

Dr. Bingxin Lu

Contact Information	Department of Cell and Developmental Biology, University College London Gower Street, London, WC1E 6BT	b.lu@ucl.ac.uk
Research Interests	Computational biology; machine learning; algorithms; statistical inference; phylogenetics; population genetics; omics; platform and pipeline development; data analysis; method development and benchmarking; modeling; evolutionary dynamics; cancer evolution; mutational pattern and process	
Employment	Postdoctoral Fellow, University College London (UCL)	01/2019 - present
	Supervisor: Prof. Chris Barnes	
	Dynamical modeling of somatic genomes	
	- Developing methods to infer tumour sample phylogeny from copy number profiles - Modelling and analysis of chromosomal instability in experimental and real patient data	
	Postdoctoral Fellow, Genome Institute of Singapore (GIS)	09/2017 - 12/2018
	Supervisor: Prof. Weiwei Zhai	
	Analyzing tumour heterogeneity and clonal evolution	
	- Developing methods to simulate sequencing data of heterogeneous tumour samples - Analysis of intratumour heterogeneity in lung and liver cancer patient data	
Qualifications	Ph.D. Computer Science, National University of Singapore (NUS)	08/2013 - 09/2017
	Supervisor: Prof. Hon Wai Leong	
	Analyzing lateral gene transfer with computational methods	
	- Predicting genomic islands in a microbial genome with machine learning - Developing algorithms related to phylogenetic networks	
	M.Eng. Computer Software and Theory, East China Normal University	09/2010 - 07/2013
	Supervisor: Prof. Zhenbing Zeng, Prof. Tielu Shi	
	Developing high-throughput biological data analysis platform	
	- Platform for transcriptomic (RNA-Seq) data analysis - Platform for proteomics (MS/MS) data analysis	
	B.Eng. Software Engineering, East China Normal University (ECNU)	09/2005 - 07/2009
Teaching Experience	Teaching Assistant, Programming Methodology	08/2015 - 11/2015
	Department of Computer Science, NUS	
	Laboratory guidance; After class consulting; Assignment marking	
	Teaching Assistant, Discrete Mathematics	02/2011 - 06/2011
	Software Engineering Institute, ECNU	
	Tutorial teaching; Assignment marking	
Awards & Funding	Travel Fellowship, ECCB, The Hague, Netherlands	2016
	Student Travel Bursary, Winter School, The University of Queensland	2014
	Research Scholarship, National University of Singapore	2013 - 2017
	Excellent Graduate Student, East China Normal University	2009
Peer Review	APBC 2020; BMC Supplements (ICIBM 2021)	
Administrative Experience	Organizing a monthly joint journal club on cancer genomics with the research groups of Dr. Maria Secrier and Dr. Simone Zaccaria, UCL	11/2019 - present
Public Engagement	Volunteer for Scratch training workshop and the Junior Category Hackathon@SG, Singapore	
	07/2015	

