

Lu Eric Zhang

Contact Information

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Work experience

- **Associate Professor (with tenure)**, Hong Kong Baptist University, HK
2024.7-now, Department of Computer Science (early promotion)
- **Assistant Professor**, Hong Kong Baptist University, HK
2019.2-2024.6, Department of Computer Science
- **Honorary Research Officer**, Imperial College London, UK
2014.8-2017.7 Department of Medicine
- **Research Assistant**, The University of Hong Kong, HK
2008.10-2010.9 Department of Paediatrics and Adolescent Medicine

Education Background

- **Postdoctoral Fellow**, Stanford University, USA
2016.6-2019.1, Department of Computer Science and Pathology
- **Postdoctoral Scholar**, City University of Hong Kong, HK
2016.2-2016.5, Department of Computer Science
- **Visiting PhD student**, UC Berkeley, USA
2015.1-2015.7, Department of Mathematics
- **PhD**, City University of Hong Kong, HK
2012.10-2016.2, Department of Computer Science
- **MPhil**, The University of Hong Kong, HK
2010.9-2012.9 Department of Paediatrics and Adolescent Medicine
- **BEng**, Tianjin University, Tianjin, China
2004.9-2008.7 School of Software Engineering

Research Interests

- Develop assembly algorithms and deep learning models for metagenomic sequencing data analysis
- Develop deep learning models for single-cell sequencing data analysis
- Develop AI-based foundation models for genomics and drug discovery

Grant

- Improved Metabolic Network Reconstruction and Metabolite Profiles Prediction using Complete and Strain-Resolved Microbial Genomes. Young Collaborative Research Grant. YCRG, RGC/C2004-23Y (**PC, 4,494,061HKD, 2024.6-2027.5**).
- Development of a target sequencing system for long-read sequencing technology based on restriction enzymes. TCFS, GHX/270/22SZ, (Supported in principle. **PI, 1,300,000HKD, not started**).
- Advancing clinical differentiation between constipation-predominant irritable bowel syndrome and functional constipation using machine learning models. HMRF, 11221026 (**PI, 487,800HKD, 2024.9-2027.9, not started**).
- Computational models for health management system using multi-source data, TCFS, GHX/133/20SZ, (**PI, 1,844,600HKD, 2022.9-2024.8**).
- 基于长读长测序技术的宏基因组组装算法研究, BGI Open Fund, BGIRSZ20220014, (**PI, 450,000RMB, 2023.1-2024.12**).
- A computational framework to prioritize disease-associated low frequency variants from Identity-By-Descent regions, ECS HKBU22201419, (**PI, 651,769HKD,**

2019.9-2023.2)

- A novel metagenome assembly algorithm by using single tube long fragment sequencing. Guangdong Basic and Applied Basic Research Foundation 2019A1515011046, **(PI, 100,000RMB, 2019.9-2022.8)**
- A graph-based diploid assembly algorithm for detecting structural variants on 10x Linked-Read sequencing. Guangdong Basic and Applied Basic Research Foundation 2021A1515012226, **(PI, 100,000RMB, 2021.9-2024.8)**
- 一种基于单体型局部组装和共有单体型分析的复杂疾病罕见变异识别算法, Shenzhen Virtual University Park (SZVUP) Special Fund 2021Szvup135, **(PI, 187,000RMB, 2021.8-2023.7).**
- A High-resolution Global Metagenome Catalog from Uncultured Human Gut Microbiota. IRCMS/19-20/D02, Interdisciplinary Research Clusters Matching Scheme **(PI, 637,500HKD, Internal grant)**
- A computational network-based framework for analyzing single-cell sequencing. Startup grant Tier 2 RC-SGT2/19-20/SCI/007, **(PI, 480,000HKD, Internal grant)**

Awards and Honors

- Excellent Paper Award, Faculty of Science, Hong Kong Baptist University, 2024
- President's Award for Outstanding Performance as Early Career Researcher, Hong Kong Baptist University, 2023
- Best Teaching Award, Department of Computer Science, Hong Kong Baptist University, 2022
- Travel Grants for Exchange Activities of Research Students, City University of Hong Kong, 2015
- University Postgraduate Fellowship, City University of Hong Kong, 2012-2015
- University Postgraduate Fellowship, The University of Hong Kong, 2010-2012
- Best practice award, Bio-IT World 2012
- Second roll of Imagine Cup 2007
- First-class prize in the China Adolescents Science and Technology Innovation Competition in 2003
- First-class prize in the China Adolescents Science and Technology Innovation Competition in 1998

Publications (†co-first author, *corresponding author)

Published Journal Papers (Impact factor of 2023)

