#### CURRICULUM VITAE

University of Pittsburgh

School of Medicine

BIOGRAPHICAL

**Name**: Xinghua Lu

**Home Address**: **Birthplace**: Shanghai, China

**Home Phone**: **Citizenship**: United States

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EDUCATION and TRAINING

# GRADUATE:

|  |  |  |  |
| --- | --- | --- | --- |
| ***Dates Attended*** | ***Name and Location of Institution*** | ***Degree and Year*** | ***Major*** |
| 1979 | Shandong Medical University | MB/M.D. 1984 | Medicine |
| 1985 | Shandong Medical University | M.S. Cln. Res., 1988 | Cardiology |
| 1993 | University of Connecticut Health Ctr. | Ph.D., 1998 | Pharmacology |
| 2001  **POSTGRADUATE:** | University of Pittsburgh | Certificate, 2003 | Biomedical Informatics |

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| ***Dates Attended*** |  | ***Name and Location of Institution*** |  | ***Program Director and Discipline*** |
|  |  |  |  |  |
| 1984-1985 |  | Resident  Shengli Central Hospital, Dongying, China |  | Internal Medicine |
| 1988-1991 |  | Chief Resident |  | Dept. of Emergency Medicine,  Shandong Provincial Hospital |
| 1998-1998 |  | Postdoctoral Fellow, |  | Signal Transduction Laboratory, National Institute of Environmental Health Sciences |
| 1998-2001 |  | Research Associate, |  | Dept. of Pharmacology, University of Pittsburgh |
| 2001-2003 |  | National Library of Medicine Fellow,  University of Pittsburgh |  | Center for Biomedical Informatics |

APPOINTMENTS and POSITIONS

**ACADEMIC:**

***Years Inclusive Name and Location of Institution Rank/Title***

1991-1993 Dept. Emergency Medicine Attending Physician

Shandong Provincial Hospital, Jinan (Cardiologist)

2003 – 2008 Dept Biostat, Bioinf & Epi., Medical Assistant Professor

University of South Carolina (MUSC)

2005 – 2010 Dept Biostat, Bioinf & Epi / Biochem Director, NLM Training

MUSC Program (NLM, NIH)

2007 – 2010 Dept Biostat, Bioinf & Epi / Biochem Director, Bioinformatics

MUSC Division

2008 – 2009 Dept Biostat, Bioinf & Epi., MUSC Associate Professor

2009 – 2010 Dept Biochemistry and Molecular Associate Professor

Biology, MUSC

2009 – 2010 Dept Biochemistry and Molecular Co-Director, GAANN

Biology, MUSC Training Program in Lipidomics and Systems Biology (funded by the Department of Education, USA)

2009 – 2010 Biochemistry, MUSC Co-Director, Biostatistics

Training for Basic Biomedical

Research Program (NIGMS)

2010 - 2016 Department of Biomedical Informatics Associate Professor

University of Pittsburgh, Pittsburgh PA

2010 - Center for Translational Co-Director

Bioinformatics, University of Pittsburgh

2014 - 2018 Center for Causal Discovery Cancer DBP Lead,

University of Pittsburgh Exec. Comm. Member

2016 - Department of Biomedical Informatics Professor

University of Pittsburgh, Pittsburgh, PA

2021/11 – 2022/03 Shenzhen Bay Laboratory, Shenzhen, China Visiting Sabbatical Scholar

**MEMBERSHIPS in PROFESSIONAL and SCIENTIFIC SOCIETIES**

* Member of Federation of American Societies for Experimental 1996-2001

Biologists (Experimental Biology and Biophysics Societies)

* Member of American Association for the Advancement of Science 1998 - 2007
* Member of International Society for Computational Biologist 2001 - present
* Member of International mathematical Statistics 2004 - 2008
* Member of American Medical Informatics Association 2003 - present

AWARDS and HONORS

* Recipient of yearly Best Student Award from Shandong Medical University. 1981-1983
* Best Teaching Award, Shandong Provincial Hospital Nursing School. 1992
* Basic Medical Science Fellowship, University of Connecticut Health Center. 1993-1998
* SmithKline Beecham Award for Outstanding Graduate Student Research at 1997

New England Pharmacologists’ Meeting. Boston, MA.

* Fogarty Fellowship Award, National Institutes of Health. 1998
* National Library of Medicine Training Fellowship 2001-2003
* Lister Hill National Center for Biomedical Communication Summer Research 2003

Participation Program Fellowship.

* International Society for Computation Biology travel award for PSB 2004 2004
* The Third International Charleston Ceramide Conference travel award 2005
* Outstanding Paper Award, 2009 American Medical Informatics Association

Summit on Translational Bioinformatics 2009

* Invited Speaker, The 175 Anniversary of National Library of Medicine Conference 2011
* 2nd Place Award, [The Sage Bionetworks-DREAM Breast Cancer Prognosis](https://sagesynapse.wordpress.com/2012/11/01/breast-cancer-challenge-team-pitttransmed-places-second-for-metabric-phase-of-the-challenge/)

[Challenge (BCC)](https://sagesynapse.wordpress.com/2012/11/01/breast-cancer-challenge-team-pitttransmed-places-second-for-metabric-phase-of-the-challenge/) 2012

* 1st Place Award, SBV IMPROVER Trans-species Network Challenge 2013
* 1st Place Award (tied with IBM Research/Center for Computational Health), 2019

[Partners HealthCare Biobank Disease Challenge](https://rc.partners.org/news-events/announcements/winners-announced-first-biobank-disease-challenge) (Xinghua Lu, Degan Hao,

