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EDUCATION

Baylor College of Medicine Houston, TX
Ph.D., Department of Biochemistry and Molecular Biology 2004 – 2010
• Thesis: “Coarse-grained Modeling of Biomolecules”
Mentor: Dr. Jianpeng Ma

Fudan University Shanghai, China
Bachelor of Science, Honor Program of Science (Major in Physics) 1999 – 2003

RESEARCH EXPERIENCE

The Jackson Laboratory Bar Harbor, ME
Assistant Professor 2016 – Present
Graduate School of Biomedical Science and Engineering, University of Maine Orono, ME
Assistant Professor 2016 – Present
The School of Graduate Biomedical Sciences, Tufts University School of Medicine Boston, MA
Assistant Professor in Genetics and Neuroscience 2017 – Present
• Research on developing random circuit perturbation methods for modeling gene regulatory circuits
• Research on integrating bottom-up mathematical modeling with top-down genome informatics
• Research on elucidating multi-step cellular state transition in cell differentiation and tumorigenesis

Center for Theoretical Biological Physics, Rice University Houston, TX
Postdoctoral Fellow (PI: Dr. José Onuchic) 2012 – 2016
Cancer Prevention Research Institute of Texas (CPRIT) Fellow 2014 - 2016
• Research on developing computational methods for modeling dynamics of gene regulatory circuits
• Research on computational modeling of a gene regulatory circuit of epithelial-mesenchymal transition (EMT) and its coupling to cell motility, metabolism and stemness
• Research on computational modeling of cell-cell communications among cancer and immune cells

Baylor College of Medicine Houston, TX
Research Assistant in Computational Structure Biology Lab (PI: Dr. Jianpeng Ma) 2004 – 2012
• Research on developing statistical potentials for modeling protein structures and their applications in structure prediction
• Research on developing coarse-grained normal mode analysis methods for modeling dynamics of supramolecular complexes
• Research on developing normal-mode-based algorithms for x-ray crystallographic refinement

FUNDING

- R35GM128717 Lu (PI) 08/01/18 – 07/31/23
National Institute of General Medical Sciences, National Institutes of Health
New Computational Systems Biology Methods for Modeling Gene Regulatory Circuits
Amount: \$1,250,000 (direct cost)
- New Investigator Grant Lu (PI) 01/01/18 – 06/30/19
Jackson Laboratory Cancer Center
Understanding reproductive toxicity of cancer therapies and developing fertoprotective treatments.
Identify signaling and transcription regulatory networks involved in ovarian response to radiation, cisplatin and doxorubicin using computational modeling and network analyses.
- New Investigator Grant Lu (PI) 03/10/17 – 03/09/18
Jackson Laboratory Cancer Center
Decoding the epigenetic regulatory mechanism of tumorigenesis in acute myeloid Leukemia
The main goal of this proposed study is to utilize computational systems biology approach to elucidate the epigenetic and genetic regulation of cancer cells during both AML initiation and recurrence.
- RP140113 Lu (co-PI) 2014 – 2016
Cancer Prevention Research Institute of Texas (CPRIT) Computational Cancer Biology Training Grant

LEADERSHIP POSITIONS/EXPERIENCE

- Thesis committee of a graduate student from University of Maine 2019 – Present
- Organizer of the JAX Computational Biology Interest Group 2017 – Present
- JAX Data Science webpage designing committee 2018 – Present
- Supervision of graduate students from the Tufts Genetics Program 2019 – Present
- Supervision of students and postdoctoral trainees from the JAX Education Program 2017 – Present
- JAX Computational Science retreat planning committee 2019
- Tufts Genetics Program retreat planning committee 2018
- Tufts Genetics Program (JAX track) graduate student recruiting committee 2018
- Coordinator of the Gulf Coast Consortia Computational Cancer Biology Training Program 2015 – 2016
- Gulf Coast Consortia Keck Seminar Planning Committee 2014 – 2016
- Interviewed and recruited Frontier in Science (FIS) summer intern undergraduate students 2013 – 2014
- Supervision of Rice CTBP graduate students and intern undergraduate students on computational modeling of genetic circuits 2012 – 2016
- Supervision of intern undergraduate students from the FIS outreach program 2013 – 2014

TEACHING EXPERIENCE

- Organizer of a JAX campus-wide workshop on mathematical modeling in Systems Biology 2019
- Director of the short course on experimental models of human cancer for Tufts Genetics students 2019
- Guest lectures on Computational Molecular Biophysics (BIOE 589), Rice University 2007 - 2012

