LUO, RUIBANG

DEC 2023

Associate Professor
Department of Computer Science
Faculty of Engineering, The University of Hong Kong
Rm422, Chow Yei Ching Bldg.
HKU, Pokfulam Rd., Hong Kong

+852-2859-2186
rbluo@cs.hku.hk
http://luo-lab.hk/

Summary of achievements

- Published 78 papers in prestigious journals including *Nature*, *Nature Biotechnology*, *Nature Machine Intelligence*, *Nature Communications*, *Communications Biology*, *Briefing in Bioinformatics*, *Genome Medicine,* etc.
  - Google Scholar statistics: Citations (over 20k excluded consortium works), h-index (32)
- Research grants (past 5 years): HKD 9M
- PC member of top bioinformatics conferences from 2017 to present including ISMB, RECOMB, RECOMB-Seq, IEEE BIBM, ACM-BCB
- Prestigious awards and recognitions:
  - 2019-23 Top 1% Scholars Worldwide by Clarivate Analytics
  - 2022, Worldwide Top 150 Chinese Young Scholars in Artificial Intelligence by Baidu Research
  - 2019, Top 10 Innovators Under 35 Asia Pacific by MIT Technology Review
  - 2018, Faculty Knowledge Exchange Award, Faculty of Engineering, HKU
  - 2017, Forbes 30 Under 30 Asia 2017: Healthcare and Science
- Widely adopted open-source bioinformatics software:
  - Over 10M downloads: SOAPdenovo2
  - Over 1M downloads: MegaHIT, SOAPdenovo-Trans
  - Over 100k downloads: Clairvoyante, Clair3, COPE, RENET, LRSim
- Graduated 5 PhD and 4 MPhil students

Area of expertise

1. Bioinformatics algorithm
2. Precision medicine application
3. Metagenomics
4. Clinical informatics

Education

Ph.D. in Computer Science Sept 2011 – Aug 2015

The University of Hong Kong, Hong Kong

B. Eng. in Bioengineering Sept 2007 – Jun 2010

South China University of Technology, Guangzhou

Professional experience

Associate Professor, The University of Hong Kong Mar 2023 – present
Assistant Professor, The University of Hong Kong Jan 2018 – Feb 2023
Postdoctoral Fellow, Johns Hopkins University Sept 2016 – Dec 2017

Awards and honors

1. 2019-23, Top 1% Scholars Worldwide by Clarivate Analytics
2. 2022, Worldwide Top 150 Chinese Young Scholars in Artificial Intelligence by Baidu Research
3. 2019, Top 10 Innovators Under 35 Asia Pacific by MIT Technology Review
4. 2018, Faculty Knowledge Exchange Award (Faculty of Engineering, HKU) for 'Bioinformatics Algorithms and Next-Generation-Sequencing (NGS) Data Analysis"
5. 2017, Forbes 30 Under 30 Asia 2017: Healthcare and Science

Peer-reviewed publications (as of Dec 2023)

In my following listing, my publications are grouped into three categories:

- Corresponding (*), co-corresponding (*), or first-authored (^) publications
- Co-first authored (#) publications
- Co-authored publications

The name of my students is underlined as "Student Name". Impact factors and citations are as of Aug 2022. The 2-year impact factor is given except for journals established for less than five years, or conferences. To get to the point quickly, papers with more than ten authors are shown with a reduced list including only the first five and last three authors. The full author list of my co-authored papers is skipped. Nonetheless, the full author list of my publications is arranged and easily accessible

from my Google Scholar profile at
https://scholar.google.com.hk/citations?user=CwGy9jsAAAAJ

Corresponding (*), co-corresponding (*), or first-authored (^) publications:

1. T. T. L. Ng, J. Su, H. Y. Lao, W. Lui, C. T. M. Chan, A. W. Leung, ..., **R. Luo***, G. K. H. Siu*. Long-read sequencing with hierarchical clustering for antiretroviral resistance profiling of mixed human immunodeficiency virus quasispecies. ***Clinical Chemistry***, 69(10), 1174-1185, 2023.
2. H. Yu, Z. Zheng, J. Su, T. Lam, R. Luo. Boosting variant-calling performance with multi-platform sequencing data using Clair3-MP. ***BMC bioinformatics***, 24(1), 308, 2023.
3. S. Li, B. Yan, T. K. Li, J. Lu, Y. Gu, Y. Tan, ..., P. Xie*, Y. Wang*, G. Lin*, R. Luo*. (2023). Ultra-low-coverage genome-wide association study—insights into gestational age using 17,844 embryo samples with preimplantation genetic testing. ***Genome Medicine***, 15(1), 10, 2023.
4. J. Su, W. Lui, Y. Lee, Z. Zheng, G. K. H. Siu, T. T. L. Ng, …, **R. Luo***. Evaluation of Mycobacterium tuberculosis enrichment in metagenomic samples using ONT adaptive sequencing and amplicon sequencing for identification and variant calling. ***Scientific reports***, 13(1), 5237, 2023.
5. S. Li, B. Yan, B. Wu, J. Su, J. Lu, T. Lam, ..., K. R. Boheler*, E. N. Y. Poon*, **R. Luo***. Integrated modeling framework reveals co-regulation of transcription factors, miRNAs and lncRNAs on cardiac developmental dynamics. ***Stem Cell Research & Therapy***, 14(1), 247, 2023.
6. L. Chen, J. Su, Z. Zheng, T. Lam, R. Luo. Large-scale Dataset and Effective Model for Variant-Disease Associations Extraction. ***ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics***, 10.1145/3584371.3612995, 2023.
7. L. Chen, J. Su, T. Lam, **R. Luo***. Exploring Pair-Aware Triangular Attention for Biomedical Relation Extraction. ***14th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics***, 10.1145/3584371.3612994, 2023.
8. Z. Zheng, S. Li, J. Su, A. W. Leung, T. Lam, **R. Luo***. Symphonizing pileup and full-alignment for deep learning-based long-read variant calling. ***Nature Computational Science***, 2(12), 797-803, 2022.
9. Q. Li, B. Yan, T. Lam, **R. Luo***. Assembly-free discovery of human novel sequences using long reads. ***DNA Research***, 29(6), dsac039, 2022.

10. Y. Zhou, A. W. Leung, S. S. Ahmed, T. Lam, **R. Luo***. Duet: SNP-assisted structural variant calling and phasing using Oxford nanopore sequencing. ***BMC bioinformatics***, 23(1), 465, 2022.
11. J. Su, Z. Zheng, S. S. Ahmed, T. Lam, **R. Luo***. Clair3-Trio: high-performance Nanopore long-read variant calling in family trios with Trio-to-Trio deep neural networks. ***Briefings in Bioinformatics (IF: 13.99)***, bbac301, 2022.
12. M. Ou, H. C. Leung, A. W. Leung, H. Luk, B. Yan, …, T. Lam*, I. F. Lo*, **R. Luo***. HKG: An open genetic variant database of 205 Hong Kong Cantonese exomes. ***NAR Genomics and Bioinformatics***, 4(1):lqac005, 2022.
13. A. W. Leung, H. C. Leung, C. Wong, Z. Zheng, W. Lui, H. Luk, I. F. Lo, **R. Luo***, T. Lam*. ECNano: A Cost-Effective Workflow for Target Enrichment Sequencing and Accurate Variant Calling on 4,800 Clinically Significant Genes Using a Single MinION Flowcell. ***BMC Medical Genomics (IF: 3.34)***, 15(1):43, 2022.
14. H. C. Leung, H. Yu, Y. Zhang, A. W. Leung, I. F. Lo, …, Y. Wong, **R. Luo***, T. Lam*. Detecting Structural Variations with Precise Breakpoints using Low-Depth WGS Data from a Single Oxford Nanopore MinION Flowcell. **Scientific Reports *(IF: 4.99)***, 12(1):4519, 2022.
15. Q. Li, S. Tian, B. Yan, C. Liu, T. Lam*, R. Li*, **R. Luo***. Building a Chinese pan-genome of 486 individuals. ***Communications Biology (IF: 6.54)***, 4(1):1016, 2021. (Citations: 6)
16. S. Xie, A. W. Leung, Z. Zheng, D. Zhang, C. Xiao*, **R. Luo***, M. Luo*, S. Zhang*. The applications and potentials of nanopore sequencing in the (epi)genome and (epi)transcriptome era. ***The Innovation***, 2(4):100153, 2021. (Citations: 9)
17. **R. Luo**^, A. Delaunay-Moisan, K. Timmis, A. Danchin*. SARS-CoV-2 biology and variants: anticipation of viral evolution and what needs to be done. ***Environmental Microbiology (IF: 5.47)***, 23(5):2339-63, 2021. (Citations: 22)
18. Y. Wu, H. Ting, T. Lam, **R. Luo***. BioNumQA-BERT: Answering Biomedical Questions Using Numerical Facts with a Deep Language Representation Model. ***ACM conference on Bioinformatics, Computational Biology and Biomedicine***, 10.1145/3388440.3412457, 2021. (Citation: 2)
19. J. Su, Y. Wu, H. Ting, T. Lam, **R. Luo***. RENET2: High-Performance Full-text Gene-Disease Relation Extraction with Iterative Training Data Expansion. ***NAR Genomics and Bioinformatics***, 3(3):lqab062, 2021. (Citations: 4)
20. Y. Zhang, C. Liu, H. C. Leung, **R. Luo***, T. Lam*. CONNET: Accurate Diploid Genome Consensus in *de novo* Assembly of Nanopore Sequencing Data via Deep Learning. ***iScience (IF: 6.10)***, 23(5):101128, 2020. (Citations: 5)