and Qiao Jin), Boston, MA 2019

PUBLICATIONS

## Refereed Journal Articles

1. **Lu, X**., Fein, A., Feinstein, M.B. and O’Rourke, F.A., (1999)  Antisense knock out of the Inositol 1,3,4,5-tetrakisphosphate receptor GAP1IP4BP in the human erythroleukemia cell line leads to the appearance of intermediate conductance K(Ca) channels that hyperpolarize the membrane and enhance calcium influx.  ***J. Gen. Physiol***.  113:81-9 (IF: 5.1).
2. Signore, A., O’Rourke, F., **Lu, X**., Feinstein, and Yeh, H. (1999)  Immunohistochemical localization of the InsP4 Receptor GTPase-Activating Protein GAP1IP4BP in the rat brain.   ***J. Neurosci. Res***. 55:321-328. (IF: 2.3).
3. Laplante JM, O'rourke F, **Lu, X**, Fein A, Olsen A, Feinstein MB  (2000) Cloning of human Ca2+ homoeostasis endoplasmic reticulum protein (CHERP): regulated expression of  antisense cDNA depletes CHERP, inhibits intracellular Ca2+ mobilization and decreases cell  proliferation. ***Biochem. J***. 348:189-99 (IF: 3.4).
4. Zhang, T., Gealy, R., **Lu, X**., Takimoto, K., and Levitan, E.S., (2000) TRH regulates Kv1.5 gene expression though a Gq-mediated PLC-independent pathway. ***Mol. Cell Endocrinol***. 25;165(1-2):33-39. (IF: 3.6).
5. Ng, K., **Lu, X**., Levitan, ES. (2002)  Physical mobilization of secretory vesicles facilitates neuropeptide release by nerve growth factor-differentiated PC12 cells.  ***J Physiol*** (London) 542 (Pt2) 395-402 (4.6) PMID:12122140 PMCID:PMC2290425.
6. Ng, Y.K., **Lu, X**. (*equal contributing author*), Walkins, S.C., Ellis-Davies, G.C. and Levitan, E.S., (2002) Nerve growth factor-induced differentiation changes the cellular organization of regulated peptide release by PC12 cells. (doi:20026395). ***J. Neurosci***. 22(10):3890-7 (IF: 8,23). PMID:12019308.
7. **Lu, X**., Ellis-Davies, G.C.R., and Levitan E.S.(2003**)** Calcium requirements for exocytosis do not delimit the releasable neuropeptide pool. ***Cell Calcium*** 33(4):267-271 (4.5) PMID:12618147.
8. Ng, Y.K., **Lu, X**., Gulacsi, A., Han, W., Saxton, M.J. and Levitan, E.S. (2003) Unexpected mobility variation among individual secretory vesicles produces an apparent refractory neuropeptide pool. (doi:10.10161/S006-3495(03)75137-6). ***Biophysical J***. 84(6):4127-34. PMID:12770915. PMCID:PMC1302991.
9. **Lu, X**., Zhai, C., Gopalakrishnan**,** V.,andBuchanan, B.G. (2004) Automatic annotation of protein motif function with Gene Ontology terms. (doi:10.1186/1471-2105-5-122). ***BMC Bioinformatics*** 5:122. PMID:15345032. PMCID:PMC517493.
10. Tao, T., Zhai, C., **Lu, X**. and Fang, H. (2004) A study of statistical methods for predicting function of protein motifs. ***Applied Bioinformatics***, 3:115-124. PMID: 15693737.
11. Cowart, L.A., Okamoto, Y., **Lu, X**. and Hannun, Y.A. (2006) Distinct roles for *de novo* versus hydrolytic pathways of sphingolipid biosynthesis in *Saccharomyces cerevisiae*. (doi:10.10421/BJ20050643). ***Biochemical J***. 393(3):733. PMID:16201964.PMCID:PMC1360726.
12. Zheng, B., McLean, D.C., and **Lu, X**. (2006) Identifying biological concepts from a protein-related corpus with a probabilistic topic model. (doi:10.1186/1471-2105-7-58). ***BMC Bioinformatics*** 7:58. PMID:16466569. PMCID:PMC1420333.
13. Chen, Y.A., Chou, C.C., **Lu, X**., Slate, E.H., Peck, K., Xu, W., Voit, E.O., and Almeida, J.S. (2006) A multivariate prediction model for microarray cross-hybridization. (doi:10.1186/1471-2105-7-101). ***BMC Bioinformatics*** 7:101. PMID:16509965. PMCID:PMC1409802. (*highly accessed paper*)
14. **Lu, X**., Zheng, B., Velivelli, A. and Zhai, C (2006) Enhancing text categorization with semantic-enriched representation and training data augmentation. ***J Am Med Inform Assoc***, 13(5):526-35. PMID:16799127. PMCID:PMC1561790.
15. Chen, Y., Zheng, B., Robbins, D.H., Lewin, DN., Mikhitarian, K, Graham, A., Rumpp, L, Glenn, T, Gillanders, WE, Cole, DJ, **Lu, X**, Hoffman, BJ. and Michael Mitas (2007) Accurate discrimination of pancreatic ductal adenocarcinoma and chronic focal pancreatitis using multi-marker expression data and samples obtained by minimally invasive fine needle aspiration. ***International Journal of Cancer***, 120(7):1511. PMID:17192896.
16. Zheng, B., and **Lu, X**. (2007) Novel metrics for evaluating the functional coherence of protein groups via protein-semantic-network. (doi[:10.1186/gb-2007-8-7-r153](http://genomebiology.com/2007/8/7/R153)). ***Genome Biology*** **8:**R153 PMID:17672896; PMCID:PMC2323239.
17. Jin, B., Muller, B., Zhai, CX, and **Lu, X** (2008) Multi-label literature classification based on the Gene Ontology graph. (doi:10.1186/1471-2105-9-525) ***BMC Bioinformatics*** 9:525. PMID:19063730. PMCID:PMC2644325.
18. Kozel, FA., Johnson, KA., Grenesko,EL., Laken, SJ., Kose, S, **Lu, X**., Pollina, D., Ryan, A and George, MS (2009) Functional MRI detection of deception after committing a mock sabotage crime. (doi:10.1111/j.1556-5029.2008.00927.x Epub 2008 Nov 29) ***J. Forensic Sciences***, 54(1):220-31. [PMID: 19067772](http://www.ncbi.nlm.nih.gov/pubmed/19067772). PMCID:PMC2735094.
19. Jin, B., Strasburger, A., Laken, SJ., Kozel, FA., Johnson, KA., George, MS., and **Lu, X**. (2009) Feature selection for fMRI-based deception detection. (doi:10.1186/1471-2105-10-S9-S15) ***BMC Bioinformatics*** **10** (Suppl 9)**:**S15 (*Outstanding Paper Award at the AMIA Summit on Translational Bioinformatics*) [PMID: 19761569](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2745686/?tool=pubmed). PMCID:PMC2745686.
20. Muller, B., Richards, AJ., Jin, B., **Lu, X**. (2009) GOGrapher; A Python library for GO graph representation and analysis.  (doi:10.1186/1756-0500-2-122) ***BMC Research Notes*** 2:122 [PMID:19583843](http://www.pubmedcentral.nih.gov/articlerender.fcgi?tool=pubmed&pubmedid=19583843). PMCID:PMC2714316.
21. Zheng, B. and **Lu, X.** (2009) Application of semantic modeling in bioinformatics domain.  In: Data Management in Semantic Web, Ed. Jin, H. and Lv, Z, Nova Science Publishers, Inc.
22. Richards, A.J., Muller, B., Shotwell, M., Cowart, L.A., Rohrer, B., and **Lu, X.** (2010) Assessing the functional coherence of gene sets with metrics based on the Gene Ontology graph. (doi:10.1093/bioinformatics/gtq203). ***Bioinformatics***, 26 (12): i79-i87.(Supplement issue for the Proceedings for the Intelligent Systems in Molecular Biology (ISMB) 2010, 19% acceptance). PMID:20529941. PMCID:PMC2881388.
23. Cowart, L.A., Shotwell, M., Worley, M.L., Richards, A.J., Montefusco, D.J., Hannun Y.A., and **Lu, X**. (2010) Revealing a signaling role of phytosphingosine-1-phosphate in yeast. (doi:10.1038/msb.2010.3. Epub 2010 Feb 16). ***Molecular Systems Biology*** 6:349 (Selected for presentation at the Highlight Track of ISMB 2010 which presents major advance in the field; invited presentation at the Gordon Research Conference 2010). [PMID: 20160710](http://www.ncbi.nlm.nih.gov/pubmed/20160710). PMCID:PMC2835565.
24. Jin, B. and **Lu, X.** (2010). Identifying informative subsets of the Gene Ontology with information bottleneck methods. (doi:10.1093/bioinformatics/btq449. Epub 2010 Aug 22). ***Bioinformatics*** 26 (19): 2445-2451. PMID:20702400. PMCID:PMC2944202.
25. Feng, H., Hu, B., Liu, K.W., **Lu, X.**, Yin, J.J., Lu, S., Keezer, S., Fenton, T., Furnari, F.B., Hamilton, R.L., Vuori, K., Nagane, M., Nishikawa, R., Cavenee, W.K. and Cheng, S.Y. (2012) Activation of Rac1 by Src-dependent phosphorylation of Dock180Y1811 mediates PDGFRα-stimulated glioma tumorigenesis in mice and humans. (doi:10.1172/JCI58559. Epub 2011 Nov 14). ***Journal of Clinical Investigation*** 121(12):4670–4684. PMID:22080864. PMCID:PMC3223070.
26. Osmanbeyoglu, H., Hartmaier, R., Oesterreich, S., and Lu, X. (2012) Improving ChIP-seq peak-calling for functional indirect co-regulator binding by integrating multiple sources of biological information. (doi:10.1186/1471-2164-13-S1-S1. Epub 2012 Jan 17). ***BMC Genomics*** 13(Suppl 1):S1. PMID:22369349. PMCID:PMC3439677.
27. Richards, A., Schwacke, J., Rohrer, B., Cowart, L.A., and **Lu, X.** (2012) Revealing functionally coherent gene subset using spectral clustering and information integration approaches. (doi:10.1186/1752-0509-6-S3-S7. Epub 2012 Dec 17). ***BMC Systems Biology*** **6** (Suppl 3) : S7. PMID:23282411. PMCID:PMC:3542577.
28. Qin, T., Tsoi, L.C., Sims K.J., **Lu, X.,** and Zheng, W.J. (2012) Signaling network prediction by the Ontology Fingerprint enhanced Bayesian network. (doi:10.1186/1752-0509-6-S3-S3). ***BMC Systems Biology*** **6** (Suppl 3): S3 (co-corresponding author). PMIC:23282239; PMCID:PMC3524013.
29. Lu, S. and **Lu, X.** (2013) Using graph model to find transcription factor modules: the hitting set problem and an exact algorithm. (doi:10.1186/1748-7188-8-2) ***Algorithms for Molecular Biology*** **8:**2 PMID:23324335. PMCID:PMC3622577.
30. Mowrey, D., Cheng, M., Liu, L., Willenbring, D., **Lu, X**., Wymore, T., Xu, Y., and Tang, P. (2013) Asymmetric ligand binding facilitates conformational transitions in pentameric ligand-gated ion channels. (doi:10.1021/ja307275v. Epub 2013 Feb 4). ***J Am Chem. Soc***. 135(6):2172-80. PMID:23339564. PMCID:PMC3582375.
31. Lu, S., Jin, B., Cowart, LA., and **Lu, X** (2013) From data towards knowledge: Revealing the architecture of signaling systems by unifying knowledge mining and data mining of systematic perturbation data. (doi:10.1371/journal.pone.0061134. Print 2013). ***PLoS One*** 8(4): e61134. PMID:23637789. PMCID:PMC3634064.
32. Chen, V.and **Lu, X.** (2013) Conceptualization of molecular findings by mining gene annotations. (doi:10.1186/1753-6561-7-S7-S2. Epub 2013 Dec 20). ***BMC Proceedings*** **7**(Suppl 7):S2. PMID:24564884. PMCID:PMC4042834.
33. Osmanbeyoglu, H., Lu, K., Oesterreich, S., Day, R.S., Benos, P.V., Coronnello, C., and **Lu, X.** (2013) Estrogen represses gene expression through chromatin reconfiguration. (doi:10.1093/nar/gkt586. Epub 2013 Jul 1). ***Nucleic Acid Research*** **41**(17): 8061-8071. PMID:23821662. PMCID:PMC3783169.
34. Montefusco, D., Chen, L., Matmati, N., Lu, S., Newcomb, B., Cooper, G.F., Hannun, Y.A., and **Lu, X**. (2013) Distinct signaling roles of ceramide species in yeast revealed through systematic perturbation and integromics analyses. (doi:10.1126/scisignal.2004515). ***Science Signaling*** 6:rs14. PMID:24170935. PMCID:PMC3974757.
35. Zhao, Z., Shen, B., **Lu, X.**, and Vongsangnak, W. (2013) Translational biomedical informatics and computational systems medicine. (doi:10.1155/2013/237465. Epub 2013 Dec 2). ***BioMed Research International***, vol. 2013, Article ID 237465, 2013. PMID:24350252. PMCID:PMC3856116.
36. Jiang X., Cai B., Xue D., **Lu X.**, Neapolitan R.E., and Cooper, G.F. (2014). A comparative analysis of methods for predicting clinical outcomes using high-dimensional genomic datasets. (doi:10.1136/amiajnl-2013-002358. Epub 2014 Apr 15). ***J Am. Medical Informatics Assoc***. 21:e312-e319. PMID:24737607. PMCID:PMC4173174.
37. Bilal, E., et al. (2014) A crowd-sourcing approach for the construction of species-specific cell signaling networks. (doi:10.1093/bioinf). ***Bioinformatics*** (This is the report of the Species Translation Challenge organized by the Systems Biology Verification Consortium ([SBV](https://sbvimprover.com/challenge-2/overview)). We were contributing authors, and our team won the first place in the challenge.)
38. Cai, C., Chen, L., Jiang, X., and **Lu, X**. (2014) Modeling signal transduction from protein phosphorylation to gene expression. (doi:10.4137/CIN.S13883. eCollection 2014 Review). ***Cancer Informatics***, 13(S1):59-67. PMID:25392684. PMCID:PMC4216050.
39. Chen, L., Cai, C., Chen, V., and **Lu, X.** (2015) Trans-species learning of cellular signaling systems with bimodal deep belief networks. (doi:10.1093/bioinformatics/btv315. Epub 2015 May 20). ***Bioinformatics*** Sept 15; 31(18): 3008-3015. PMID:25995230. PMCID:PMC4668779.
40. Lu, S., Lu, K.N., Cheng, S., Ma, X., Nystrom, N., and **Lu, X**. (2015) Identifying driver genomic alterations in cancers by searching minimum-weight, mutually exclusive sets. (doi:10.1371/journal.pcbi.1004257. eCollection 2015 Aug). ***PLoS Computational Biology*** Aug 28; 11(8):e1004257. (Highlighted at the ISMB 2015). PMID:26317382. PMCID:PMC4552843.