SELECTED PRESENTATIONS

- Invited Talk, Annual Society of Mathematical Biology meeting, Montreal, Canada 7/2019
- Invited Talk, Genetics in Sackler School, Tufts University, Boston, MA, 11/2018
- Invited Talk, The 11th European Conference on Mathematical and Theoretical Biology, Lisbon, Portugal, 7/2018
- Talk, the JAX Scientific Symposium, Farmington, CT 5/2018
- Invited Talk, 2nd International Conference on Genomic Medicine, Houston, TX 2/2018
- Invited Talk, Jose Onuchic 60th Birthday Symposium, Houston, TX 1/2018
- Invited Talk, CTBP Seminar, Rice University, Houston, TX 9/2017
- Invited Talk, the 2nd International Conference Computational Genetics and Proteomics, Panama 8/2017
- Invited Talk, Gordon Research Conference on Stochastic Physics in Biology, Ventura, CA 1/2017
- Invited Talk, Phsycis Department, Nanjing University, Nanjing 11/2016
- Invited Talk, Shanghai Institue of Materia Medica, Chinese Academy of Sciences, Shanghai 11/2016
- Contributed Talk, Frontiers in Single Cell Genomics, Cold Spring Harbor Asia, Suzhou 11/2016
- Invited Talk, Physics Department, Fudan University , Shanghai 11/2016
- Invited Talk, The 1st International Conference on Compuataional Genomics and Proteomics, Costa Rica 10/2016

JOURNALS REFEREED

PNAS, BMC Systems Biology, PLOS ONE, PLOS Computational Biology, PEDS, Journal of Physics D: Applied Physics, Proteomics, Scientific Reports, Physical Biology, iScience, Frontiers in Oncology

PUBLICATIONS SUBMITTED OR IN PREPARATION

1. A. Katebi, V. Kohar, & **M. Lu**. Random Parametric Perturbations of Gene Regulatory Circuit Uncover State Transitions in Cell Cycle. *bioRxiv* (2019) doi:<https://doi.org/10.1101/799965>.
2. D. Ramirez, V. Kohar, A. Katebi, and **M. Lu**, Modeling a gene regulatory network of EMT hybrid states for mouse embryonic skin cells. *bioRxiv* (2019) doi:<https://doi.org/10.1101/799908>.
3. V. Kohar, D. Gordin, A. Ketabi and **M. Lu**, Gene Circuit Explorer (GeneEx): an interactive web-app and database for visualizing, simulating and analyzing gene regulatory circuits. (in prep)
4. K. Su, V. Kohar, A. Katebi, D. Gordin, Z. Qin, K. Karuturi, S. Li, and **M. Lu**, NetAct: a computational algorithm to construct core transcription factor regulatory networks using gene activity (in prep)

PUBLICATIONS

5. D. Jia, **M. Lu**, K.H. Jung, J.H. Park, L. Yu, J. Onuchic, B.A. Kaipparettu, H. Levine. (2019) Elucidating Cancer Metabolic Plasticity by Coupling Gene Regulation with Metabolic Pathways, *Proc. Natl. Acad. Sci. U.S.A.* 116 (9) 3909-18
6. D. Jia, J. George, S. Tripathi, D. Kundnani, **M. Lu**, S. Hanash, J. Onuchic, M.K. Jolly, H. Levine. (2019) Testing the gene expression classification of the EMT spectrum. *Physical Biology*. 16(2): 025002
7. V. Kohar and **M. Lu**. (2018) Role of noise and parametric variation in the dynamics of gene regulatory circuits. *NPJ Syst. boil. Appl.* 4: 40
8. B. Huang, D. Jia, J. Feng, H. Levine, J.N Onuchic, **M. Lu**. (2018) RACIPE: a computational tool for modeling gene regualtory circuits using randomization. *BMC Syst. Biol.* 12(1): 74
9. F. Bocci, Y. Suzuki, **M. Lu**, J.N. Onuchic. (2018) Role of metabolic spatiotemporal dynamics in regulating biofilm colony expansion. *Proc. Natl. Acad. Sci. U.S.A.* doi:10.1073/pnas.1706920115
10. F. Ye, D. Jia, **M. Lu**, H. H. Levine, M. W. Deem. (2018) Modularity of the metabolic gene network as a prognostic biomarker for hepatocellular carcinoma. *Oncotarget*. 9(19): 15015-26