Under Review

1. Chao Yang[†], Jingjing Wang[†], Debajyoti Chowdhury, Yijing Zhang, Lixiang Zhai, Yufen Huang, Yuanwei Zhang, Xiaodong Fang, ZhaoXiang Bian, **Lu Zhang***. Integrated analysis of gut microbiome compositional and genomic alterations reveals strain diversity and actionable biomarkers across multiple colorectal cancer cohorts. Submitted to **Microbiome (Q1, IF: 13.8)**
2. Zeming Li[†], Xuwei Luo[†], Zhenhua Yang[†], Huayu Zhang, Long Ge, Zhaoxiang Bian, James Zou*, Yaolong Chen*, **Lu Zhang***, on behalf of the ADVANCED working group. RAPID: Reliable and efficient automatic generation of submission reporting checklists with large language models. Submitted to **Nature Machine Intelligence (Q1, IF: 18.8)**
3. Guo Mao, Hiu Fung Yip, **Lu Zhang***. IDCLP: A Deep Learning Framework for Predicting Chemical-Induced Gene Expression Profiles through Multisource Data Integration. Submitted to **Nucleic Acids Research (Q1, IF: 13.6)**
4. Juan Shen, Weiming Liang, Ruizhen Zhao, Yang Chen, Yaming Liu, Wei Cheng,

Tailiang Chai, Yin Zhang, Silian Chen, Jiazhe Liu, Xueting Chen, Yusheng Deng, Zhao Zhang, Yufen Huang, Huanjie Yang, Li Pang, Qinwei Qiu, Haohao Deng, Shanshan Pan, Linying Wang, Jingjing Ye, Wen Luo, Xuanning Jiang, Xiao Huang, Wanshun Li, Lixian Liang, **Lu Zhang**, Li Huang, Zhimin Yang, Rouxi Chen, Junpu Mei, Zhen Yue, Hong Wei, Karsten Kristiansen, Lijuan Han, Xiaodong Fang. Cross-tissue multi-omics analyses reveal the gut microbiota's absence impacts organ morphology, immune homeostasis, bile acid, and lipid metabolism. Major Revision in **iMeta (Q1, IF: 23.8)**

5. Honghao Lai, Jiayi Liu, Danni Xia, Chunyang Bai, Mingyao Sun, Bei Pan, Jiajie Huang, Liangying Hou, Weilong Zhao, Jinhui Tian, Yaolong Chen, **Lu Zhang**, Janne Estill, Jie Liu, Xing Liao, Nannan Shi, Xin Sun, Hongcai Shang, Zhaoxiang Bian, Kehu Yang, Luqi Huang, Long Ge. Language Models for Data Extraction and Risk of Bias Assessment in Complementary Medicine. Major Revision in **Npj Digital Medicine (Q1, IF:12.4)**
6. Zirui Wang, Ke Xu, Yang Liu, Yu Xu, **Lu Zhang***. Mitigation of multi-scale biases in cell-type deconvolution for spatially resolved transcriptomics using HarmoDecon. Under Review in **PNAS (Q1, IF:10.1)**. doi: 10.1101/2024.10.02.616209v1
7. Zhenmiao Zhang, Mingxing Rao, Yufen Huang, **Lu Zhang***. A graph-based Gaussian Mixture Variational Autoencoder improves metagenome binning for short contigs. Major revision in **Nature Communications (Q1, IF:14.7)**. doi: 10.21203/rs.3.rs-3308172/v1
8. Chonghao Wang, Werner Pieter Veldsman, **Lu Zhang***. Detection of short identity by descent segments using low-frequency variants. Major revision in **Genome Research (Q1, IF:6.2)**. doi: 10.1101/2023.09.26.559464
9. Ke Xu, Yu Xu, Zirui Wang, Xin Zhou*, **Lu Zhang***. stDyer enables spatial domain clustering with dynamic graph embedding. Major revision in **Genome Biology (Q1, IF:10.1)**. doi.org/10.1101/2024.05.08.593252
10. Yu Xu, Chonghao Wang, Ke Xu, Yi Ding, Aiping Lyu*, **Lu Zhang***. TRAFICA: An Open Chromatin Language Model to Improve Transcription Factor Binding Affinity Prediction. Under Review in **Nature Communications (Q1, IF:14.7)**. doi.org/10.1101/2023.11.02.565416
11. Xufei Luo[†], Zeming Li[†], Zhenhua Yang[†], Yanfang Ma, Fengxian Chen, Qi Wang, Long Ge, James Zou*, **Lu Zhang***, Yaolong Chen*, Zhaoxiang Bian, on behalf of the ADVANCED working group. Using large language models to assess the consistency of randomized controlled trials on AI interventions with CONSORT-AI: a cross-sectional survey. Major Review in **International Journal of Surgery (Q1, IF:12.5)**.
12. Xiangzhe Yuan, Chonghao Wang, **Lu Zhang***, DBNL: A Machine Learning Method for Ensembling Polygenic Risk Scores and Non-Genetic Factors. Under Review in **IEEE/ACM Transactions on Computational Biology and Bioinformatics (Q1, 3.6)**.
13. Werner Pieter Veldsman, Qi Zhang, Qian Zhao, **Lu Zhang***. The antimicrobial peptides pipeline: a bacteria-centric AMP predictor. Minor Revision in **Current Gene Therapy (Q2, IF: 3.8)**. doi: 10.1101/2024.05.26.595993