## Ogoe, H.A., Visweswaran, S., Lu, X., and Gopalakrishnan, V. (2015) Knowledge transfer via classification rules using functional mapping for integrative modeling of gene expression data. (doi:10.1186/s12859-015-0643-8). *BMC Bioinformatics* Jul 23; 16:226. (Highly Accessed paper) PMID:26202217. PMCID:PMC4512094.

## Chen, L., Cai, C., Chen, V., and Lu, X. (2016) Learning a hierarchical representation of the yeast transcriptomic machinery using an autoencoder model. (doi:10.1186/s12859-015-0852-1). *BMC Bioinformatics* Jan 11;17(Suppl 1):9 DOI: 10.1186/s12859-015-0852-1. PMID:26818848. PMCID:PMC4905523.

1. Hill, S.M., Heiser, L.M., Cokelaer, T., Unger, M. Nesser, N.K., Carlin, D.E., Zhang, Y., Sokolov, A., Paull, E.O., Wong, C.D., Graim, K., Bivol, A., Wang, H., Zhu, F., Afsari, B., Danilova, L.V., Favorov, A.V., Lee, W.S., Taylor, D., Hu, C.W., Long, B.I., Noren, D.P., e*t al*. (2016) Inferring causal molecular networks: empirical assessment through a community-based effort. (doi:10.1038/nmeth.3773. Epub 2016 Feb 22). ***Nature Methods*.** Apr 13; 4:310–318. PMID:26901648. PMCID:PMC4895523.
2. Lu, S., Mandava, G., Yan, G., and **Lu, X.** (2016) An exact algorithm for finding cancer driver somatic genome alterations: the weighted mutually exclusive maximum set cover problem. (doi:10.1186/s13015-016-0073-9. eCollection 2016). ***Algorithm for Molecular Biology*** May 4;**11**:11. PMID:27148394. PMCID:PMC4855522.
3. Huang, T., Alvarez, A.A., Pangeni, R.P., Horbinski, C., Lu, S., Kim, S.K., James, C.D., Raizer, J., Kessler, J., Brenann, C.W., Sulman, E.P., Finocchiaro, G., Tan, M., Nishikawa, R., **Lu, X**., Nakano, I., Hu1, B., and Cheng, S.Y. (2016) A regulatory circuit of miR-125b/miR-20b and Wnt signaling controls glioblastoma phenotypes through FZD6-mediated pathways. (doi:10.1038/ncommus12885). ***Nature Communication,*** Oct 4; 7:12885. PMID:27698350. PMCID:PMC5059456.
4. Lu, S., Cai, C., Yan, G., Zhou, Z., Wan, Y., Chen, V., Chen, L., Cooper, G.F., Obeid, L.M., Hannun, Y.A., Lee, A.V., and **Lu, X.** (2016) Signal-oriented pathway analyses reveal a signaling complex as a synthetic lethal target for p53 mutations. (Epub 2016 Oct 10). ***Cancer Research.*** *Dec 1;* 76 (23), 6785-6794. PMID:27758891. PMCID:PMC5165695.
5. Chen, V., Paisley, J., and **Lu, X.** (2017) Revealing common disease mechanisms shared by tumors of different tissues of origin through semantic representation of genomic alterations and topic modeling. (doi:10.1186/s12864-017-3494-a). ***BMC Genomics*** Mar 14;18 (Suppl 2):105. PMID:29361690. PMCID:PMC5374647.
6. Young, J.D., Cai, C., and **Lu, X.** (2017) Unsupervised deep learning reveals prognostically relevant subtypes of glioblastoma. (doi:10.1038/s12859-017-1798-2). ***BMC Bioinformatics*** Oct 3; 18 (Suppl 11):381. PMID:28984190. PMCID:PMC5629551.
7. Watters, R.J, Hartmaier, R.J., Osmanbeyoglu, H.U., Gillihan, R.M., Rae, J., Liao, L., Chen, K., Li, W., **Lu, X.**, and Oesterreich, S. (2017) Steroid receptor coactivator-1 can regulate osteoblastogenesis independently of estrogen. ([http://dx.doi.org/10.1016/j.mce.2017.03.005. Epub 2017 Mar 4)](http://dx.doi.org/10.1016/j.mce.2017.03.005.%20Epub%202017%20Mar%204)). ***Molecular and Cellular Endocrinology*** Jun15; 448:21-27.(PMCID In Process)
8. Yan, G., Chen, V., **Lu, X.**, and Lu, S. (2017) A signal-based method for finding driver modules of breast cancer metastasis to the lung. (doi:10.1038/241598-017-009951-2). ***Scientific Reports***. Aug 30; 7: 10023. PMID:28855549. PMCID:PMC5577160.
9. Huang, T., Kim, C.K., Alvarez, A.A., Pangeni, R.P., Shi, T., Sastry, N., Lu, S., Horbinski, C., Kessler, J., Nishikawa, R., Nakano, I., **Lu, X.**, James, C.D., Ying, X.M., Hu, B., and Cheng, S.Y. (2017) MST4 phosphorylation of ATG4B regulates autophagic activity, tumorigenicity and radioresistance in glioblastoma. (doi:10.1016/j.ccell.2017.11.005). ***Cancer Cell*** Dec 11;32:840-855. PMID: 29232556. PMCID:PMC5734934.
10. Sadahiro, H., Kang, K., Gibson, J.T, Minata, M., Yu, H., Shi, J., Chhipa. R.R., Chen, Z., Lu, S., Simoni, Y., Furuta, T., Sabit, H., Zhang, S., Bastola, S., Yamaguchi, S., Alsheikh, H., Komarova, S., Wang, J., Kim, S.H., Hambardzumyan, D., **Lu, X**., Newell, E.W., Dasgupta B., Nakada, M., Lee, L.J., Nabors, B, Norian, L.A., and Nakano, I. (2018). Activation of the receptor tyrosine kinase AXL regulates the immune microenvironment in glioblastoma. (doi:10.1021/acsnano.8b02264. Epub 2018 Jun 1). ***Cancer Research*** Jun 1; 78(11):3002-3013. PMID:29531161. PMCID:PMC5984695.
11. Pangeni, R., Zhang, Z., Alvarez, A.A., Wan, X., Sastry, N., Lu, S., Shi, T., Huang, T., Lei, C.X., James, C.D., Kessler, J.A., Brennan, C.W., Nakano, I., **Lu, X**., Hu, B., Zhang, W., and Cheng, S.Y. (2018) Genome-wide methylomic and transcriptomic analyses identify subtype-specific epigenetic signatures commonly dysregulated in glioma stem cells and glioblastoma. (doi:10.1080/15592294.2018.1469892. Epub 2018 Aug 6). ***Epigenetics*** 13(4): 432-448. PMID: 29927689. PMCID:PMC6140806.
12. Ding, M.Q., Chen, L., Cooper, G.F., Young, J.D., and **Lu, X**. (2018) Precision oncology beyond targeted therapy: Combining omics data with machine learning matches the majority of cancer cells to effective therapeutics. (doi:10.1158/1541-7786.MCR-17-0378. Epub 2017 Nov 13). ***Molecular Cancer Research*** 16(2):269-278. PMID:29133589; PMCID:PMC5821274.

