

Dr. Bingxin Lu

| | | |
|----------------------------|---|--|
| Contact Information | School of Biosciences, 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 | Surrey Future Fellow , University of Surrey | 06/2023 - |
| | Postdoctoral Fellow , 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 |
| | Postdoctoral Fellow , 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 |
| Education | Ph.D. Computer Science , 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 |
| | M.Eng. Computer Software and Theory , East China Normal University 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 | 09/2010 - 07/2013 |
| | B.Eng. Software Engineering , East China Normal University (ECNU) | 09/2005 - 07/2009 |
| Teaching | Teaching Assistant , School of Biosciences, University of Surrey Module: Systems Biology (undergraduate) Role: Practical sessions on using MATLAB, COPASI, and OptFlux to model biological processes | 02/2024, 10/2024 |
| | Teaching Assistant , Department of Computer Science, NUS Module: Programming Methodology (undergraduate) Role: Laboratory guidance on programming exercises; After class support; Assignment marking | 08/2015 - 11/2015 |
| | Teaching Assistant , Software Engineering Institute, ECNU Module: Discrete Mathematics (undergraduate) Role: Tutorial on explaining solutions to exercises; Assignment and exam marking | 02/2011 - 06/2011 |
| Student Mentoring | finished (including co-supervised): 6 Master thesis, 4 Undergraduate thesis, 3 Undergraduate intern projects ongoing: 1 Master thesis, 3 Undergraduate thesis, 2 Undergraduate intern projects | |

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, 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.

| | | |
|-----------------------------|---|--|
| | <p>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. <i>Science China Life Sciences</i>, 56(2), 143-155.</p> | |
| Papers submitted | <p>Bingxin Lu, Samuel Winnall, William Cross, Chris P. Barnes (2024). Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability. <i>bioRxiv</i>: 10.1101/2024.01.03.574048.</p> <p>Cheng Zhao, Darren P. Ennis, Bingxin Lu, et al. (2024). The genomic trajectory of ovarian high grade serous carcinoma is determined in STIC lesions. <i>bioRxiv</i>: 10.1101/2024.03.11.584384.</p> <p>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. <i>bioRxiv</i>: 10.1101/2020.03.26.007138. (* co-first authors)</p> | |
| Posters | <p>Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability, Bingxin Lu, Samuel Winnall, William Cross, Chris P. Barnes, <i>ISMB</i>, Montreal, Canada, 07/2024.</p> <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>Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability. <i>MASAMB</i>, London, UK 08/2024</p> <p>Dynamic modeling of chromosomal instability in somatic genomes. <i>APBioNETTalks</i>, online 06/2024</p> <p>Tumour phylogeny reconstruction from copy number profiles of multiple samples. <i>Shandong University</i>, Qingdao, China 12/2023</p> <p>A computational model of double strand breaks and repair characterizes the generation of somatic structural variants. <i>CSHA</i>, Suzhou, China 12/2023</p> <p>Dynamic modeling of chromosomal instability in somatic genomes. <i>Institute of Zoology Chinese Academy of Sciences</i>, Beijing, China 11/2023</p> <p>GI-Cluster: detecting genomic islands via consensus clustering on multiple features. <i>GIW</i>, Seoul, Korea 10/2017</p> <p>A program to compute the soft Robinson–Foulds distance between phylogenetic networks. <i>APBC</i>, Shenzhen, China 01/2017</p> <p>A program for verification of phylogenetic network models. <i>ECCB</i>, The Hague, Netherlands 09/2016</p> <p>GI-SVM: A sensitive method for predicting genomic islands based on unannotated sequence of a single genome. <i>CSbio</i>, Bangkok, Thailand 11/2015</p> | |
| Awards & Funding | <p>MRC New Investigator Grant, UKRI, UK 2025 - 2028</p> <p>Travel Fellowship, ECCB, The Hague, Netherlands 2016</p> <p>Student Travel Bursary, Winter School, The University of Queensland 2014</p> <p>Research Scholarship, National University of Singapore 2013 - 2017</p> <p>Excellent Graduate Student, East China Normal University 2009</p> | |

| | | |
|----------------------------|---|------------------------------|
| 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 |
| 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 |
| | Department of Cell and Developmental Biology, UCL | christopher.barnes@ucl.ac.uk |
| | 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 |