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 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 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. *bioRxiv*: 2020.03.26.007138. (* co-first authors)

Posters

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

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

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

Service

Peer Review: APBC 2020; BMC Supplements (ICIBM 2021)	
Editing: PLOS One, guest editor	2023 -
Co-organizing a monthly joint journal club on cancer genomics with the research groups of Dr. Maria Secrier and Dr. Simone Zaccaria, 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

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