# 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. (doi:10.1371/journal.pone.0203871. eCollection 2018). *PLoS One* Sept 12; 13(9): e0203871. PMID:30208101. PMCID:PMC6135403.

# Chen, L. and Lu, X. (2018) Discovering functional impacts of microRNAs in cancers using a causal deep learning model. (doi: 10.1186/s12920-018-0432-0). Proceedings of the 29th International Conference on Genome Informatics (GIW 2018): Medical Genomics. *BMC Medical Genomics* 11(S6):53-112. (doi:10.1186/s12920-018-0432-0). PMID:30598118 PMCID:PMC6311958

1. Cooper, G.F., Cai C., and **Lu, X.** (2018) Tumor-specific causal inference (TCI): A Bayesian method for identifying causative genome alterations with individual tumors. (doi:10.1101/225631). **BioRxiv** (preprint server for Biology).
2. Liang, L., Chen, V., Zhu, K., Fan, X., **Lu, X**, and Lu, S. (2019) Integrating data and knowledge to identify functional modules of genes: A multilayer approach. (doi:10.1186/s12859-019-2800-y). ***BMC Bioinformatics*** 20(1; May):225. PMID: 31046665. PMCID:PMC6498600.
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5. Xue, Y., Cooper, G.F., Cai, C., Lu, S., Hu, B., Ma, X., and **Lu, X**. (2019) Tumour-specific causal inference discovers distinct disease mechanisms underlying cancer subtypes. **Scientific Reports** 2019DOI **:**10.1038/s41598-019-48318-7
6. Liu, J., Ma, X., Cooper, GF, and **Lu, X** (2020) Explicit representation of protein kinase activity states significantly improve causal discovery of protein phosphorylation networks. ***BMC Bioinformatics,*** *21, 379 (2020)*
7. Xue, Y., Ding, M., **Lu, X.** Learning to encode cellular response to systematic perturbations with deep generative models. ***npj Syst Biol Appl*** 6,35 (2020).
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7. Cai, M., Yue, M., Chen, T., Liu, J., Forno, E., **Lu, X**., Billiar, T., Celedon, J., McKennan, C., Chen., W., and Wang, J.. (2022) Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution. ***Bioinformatics*** DOI: <https://doi.org/10.1093/bioinformatics/btac279>
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1. Rahman M.A.\*, Cai C, McNamara D, Ding Y, Cooper G.F., Lu X, Liu J. (2023) An individualized Bayesian method for estimating genomic variants of hypertension. ***BMC Genomics***. 23(Suppl 5):863. PMID: **37936055,** PMCID: [PMC10631115](http://www.ncbi.nlm.nih.gov/pmc/articles/pmc10631115/), doi: <https://doi.org/10.1101/2022.06.25.22276897>.
2. Fu, Z., Chen, S., Zhu, Y., Zhang, D., Xie, P., Jiao, Q., Chi, J., Xu, S., **Xue, Y**., Lu, X., Song, X., Cristofanilli, , M., Gradishar, W., Kalinsky, K., Yin, Y., Zhang, B., and Wan, Y. (2023) Proteolytic regulation of CD73 by TRIM21 orchestrates tumor immunogenicity. ***Science Advances***, 9(1): eadd6626
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4. Zhang, H., Lu, X., Lu, B., and Chen, L.. (2023) scGEM: Unveiling the nested tree-structured gene co-expressing modules in single-cell transcriptome data. ***Cancers*** 15(17), 4277; <https://doi.org/10.3390/cancers15174277>
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6. Chen, L, Wang, Y, Cai, C, Ding, Y, Kim, RS., Lipchik, C, Gavin, PG., Yothers, G, Allegra, CJ, Petrelli, NJ, Suga, JM., Hopkins, JO., Saito, NG., Evans, T., Jujjavarapu, S., Wolmark, N., Lucas, PC., Paik, S., Sun, M., Pogue-Geile, KL., **Lu, X**. (2023) Machine Learning Predicts Oxaliplatin Benefit in Early Colon Cancer. Accepted by the ***Journal of Clinical Oncology***
7. Huang, P, Cai, M, **Lu, X**, McKennan, C., and Wang, J (2023). Accurate estimation of rare cell type fractions from tissue omics data via hierarchical deconvolution. Accepted by the ***Annals of Applied Statistics***
8. Hu, J., Gao, C., Ge, H., Kuan, SF., Cai, C., Lu, X., Esni, F., Schoen, R., Wang, J., and Chu, E. (2023) FAK loss reduces BRAFV600E-induced ERK phosphorylation to promote intestinal stemness and cecal tumor formation (accepted by ***eLife***)

**Refereed Conference Proceeding Papers**

1. Tao, T., Zhai, C., **Lu, X**. and Fang, H. (2003) A study of statistical methods for predicting function of protein motifs. In ***Proceedings of Biological Language Conference*** 2003, Pittsburgh, PA
2. **Lu, X**., Hauskrecht, M. and Day, R.S. (2004) Modeling Cellular Processes with Variational Bayesian Cooperative Vector Quantizer. In: ***Proceedings of Pacific Symposium on Biocomputing***, pp.533.
3. Jin, B. and **Lu, X.** (2009) Enhancing GO-graph-based multi-label classification using semantic-rich GO terms.  Proceedings of the Annual Meeting of the ISMB BioLINK Workshop 2009.
4. Lu, S. and **Lu, X.** (2011). A graph model and an exact algorithm for finding cooperative transcription factor modules. ***Proceedings of ACM Bioinformatics and Computational Biology*** 2011.
5. Jin, B., Chen, V., Chen, L., and **Lu, X**. (2011) Mapping annotations with textual evidence using an scLDA model. (Epub 2011 Oct 22). ***Proceedings of AMIA Annual Symposium*** **2011**, Washington DC. PMId:22195141. PMCID:PMC3243146.
6. Lu, S. and **Lu, X** (2012) Integrating genome and functional genomics data to reveal perturbed signaling pathways in ovarian cancers. ***Proceedings of AMIA Summit on Translational Bioinformatics***, San Francisco. (Epub 2012 Mar 19). PMID:22779056. PMCID:PMC3392049.
7. Jin, Q., Dhingra, B., Cohen, W., and **Lu, X**. (2018) AttentionMeSH: Simple, Effective and Interpretable Automatic MeSH Indexer. <http://www.aclweb.org/anthology/W18-5306> ***Proceedings of the Conference on Empirical Methods in Natural Language Processing 2018,*** Brussel, Belgium, October 31-Nov 4.
8. Jin, Q., Dhingra, B., Cohen, W., and Lu, X. (2019) Probing Biomedical Embeddings from Language Models [[arXiv]](https://arxiv.org/pdf/1904.02181.pdf) [[pdf]](https://andy-jqa.github.io/doc/probing.pdf) [[code]](https://github.com/Andy-jqa/bioelmo) ***Proceedings of NAACL RepEval***, 2019
9. Jin, Q., Liu, J., Lu, X., (2019) Deep Contextualized Biomedical Abbreviation Expansion. ***Proceedings of ACL BioNLP 2019.*** [arXiv:1909.06146v1](https://arxiv.org/abs/1909.06146v1) [cs.CL]
10. Jin, Q., Dhingra B., Liu, Z., Cohen, WW and Lu, X (2019) PubMedQA: A dataset for biomedical research question answering. ***EMNLP 2019***
11. Tao, Y., Cai, C., Cohen, W., and Lu, X (2019) From genome to phenome: Predicting multiple cancer phenotypes based on somatic genomic alterations via the genomic impact transformer. Proceedings of ***Pacific Symposium on Biocomputing.*** arXiv902.00078 (q\_bio.MN)
12. Y Tao, S Ren, MQ Ding, R Schwartz, X Lu. Predicting Drug Sensitivity of Cancer Cell Lines via Collaborative Filtering with Contextual Attention. ***Proceedings of******Machine Learning Research*** 1-A7, 2020
13. Young, JD., Andrews, B., Cooper, GF., and **Lu, X** (2020) Learning Latent Causal Structures with a Redundant Input Neural Network, Proceedings of the 2020 KDD Workshop on Causal Discovery. [PMLR 127:62-91](http://proceedings.mlr.press/v127/young20a/young20a.pdf)
14. Lu, S., Wei, W., Belovsky, M., and Lu, X., (2021) Understanding heart failure patients EHR clinical features via SHAP interpretation of tree-based machine learning model predictions. ***Annual Symposium of AMIA***, San Diego, CA
15. Ren, S., Tao, Y., Yu, K., Xue, Y., Schwartz, R., Lu, X. (2022) *De novo* prediction of cell-drug sensitivities using deep learning-based graph regularized matrix factorization. ***Pacific Symposium on Biocomputing 2022***. bioRxiv: <https://www.biorxiv.org/content/10.1101/2021.10.11.462450v1>
16. Zhang, H., Lu, X., Lu, B., and Chen, L.. (2023) scGEM: unveiling the nested tree-structured gene co-expressing modules in single-cell transcriptome data. ***International Conference on Intelligent Biology and Medicine (ICIBM).***