2024

1. Bohao Zou, JingJing Wang, Yi Ding, Zhenmiao Zhang, Yufen Huang, Xiaodong Fang, Ka Chun Cheung, Simon See and **Lu Zhang***. A multi-modal deep language model to contaminant removal contamination from metagenome-assembled genomes. **Nature Machine Intelligence (Q1, IF:18.8)**. doi: 10.1038/s42256-024-

2. Luo Xufei, Lyu Han, Song Zaiwei, Liu Hui, Wang Zhixiang, Li Haodong, Wang Ye, Zhu Di, **Lu Zhang***, Chen Yaolong*. The Impact of Generative Artificial Intelligence on the Development, Evaluation, and Application of Clinical Practice Guidelines. **Medical Journal of Peking Union Medical College Hospital**. doi: 10.12290/xhyxzz.2024-0602
3. Chao Yang, Zhenmiao Zhang, Yufen Huang, Xuefeng Xie, Herui Liao, Jin Xiao, Werner Pieter Veldsman, Kejing Yin, Xiaodong Fang*, **Lu Zhang***. LRTK: A platform agnostic toolkit for linked-read analysis of both human genomes and metagenomes. **GigaScience (Q1, IF: 11.8)**. doi: 10.1093/gigascience/giae028
4. Zhenmiao Zhang, Jin Xiao, Hongbo Wang, Chao Yang, Yufeng Huang, Zhen Yue, Yang Chen, Lijuan Han, Aiping Lyu, Xiaodong Fang, **Lu Zhang***. Exploring high-quality microbial genomes by assembling short-reads with long-range connectivity. **Nature Communications (Q1, IF: 14.7)**. doi: 10.1038/s41467-024-49060-z
5. Werner Pieter Veldsman, Chao Yang, Zhenmiao Zhang, Yufen Huang, Debajyoti Chowdhury and **Lu Zhang***. Structural and Functional Disparities within the Human Gut Virome in terms of Genome Topology and Representative Genome Selection. **Viruses-Basel (Q1, IF: 3.8)**. doi:10.3390/v16010134

2023

1. Zhenmiao Zhang, Chao Yang, Werner Pieter Veldsman, Xiaodong Fang, **Lu Zhang***. Benchmarking genome assembly methods on metagenomic sequencing data. **Briefings in Bioinformatics (Q1, IF: 6.8)**. doi: 10.1093/bib/bbad087
2. Jingjing Wang, Werner Pieter Veldsman, Xiaodong Fang, Yufen Huang, Xuefeng Xie, Aiping Lyu, **Lu Zhang***. Benchmarking multi-platform sequencing technologies for human genome assembly. **Briefings in Bioinformatics (Q1, IF: 6.8)**. doi: 10.1093/bib/bbad3
3. Ke Xu, ChinWang Cheong, Werner Pieter Veldsman, Aiping Lyu*, William K. Cheung*, **Lu Zhang***. Accurate and interpretable gene expression imputation on scRNA-seq data using IGSimpute. **Briefings in Bioinformatics (Q1, IF: 6.8)**. doi:10.1093/bib/bbad124
4. Lixiang Zhai, Haitao Xiao, Chengyuan Lin, Yan Y Lam, Hoi Leong Xavier Wong, Mengxue Gong, Guojun Wu, Yusheng Deng, Ziwan Ning, Chunhua Huang, Yijing Zhang, Min Zhuang, Chao Yang, **Lu Zhang**, Ling Zhao, Chenhong Zhang, Xiaodong Fang, Wei Jia, Liping Zhao, Zhao-xiang Bian. Gut microbiota-derived tryptamine impairs insulin sensitivity. **Nature Communications (Q1, IF: 14.7)**. doi: 10.1038/s41467-023-40552-y
5. Werner P. Veldsman, Xin Maizie Zhou, Yuanwei Zhang, Bailiang Li, **Lu Zhang***. Editorial: Predicting high-risk individuals for common diseases using multi-omics and epidemiological data, volume II. **Frontiers in Genetics (Q2, IF: 2.8)**. doi: 10.3389/fgene.2023.1280648

