

Dr. Bingxin Lu

Contact Information	School of Biosciences, University of Surrey Stag Hill Campus 15AX02, Surrey, GU2 7XH	b.lu@surrey.ac.uk
Research Interests	Computational biology; machine learning; algorithms; pattern recognition; statistical inference; phylogenetics; population genetics; omics; platform and pipeline development; data analysis; method development and benchmarking; modelling; evolutionary dynamics; mutational pattern and process	
Employment	Surrey Future Fellow , University of Surrey	06/2023 -
	Postdoctoral Fellow , University College London (UCL)	01/2019 - 05/2023
	Principle Investigator: Prof. Chris Barnes Project: Dynamical modelling 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
	Principle Investigator: Prof. Weiwei Zhai Project: Analyzing tumour heterogeneity and clonal evolution - Developing methods to simulate sequencing data of heterogeneous tumour samples - Analysis of intra-tumour heterogeneity in lung and liver cancer patient data	
Education	Ph.D. Computer Science , National University of Singapore (NUS)	08/2013 - 09/2017
	Supervisor: Prof. Hon Wai Leong Project: 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 Project: 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	Teaching Assistant , Department of Computer Science, NUS	08/2015 - 11/2015
	Module: Programming Methodology (undergraduate) Role: Laboratory guidance on programming exercises; After class support; Assignment marking	
	Teaching Assistant , Software Engineering Institute, ECNU	02/2011 - 06/2011
	Module: Discrete Mathematics (undergraduate) Role: Tutorial on explaining solutions to exercises; Assignment and exam marking	
Student Mentoring	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 PSiTE

Mengge Wang (Undergraduate intern project), 11/2016 – 05/2017, NUS, Analysing features related to the prediction of genomics islands

Naiqi Qiu (Undergraduate), 12/2012 – 05/2013, ECNU, The integration of PRIDE-tools and the MS-analysis-platform based on Galaxy

Publications

Full list at [google scholar](#)

Bingxin Lu, Kit Curtius, Trevor A. Graham, Ziheng Yang, Chris P. Barnes (2023). CNETML: Maximum likelihood inference of phylogeny from copy number profiles of spatio-temporal samples. *Genome Biology*, 24, 144.

Kasper Karlsson, Moritz Przybilla, Eran Kotler, Aziz Khan, Hang Xu, Kremena Karagyzova, Alexandra Sockell, Wing H. Wong, Katherine Liu, Amanda Mah, Yuan-Hung Lo, **Bingxin Lu**, et al. (2023). Deterministic evolution and stringent selection during preneoplasia. *Nature*, 618, 383–393.

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. *National Science Review*, 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. *Nature Genetics*, 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. *Nature Genetics*, 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. *Bioinformatics*, 35(17), 3148–3150.

Andreas D.M. Gunawan, **Bingxin Lu**, Louxin Zhang (2018). Fast methods for solving the Cluster Containment Problem for phylogenetic networks. *arXiv:1801.04498*.

Bingxin Lu, Hon Wai Leong (2018). GI-Cluster: detecting genomic islands via consensus clustering on multiple features. *Journal of Bioinformatics and Computational Biology*, 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. *Nature Biotechnology*, 35(5), 409–412.

Bingxin Lu, Louxin Zhang, Hon Wai Leong (2017). A program to compute the soft Robinson–Foulds distance between phylogenetic networks. *BMC Genomics*, 18(2), 111.

Andreas D.M. Gunawan*, **Bingxin Lu***, Louxin Zhang (2016). A program for verification of phylogenetic network models. *Bioinformatics*, 32(17), i503–i510. (* co-first authors)

Bingxin Lu, Hon Wai Leong (2016). Computational methods for predicting genomic islands in microbial genomes. *Computational and Structural Biotechnology Journal*, 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.

Papers submitted	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)	
Posters	<p>A computational model of double strand breaks and repair characterizes the generation of structural variants, Bingxin Lu and Chris P. Barnes, <i>ECCB</i>, Barcelona, Spain, 09/2022.</p> <p>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)</p> <p>Fast Algorithms for the Cluster Containment Problem, Andreas D.M Gunawan, Bingxin Lu, and Louxin Zhang, <i>RECOMB</i>, Paris, France, 04/2018.</p> <p>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.</p> <p>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.</p>	
Talks	<p>GI-Cluster: detecting genomic islands via consensus clustering on multiple features. <i>GIW</i>, Seoul, Korea</p> <p>A program to compute the soft Robinson–Foulds distance between phylogenetic networks. <i>APBC</i>, Shenzhen, China</p> <p>A program for verification of phylogenetic network models. <i>ECCB</i>, The Hague, Netherlands</p> <p>GI-SVM: A sensitive method for predicting genomic islands based on unannotated sequence of a single genome. <i>CSbio</i>, Bangkok, Thailand</p>	<p>10/2017</p> <p>01/2017</p> <p>09/2016</p> <p>11/2015</p>
Awards & Funding	<p>Travel Fellowship, ECCB, The Hague, Netherlands</p> <p>Student Travel Bursary, Winter School, The University of Queensland</p> <p>Research Scholarship, National University of Singapore</p> <p>Excellent Graduate Student, East China Normal University</p>	<p>2016</p> <p>2014</p> <p>2013 - 2017</p> <p>2009</p>
Service	<p>Peer Review: APBC 2020; BMC Supplements (ICIBM 2021)</p> <p>Editing: PLOS One, guest editor</p> <p>Co-organizing a monthly joint journal club on cancer genomics with the research groups of Dr. Maria Secrier and Dr. Simone Zaccaria, UCL</p> <p>Volunteer for CGM (Chinese Genomics Meet-up) Europe</p>	<p>2023 -</p> <p>11/2019 - 05/2022</p> <p>11/2022 - 07/2023</p>
Public Engagement	<p>Volunteer for Soapbox Science, London</p> <p>Volunteer for Scratch training workshop and the Junior Category Hackathon@SG, Singapore</p>	<p>05/2023</p> <p>07/2015</p>
Industry Experience	<p>Software developer (C#), Jingchu Technologies Inc. (Beijing)</p> <p>Software developer (C++), Luban Software Co. Ltd. (Shanghai)</p> <p>Software developer (Java), Carestream Health, Inc. (Shanghai)</p>	<p>05/2010 - 08/2010</p> <p>04/2009 - 08/2009</p> <p>07/2008 - 10/2008</p>
References	<p>Prof. Chris P. Barnes Department of Cell and Developmental Biology, UCL</p> <p>Prof. Trevor A. Graham The Institute of Cancer Research</p> <p>Prof. Weiwei Zhai Institute of Zoology, Chinese Academy of Sciences</p> <p>Prof. Hon Wai Leong Department of Computer Science, NUS</p> <p>Prof. Louxin Zhang Department of Mathematics, NUS</p>	
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