**Unrefereed Preprints**

1. Liang, L, **Lu X**, Lu S.  PEAK2VEC ENABLES INFERRENCE OF TRANSCRIPTIONAL REGULATION FROM ATAC-SEQ.  **bioRxiv** 2021.09.29.462455; doi: <https://doi.org/10.1101/2021.09.29.462455>
2. Tao Y, Ma X, Lalio GI, Zuniga AG, Palmer D, Toska E, Schwartz R, **Lu X**, Osmanbeyoglu HU.  [Interpretable deep learning for chromatin-informed inference of transcriptional programs driven by somatic alterations across cancers](https://www.biorxiv.org/content/10.1101/2021.09.07.459263.abstract).  **bioRxiv** 2021.09.07.459263; doi: <https://doi.org/10.1101/2021.09.07.459263>
3. Liang L**, Lu X**, Lu S.  [New Gene Embedding Learned from Biomedical Literature and Its Application in Identifying Cancer Drivers](file:///C:/Users/Linda/AppData/Local/Microsoft/Windows/INetCache/Content.Outlook/4E3OW9Y2/New%20Gene%20Embedding%20Learned%20from%20Biomedical%20Literature%20and%20Its%20Application%20in%20Identifying%20Cancer%20Drivers). **bioRxiv** 2021.01.13.426600; doi: <https://doi.org/10.1101/2021.01.13.426600>
4. Chen, X., Chen., L., Kurten, C., Jabbari, F., Vujanovic, L., Ding, Y., Kulkarni., A., Tabib., T., Lafyatis, R., Cooper, GF., Ferris, R., Lu, X. (2021) An instance-specific causal framework for learning intercellular communication networks that define microenvironments of individual tumors. ***Cell Report Methods*** (under review), Preprint: <https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3925258>

**Books, Editorials, Chapters, Reviews, Non-refereed Invited Published Papers, Non-refereed Proceedings of Conference and Symposia, Unpublished Technical Reports, Monographs, Books and Book Chapters**

1. Wei, C., Li, X., Zhang, Z. and **Lu, X**. *et al* Ed. (1992) *Intensive Care of Critical Diseases*. Yellow River Press Inc. Shandong, China
2. **Lu, X**., Zhai, C.X., Gopalakrishnan, V., and Buchanan, B.G.. (2002) Predicting functions of protein motifs by mining the knowledge base of Gene Ontology. Center for Biomedical Informatics Technical Report, University of Pittsburgh, Series Number: CBMI-02-180
3. **Lu, X**., Day, R.S. and Hauskrecht, M. (2002) Variational Bayesian learning of a multiple causal model – Part I: The Theory Center for Biomedical Informatics Technical Report, University of Pittsburgh, Series Number: CBMI-02-181
4. Zhai, C., **Lu, X**., Ling, X., He, X., Velivelli, A., Wang, X., Fang, H., and Shakery, A. (2005) UIUC/MUSC at TREC 2005 Genomics Track. Proceedings of the Text Retrieval Conference 2005 (*TREC is an international conference allowing researchers over the world to report their results on information retrieval challenges. Our results in 2005 genomic track were the best in several categories of the challenges*).
5. **Lu, X**., Zheng, W.J., Hannun, Y.A. (2015) Systems biology approaches for studying sphingolipid signaling. In ***Sphingolipids in Cancers****.* Ed by Hannun, YA et al.
6. Cooper, G.F., Bahar, I., Becich, M.J., Benos, P.V., Berg, J., Espino, J.U., Glymour, C., Jacobson, R.C., Kienholz, M., Lee, AV., Scheines, R., **Lu, X**., and the Center for Causal Discovery team (2015) The Center for Causal Discovery of Biomedical Knowledge from Big Data. ***JAMIA*** 22(6):1132 – 1136.
7. Cooper, G.F., Cai, C., **Lu, X**. (2017) Tumor-specific Causal Inference (TCI): A Bayesian method for identifying causative genome alterations within individual tumors. BioRxiv. Doi: http//dx.doi.org/10.1101/225631.
8. Chen, L. and **Lu, X.** (2018) Making deep learning models transparent. Invited Editorial (doi: 10.21037/jmai.2018.07.01) ***Journal of Medical Artificial Intelligence*** 1:5
9. Cai, C., Cooper, G.F., Lu, K., Ma, X., Xu, S., Zhao, Z., Chen, X., Xue, Y., Lee, A.V., Clark, N., Chen, V., Lu, S., Chen, L., Yu, L., Hochheiser, H.S., Jiang, X., Wang, Q.J., and **Lu, X**. Systematic Discovery of the Functional Impact of Somatic Genome Alterations in Individual Tumors through Tumor-specific Causal Inference. [Internet]. bioRxiv2018 May. 54 pages. Available from: https://www.biorxiv.org/content/early/2018/05/24/329375. DOI: 10.1101/329375

## Invited or Selected Plenary Presentations at Conferences

1. **Lu, X**., Zhai, C., Gopalakrishnan**,** V.,andBuchanan, B.G. Automatic annotation of protein motif function with Gene Ontology terms. Intelligence Systems of Molecular Biology, 2002, Edmonton, CA
2. **Lu, X**., Hauskrecht, M. and Day, R.S. Modeling Cellular Processes with Variational Bayesian Cooperative Vector Quantizer. Plenary presentation at the Pacific Symposium on Biocomputing Conference, 2004, Big Island, HI
3. **Lu, X**, Zheng, B. and McClean, D. Text mining with hierarchical probabilistic topic model. Biannual Conference of IMS, 2005, Beijing
4. Zheng, B., **Lu, X** . Evaluating protein functional coherence via protein-semantic network. International Conference of Systems Biology, 2006, Yokohama, Japan.**Lu, X**. Automatically extracting GO annotation evidence with a latent topic model. Intelligent Systems in Molecular Biology, 2007, Vienna, Austria
5. **Lu, X**. Graph-theory-based metrics for evaluating the functional coherence of genes. AMIA Fall Symposium 2007, Chicago
6. Muller, B., Richards, A., Tsoi, L, Jin, B., and **Lu, X**. (2008) GOGrapher: A Python library for GO network graph analysis. The Intelligent Systems for Molecular Biology. August, 2008, Toronto, Canada
7. Richards, A., Rohrer, B., Tsoi, L, Muller, B., Shotwell, M., and **Lu, X**.. (2008) GOSteiner: a graph theoretic measure of protein functional coherence. The Intelligent Systems for Molecular Biology. August, 2008, Toronto, Canada
8. Jin\*, B. Strasburger, A., Laken, SJ., Kozel, FA., Johnson, KA., George, MS., and **Lu, X**.. (2009)  Feature Selection for fMRI-based Deception Detection, Plenary presentation at the Summit on Translational Bioinformatics 2009, San Francisco, CA (with outstanding paper award)
9. Jin, B., and **Lu, X** (2009) Enhancing graph-based multi-label text classification with semantic-rich GO terms. Plenary presentation at BioLink’09 Workshop
10. Jin, B. and **Lu, X** (2010) Identify informative subset of the Gene Ontology using information bottleneck methods. ISMB 2010, Boston, MA
11. Richards, AJ., Schwacke, JH., Cowart, LA., Rohrer, B., and **Lu, X** (2010) A spectral clustering and information integration framework to mine gene sets using heterogeneous data sources. ISMB 2010, Boston, MA
12. **Lu, X**, Cowart, LA (2010) Modeling the role of sphingolipids in gene expression systems in yeast. The Yeast Genetics and Molecular Biology conference, Vancouver, BC, Canada, July 2010
13. **Lu, X** (2014) Treat the undruggables: Identification of p53-center pathway reveals a therapeutic strategy for treating tumors with p53 mutations. Invited seminar, Stony Brook University, Stony Brook, NY
14. Lu, S., and **Lu, X**. (2015) Identifying driver genomic alterations in cancers by searching minimum-weight, mutually exclusive sets. Late Break Plenary Presentation (selected) at ISMB 2015
15. **Lu. X**. Personalized Precision Medicine for Cancers: a Big Data Approach. Keynote Lecture at the 9th International Conference on Bioinformatics and Biomedical Engineering (iCBBE 2015). Shanghai, China
16. **LuX.** Precision Oncology in a Big Data Era. The 6th BIT World DNA Day Conferences. Dalian, China, April 26th, 2016
17. **Lu, X.**. From big data to bedside (DB2B): A computational perspective for precision oncology. Invited speaker, 7th International Workshop on Cancer Systems Biology, Zhuhai, China, June, 2017
18. **Lu, X.** From Big Data to Bedside (DB2B): Precision oncology in an era of artificial intelligence. ICIBM 2018 Eminent Scholar Lecture, Los Angeles, CA.

