

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), 01/2021 – 10/2021, UCL, Comparison of phylogenetic tree reconstruction methods using metastatic breast cancer data	
	Abbie Duan (Undergraduate), 10/2020 – 05/2021, UCL, Finding underlying patterns in copy number alteration data of gastric and colon cancers	
	Lisa Doetsch (Undergraduate summer project), 07/2020 – 10/2020, UCL, Finding underlying patterns in copy number alteration data of gastric and colon cancers	
	Simone De Angelis (MSc Genetics of Human Disease), 01/2020 – 09/2020, UCL, Evaluating tree building methods for tumour copy number profiles	
	Samuel Winnall (MSc Biological Physics), 10/2019 – 09/2020, UCL, Dynamical modelling of the evolution of structural variation in cancer genomes	
	Rachel Muir (MSc Genetics of Human Disease), 01/2019 – 09/2019, UCL, Evaluating phylogenetic inference of multi-region tumour data using copy number profiles	
	Abner Herbert Lim (Undergraduate intern project), 01/2018 – 06/2018, GIS, Simulating next-generation sequencing data of tumour samples with P <i>SiTE</i>	
	Mengge Wang (Undergraduate intern project), 11/2016 – 05/2017, NUS, Analysing features related to the prediction of genomics islands	
Industry Experience	Naiqi Qiu (Undergraduate), 12/2012 – 05/2013, 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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	Prof. Trevor A. Graham	(+44) 020 3437 6849
	The Institute of Cancer Research	trevor.graham@icr.ac.uk
	Prof. Weiwei Zhai	(+86) 010 6480 1720
	Institute of Zoology, Chinese Academy of Sciences	weiweizhai@ioz.ac.cn
Posters	Prof. Hon Wai Leong	(+65) 6516-2903
	Department of Computer Science, NUS	leonghw@comp.nus.edu.sg
	Prof. Louxin Zhang	(+65) 6516-6579
	Department of Mathematics, NUS	matzlx@nus.edu.sg
	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 Karagyozeva, 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, Peiying 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.