2022

1. Lixiang Zhai, Chunhua Huang, Ziwan Ning, Yijing Zhang, Min Zhuang, Wei Yang, Xiaolei Wang, Jingjing Wang, **Lu Zhang**, Haitao Xiao, Ling Zhao, Yan Y Lam, Chi Fung Willis Chow, Jiandong Huang, Shuofeng Yuan, Kui Ming Chan, Hoi Leong Xavier Wong, Zhao-xiang Bian. Ruminococcus gnavus plays a pathogenic role in diarrhea-predominant irritable bowel syndrome by increasing serotonin biosynthesis. **Cell Host and Microbe (Q1, IF: 31.3)**. doi: 10.1016/j.chom.2022.11.006

2. Chonghao Wang, Jing Zhang, Xin Zhou, **Lu Zhang***. A comprehensive investigation of the statistical and machine learning approaches for human complex disease prediction. **Briefings in Bioinformatics (Q1, IF: 6.8)**. doi: 10.1093/bib/bbac552
3. Yu Xu, Jiaying Chen, Aiping Lyu, William K Cheung, **Lu Zhang***. dynDeepDRIM: a dynamic deep learning model to infer direct regulatory interactions using single cell time-course gene expression data. **Briefings in Bioinformatics (Q1, IF: 6.8)**. doi: 10.1093/bib/bbac424
4. FengShi, Delbert Almerick T Boncanc, Hin Ting Wan, Ting Fung Chan, **Lu Zhang**, Keng Po Lai, Chris Kong-Chu Wong. Hepatic metabolism gene expression and gut microbes in offspring, subjected to in-utero PFOS exposure and postnatal diet challenges. **Chemosphere (Q1, IF: 8.1)**. doi: 10.1016/j.chemosphere.2022.136196.
5. WANG Hongbo, Hin Ting WAN, WU Bin, JIAN Jianbo, HM Alice, Claire Yik-Lok CHUNG, Eugene Yui-Ching CHOW, Jizhou ZHANG, OL Anderson, Keng Po LAI, Ting Fung CHAN, **Lu Zhang***, Chris Kong-Chu WONG*. A Chromosome-level Assembly of the Japanese Eel Genome, Insights into Gene Duplication and Chromosomal Reorganization. **GigaScience (Q1, IF: 11.8)**. doi: 10.1093/gigascience/giac120
6. Yunfei Hu, Sanidhya Mangal, **Lu Zhang**, Xin Zhou. Automated filtering of genome-wide large deletions through an ensemble deep learning framework. **Methods (Q1, IF: 4.2)**. doi:10.1016/j.ymeth.2022.08.001

2021

1. Chao Yang, Debajyoti Chowdhury, Zhenmiao Zhang, William K. Cheung, Aiping Lu, ZhaoXiang Bian, **Lu Zhang***. A review of computational tools for generating metagenome-assembled genomes from metagenomic sequencing data. **Computational and Structural Biotechnology Journal (Q1, IF: 4.4)**. doi: 10.1016/j.csbj.2021.11.028
2. Zi-Hang Wen, Jeremy L. Langsam, **Lu Zhang**, Wenjun Shen, Xin Zhou. A Bayesian factorization method to recover single-cell RNA sequencing data. **Cell Reports Methods (Q2, IF: 4.3)**. doi: 10.2139/ssrn.3867727
3. Li Song, **Lu Zhang***, Xiaodong Fang*. Characterizing enterotypes in human metagenomics: a viral perspective. **Frontiers in Microbiology (Q2, IF: 4)**. doi: 10.3389/fmicb.2021.740990
4. Yichen Henry Liu, Griffin L. Grubbs, **Lu Zhang**, Xiaodong Fang, David L. Dill, Arend Sidow, Xin Zhou. Aquila_stLFR: diploid genome assembly based structural variant calling package for stLFR linked-read. **Bioinformatics Advances (Q4, IF: 2.4)**. doi:10.1093/bioadv/vbab007/6300508.
5. Debajyoti Chowdhury, Maizie (Xin) Zhou, Bailiang Li, Yuanwei Zhang, William K Cheung, Aiping Lu, **Lu Zhang***. Predicting High-Risk Individuals for Common Diseases Using Multi-Omics and Epidemiological Data. **Frontiers in Genetics (Q2, IF: 2.8)**. doi: 10.3389/fgene.2021.737598.
6. Jiaying Chen, Chinwang Cheong, Liang Lan, Xin Zhou, Jiming Liu, Aiping Lyu, William K Cheung*, **Lu Zhang***. DeepDRIM: a deep neural network to reconstruct cell-type-specific gene regulatory network using single-cell RNA-Seq Data. **Briefings in Bioinformatics (Q1, IF: 6.8)**. doi: 10.1093/bib/bbab325.
7. Md Selim Reza, Yunpeng Cai, **Lu Zhang**, Xingyu Zhang, Yanjie Wei. Computational Solutions for Microbiome and Metagenomics Sequencing Analyses. **Frontiers in Molecular Biosciences (Q1, IF: 3.9)**. doi: 10.3389/fmolb.2021.698384.
8. Zhenmiao Zhang, **Lu Zhang***. METAMVGL: a multi-view graph-based