Mentoring Experience	Christos Magkos (MSc Genetics of Human Disease), 2021, UCL, Comparison of phylogenetic tree reconstruction methods using metastatic breast cancer data	
	Abbie Duan (Undergraduate), 2021, UCL, Finding underlying patterns in copy number alteration data of gastric and colon cancers	
	Lisa Doetsch (Undergraduate summer project), 2020, UCL, Finding underlying patterns in copy number alteration data of gastric and colon cancers	
	Samuel Winnall (MSc Biological Physics), 2020, UCL, Dynamical modelling of the evolution of structural variation in cancer genomes	
	Simone De Angelis (MSc Genetics of Human Disease), 2020, UCL, Evaluating tree building methods for tumour copy number profiles	
	Rachel Muir (MSc Genetics of Human Disease), 2019, UCL, Evaluating phylogenetic inference of multi-region tumour data using copy number profiles	
	Abner Herbert Lim (Undergraduate intern project), 2018, GIS, Simulating next-generation sequencing data of tumour samples with PSiTE	
	Mengge Wang (Undergraduate intern project), 2017, NUS, Analysing features related to the prediction of genomics islands	
Industry Experience	Naiqi Qiu (Undergraduate), 2013, ECNU, The integration of PRIDE-tools and the MS-analysis-platform based on Galaxy	
	Software developer (C#), Jingchu Technologies Inc. (Beijing)	05/2010 - 08/2010
	Software developer (C++), Luban Software Co. Ltd. (Shanghai)	04/2009 - 08/2009
References	Software developer (Java), Carestream Health, Inc. (Shanghai)	
	07/2008 - 10/2008	
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	Department of Computer Science, NUS	leonghw@comp.nus.edu.sg
	Prof. Louxin Zhang	(+65) 6516-6579
	Department of Mathematics, NUS	matzlx@nus.edu.sg
	Prof. Weiwei Zhai	(+86) 010 6480 1720
	Institute of Zoology, Chinese Academy of Sciences	weiweizhai@ioz.ac.cn
Posters	Prof. Chris P. Barnes	(+44) 020 3108 2415
	Department of Cell and Developmental Biology, UCL	christopher.barnes@ucl.ac.uk
	Prof. Trevor A. Graham	(+44) 020 3437 6849
	The Institute of Cancer Research	trevor.graham@icr.ac.uk
	Tumour phylogeny reconstruction from copy number profiles of temporal multi-region samples, Bingxin Lu , Kit Curtius, Kane Smith, Ibrahim Al Bakir, Trevor A. Graham, Chris P. Barnes, <i>Evolution and Ecology of Cancer</i> , Hinxton, UK, 07/2019. (with lightning talk)	
	Fast Algorithms for the Cluster Containment Problem, Andreas D.M Gunawan, Bingxin Lu , and Louxin Zhang, <i>RECOMB</i> , Paris, France, 04/2018.	
	Computer program for verification of phylogenetic networks, Andreas D.M Gunawan, Bingxin Lu , Hon Wai Leong and Louxin Zhang, <i>RECOMB</i> , Hong Kong, China, 05/2017.	
	GI-Cluster: Detecting genomic islands in newly sequenced microbial genomes via consensus clustering on multiple features, Bingxin Lu and Hon Wai Leong, <i>RECOMB</i> , Hong Kong, China, 05/2017.	