11. D. Jia, M.K. Jolly, S.C. Tripathi, P.D. Hollander, B. Huang, **M. Lu**, M. Celiktas, E. Ramirez-Peña, E. Ben-Jacob, J.N. Onuchic, S.M. Hanash, S.A. Mani, H. Levine. (2017) Distinguishing mechanisms underlying EMT tristability. *Cancer Converg.* 1:2. <https://doi.org/10.1186/s41236-017-0005-8>
12. X. Tian, B. Huang, X. Zhang, **M. Lu**, F. Liu, J. Onuchic, W. Wang. (2017) Modeling the response of a tumor-suppressive network to mitogenic and oncogenic signals. *Proc. Natl. Acad. Sci. U.S.A.* 114(21):5337-42
13. B. Huang*, **M. Lu***, D. Jia, E. Ben-Jacob, H. Levine, J. Onuchic. (2017) Interrogating the topological robustness of gene regulatory circuits by randomization. *PLoS Comput Biol.* 13(3):e1005456 (*equal contribution)
14. L. Yu*, **M. Lu***, D. Jia*, J. Ma, E. Ben-Jacob, H. Levine, B.A. Kaipparettu, J. Onuchic. (2017) Modeling the Genetic Regulation of Cancer Metabolism: Interplay Between Glycolysis and Oxidative Phosphorylation. *Cancer Res.* 77(7): 1564 (*equal contribution, *co-corresponding author)
15. M. Darash-Yahana*, Y. Pozniak*, **M. Lu***, Y-S. Sohn, O. Karmi, S. Tamir, *et al.* Breast cancer tumorigenicity is dependent on high expression levels of NAF-1 and the lability of its Fe-S clusters. *PNAS* 113(39):10890–5. (*equal contribution)
16. Y. Suzuki*, **M. Lu***, E. Ben-Jacob, and J. Onuchic. Periodic, quasi-periodic and chaotic dynamics in simple gene elements with time delays. (2016) *Sci. Rep.* 6: 21037 (*equal contribution)
17. B. Huang, M. Jolly, **M. Lu**, E. Ben-Jacob, I. Tsarfaty, and J. Onuchic. (2015) Modeling the transition between collective and solitary migration phenotypes in cancer metastasis. *Sci. Rep.* 5:17379
18. M. Jolly, M. Boareto, B. Huang, D. Jia, **M. Lu**, J. Onuchic, H. Levine, and E. Ben-Jacob. (2015) Implications of the hybrid epithelial/mesenchymal phenotype in metastasis. *Front. Oncol.* 5:155
19. M. Jolly, M. Boareto, **M. Lu**, J. Onuchic, C. Clementi, and E. Ben-Jacob. (2015) Operating principles of Notch–Delta–Jagged module of cell–cell communication. *New J. Phys.* 17 (5):055021
20. M. Boareto, M. Jolly, **M. Lu**, J. Onuchic, C. Clementi, and E. Ben-Jacob. (2015) Jagged-Delta asymmetry in Notch signaling can give rise to a sender/receiver hybrid phenotype. *Proc. Natl. Acad. Sci. U.S.A.* 112(5):E402-9
21. E. Ben-Jacob, **M. Lu**, D. Schultz, J. Onuchic. (2015) The physics of bacterial decision making. *Front. Cell. Infect. Microbiol.* 4: 154
22. **M. Lu**, B. Huang, S. Hanash, J. Onuchic and E. Ben-Jacob. (2014) Modeling putative therapeutic implications of exosome exchange between tumor and immune Cells. *Proc. Natl. Acad. Sci. U.S.A.* 111(40):E4165-74
23. **M. Lu**, M. Jolly, J. Onuchic and E. Ben-Jacob. (2014) Toward decoding the principles of cancer metastasis circuits. *Cancer Res.* 74(17):4574-4587
24. **M. Lu**, J. Onuchic and E. Ben-Jacob. (2014) Construction of an Effective Landscape for Multistate Genetic Switches. *Phys. Rev. Lett.* 113 (7): 078102
25. M. Jolly, B. Huang, **M. Lu**, S. Mani, H. Levine and E. Ben-Jacob. (2014) Towards elucidating the connection between epithelial-mesenchymal transitions and stemness. *J. R. Soc. Interface.* 11:20140962
26. B. Huang, **M. Lu**, M. Jolly, I. Tsarfaty, J. Onuchic and E. Ben-Jacob. (2014) The three-way switch operation of Rac1/RhoA GTPase-based circuit controlling amoeboid-hybrid-mesenchymal transition. *Sci. Rep.* 4:6449
27. **M. Lu**, M. Jolly, H. Levine, J. Onuchic and E. Ben-Jacob. (2013) MicroRNA-based regulation of epithelial–hybrid–mesenchymal fate determination. *Proc. Natl. Acad. Sci. U.S.A.* 110(45):18144-9
28. **M. Lu**, M. Jolly, R. Gomoto, B. Huang, J. Onuchic and E. Ben-Jacob. (2013) Tristability in Cancer-Associated MicroRNA-TF Chimera Toggle Switch. *J. Phys. Chem. B.* 117:13164-13174
29. D. Schultz*, **M. Lu***, T. Stavropoulos, J. Onuchic and E. Ben-Jacob. (2013) Turning Oscillations Into Opportunity Spikes: A Lesson from Bacterial Decision Gate. *Sci. Rep.* 3:1668 (*equal contribution)