PROFESSIONAL ACTIVITIES

## TEACHING:

**Courses Taught**

* . **Machine Learning and Data Mining**

This 3 credit hour course is established by Dr. Xinghua Lu, which is now a required course in the

Bioinformatics Graduate Program.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Years Offered** | **Credit Hours** | **Students** | **Contact Hours** | **[[1]](#footnote-2)Course PACE Score** | **Instructor PACE Score** |
| 2005, Spring | 3 | 3 | 3×15 | 97 | 98 |
| 2006, Spring | 3 | 5 | 3×15 | 91 | 92 |
| 2008, Spring | 3 | 5 | 3x15 | 95 | 96 |
| 2009, Spring | 3 | 4 | 3x15 | 4.5 (new scale, with 5 as the highest) | 4.5 |

* **Introduction to Bioinformatics**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Years Offered** | **Credit Hours** | **Students** | **Contact Hours** | **Course PACE Score** | **Instructor PACE Score** |
| 2006, Fall | 6 | 35 | 4 |  |  |
| 2015, Fall | 3 | 7 |  |  |  |

* **Principles of Bioinformatics Algorithms**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Years Offered** | **Credit Hours** | **Students** | **Contact Hours** | **Course PACE Score** | **Instructor PACE Score** |
| 2007, Spring | 3 | 5 | 3×15 | 83 | 92 |
| 2010, Spring | 3 | 4 | 3x15 | NA | NA |

* **Journal Club for Statistical and Computational Biology**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Years Offered** | **Credit Hours** | **Students** | **Contact Hours** | **Course PACE Score** | **Instructor PACE Score** |
| 2007, Fall | 1 | 7 | 1×15 |  |  |
| 2008, Spring | 1 | 7 | 1x15 |  |  |
| 2008, Fall | 1 | 8 | 1x15 |  |  |
| 2009, Spring | 1 | 5 | 1x15 |  |  |
| 2009, Fall | 1 | 5 | 1x15 |  |  |

* **Natural Language Processing and Information Retrieval**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Years Offered** | **Credit Hours** | **Students** | **Contact Hours** | **Course EVAL Score** | **Instructor EVAL Score** |
| 2009, Spring | 2 | 4 | 2×15 | 4.5 | 4.5 |

* **Translational Bioinformatics**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Years Offered** | **Credit Hours** | **Students** | **Contact Hours** | **Course EVAL Score** | **Instructor EVAL Score** |
| 2012, Spring | 3 | 5 | 3×16 |  |  |

# Graduate Student Advisorships, Thesis and Dissertation Committees

**Graduate Degree Students**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Name** | **Program** | **Institute** | **Role** | **Duration** | **Current Position** |
| Yian Ann Chen | PhD | Medical University of South Carolina | Member, Dissertation committee | 2003-2006 | Res. Assistant Prof. Texas A&M University |
| Liuhong Jiang | MS | Medical University of South Carolina | Member, Thesis Committee | 2003-2006 | FBI |
| Robert Eric Gorilitsky | PhD | Medical University of South Carolina | Member, Dissertation Committee | 2003-2007 | Benefit.com, Charleston, SC |
| Yuliva V. Karplevitch | PhD | Medical University of South Carolina | Co-Chair, Dissertation Committee | 2003-2007 | Res. Assistant Prof. Texas A&M University |
| Kellie Sims | PhD | Medical University of South Carolina | Co-Chair, Dissertation Committee | 2003-2008 | Postdoctoral Fellow, MUSC |
| Adam Richards | PhD | Medical University of South Carolina | Chair, Program Study Committee/Dissertation Committee | 2005-2010 | University of Colorado |
| Lam Tsoi | PhD | Medical University of South Carolina | Member, Program Study Committee | 2005-2008 | University of Michigan |
| Joshua Swearingen | PhD | Medical University of South Carolina | Chair, Program Study Committee; Co-Chair, Dissertation Committee | 2006-2010 |  |
| Alvin Strasburger | MS | Medical University of South Carolina | Chair, Thesis Research Committee | 2005-2010 | Medical School, University of South Carolina |
| Chris Demos | MS | Medical University of South Carolina | Member, Thesis Committee | 2007-2008 | Research Technician, Medical University of South Carolina |
| Brian Muller | MS | Medical University of South Carolina | Chair, Thesis Committee | 2007-2009 | IT Manager, The-diplomat.com |
| Jessica Ross | PhD | Medical University of South Carolina | Member, Dissertation Committee | 2007-2010 |  |
| Bethany Wolf | PhD | Medical University of South Carolina | Member, Dissertation Committee | 2007-2009 | Postdoctoral Fellow, Medical University of South Carolina |
| Matthew Shotwell | PhD | Medical University of South Carolina | Member, Program Study; Member, Dissertation Committee | 2007-2010 | Assistant. Prof., Vanderbilt University |
| Hattice Osmanbeyoglu | PhD | University of Pittsburgh, Biomedical Informatics | Chair, Dissertation Committee | 2011-2012 | Assistant Prof., University of Pittsburgh |
| Song Chi | PhD | University of Pittsburgh | Member, Research Committee | 2011-2012 | Postdoctoral Fellow, Yale University |
| Eric Williams | PhD | University of Pittsburgh, Biomedical Informatics | Member, Research Committee | 2011-2013 |  |
| Jonathan Young | MS | University of Pittsburgh, Intelligent Systems Program | Chair, Research Committee | 2015-2017 |  |
| Lujia Chen | PhD | University of Pittsburgh, Biomedical Informatics | Chair, Research Committee | 2009-2017 |  |
| Vicky Chen | PhD | University of Pittsburgh, Biomedical Informatics | Chair, Research Committee | 2009-2017 |  |
| Kevin McDade | PhD | University of Pittsburgh, Biomedical Informatics | Member, Dissertation Committee | 2010-2016 |  |
| Joyeeta Dutta-Muscato | PhD | University of Pittsburgh, Biomedical Informatics | Member, Research Committee | 2011-2016 |  |
| Henry Ogoe | PhD | University of Pittsburgh, Biomedical Informatics | Member, Research Committee | 2011-2019 |  |
| Michael Ding | PhD | University of Pittsburgh, Biomedical Informatics | Member, Research Committee; Chair, Dissertation Committee | 2014-2020 |  |
| Mahganeh Eshaghzadeh- Torbati | PhD | University of Pittsburgh, Intelligent Systems Program | Member, Dissertation Committee | 2014-2019 |  |
| Sanghoon Lee | PhD | University of Pittsburgh, Biomedical Informatics | Research Advisor; Member, Dissertation Committee | 2015-2021 |  |
| Xueer Chen | PhD | University of Pittsburgh, Biomedical Informatics | Chair, Research Committee | 2015-2020 |  |
| Yifan Xue | PhD | University of Pittsburgh, Biomedical Informatics | Chair, Research Committee | 2016-2021 |  |
| Giacomo Nebbie | PhD | University of Pittsburgh, Intelligent Systems Program | Chair, Research Committee | 2016-2018 |  |
| Yifeng Tao | PhD | Joint Carnegie Mellon University and University of Pittsburgh, Computational Biology | Co-Advisor, Research Committee; Member, Dissertation Committee | 2016-2021 |  |
| Lifan Liang | PhD | University of Pittsburgh, Biomedical Informatics | Member, MS Dissertation Committee | 2016-2021 |  |
| Shuangxia Ren | PhD | University of Pittsburgh, Intelligent Systems Program | Chair, Research Committee | 2018-present |  |
| Ryan Hausler | MS | University of Pittsburgh, Biomedical Informatics | Academic Advisor | 2018-2020 |  |
| Fattaneh Jabbari | PhD | University of Pittsburgh, Intelligent Systems Program | Member, Dissertation Committee | 2018-2020 |  |
| Jing, Yankang | PhD | University of Pittsburgh, Pharmacy Program | Member, Dissertation Committee | 2019-2021 |  |
| Deyi Eric Li | MS | CMU Computational Biology | Research course advisor | 2022 – 2022 |  |
| Hejie Cui | MS | CMU Computational Biology | Research course advisor | 2022 – 2022 |  |
| Han Zhang | PhD | University of Pittsburgh, Biomedical Informatics | Research advisor and committee member | 2022 - |  |