21. H. C. Leung*, D. Li, Y. Xin, W. Law, Y. Zhang, H. Ting, **R. Luo***, T. Lam*. MegaPath: sensitive and rapid pathogen detection using metagenomic NGS data. ***BMC Genomics (IF: 4.26)***, 21(Suppl 6):500, 2020. (Citation: 2)
22. **R Luo***^, C. Wong, Y. Wong, C. Tang, C. Liu, H. C. Leung, T. Lam*. Exploring the limit of using a deep neural network on pileup data for germline variant calling. ***Nature Machine Intelligence (IF: 25.89)***, 2:220-7, 2020. (Citations: 64)
23. W. Lui, A. W. Leung, H. C. Leung, Y. Xin. J. L. Teng, P. C. Woo, T. Lam, **R. Luo***. MegaPath-Nano: Accurate Compositional Analysis and Drug-level Antimicrobial Resistance Detection Software for Oxford Nanopore Long-read Metagenomics. ***IEEE International Conference on Bioinformatics and Biomedicine***, 10.1109/BIBM49941.2020.9313313, 2020.
24. X. Cao, F. Lan, C. Liu, T. Lam, **R. Luo***. ChromSeg: Two-Stage Framework for Overlapping Chromosome Segmentation and Reconstruction. ***IEEE International Conference on Bioinformatics and Biomedicine***, 10.1109/BIBM49941.2020.9313458, 2020. (Citation: 2)
25. **R. Luo***^, T. Lam, M. C. Schatz. Skyhawk: An Artificial Neural Network-based discriminator for reviewing clinically significant genomic variants. ***International Journal of Computational Biology and Drug Design***, 13(5-6):431-7, 2020. (Citation: 6)
26. **R. Luo***^, F. J. Sedlazeck, T. Lam, M. C. Schatz. A multi-task convolutional deep neural network for variant calling in single molecule sequencing. ***Nature Communications (IF: 17.69)***, 10(1):998, 2019. (Citations: 110)
27. **R. Luo***^, F. J. Sedlazeck, C. A. Darby, S. M. Kelly, M. C. Schatz. LRSim: a Linked Reads Simulator generating insights for better genome partitioning. ***Computational and Structural Biotechnology (IF: 6.15)***, 15:478-84, 2017. (Citation: 31)
28. **R. Luo**^, A Zimin, R. Workman, Y. Fan, G. Pertea, …, W. Timp, S. X. Zhang, S. L. Salzberg*. First Draft Genome Sequence of the Pathogenic Fungus Lomentospora prolificans (Formerly *Scedosporium prolificans*). ***G3 Genes|Genomes|Genetics (IF: 2.78)***, 7(11):3831-36, 2017. (Citation: 10)
29. **R. Luo***^, M. C. Schatz, S. L. Salzberg. 16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. ***GigaScience (IF: 7.65)***, 6(7):1-4, 2017. (Citation: 19)
30. B. Liu, C. Liu, D. Li, Y. Li, H. Ting, S. Yiu, **R. Luo***, T. Lam*. BASE: a practical de novo assembler for large genomes using long NGS reads. ***BMC Genomics***, 17(Suppl 5):499, 2016. (Citation: 12)

