LINYING ZHANG

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EDUCATION

Columbia University in the City of New York *August 2018 - Present*
Ph.D. in Biomedical Informatics — GPA: 3.85/4.0
Advisors: George Hripcsak and David Blei

Harvard. T.H.Chan School of Public Health *August 2016 - May 2018*
M.S. in Computational Biology and Quantitative Genetics (CBQG) — GPA: 3.79/4.0
Advisor: Giovanni Parmigiani
CBQG Program Student Committee Co-chair.
Thesis: *Interactions between multiple myeloma cells and bone marrow stromal cells impact epigenetic profiles of multiple myeloma.*

Boston University *August 2011 - May 2014*
B.A. with Honors (Summa Cum Laude) in Biochemistry and Molecular Biology — GPA: 3.74/4.0
Advisor: Ulla Hansen
Awards: Dean's List (6 semesters); Senior Book Award.
Thesis: *Establishing hepatocellular carcinoma cell lines with inducible expression of degradable LSF to investigate LSF regulation in cell cycle.*

RESEARCH EXPERIENCE

Dana-Farber Cancer Institute April 2017 - May 2018
Graduate Researcher (Advisor: Giovanni Parmigiani)

· Investigated the impact of interactions between multiple myeloma (MM) cells and bone marrow stromal cells (BMSC).
· Built a pipeline for ChIP-Seq and RNA-Seq analysis in Linux and R.
· Identified epigenetic changes in both MM and BMSC via differential binding analysis and motif analysis.
· Integrated expression data and epigenetic data to study the impact of epigenetic changes on gene regulation.

Alnylam Pharmaceuticals Inc. June 2014 - June 2016
Research Scientist (Supervisor: Stuart Milstein)

· Supported drug candidate selection by performing high-throughput screening and data analysis.
· Supported Clinical Trial Application filling of ALN-AAT by assay development.
· Investigated the possibility of targeting APP with siRNA for treatment of Alzheimers disease.

Boston University March 2013 - May 2014
Undergraduate Researcher (Advisor: Ulla Hansen)

· Identified the role of transcription factor LSF in cell cycle progression in liver cancer cells.
· Initiated the establishment of an inducible cell line by optimizing transfection condition.
· Designed DNA constructs to achieve instant protein degradation in cell cycle by PCR.

PUBLICATIONS & PREPRINTS

L. Zhang, Y. Wang, A. Ostropolets, J. J. Mulgrave, D. M. Blei, and G. Hripcsak. The medical deconfounder: Assessing treatment effects with electronic health records. In *Proceedings of the 4th Machine Learning for Healthcare Conference*, volume 106 of *Proceedings of Machine Learning Research*, pages 490-512, Ann Arbor, Michigan, 2019.

O. Gottesman, F. Johansson, J. Meier, J. Dent, D. Lee, S. Srinivasan, **L. Zhang**, Y. Ding, D. Wihl, X. Peng, J. Yao, I. Lage, C. Mosch, L.H. Lehman, M. Komorowski, A. Faisal, L. Celi, D. Sontag, F. Doshi-Velez. Evaluating reinforcement learning algorithms in observational health settings. *Arxiv preprint*, 2018.

PRESENTATIONS & POSTERS

L. Zhang, Y. Wang, A. Ostropolets, J.J. Mulgrave, D.M. Blei, and G. Hripcsak. The Medical Deconfounder: Assessing Treatment Effect with Electronic Health Records. *Women in Machine Learning Workshop.* Vancouver, Canada. 2019. [Poster]

L. Zhang, Y. Wang, A. Ostropolets, J.J. Mulgrave, D.M. Blei, and G. Hripcsak. The Medical Deconfounder: Assessing Treatment Effect with Electronic Health Records. *Machine Learning for Health Workshop.* Vancouver, Canada. 2019. [Poster]

L. Zhang, M.K. Samur, R. Szalat, C.B. Epstein, R. Prabhala, M. Fulciniti, N.C. Munshi*, G. Parmigiani*. Interactions between multiple myeloma cells and bone marrow stromal cells impact epigenetic profiles of multiple myeloma. *Program in Quantitative Genomics Conference.* Boston, MA. 2017. [Poster]

L. Zhang, M.K. Samur, R. Szalat, C.B. Epstein, R. Prabhala, M. Fulciniti, N.C. Munshi*, G. Parmigiani*. Interactions between multiple myeloma cells and bone marrow stromal cells impact epigenetic profiles of multiple myeloma. *Dana-Farber/Harvard Cancer Center Celebration of Junior Investigators.* Boston, USA. 2017. [Poster]

R. Szalat, M.K. Samur, C.J. Ott, M. Lawlor, C. Epstein, B.J. Abraham, C.Y. Lin, **L. Zhang**, R. Prabhala, N. Farrell, K. Wes, Y.T. Tai, M. Fulciniti, G. Parmigiani, R.A. Young, K.C. Anderson, and N.C. Munshi. Integrative Oncogenomic Analysis Combining Whole Genome, Transcriptome and Epigenome Identifies Altered Chromatin Accessibility Landscape in Multiple Myeloma. *American Society of Hematology Annual Meeting.* 2018. [Oral presentation]

PROFESSIONAL SERVICE

Reviewer for International Conference on Machine Learning (ICML) 2020.

Reviewer for Women in Machine Learning (WiML) 2019.

Reviewer for Machine Learning for Health (ML4H) 2019.

TEACHING EXPERIENCE

Computational Methods. *Columbia University.* Spring 2020.

Computer Applications in Health Care Biomedicine. *Columbia University.* Fall 2019.

Principles of Biostatistics III. *Harvard T.H.Chan School of Public Health.* Summer 2017.

RELEVANT COURSES

Statistics	**Computer Science**
Probability (Biostatistics PhD core courses)	Machine Learning
Statistical Inference (Biostatistics PhD core courses)	Data Science

Methods (Biostatistics PhD core courses)	Deep learning
Longitudinal Analysis	Foundations of Graphical Models
Calculus I&II and Linear Algebra	Reinforcement Learning

INTERESTS

Ballroom dancing: 1st place at BADC 2016 at Columbia University; 3rd place at MIT Open 2017.

Piano: won the highest amateur level certificate from Chinese Musicians Association at age 15.

Scuba diving: Certified Open Water diver since 2015.