**Postdoctoral Fellows**

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| --- | --- | --- |
| Name | Duration | Current Position |
| David McLean, PhD | 2003 - 2005 | Assist Prof, Claflin Univ. |
| Bin Zheng, MD, PhD | 2004 - 2006 | Staff Scientist, Harvard Univ. |
| Thomas Asbury, PhD | 2006 - 2008 | Senior Scientist, Affymetrix |
| Bo Jin, PhD | 2007 - | Senior Scientist, Sigma |
| Atulya Velivelli | 2007-2008 | IT professional |
| Songjian Lu | 2009-1015 | Assist Prof. Univ. Pitt |
| Chunhui Cai | 2012 - 2019 | Staff Scientist, Pitt |
| Huichen Feng | 2013-2014 | NLM Postdoc Fellow, Pitt |
| Jonathan Young  Jinling Liu | 2013 – 2020  2017 – 2020 | NLM Postdoc Fellow, Pitt, Intelligent Systems  NLM Postdoc Fellow, Pitt |
| Lujia Chen | 2017 -2021 | Assist Prof, Pitt |

**Tsinghua University School of Medicine and University of Pittsburgh Biomedical Partnership, Academic Affairs, Health Sciences Visiting Scholars (M.D. students)**

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| Name | Duration |
| Qiao Jin  Zhengping Liu | 2017-2019  2018-2020 |

**Beijing Information Science and Technology University, Visiting Scholar (PhD student)**

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| Name | Duration |
| Ruoyu Chen | 2018-2020 |

**Undergraduate and high school scholar**

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| --- | --- | --- | --- |
| **Student Name** | **Program** | **Role** | **Duration** |
| Mitchell Worley | SURP | Advisor | June-Aug, 2008 |
| Perry Spyropoulos | SURP | Advisor | June-Aug, 2009, 2010 |
| Taylor Raffield | SURP | Advisor | June-Aug, 2009 |
| Ashwin Bhat | SURP | Advisor | June – Aug, 2010 |
| James Segars | SURP | Advisor | June – Aug, 2010 |
| Lukas Schmidt  Joyetta Dutta-Muscato | CoSBBI  CoSBBI | Advisor  Advisor | June – Aug, 2015  June – Aug, 2015 |
| Albert Kim  Binfeng Lu  Amanda Zeng  Cecelia Baek  Samuel Ding  Eddie Perez-Claudio | CoSBBI  CoSBBI  CoSBBI  CoSBBI  CoSBBI  IBRIC | Advisor  Advisor  Advisor  Advisor  Advisor  Co-mentor   |  |  | | --- | --- | |  |  | | June – Aug, 2015  June – Aug, 2016  June – Aug, 2016  June – Aug, 2017  June – Aug, 2018  June – Aug. 2019 |
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**RESEARCH GRANTS:**

**Active Grant Supports**

5R01 LM012011-06 (Lu) 04/01/2015 – 03/31/2024 3.60 calendar

NLM $202,500

Interpretable deep learning models for translational research

5R01 CA215481-04 (Yu) 01/01/2018 – 12/31/2022 0.60 calendar

NCI $300,244

Translation addiction and targeting in colon cancer

5R01 CA229431-02 (Wang) 07/02/2019 – 06/30/2024 0.60 calendar

NCI $235,380

Title of Project: A novel mitotic regulatory axis in neuroendocrine prostate cancer

1R01 CA254274-01A1 (Lu, B) 06/16/2021 – 05/31/2026 0.60 calendar

NCI $253,109

Study of the IL-33-driven immune cell organization underpinning responses to immune

checkpoint blockade cancer therapy

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| **Completed Grant**  U54HG008540  NHGRI | Center of Causal Discovery (NIH Big Data to Knowledge Center) | Cancer Pathway DBP Lead (15%) | 09/14 – 08/18 (NCE) | $12M (total) |
| 1 R01LM012011  NLM | Deciphering cellular signaling system by deep mining a comprehensive genomic  Compendium. | **PI** (30%) | 04/15-03/19 | $ 1,508,636 |
| Dept. of Health, PA  Grant #: 4100070287 | Big Data for Better Health (PA CURE grant) | **Project Lead**, **Co-I** (15%) | 07/15 – 06/18 (NEC) | $5,042,791 |
| UPMC/Pitt, ITTC Program | Tumor-specific driver identification | **Co-PI** (Lu (25%), **co-PI**: Cooper | 01/18 – 12/19 | $3M |
| P30CA047904 (Pilot Project) | Developing an AI-based Clinical Decision Support System for Precision Oncology   |  | | --- | |  | | **PI** | 05/18 – 04/19 | $50,000 |

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| 1R01LM011663  NLM | A new generation clinical decision support system | **Co-I** (5%) | 06/14 – 05/18 | $2,331,264 |
| 1R01LM 011155  NLM | Ontology-Driven Methods for Knowledge Acquisition and Knowledge Discovery | **PI**, (30%) | 09/2011-08/2015 | $1,475,062 |
| 1U01HL112707  NHLBI | Sarcoidosis and A1AT Genomics & Informatics Center | Co-I (5%) | 2012-2015 | $2,447,769 x 3 |
| 1R01GM100387 | Transfer Rule Learning for Knowledge Based Biomarker Discovery and Predictive Biology | Co-I (5%) | 2012-2015 | $901,746 |
| 1 R01 LM 010144 | Statistical methods for integromics discoveries. | **PI** | 09/09 -08/14 | $1,828,806 |
| 1 R01 LM009153 | Automatic Literature-Based Protein Annotation | PI | 07/07 –07/10 | $846,721 |
| 5R01LM009153-03S2 | Administrative supplement of the NLM R01 grant 3R01LM009153-02 | PI | 07/2009-07/2010 (no-cost ext. until 07/2011 | $138,415 |
| R01LM009153-02S1 | Summer Research supplement associated with the NLM R01 grant 3R01LM009153-02 | **PI** | 05/2009-07/2010 (no-cost ext. until 07/2011) | $39,294 |
| 2 P20 RR017677 | COBRE in Lipidomics & Pathobiology: Modeling the roles of bioactive lipids in gene expression systems | **PI** | 07/07 - 06/10 | $300,000 (total project: $10,730,000) |
| VA Merit Award | Sphingolipid- mediated skeletal muscle pathology in response to free fatty acids | Co-I | 04/2009 – 03/2012 | VA $775,000 |
| T15 LM07438-02 | Training of Toolmakers for Bio-Medical Informatics | PI | 07/02 - 06/10 | $1,727,872 |
| Cephos Inc | Developing statistical methodology for functional MRI-based deception detection | PI | 01/07 - 12/07 | $25,000 |
| 5 P20 RR016434-04 | SC COBRE for Cardiovascular Disease: Admin Core A4 - Pilot Program and Recruitment | Co-I | 9/2001 – 6/2006 | $300,000 |
| Department of Health of Shandong Province | Evaluation of thrombolytic therapy in unstable angina | **PI** | 1992 | Department of Health, Shandong Province, China |