metagenomic contig binning algorithm by integrating assembly and paired-end graphs. **BMC Bioinformatics (Q1, IF: 2.9)**. doi: 10.1186/s12859-021-04284-4.

9. Xin Zhou, **Lu Zhang**, Ziming Weng, David L. Dill, Arend Sidow. Aquila enables reference-assisted diploid personal genome assembly and comprehensive variant detection based on linked reads. **Nature Communications (Q1, IF: 14.7)**. doi: 10.1038/s41467-021-21395-x

2020

1. **Lu Zhang**^{*}, Xiaodong Fang et al. A Comprehensive Investigation of Metagenome Assembly by Linked-Read Sequencing. **Microbiome (Q1, IF: 13.8)**. doi: 10.1186/s40168-020-00929-3.
2. **Lu Zhang**[†], Xin Zhou[†], Ziming Weng, Arend Sidow. De novo diploid genome assembly for genome-wide structural variant detection. **NAR Genomics and Bioinformatics (Q1, IF: 4)**. doi: 10.1093/nargab/lqz018

2019

1. **Lu Zhang**[†], Xin Zhou[†], Ziming Weng, Arend Sidow. Assessment of human diploid genome assembly with 10x Linked-Reads data. **GigaScience (Q1, IF: 11.8)**. doi: 10.1093/gigascience/giz141

2018

1. JiFeng Guo[†], **Lu Zhang**[†] et al. De novo coding mutations contribute to early onset Parkinson's disease. **Proceedings of the National Academy of Sciences of the United States of America (Q1, IF: 9.4)**. doi: 10.1073/pnas.1809969115.
2. Xin Zhou, Serafim Batzoglou, Arend Sidow, **Lu Zhang**^{*}. HAPDeNovo: a haplotype-based approach for filtering and phasing de novo mutations in linked read sequencing data. **BMC Genomics (Q2, IF: 3.5)**. doi:10.1186/s12864-018-4867-7.

2017

1. Lu Liu[†], **Lu Zhang**[†] et al. The SNP-set based association study identifies *ITGAI* as a susceptibility gene of attention-deficit/hyperactivity disorder in Han Chinese. **Translational Psychiatry (Q1, IF: 5.8)**. doi:10.1038/tp.2017.156.
2. **Lu Zhang**[†], Cheng Qin[†], Junpu Mei[†], et al. Identification of microRNA Targets of Capsicum spp. using MiRTrans—a trans-omics approach. **Frontiers in Plant Science (Q1, IF: 4.1)**. doi: 10.3389/fpls.2017.00495.

2016

1. Zhifan Zhou, Zhengmao Hu, **Lu Zhang** et al. Identification of RELN variation p.Thr3192Ser in a Chinese family with autosomal-dominant schizophrenia. **Scientific Reports (Q1, IF: 3.8)**. doi:10.1038/srep24327.

2015

1. Xueyan Li[†], Dingding Fan[†], Wei Zhang[†], Guichun Liu[†], **Lu Zhang**[†], et al. Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. **Nature Communications (Q1, IF: 14.7)**. doi:10.1038/ncomms9212.
2. **Lu Zhang**, Xikang Feng, Yen Kaow Ng and Shuai Cheng Li. Reconstructing directed gene regulatory network by only gene expression data. **BMC Genomics (Q2, IF: 3.5)**. doi: 10.1186/s12864-016-2791-2.
3. Jing Zhang[†], **Lu Zhang**[†], Jiaxu Hong, Dan Wu, Jianjiang Xu. Association of Common Variants in *LOX* with Keratoconus: A Meta-Analysis. **PLOS One (Q2, IF: 2.9)**. doi: 10.1371/journal.pone.0145815.
4. Huashui Ai, Xiaodong Fang, Bin Yang, Zhiyong Huang, Hao Chen, Likai Mao, Feng Zhang, **Lu Zhang**, et al. Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. **Nature Genetics**