30. M. Lu, and J. Ma. (2013) PIM: Phase Integrated Method for Normal Mode Analysis of Biomolecules in Crystalline Environment. *J. Mol. Biol.* 425: 1082-1098
31. M. Lu, D. Ming and J. Ma. (2012) fSUB: Normal Mode Analysis with Flexible Substructures. *J. Phys. Chem. B.* 116(29): 8636-45
32. M. Lu and J. Ma. (2011) Normal mode analysis with molecular geometry restraints: Bridging molecular mechanics and elastic models. *Arch. Biochem. Biophys.* 508 (1): 64-71
33. M. Lu and J. Ma. (2009) A Minimalist Network Model for Studying Biomolecular Vibration. Book Chapter in *Proteins: Energy, Heat and Signal Flow*. CRC Press: 229 - 245.
34. X. Chen, M. Lu, B. K. Poon, Q. Wang, and J. Ma. (2009) Structural improvement of unliganded simian immunodeficiency virus gp120 core by normal-mode-based X-ray crystallographic refinement. *Acta D* 65:339-347.
35. Wang, Q. H., F. Cheng, M. Lu, X. Tian, and J. P. Ma. (2008) Crystal structure of unliganded influenza B virus hemagglutinin. *J. Virol.* 82:3011-3020.
36. M. Lu and J. Ma. (2008) A minimalist network model for coarse-grained normal mode analysis and its application to biomolecular x-ray crystallography. *Proc. Natl. Acad. Sci. U.S.A.* 105(40):15358-63.
37. M. Lu, A. D. Dousis, and J. Ma. (2008) OPUS-Rota: A fast and accurate method for side-chain modeling. *Protein Sci.* 17:1576-1585.
38. M. Lu, A. D. Dousis, and J. Ma. (2008) OPUS-PSP: An orientation-dependent statistical all-atom potential derived from side-chain packing. *J. Mol. Biol.* 376:288-301.
39. B.K. Poon, X. Chen, M. Lu, N. K. Vyas, F. A. Quiocco, Q. Wang, and J. Ma. (2007) Normal mode refinement of anisotropic thermal parameters for a supramolecular complex at 3.42-A crystallographic resolution. *Proc. Natl. Acad. Sci. U.S.A.* 104(19):7869-74.
40. Y. Wu*, M. Lu*, M. Chen, J. Li, and J. Ma. (2007) OPUS-Ca: A knowledge-based potential function requiring only C alpha positions. *Protein Sci.* 16:1449-1463. (*equal contribution)
41. M. Lu, B.K. Poon, and J. Ma. (2006) A new method for coarse-grained elastic normal-mode analysis. *J. Chem. Theory and Comput.* 2:464-471.
42. Y. Wu, X. Tian, M. Lu, M. Chen, Q. Wang, and J. Ma. (2005) Folding of small helical proteins assisted by small-angle X-ray scattering profiles. *Structure* 13:1587-1597.
43. M. Lu and J. Ma. (2005) The role of shape in determining molecular motions. *Biophys. J.* 89:2395-2401.
44. Y. Wu, M. Chen, M. Lu, Q. Wang, and J. Ma. (2005) Determining protein topology from skeletons of secondary structures. *J. Mol. Biol.* 350:571-586.
45. Eichinger, et.al. (2005) The genome of the social amoeba Dictyostelium discoideum. *Nature* 435:43-57.