

**FULL NAME AND DEGREE/S: Mingyang Lu, Ph.D.**  
**CURRENT ADMINISTRATIVE TITLE: The Jackson Laboratory**  
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**FAX ADDRESS: 207-288-6757**

**EDUCATION**

Undergraduate

<i>Year of Degree</i>	<i>Degree</i>	<i>Institution</i>
2003	B.S.	Fudan University

Medical School and/or Graduate School

<i>Year of Degree</i>	<i>Degree</i>	<i>Institution</i>
2010	Ph.D.	Baylor College of Medicine

**POSTDOCTORAL TRAINING**

**Fellowships: CPRIT Computational Cancer Biology Training Grant**

<i>Date</i>	<i>Specialty</i>	<i>Institutions</i>
2014-2016	Computational Biology	Rice University

<i>Date</i>	<i>Specialty</i>	<i>Institutions</i>
2010-2012	Computational Biology	Baylor College of Medicine

<i>Date</i>	<i>Specialty</i>	<i>Institutions</i>
2012-2014	Computational Biology	Rice University

**ACADEMIC APPOINTMENTS** (old and new)

2016 – present	Assistant Professor, Jackson Laboratory
2016 – present	Assistant Professor, Graduate School of Biomedical Science and Engineering, University of Maine

**AWARDS AND HONORS**

2016 - present	Assistant Professor, University of Maine, Graduate of Biomedical Science and Engineering, Orono, ME
2016 - present	Assistant Professor, The Jackson Laboratory, Bar Harbor, ME
2014 - 2016	Cancer Prevention Research Institute of Texas (CPRIT) Computational Cancer Biology Training Grant RP140113
2015	Excellent Poster Award from Gordon Research Conference: Stochastic Physics in Biology
2013	Teaching Award at Rice University
2008	Government Award for Chinese Outstanding Students Abroad

## **TRAINING OF GRADUATE STUDENTS/POST DOCTORAL**

### **Graduate Students:**

2017-present	Ataur Katebi, Postdoctoral Fellow at Jackson Laboratory
2012-2016	Bin Huang, Chemistry Department, Rice University
2013	Ryan Gomoto, Program in Structural and Computational Biology and Molecular Biology (SCBMB), Baylor College of Medicine
2013-2014	Marcelo Boareto, Center for Theoretical Biological Physics (CTBP), Rice University; Institute of Physics, University of São Paulo
2014-2016	Linglin Yu, Applied Physics Program, Rice University; Department of Biochemistry and Molecular Biology, Baylor College of Medicine
2015-2016	Dongya Jia, PhD Program in Systems, Synthetic, and Physical Biology, Rice University
2015-2016	Federico Bocci, Chemistry Department, Rice University

### **Summer undergraduate students:**

2013	Tristan Walker, Frontier in Science (FIS) Program, Center for Theoretical Biological Physics (CTBP), Rice University; Physics Department, University of Houston
2014	Steven Dang, Frontier in Science (FIS) Program, Center for Theoretical Biological Physics (CTBP), Rice University; Physics Department, University of Houston
2014	Albert Ge, Center for Theoretical Biological Physics (CTBP), Rice University; Department of Computational and Neural Systems, California Institute of Technology

## **TEACHING RESPONSIBILITIES**

9/2007-12/2007	BIOE 589, Two lectures: protein structure, side-chain modeling (Teaching Assistant, Computational Molecular Biophysics, Rice University)
9/2008-12/2008	BIOE 589, Four lectures: coarse-graining, potential, NMA, x-ray (Teaching Assistant, Computation Molecular Biophysics, Rice University)
9/2009-12/2009	BIOE 589, Four lectures: 2 NMA, 2 potential (Teaching Assistant, Computational Molecular Biophysics, Rice University)
9/2010-12/2010	BIOE 589, Two lectures: Statistical potentials for protein structure prediction (Teaching Assistant, Computational Molecular Biophysics, Rice University)
9/2012-12/2012	BIOE 589, Four lectures: MD, potentials, NMA, x-ray (Teaching Assistant, Computational Molecular Biophysics, Rice University)