-
- (Q1, IF: 31.7). doi:10.1038/ng.3199.
5. Jing Zhang, **Lu Zhang**, et al. Gene-based meta-analysis of GWAS data identifies independent SNPs in ANXA6 as associated with SLE in Asian populations. **Arthritis & Rheumatology** (Q1, IF: 11.4). doi:10.1002/art.39275.
 6. Dingge Ying, Pak Chung Sham, David Keith Smith, **Lu Zhang**, Yu Lung Lau and Wanling Yang. HaploShare: identification of extended haplotypes shared by cases and evaluation against controls. **Genome Biology** (Q1, IF: 10.1). doi:10.1186/s13059-015-0662-9.
 7. Yan Zhang, Yong-Fei Wang, Jing Yang, Jing Zhang, Liangdan Sun, Nattiya Hirankarn, Hai-Feng Pan, Chak Sing Lau, Tak Mao Chan, Tsz Leung Lee, Alexander Moon Ho Leung, Chi Chiu Mok, **Lu Zhang**, et al. Meta-analysis of two Chinese populations identifies an autoimmune disease risk allele in 22q11.21 as associated with systemic lupus erythematosus. **Arthritis Research & Therapy** (Q1, IF: 4.4). doi:10.1186/s13075-015-0577-6.
 8. Yan Zhang, Jing Yang, Jing Zhang, Liangdan Sun, Nattiya Hirankarn, Hai-Feng Pan, Chak Sing Lau, Tak Mao Chan, Tsz Leung Lee, Alexander Moon Ho Leung, Chi Chiu Mok, **Lu Zhang**, et al. Genome-wide search followed by replication reveals genetic interaction of CD80 and ALOX5AP associated with systemic lupus erythematosus in Asian populations. **Annals of the Rheumatic Diseases** (Q1, IF: 20.3). doi:10.1136/annrheumdis-2014-206367.

2014

1. Yan Zhang, Jing Zhang, Jing Yang, Yongfei Wang, **Lu Zhang**, et al. 2014 Meta-analysis of GWAS on two Chinese populations followed by replication identifies novel genetic variants on the X chromosome associated with systemic lupus erythematosus. **Human Molecular Genetics** (Q2, IF: 3.1). doi:10.1093/hmg/ddu429.
2. Xiaodong Fang, Eviatar Nevo, Lijuan Han, Erez Y Levanon, Jing Zhao, Aaron Avivi, Denis Larkin, Xuanning Jiang, Sergey Feranchuk, Yabing Zhu, Alla Fishman, Yue Feng, Noa Sher, Zhiqiang Xiong, Thomas Hankeln, Zhiyong Huang, Vera Gorbunova, **Lu Zhang**, et al. Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. **Nature Communications** (Q1, IF: 14.7). doi:10.1038/ncomms4966.
3. Cheng Qin, Changshui Yu, Yaou Shen, Xiaodong Fang, Lang Chen, Jiumeng Min, Jiaowen Cheng, Shancen Zhao, Meng Xu, Yong Luo, Yulan Yang, Zhiming Wu, Likai Mao, Haiyang Wu, Changying Ling-Hu, Huangkai Zhou, Haijian Lin, Sandra González-Morales, Diana L Trejo-Saavedra, Hao Tian, Xin Tang, Maojun Zhao, Zhiyong Huang, Anwei Zhou, Xiaoming Yao, Junjie Cui, Wenqi Li, Zhe Chen, Yongqiang Feng, Yongchao Niu, Shimin Bi, Xiuwei Yang, Weipeng Li, Huimin Cai, Xirong Luo, Salvador Montes-Hernández, Marco A Leyva-González, Zhiqiang Xiong, Xiujing He, Lijun Bai, Shu Tan, Xiangqun Tang, Dan Liu, Jinwen Liu, Shangxing Zhang, Maoshan Chen, **Lu Zhang**, et al. Whole-genome sequencing of cultivated and wild peppers provides insights into Capsicum domestication and specialization. **Proceedings of the National Academy of Sciences of the United States of America** (Q1, IF: 9.4). doi: 10.1073/pnas.1400975111.

2013

1. **Lu Zhang**, Jing Zhang, Jing Yang, Dingge Ying, Yu lung Lau, Wanling Yang. PriVar: a flexible toolkit for prioritizing SNV and indel from next generation sequencing data. **Bioinformatics** (Q1, IF: 4.4). doi:10.1093/bioinformatics/bts627.
2. Jing Zhang, Yan Zhang, **Lu Zhang**, Jing Yang et al. Epistatic interaction between

genetic variants in susceptibility gene ETS1 correlates with IL-17 levels in SLE patients. **Annals of human genetics (Q3, IF: 1)**. doi:10.1111/ahg.12018.

