxiv*.
9. Ruan, H., Li, X., Xu, X., Leibowitz, B.J., Tong, J., **Chen, L.**, Ao, L., Xing, W., Luo, J., Yu, Y. and Schoen, R.E. (2020) eIF4ES209 phosphorylation licenses Myc-and stress-driven oncogenesis, *eLife*.
10. Cai, C., Cooper, G.F., Lu, K.N., Ma, X., Xu, S., Zhao, Z., Chen, X., Xue, Y., Lee, A.V., Clark, N., Chen, V., Lu, S., **Chen, L.**, Lu X. (2019) Systematic Discovery of the Functional Impact of Somatic Genome Alterations in Individual Tumors through Tumor-specific Causal Inference, *PLoS Comput Biol*.
11. **Chen, L.**, Lu, X. (2018) Discovering functional impacts of miRNAs in cancers using a causal deep learning model, *BMC medical genomics*, 11, 116.
12. **Chen, L.**, Lu, X. (2018) Making deep learning models transparent, *J of Med Artif Intell*, 1, 5.
13. Ding, M.Q., **Chen, L.**, Cooper G.F., Young, J.D., Lu X. (2018) Precision Oncology beyond Targeted Therapy: Combining Omics Data with Machine Learning Matches the Majority of Cancer Cells to Effective Therapeutics, *Molecular cancer research : MCR*, 16, 269-278.
14. Lu, S., Fan, X., **Chen, L.**, Lu, X. (2018) A novel method of using Deep Belief Networks and genetic perturbation data to search for yeast signaling pathways, *Plos One*, 13, 9.
15. **Chen, L.**, Cai C., Chen V., Lu X. (2016) Learning a hierarchical representation of the yeast transcriptomic machinery using an autoencoder model, *BMC bioinformatics*, 17 Suppl 1, 9.
16. Lu, S., Cai C., Yan, G., Zhou, Z., Wan, Y., Chen, V., **Chen, L.**, Cooper GF., Oveid LM., Hannun Y.A., Lee A.V., Lu, X. (2016) Signal-Oriented Pathway Analyses Reveal a Signaling Complex as a Synthetic Lethal Target for p53 Mutations, *Cancer research*, 76, 6785-6794.
17. Hill, S.M., et al. (2016) Inferring causal molecular networks: empirical assessment through a community-based effort, *Nat Methods*, 13, 310-318.
18. **Chen, L.**, Cai C., Chen V., Lu X. (2015) Trans-species learning of cellular signaling systems with bimodal deep belief networks, *Bioinformatics*, 31, 3008-3015.
19. Cai, C., **Chen, L.**, Jiang, X., Lu X. (2014) Modeling signal transduction from protein phosphorylation to gene expression, *Cancer informatics*, 13, 59-67.
20. Montefusco, D.J.*, **Chen, L.***, Matmati N., Lu S., Newcomb B., Cooper G.F., Hannun Y.A., Lu X. (2013) Distinct signaling roles of ceramide species in yeast revealed through systematic perturbation and systems biology analyses, *Science signaling*, 6, rs14. (* indicates co-first author)
21. Jin, B., Chen, V., **Chen, L.**, Lu, X. (2011) Mapping annotations with textual evidence using an scLDA model, *AMIA ... Annual Symposium proceedings. AMIA Symposium*, 2011, 834-842.

Complete List of papers in production

1. **Chen, L.**, et al (2023). Machine Learning Predicts Oxaliplatin Benefit in Early Colon Cancer. *Journal of Clinical Oncology*. In Production.
2. Zhang, H., Lu, X., **Chen, L.** Insights into the TME from integrative analysis of single-cell RNA-seq, bulk RNA-seq, and spatial transcriptomic data. In production.

Complete List of papers under review

1. Shuang, X., **Chen, L.**, Cooper, G., Lu, X., et al. (2023) An interpretable deep learning framework for genome-informed precision oncology. *Nature Machine Intelligence*.
2. Zhang, H., Lu, B., Cooper, G., Lu, X., **Chen, L.** (2023) Deconvolving single-cell transcriptomics reveal cellular programs regulated by cell-cell communication in the colorectal cancer. *Nature Cancer*.