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Invited Lectureships

1. ***Identifying biological concepts from a protein-related corpus***. Bioinformatics Seminar Series, UIUC, Urbana, IL, April, 2005
2. ***Determining functional coherence of proteins via protein-semantic network***. USC Bioinformatics Seminar Series, Columbia, SC, January 2006
3. ***Identifying gene expression modules via information integration***. Clemson University Genomic Institute, December 2006
4. ***Integrating multiple type information to identify gene expression modules***. Rosetta Pharmainformatics, Merck Research, Seattle, December 2006
5. ***Biomarker identification for fMRI-based deception detection***. Invited speaker for IEEE International Conference on Biomedical Engineering and Informatics, Sanya, China. May, 2008
6. ***Revealing a role for phytosphingosine-1-phosphate in HAP complex-mediated gene regulation in yeast by an ‘integromics’ approach***. University of South Carolina, Columbia, December 2008
7. ***Integromics approaches for biological discoveries***. University of Texas Health Science Center, Houston, TX, April, 2009
8. ***A signaling role of sphingosine-1-phosphate revealed by an ‘integromics’ approach***. Third South Carolina Symposium of Bioinformatics, April 15th ,Columbia, SC
9. ***Modeling cellular signaling systems with integromics approaches***. Invited seminar at the Department of Biomedical Informatics, University of Pittsburgh, Jan, 2010
10. ***Modeling sphingolipid-mediated signal transduction in yeast gene expression systems***. Invited presentation at the Eleventh Gordon Research Conference on Glycolipid and Sphingolipid Biology. Ventura, CA, Feb 2010
11. ***Modeling semantic information of the Gene Ontology and protein annotation***. University of Delaware, April, 2010
12. ***Revealing signal transduction pathways by unifying knowledge mining and data mining***. Center for Computational Biology and Bioinformatics, Indiana University, 2012
13. ***Identifying informative modular features for predicting cancer outcomes***. Invited presentation as the second best performing team, DREAM Conference, San Francisco, Nov, 2012
14. ***Revealing signaling pathways through integrating knowledge mining and data mining of systematic perturbation data***. Invited plenary presentation, The 5th Chinese Conference on Bioinformatics and Systems Biology, Harbin, China, August, 2012
15. ***Identifying signaling pathways through integrating knowledge mining and data mining.*** Invited Keynote Speaker, The International Conference on Translational Bioinformatics, Taicang, China, Dec 2012
16. ***From data towards knowledge: Reverse engineering and representing the signaling systems using systematic perturbation data***. Invited seminarStony Brook University, New York, Feb 2013
17. ***Identifying pathway-oriented molecular features for translational cancer medicine***. Invited Keynote Speaker, ACBIT’2013 Conference, Aizu, Japan
18. ***Treating the undruggables: A pathway-oriented analysis revealed novel therapeutic strategies for treating p53 mutations in cancer***. Invited seminar at the Stony Brook University Cancer Center, March, 2014.
19. ***Treating the undruggables: A pathway-oriented analysis revealed novel therapeutic strategies for treating p53 mutations in cancer***. Invited seminar at the School of Biomedical Informatics, the University of Texas at Houston, May 2014.
20. ***Personalized Precision Medicine for Cancers: a Big Data Approach***. Invited Keynote speaker, The 4th International Conference on Bioinformatics and Biomedical Engineering (ICBBE 2015), Shanghai, Sept 2015
21. ***Big data to bedside***: Cancer precision medicine in a big data era. Invited seminar at the University of Hawaii Cancer Center. Honolulu, HI, Nov, 2015
22. ***Big Data to Bedside (BD2B): Cancer Precision Medicine in the Big Data Era.***  The Center for BD2K (KnowEng) at the University of Illinois at Ubana-Chaimpaign. April, 2016.
23. ***Big Data to Bedside (BD2B): Cancer Precision Medicine in the Big Data Era.*** The University of West Virginia. Morgantown, November, 2016.
24. **From big data to bedside (DB2B): A computational perspective for precision oncology. Invited lecture at the University of Technology**, The International Workshop of Cancer Systems Biology, Zhuhai, China, June, 2017.
25. **From big data to bedside (DB2B): A computational perspective for precision oncology.** Invited lecture at the University of Technology, Sydney, August, 2017.
26. **From big data to bedside (DB2B):** **Towards AI-based clinical decision support for precision oncology,** Science 2018, From A to Z, University of Pittsburgh, October 18, 2018.
27. **From bid data to bedside (DB2B).** Head and Neck SPORE meeting, UPMC, Department of Otolaryngology, January 29, 2019.

Professional Services

## Member of Journal Editorial Board

* 2007-- present Associate Editor, ***BMC Research Notes***
* 2009 – 2014 Editorial Board Member, ***Open Systems Biology***
* 2013 – present Editorial Board, ***DNA Repair***
* 2016 - present Editorial Board, ***BMC* *Big Data Analytics***

## Journal/Conference Reviewer

* Applied Bioinformatics, Acta Biochimica et Biophysica Sinica, BMC Bioinformatics, IEEE Transactions on Neural Network IEEE Transactions on Information Sciences, International Journal of Psychiatry in Medicine, Journal of Biomedical Semantics Research, Journal of American Medical Informatics Association, Molecular Systems Biology,
* Program Committee, IEEE 7th International Symposium on Bioinformatics & Bioengineering (BIBE 2007)
* Chair, Special Session on Statistical Methods in Biomarker Identification, IEEE International Conference on Biomedical Engineering and Informatics, 2008 (BMEI 2008). Program Committee
* The International Conference on Models in Life Sciences, 2011
* Program Committee Member, The Fourth Summit on Systems Biology: Molecular Networks and Disease (2011)
* Program Committee Member, 2011 International Symposium on Computational Models for Life Sciences
* 2011 AMIA conference.
* Program Committee Member, 2012, the 12th Workshop on Algorithms in Bioinformatics, Lubljana, Slovenia.
* Program Committee Member, 2012, The International Conference on Translational Bioinformatics, Taicang, China
* Program Committee Member, 2013, The International Conference on Intelligent Biology and Medicine
* Program Committee Member, 2013, The First Aizu Conference on Biomedical Informatics and Technology (ACBIT'2013)
* Program Committee, 2014, BioVis 2014
* Program Committee, 2015, 2016, 2017, APBC 2016

## NIH Grant Study Sections

* 2008 – 2010 NIH/NLM Biomedical Library and Informatics Research Committee (BLIRC) study

section: a regular member of the study section, resigned because my move to Pitt created conflict of interests

* 2007 – 2012 Member, NLM Special Panel Study Section ZLM1 ZH-L. Meeting Sessions:

April , 2007; July, 2007; October, 2007; Feb, 2008; April, 2008; Sept, 2011; Jan, 2012; May, 2012

* 2011 Member, 2012/01 ZRG1 BST-H (40) P41 Review Panel
* 2112 Special Study Section on Climate Change and Health
* 2014 External Reviewer, Research Grants Council (RGC) of Hong Kong
* 2014 NLM Special panel on G08 Informatics Resource
* 2014 Special Study Section on the Centers of Biomedical Research Excellence
* 2015 NIGMS Centers of Pharmacogenomics, ZRG1BST-U(50), ZLM1-ZH-C-01
* 2016 ZMD1-MLS-11, BDMA (ad hoc member in Feb study section), ZGM1 TRN-3 (CO),

ZGM1-TRN-3-CO,  ZLM1-ZH-C-01, ZDK1-GRB-J-M1

* 2020 – 2024 Biomedical Informatics, Library and Data Sciences (BILDS) study section

**International Grant Review**

2020 Singapore National Research Foundation (NRF) Competitive Research Programme (CRP)

2021 Health Research Council of New Zealand (HRC)

# Academic Research Activities

# LIST OF CURRENT RESEARCH INTERESTS:

* Biomedical Informatics
* Cancer Genomics
* Bioinformatics
* Systems biology
* Machine learning and statistics
* Artificial intelligence
* Translational bioinformatics

### **SERVICE:**

###### **Medical University of South Carolina, Charleston, SC**

**University:**

2007 – 2009 CTSA Biomedical Informatics Workgroup

2007 – 2010 Member, Biomolecular Computing Resource Center, Steering Committee

2008 – 2010 Member, University Research Council.

**College:**

2007 – 2009 Member, First Year Curriculum Steering Committee

2005 – 2010 Training program directors, NLM training program, BTBBR training program, and GAANN training program

**Department:**

2003 – 2010 Student Progress Committee

2003 – 2010 Bioinformatics Curriculum Committee

2004 – 2008 Library Committee

2004 – 2010 Departmental IT committee

###### **University of Pittsburgh, Pittsburgh, Pennsylvania**

**University:**

2010- 2015 Co-Director, Center for Translational Bioinformatics,

2010 - present Member, UPCI Molecular and Cell Biology Program

2015 - 2019 Executive Committee member, The Center for Causal Discovery

**Department:**

2010 - 2017 Core Curriculum Committee

2011 - 2013 Preliminary Exam Committee

2015 - present Faculty Search Committee

2014 Department Colloquium/Seminar Coordinator

2014 - present Department Journal Club Coordinator, spring term

2015 – 2020 Department Strategic Planning Committee

1. PAGE score was an teaching evaluation score system used by the Medical University of South Carolina with 100 being the highest score before 2009 and 5 after 2009 [↑](#footnote-ref-2)