3. Wanling Yang, Huayang Tang, Yan Zhang, Xianfa Tang, Jing Zhang, Liangdan Sun, Jing Yang, Yong Cui, **Lu Zhang** et al. Meta-Analysis and replication identify CDKN1B, TET3, CD80, DRAM1, and ARID5B as susceptibility genes for systemic lupus erythematosus in Asians. **The American Journal of Human Genetics (Q1, IF: 8.1)**. doi:10.1016/j.ajhg.2012.11.018.

2011

1. **Lu Zhang**, Wanling Yang, Dingge Ying, Stacey S. Cherny, Friedhelm Hildebrandt, Pak Chung Sham, Yu lung Lau. Homozygosity mapping on a single patient identification of homozygous regions of recent common ancestry by using population data. **Human Mutation (Q1, IF: 3.3)**. doi:10.1002/humu.21432.

Before 2011

1. Wanling Yang, Nan Shen, Dong-Qing Ye, Qiji Liu, Yan Zhang, Xiao-Xia Qian, Nattiya Hirankarn, Dingge Ying, Hai-Feng Pan, Chi Chiu Mok, Tak Mao Chan, Raymond Woon Sing Wong, Ka Wing Lee, Mo Yin Mok, Sik Nin Wong, Alexander Moon Ho Leung, Xiang-Pei Li, Yingyos Avihingsanon, Chun-Ming Wong, Tsz Leung Lee, Marco Hok Kung Ho, Pamela Pui Wah Lee, Yuk Kwan Chang, Philip H. Li, Ruo-Jie Li, **Lu Zhang**, et al. Genome-wide association study in Asian populations identifies variants in ETS1 and WDFY4 associated with systemic lupus erythematosus. **PLOS Genetics (Q1, IF: 4)**. doi:10.1371/journal.pgen.1000841.
2. Weidi Dai, **Lu Zhang**, Wenjun Wang, Yuexin Hou. Clustering Algorithm based on Grid's Density and Distance. **Journal of South China University of Technology** (in Chinese).
3. Yunpeng Zhang, **Lu Zhang**, Zhengjun Zhai, Chunyan Ma, Weidi Dai. A Much Different Parallel Construction Density Tree Clustering (PCDTC) Algorithm Based on Data Partitioning. **Journal of Northwestern Polytechnical University** (in Chinese).
4. Weidi Dai, Wenjun Wang, Yuexian Hou, Ying Wang, **Lu Zhang**. Document Clustering Based on Building Density Tree. **Transactions of Tianjin University**. doi: 10.1007/s12209-008-0005-y.

Conference paper

1. Zeming Li, Yu Xu, Debajyoti Chowdhury, Hip Fung Yip, Chonghao Wang, **Lu Zhang***. Med-PRSIMD: Enhanced Complex Disease Risk Prediction through Integrative Analysis of Multi-Type Data and Medical History Records. **ACM-BCB**.
2. Xuan Li, Zhanke Zhou, Jiangchao Yao, Yu Rong, **Lu Zhang**, Bo Han. Neural Atoms: Propagating Long-range Interaction in Molecular Graphs through Efficient Communication Channel. **ICLR 2024**. doi: /10.48550/arXiv.2311.01276
3. Zhenmiao Zhang, Hongbo Wang, Chao Yang, Yufen Huang, Zhen Yue, Yang Chen, Lijuan Han, Aiping Lyu, Xiaodong Fang and **Lu Zhang***. Exploring High-Quality Microbial Genomes by Assembly of Linked-Reads with High Barcode Specificity Using Deep Learning. **RECOMB-Seq 2023**. doi: 10.1101/2022.09.07.506963
4. Yu Xu, Chonghao Wang, William K Cheung, Jiming Liu, Aiping Lyu, **Lu Zhang***. PRSIMD: Disease risk prediction by integrating multi-source data. **IEEE International Conference on Bioinformatics and Biomedicine 2022 (BIBM 2022)**. doi: 10.1109/BIBM55620.2022.9994925
5. Yunfei Hu, Sanidhya V Mangal, **Lu Zhang**, Xin Zhou. An ensemble deep learning framework to refine large deletions in linked-reads. **IEEE International Conference on Bioinformatics and Biomedicine 2021 (BIBM 2021)**. doi:

