Dr. Bingxin Lu

Contact Information	School of Biosciences, PAI Institute, University of Surrey Stag Hill Campus 12BA02, 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

Lecturer, University of Surrey — 07/2025 -

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. Tieliu 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, School of Biosciences, University of Surrey

Module: Analytical and Clinical Biochemistry (undergraduate) — 02/2025
Role: Lectures on statistics and data analysis

Module: Systems Biology (undergraduate) — 02/2024, 10/2024
Role: Practical sessions on using MATLAB, COPASI, and OptFlux to model biological processes

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: Tutorials on explaining solutions to exercises; Assignment and exam marking

Student Mentoring

finished (including co-supervised): 7 Master thesis, 5 Undergraduate thesis, 4 Undergraduate intern projects

ongoing: 3 Master thesis, 1 Undergraduate intern project

Awards & Funding	MRC New Investigator Grant (£606K), UKRI, UK	2025 - 2028
	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

Publications

Full list at google scholar

Bingxin Lu, Samuel Winnall, William Cross, Chris P. Barnes (2025). Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability. *Nature Communications*, 16, 3033.

Bingxin Lu. (2025). Cancer phylogenetic inference using copy number alterations detected from DNA sequencing data. *Cancer Pathogenesis and Therapy*, 3, 16-29.

Cheng Zhao, Darren P. Ennis, **Bingxin Lu**, Hasan B. Mirza, Chishimba Sokota, Baljeet Kaur, Naveena Singh et al. (2024). The genomic trajectory of ovarian high grade serous carcinoma can be observed in STIC lesions. *The Journal of Pathology*, 264, 42-54.

Jianbin Chen, Neslihan Arife Kaya, Ying Zhang, Raden Indah Kendarsari, Karthik Sekar, Shay Lee Chong, Veerabrahma Pratap Seshachalam, Wen Huan Ling, Cheryl Zi Jin Phua, Hannah Lai, Hechuan Yang, **Bingxin Lu** et al. (2024). A multimodal atlas of hepatocellular carcinoma reveals convergent evolutionary paths and 'bad apple' effect on clinical trajectory. *Journal of Hepatology*, 4(81), 667-678.

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 Karagyozova, 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, Tieliu 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**, Tieliu 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, Tieliu 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 accepted	William Cross[*], Salpie Nowinski[*], George Cresswell[*], Maximilian Mossner[*], Abhirup Banerjee[*], **Bingxin Lu**[*], et al. (2024). Negative selection may cause grossly altered but broadly stable karyotypes in metastatic colorectal cancer. *bioRxiv*: 10.1101/2020.03.26.007138. (* co-first authors)
Posters	Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability, **Bingxin Lu**, Samuel Winnall, William Cross, Chris P. Barnes, *ISMB*, Montreal, Canada, 07/2024.
	A computational model of double strand breaks and repair characterizes the generation of structural variants, **Bingxin Lu** and Chris P. Barnes, *ECCB*, Barcelona, Spain, 09/2022.
	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, *Evolution and Ecology of Cancer*, Hinxton, UK, 07/2019. (with lightning talk)
	Fast Algorithms for the Cluster Containment Problem, Andreas D.M Gunawan, **Bingxin Lu**, and Louxin Zhang, *RECOMB*, Paris, France, 04/2018.
	Computer program for verification of phylogenetic networks, Andreas D.M Gunawan, **Bingxin Lu**, Hon Wai Leong and Louxin Zhang, *RECOMB*, 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, *RECOMB*, Hong Kong, China, 05/2017.
Talks	Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability. *MASAMB*, London, UK 08/2024
	Dynamic modeling of chromosomal instability in somatic genomes. *APBioNETTalks*, online 06/2024
	Tumour phylogeny reconstruction from copy number profiles of multiple samples. *Shandong University*, Qingdao, China 12/2023
	A computational model of double strand breaks and repair characterizes the generation of somatic structural variants. *CSHA*, Suzhou, China 12/2023
	Dynamic modeling of chromosomal instability in somatic genomes. *Institute of Zoology Chinese Academy of Sciences*, Beijing, China 11/2023
	GI-Cluster: detecting genomic islands via consensus clustering on multiple features. *GIW*, Seoul, Korea 10/2017
	A program to compute the soft Robinson–Foulds distance between phylogenetic networks. *APBC*, Shenzhen, China 01/2017
	A program for verification of phylogenetic network models. *ECCB*, The Hague, Netherlands 09/2016
	GI-SVM: A sensitive method for predicting genomic islands based on unannotated sequence of a single genome. *CSbio*, Bangkok, Thailand 11/2015

Service	Peer Review: APBC 2020; BMC Supplements (ICIBM 2021); CSBJ; Functional & Integrative Genomics; BioData Mining; BMC Bioinformatics, PLOS One	
	Editing: PLOS One, guest editor	2023 -
	EDI: committee member, School of Biosciences, University of Surrey	08/2024 -
	Co-organized a monthly joint journal club on cancer genomics at UCL	11/2019 - 05/2022
	Volunteer for CGM (Chinese Genomics Meet-up) Europe	11/2022 - 07/2023
Public Engagement	Volunteer for Soapbox Science, London	05/2023
	Volunteer for Scratch training workshop and the Junior Category Hackathon@SG, Singapore 07/2015	
Industry Experience	Software developer (C#), Jingchu Technologies Inc. (Beijing)	05/2010 - 08/2010
	Software developer (C++), Luban Software Co. Ltd. (Shanghai)	04/2009 - 08/2009
	Software developer (Java), Carestream Health, Inc. (Shanghai)	07/2008 - 10/2008
References	Prof. Chris P. Barnes	(+44) 020 3108 2415
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	Prof. Weiwei Zhai	(+86) 010 6480 1720
	Institute of Zoology, Chinese Academy of Sciences	weiweizhai@ioz.ac.cn
	Prof. Hon Wai Leong	(+65) 6516 2903
	Department of Computer Science, NUS	leonghw@comp.nus.edu.sg