## **PROFESSIONAL SOCIETIES**

Biophysics Society (BPS) Member  
American Physical Society (APS) Member  
American Association for the Advancement of Science (AAAS) Member  
American Association for Cancer Research (AACR) Member

## **MAJOR RESEARCH INTERESTS**

In the Lu lab at The Jackson Laboratory, we are passionate about the development and application of computational modeling methods to study the operating mechanisms of cancer genetic networks. Specifically, we use systems biology approaches to integrate computational modeling and data analysis to elucidate the relationship among robustness of network dynamics, stochasticity in gene expression and heterogeneity in cancer evolution. We are interested in the fundamental question of how cancer evolves through genetic and epigenetic alterations, especially how tumorigenesis is shaped by the architecture of gene regulatory networks. We aim to extend the scope of existing modeling scheme to large systems, and to take advantage of current available big data in the cancer biology community. Our studies will contribute to a systems-level understanding of cancer and will eventually lead to the design of personalized therapies for cancer patients.

## **RESEARCH SUPPORT**

### Current:

*Grant Title:* New Investigator Grant

*Funding Agency:* Jackson Laboratory Cancer Center

*Amount:* \$

*Period:* 2017 - 2018

*Role:* P.I.

### Completed

*Grant Title:* Computational Cancer Biology Training Grant (Theoretical and Experimental Studies at Population level of Epithelial-Mesenchymal Transitions in Metastatic Cancer)

*Funding Agency:* CPRIT

*Amount:* \$96,436 + health benefits and travel supports

*Period:* 2014 – 2016

*Role:* Co-P.I.

*Grant Title:* Center for Theoretical Biological Physics

*Funding Agency:* NSF

*Amount:* Salary Only

*Period:* 2014 – 2016

*Role:* Postdoctoral Fellow (P.I. Jose Onuchic)

*Grant Title:* Novel Statistical Energy Function and Its Applications to Side-chain Modeling and Fold Recognition

*Funding Agency:* NSF

*Amount:* Salary Only

*Period:* 2008 – 2012

*Role:* Research Associate (P.I. Jianpeng Ma)

*Grant Title:* New Simulation Methods at Multi-scale and –resolutions

*Funding Agency:* NIH

*Amount:* Salary Only

*Period:* 2008 – 2012

*Role:* Research Associate (P.I. Jianpeng Ma)

## **EDITORIAL BOARDS AND ACTIVITY**

### *Ad hoc Manuscript Reviews for Peer Reviewed Journals*

PNAS, BMC Systems Biology, PLoS One, PLoS Computational Biology, Scientific Reports, Journal of Physics D: Applied Physics, Proteomics, PEDS (Protein Engineering, Design & Selection)

### **\*BIBLIOGRAPHY**

#### *a) Refereed (i.e., peer-reviewed) papers*

1. Tian X, Huang B, Zhang XP, **Lu M**, Liu F, Onuchic JN, Wang W. Modeling the response of a tumor-suppressive network to mitogenic and oncogenic signals. *Proc. Natl Acad Sci USA*, 2017 May 23; 114(21):5337-5342. Doi: 10.1073/pnas.1702412114
2. Huang B, **Lu M**, Jia D, Ben-Jacob E, Levine H, Onuchic JN. Interrogating the topological robustness of gene regulatory circuits by randomization. *PLoS Comput Biol*. 2017 Mar 31; 13(3):e1005456. Doi: 10.1371/journal.pcbi.1005456. eCollection 2017 Mar.
3. Yu L, Lu M, Jia D, Ma J, Ben-Jacob E, Levine H, Kaiparettu BA, Onuchic JN. Modeling the Genetic Regulations of Cancer Metabolism: Interplay between Glycolysis and Oxidative Phosphorlation. *Cancer Res*. 2017 Apr 1;77(7):1564-1574. Doi: 10.1158/0008-5472.CAN-16-2074. Epub 2017 Feb 15.
4. Darash-Yahana M\*, Pozniak Y\*, **Lu M\***, Sohn Y-S, Karmi O, Tamir S, et al. Breast cancer tumorigenicity is dependent on high expression levels of NAF-1 and the lability of its Fe-S clusters. *PNAS* 2016;113:10890–5. (\* equal contribution)
5. 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)
6. B. Huang, M. Jolly, **M. Lu**, E. Ben-Jacob, I. Tsarfaty, and J. Onuchic. Modeling the transition between collective and solitary migration phenotypes in cancer metastasis. (2015) *Sci. Rep.* 5:17379
7. 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
8. 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.* doi: 10.1073/pnas.1416287112
9. **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.* doi: 10.1073/pnas.1416745111
10. **M. Lu**, J. Onuchic and E. Ben-Jacob. (2014) Construction of an Effective Landscape for Multistate Genetic Switches. *Phys. Rev. Lett.* 113 (7): 078102
11. 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
12. 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
13. **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.* 110:18144-18149
14. **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
15. 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)
16. **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
17. **M. Lu**, D.Ming and J. Ma. (2012) fSUB: Normal Mode Analysis with Flexible Substructures. *J. Phys. Chem. B.* 116(29): 8636-45
18. **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
19. 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.

