

## Dr. Bingxin Lu

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<b>Contact Information</b>	School of Biosciences, PAI Institute, University of Surrey Stag Hill Campus 12BA02, Surrey, GU2 7XH	b.lu@surrey.ac.uk
<b>Research Interests</b>	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	
<b>Employment</b>	<b>Surrey Future Fellow</b> , University of Surrey	06/2023 -
	<b>Postdoctoral Fellow</b> , University College London (UCL) 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	01/2019 - 05/2023
	<b>Postdoctoral Fellow</b> , Genome Institute of Singapore (GIS) 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	09/2017 - 12/2018
<b>Education</b>	<b>Ph.D. Computer Science</b> , National University of Singapore (NUS) 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	08/2013 - 09/2017
	<b>M.Eng. Computer Software and Theory</b> , East China Normal University 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	09/2010 - 07/2013
	<b>B.Eng. Software Engineering</b> , East China Normal University (ECNU)	09/2005 - 07/2009
<b>Teaching</b>	<b>Teaching Assistant</b> , School of Biosciences, University of Surrey Module: Analytical and Clinical Biochemistry (undergraduate) Role: Lectures on statistics and data analysis	02/2025
	Module: Systems Biology (undergraduate) Role: Practical sessions on using MATLAB, COPASI, and OptFlux to model biological processes	02/2024, 10/2024
	<b>Teaching Assistant</b> , Department of Computer Science, NUS Module: Programming Methodology (undergraduate) Role: Laboratory guidance on programming exercises; After class support; Assignment marking	08/2015 - 11/2015
	<b>Teaching Assistant</b> , Software Engineering Institute, ECNU Module: Discrete Mathematics (undergraduate) Role: Tutorials on explaining solutions to exercises; Assignment and exam marking	02/2011 - 06/2011
<b>Student Mentoring</b>	finished (including co-supervised): 6 Master thesis, 4 Undergraduate thesis, 4 Undergraduate intern projects ongoing: 4 Master thesis, 3 Undergraduate thesis, 1 Undergraduate intern project	
<b>Awards &amp; Funding</b>	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](#)

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*.

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*.

**Bingxin Lu**. (2024). Cancer phylogenetic inference using copy number alterations detected from DNA sequencing data. *Cancer Pathogenesis and Therapy*, 2, E27-E77.

**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 Karagyozyova, 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, Lidiana 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 submitted**

**Bingxin Lu**, Samuel Winnall, William Cross, Chris P. Barnes (2024). Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability. *bioRxiv*: 10.1101/2024.01.03.574048. (accepted by *Nature Communications*)

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

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

<b>Public Engagement</b>	Volunteer for Soapbox Science, London	05/2023
	Volunteer for Scratch training workshop and the Junior Category Hackathon@SG, Singapore	07/2015
<b>Industry Experience</b>	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
<b>References</b>	Prof. Chris P. Barnes Department of Cell and Developmental Biology, UCL	(+44) 020 3108 2415 christopher.barnes@ucl.ac.uk
	Prof. Weiwei Zhai Institute of Zoology, Chinese Academy of Sciences	(+86) 010 6480 1720 weiweizhai@ioz.ac.cn
	Prof. Hon Wai Leong Department of Computer Science, NUS	(+65) 6516 2903 leonghw@comp.nus.edu.sg