Talks	GI-Cluster: detecting genomic islands via consensus clustering on multiple features. <i>GIW</i> , Seoul, Korea	10/2017
	A program to compute the soft Robinson–Foulds distance between phylogenetic networks. <i>APBC</i> , Shenzhen, China	01/2017
	A program for verification of phylogenetic network models. <i>ECCB</i> , The Hague, Netherlands	09/2016
	GI-SVM: A sensitive method for predicting genomic islands based on unannotated sequence of a single genome. <i>CSbio</i> , Bangkok, Thailand	11/2015
Papers submitted	Kasper Karlsson, Moritz Przybilla, Hang Xu, Eran Kotler, Kremena Karagyozyova, Alexandra Sockell, Katherine Liu, Amanda Mah, Yuan-Hung Lo, Bingxin Lu , et al. (2022). Experimental evolution in TP53 deficient human gastric organoids recapitulates tumorigenesis. <i>bioRxiv</i> : 2022.04.09.487529.	
	Bingxin Lu , Kit Curtius, Trevor A. Graham, Ziheng Yang, Chris P. Barnes (2022). CNETML: Maximum likelihood inference of phylogeny from copy number profiles of spatio-temporal samples. <i>bioRxiv</i> : 2022.03.18.484889.	
	William Cross [*] , Salpie Nowinski [*] , George Cresswell [*] , Maximilian Mossner [*] , Abhirup Banerjee [*] , Bingxin Lu [*] , et al. (2022). Evidence for stabilising selection causing grossly altered but broadly stable karyotypes in metastatic colorectal cancer. <i>bioRxiv</i> : 2020.03.26.007138. (* co-first authors)	
Publications	Full list at google scholar	
	Weiwei Zhai [*] , Hannah Lai [*] , Neslihan Arife Kaya [*] , Jianbin Chen [*] , Hechuan Yang [*] , Bingxin Lu [*] , et al. (2022). Dynamic phenotypic heterogeneity and the evolution of multiple RNA subtypes in Hepatocellular Carcinoma: the PLANET study. <i>National Science Review</i> , 9(3), nwab192. (* co-first authors)	
	Yannik Bollen, Ellen Stelloo, Petra van Leenen, Bas Ponsioen, Myrna van den Bos, Bingxin Lu , et al. (2021). Reconstructing single-cell karyotype alterations in colorectal cancer identifies punctuated and gradual diversification patterns. <i>Nature Genetics</i> , 53(8), 1187-1195.	
	Jianbin Chen, Hechuan Yang, Audrey Su Min Teo, Lidyana Bte Amer, Faranak Ghazi Sherbaf, Chu Quan Tan, Jacob Josiah Santiago Alvarez, Bingxin Lu , et al. (2020). Genomic landscape and ethnic specificity of lung adenocarcinoma in Asia. <i>Nature Genetics</i> , 52(2), 177-186.	
	Hechuan Yang, Bingxin Lu , Lan Huong Lai, Abner Herbert Lim, Jacob Josiah Santiago Alvarez, Weiwei Zhai (2019). PSiTE: A phylogeny guided simulator for tumor evolution. <i>Bioinformatics</i> , 35(17), 3148-3150.	
	Andreas D.M. Gunawan, Bingxin Lu , Louxin Zhang (2018). Fast methods for solving the Cluster Containment Problem for phylogenetic networks. <i>arXiv</i> :1801.04498.	
	Bingxin Lu , Hon Wai Leong (2018). GI-Cluster: detecting genomic islands via consensus clustering on multiple features. <i>Journal of Bioinformatics and Computational Biology</i> , 16(03), 1840010.	
	Jinwen Feng, Chen Ding, Naiqi Qiu, Xiaotian Ni, Dongdong Zhan, Wanlin Liu, Xia Xia, Peng Li, Bingxin Lu , et al. (2017). Firmiana: Towards a one-stop proteomic cloud platform for data processing and analysis. <i>Nature Biotechnology</i> , 35(5), 409-412.	
	Bingxin Lu , Louxin Zhang, Hon Wai Leong (2017). A program to compute the soft Robinson–Foulds distance between phylogenetic networks. <i>BMC Genomics</i> , 18(2), 111.	
	Andreas D.M. Gunawan [*] , Bingxin Lu [*] , Louxin Zhang (2016). A program for verification of phylogenetic network models. <i>Bioinformatics</i> , 32(17), i503-i510. (* co-first authors)	
	Bingxin Lu , Hon Wai Leong (2016). Computational methods for predicting genomic islands in microbial genomes. <i>Computational and Structural Biotechnology Journal</i> , 14:200-206.	

Bingxin Lu, Hon Wai Leong (2016). GI-SVM: A sensitive method for predicting genomic islands based on unannotated sequence of a single genome. *Journal of Bioinformatics and Computational Biology*, 14(01), 1640003.

Zhao Fang, **Bingxin Lu**, Mingyao Liu, Meixia Zhang, Zhenghui Yi, Chengping Wen, Tielu Shi (2013). Evaluating the pharmacological mechanism of Chinese medicine Si-Wu-Tang through multi-level data integration. *PLoS ONE*, 8(11), e72334.

Geng Chen, Charles Wang, Leming Shi, Weida Tong, Xiongfei Qu, Jiwei Chen, Jianmin Yang, Caiping Shi, Long Chen, Peiyong Zhou, **Bingxin Lu**, Tielu Shi. Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. *Human Genetics*, 132(8):899-911, 2013.

Bingxin Lu, Zhenbing Zeng, Tielu Shi (2013). Comparative study of de novo assembly and genome-guided assembly strategies for transcriptome reconstruction based on RNA-Seq. *Science China Life Sciences*, 56(2), 143-155.