10.1109/BIBM52615.2021.9669571

6. Jiaxing Chen, Chinwang Cheong, Liang Lan, Xin Zhou, Jiming Liu, Aiping Lyu, William K Cheung*, **Lu Zhang***. DeepDRIM: a deep neural network to reconstruct cell-type-specific gene regulatory network using single-cell RNA-Seq Data. **RECOMB-Seq 2021**. doi: 10.1101/2021.02.03.429484
7. Zhenmiao Zhang, **Lu Zhang***. METAMVGL: a multi-view graph-based metagenomic contig binning algorithm by integrating assembly and paired-end graphs. Asia Pacific Bioinformatics Conference 2021 (**APBC 2021**). doi: 10.1101/2020.10.18.344697
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Teaching experience

2024 Fall **COMP7990** Principles and Practices of Data Analytics
2024 Spring **COMP3115** Exploratory Data Analysis and Visualization
2023 Fall **COMP1007** Introduction to Python and Its Applications
2023 Fall **COMP7990** Principles and Practices of Data Analytics
2023 Spring **COMP1007** Introduction to Python and Its Applications
2023 Spring **COMP3115** Exploratory Data Analysis and Visualization
2022 Fall **COMP7990** Principles and Practices of Data Analytics
2022 Spring **COMP1007** Introduction to Python and Its Applications
2022 Spring **COMP3115** Exploratory Data Analysis and Visualization
2021 Fall **COMP7990** Principles and Practices of Data Analytics
2020 Fall **COMP1007** Introduction to Python and Its Applications
2020 Fall **COMP7990** Principles and Practices of Data Analytics
2019 Fall **COMP1007** Introduction to Python and Its Applications
2019 Fall **COMP7990** Principles and Practices of Data Analytics
2013 Spring (TA) **CS2312** Problem Solving and Programming
2013 Fall (TA) **CS4335** Design and Analysis of Algorithms
2014 Spring (TA) **CS2312** Problem Solving and Programming
2015 Fall (TA) **GE2334** The Art and Science of Data

Service

- Program management committee member of BSc (Hons) in computer science (2022-now)
- Program management committee member of MSc in Data Analytics and Artificial

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- Intelligence (2022-now)
 - Program management committee member of MSc in Information Technology Management (2022-now)
 - Program management committee member of BSc (Hons) in innovation in Health/Well Being (2022-2024)
 - Department Coordinator of RAE 2026.
 - Department Coordinator of Computer Facility

Conference organization and committee members

- PC members of GIW2023, BIBM (2020-2024), ISBRA (2020-2024), ISDH 2019, ICBPB 2019, IJCAI (2020, 2021), BDAI 2020, ICHI (2020, 2021), ICBBS 2024
- Organization committee member, 2019 International Symposium on Digital Health
- Organization Chair of “Computational methods and their applications on single cell multiomic data” workshop in BIBM2021
- Organization Chair of “Computational methods to characterize genomic variants using high-throughput sequencing data” workshop in BIBM2022
- AI leader and co-founder of ADVANCED (AI-empowered Development and Assessment of medical guidelines and standards) working group
- Member of international RIGHT (Reporting Items for Practice Guidelines in Healthcare) working group
- Member of PREPARE (Practice Guideline Registration and Transparency) platform working group
- Member of STAR (Scientific, Transparent and Applicable Rankings tool) working group

Editorial members

- Associate Editor, Computational and Structural Biotechnology Reports
- Editorial Board member, BMC Methods.
- Editorial Board member, Current Gene Therapy.
- Guest Editor, Life, Advances in Computational Genomics, 2022.
- Guest Editor, Frontiers in Genetics, Predicting High-Risk Individuals for Common Diseases Using Multi-Omics and Epidemiological Data I, 2019
- Guest Editor, Frontiers in Molecular Biosciences, Computational Solutions for Microbiome and Metagenomics Sequencing Analyses I, 2020
- Guest Editor, Frontiers in Genetics, Predicting High-Risk Individuals for Common Diseases Using Multi-Omics and Epidemiological Data II, 2022
- Guest Editor, Frontiers in Molecular Biosciences, Computational Solutions for Microbiome and Metagenomics Sequencing Analyses II, 2021
- Guest Editor, Health Information Science and Systems, Integrative multi-omics for human health and disease studies, 2022

Reviewers

Nature Communications, Genomics, Proteomics & Bioinformatics, Genome Biology, Genome Research, Genome Medicine, GigaScience, Bioinformatics, iScience, Briefings in Bioinformatics, Npj Precision Oncology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, National Science Review, Frontiers in Genetics, Knowledge-Based Systems, Aging, Computational Biology and Chemistry