20. 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.
21. **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.* 105:15358-15363.
22. **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.
23. **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.
24. B.K. Poon, X. Chen, **M. Lu**, N. K. Vyas, F. A. Quiocho, Q. Wang, and J. Ma. (2007) Normal mode refinement of anisotropic thermal parameters for a supramolecular complex at 3.42-Å crystallographic resolution. *Proc. Natl. Acad. Sci. U.S.A.* 104:7869-7874.
25. 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)
26. **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.
27. 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.
28. **M. Lu** and J. Ma. (2005) The role of shape in determining molecular motions. *Biophys. J.* 89:2395-2401.
29. 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.
30. Eichinger, et.al. (2005) The genome of the social amoeba *Dictyostelium discoideum*. *Nature* 435:43-57.
31. 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
32. E. Ben-Jacob, **M. Lu**, D. Schultz, J. Onuchic. (2015) The physics of bacterial decision making. *Front. Cell. Infect. Microbiol.* 4: 154
33. **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
34. **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.

### **Book chapters/Invited reviews**

1. Ben-Jacob E, Lu M, Schultz D, Onuchic JN. The physics of bacterial decision making. *Front Cell Infect Microbiol.* 2014;4:154. doi: 10.3389/fcimb.2014.00154. Review. PMID: PMC4214203
2. Jolly MK, Boareto M, Huang B, Jia D, Lu M, Ben-Jacob E, Onuchic JN, Levine H. Implications of the Hybrid Epithelial/Mesenchymal Phenotype in Metastasis. *Front Oncol.* 2015;5:155. doi: 10.3389/fonc.2015.00155. Review. PMID: PMC4507461

### **Thesis**

Lu M. Coarse-grained Modeling of Biomolecules. 2010.

### **Invited lectures (last 3 years only)**

1. Invited Talk, Seminar at Center for Theoretical Biological Physics, Rice University, Houston, TX, 9/2017
2. Invited Talk, The 2st International Conference on Computational Genomics and Proteomics, Panama, 8/2017
3. Invited Talk, Gordon Research Conference on Stochastic Physics in Biology, Ventura, CA, 1/2017
4. Invited Talk, Physics Department, Nanjing University, Nanjing, 11/2016

5. Invited Talk, Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai, 11/2016
6. Invited Talk, Physics Department, Fudan University, Shanghai, 11/2016
7. Invited Talk, The 1<sup>st</sup> International Conference on Computational Genomics and Proteomics, Costa Rica, 10/2016
8. Invited Talk, University of Texas at Dallas, Dallas, TX, 3/2016
9. Invited Talk, Northeastern University, Boston, MA, 2/2016
10. Invited Talk, University of Houston, Houston, TX, 2/2016
11. Invited Talk, Louisiana State University, Baton Rouge, LA, 2/2016
12. Invited Talk, Tel Aviv University, Israel, 12/2014