31. **R. Luo**^, J. Cheung, E. Wu, H. Wang, S. Chan, …, X. Zhu, S. Peng, **T. Lam***. MICA: A fast short-read aligner that takes full advantage of Intel Many Integrated Core Architecture (MIC). ***BMC Bioinformatics (IF: 3.32)***, 6(Suppl 7):S10, 2015. (Citation: 41)
32. M. Ou, R. Ma, J. Cheung, K. Lo, P. Yee, …, A. Kwong, **R. Luo***, T. Lam*. database.bio: a web application for interpreting human variations. ***Bioinformatics (IF: 6.93)***, 31(24):4035-7, 2015. (Citation: 12)
33. **R. Luo**^, Y. Wong, W. Law, L. Lee, J. Cheung, C. Liu, T. Lam*. BALSA**:** integrated secondary analysis for whole-genome and whole-exome sequencing, accelerated by GPU. ***PeerJ (IF: 3.061)***, 2:e421, 2014. (Citation: 20)
34. **R. Luo**^, T. Wong, J. Zhu, C. Liu, X. Zhu, …, Y. Li*, R. Li*, T. Lam*. SOAP3-dp: Fast, Accurate and Sensitive GPU-based Short Read Aligner, ***PLoS ONE (IF: 3.752)***, 8(5):e65632, 2013. (Citation: 140)
35. **R. Luo**^, B. Liu, Y. Xie, Z. Li, W. Huang, …, Ji. Wang, T. Lam*, Ju. Wang*. SOAPdenovo2**:** An empirically improved memory-efficient short-read *de novo* assembler. ***GigaScience (IF: 7.65)***, 1(1):18, 2012. (Citation: 4229)
36. **R. Luo**^, C. Yu, C. Liu, T. Lam, T. Wong, S. Yiu, R. Li, H. Ting*. Efficient SNP-sensitive alignment and database-assisted SNP calling for low coverage samples. ***ACM Conference on Bioinformatics, Computational Biology and Biomedicine***, 10.1145/2382936.2382957, 2012. (Citation: 1)
37. B. Liu, J. Yuan, S. Yiu, Z. Li, Y. Xie, …, Y. Li, T. Lam*, **R. Luo***. COPE**:** an accurate k-mer-based pair-end reads connection tool to facilitate genome assembly. ***Bioinformatics (IF: 6.93)***, 28(22):2870-4, 2012. (Citation: 173)

Co-first authored (#) publications:

38. J. L. Teng, Y. Ma, J. H. Chen, **R. Luo**#, C. Foo, …, K. S. Fung, S. K. Lau*, P. C. Woo*. Streptococcus oriscaviae sp. nov. Infection Associated with Guinea Pigs. ***Microbiology Spectrum (IF: 9.04)***, 10(3):e14-22, 2022.
39. J. L. Teng, **R. Luo**#, B. S. Tang, J. Y. Fong, L. Wang, …, M. Yeung, S. K. Lau*, P. C. Woo*. High Prevalence and Mechanism Associated With Extended Spectrum Beta-Lactamase-Positive Phenotype in *Laribacter hongkongensis*, ***Frontiers in Microbiology (IF: 6.06)***, 12:618894, 2022.
40. Y. Wu, **R. Luo**#, H. C. Leung, H. Ting, T. Lam*. RENET: A Deep Learning Approach for Extracting Gene-Disease Associations from Literature. ***RECOMB (REsearch in COmputational Molecular Biology) Conference***, 10.1007/978-3-030-17083-7_17, 2019. (Citation: 47)

41. F. H. Shek, **R. Luo**[#], B. Y. Lam, W. Sung, T. Lam, …, C. Chan, R. T. Poon, N. P. Lee[*]. Serine peptidase inhibitor, Kazal type 1 (SPINK1) as a novel downstream effector of the tumorigenic cadherin-17/ß-catenin axis in hepatocellular carcinoma. ***Cellular Oncology (IF: 7.05)***, 40(5):443-56, 2017. (Citation: 13)
42. D. Li, **R. Luo**[#], C. Liu, H. Ting, K. Sadakane, H. Yamashita, T. Lam[*]. MEGAHIT v1.0: A fast and scalable metagenome assembler driven by advanced methodologies and community practices. ***Methods (IF: 4.64)***, 102:3-11, 2016. (Citation: 763)
43. H. Cao, H. Wu, **R. Luo**[#], S. Huang, Y. Sun, …, Y. Li[*], G. K Wong[*], J. Wang[*]. *De novo* assembly of a haplotype-resolved human genome. ***Nature Biotechnology (IF: 68.16)***, 33(6):617-22, 2015. (Citation: 73)
44. D. Li, C. Liu, **R. Luo**[#], K. Sadakane, T. Lam[*]. MEGAHIT**:** An ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph. ***Bioinformatics (IF: 6.93)***, 31(10):1674-6, 2015. (Citation: 2855)
45. A. H. Ramos, **R. Luo**[#], J. Feala, B. Liu, L. Gong, M Warmuth, P. Zhu, P. Smith, L. Yu[*]. Exome sequencing of tumor cell lines: Optimizing for cancer variants. ***Cancer Research (IF: 12.70)***, 74(19_Supplement):4269, 2014.
46. C Liu, **R. Luo**[#], T. Lam[*]. GPU-Accelerated BWT Construction for Large Collection of Short Reads, ***Arxiv***, 1401.7457, 2014. (Citation: 19)
47. Y. Xie, G. Wu, J. Tang, **R. Luo**[#], J. Patterson, …, X. Xu, G. K. Wong[*], J. Wang[*]. SOAPdenovo-Trans: *de novo* transcriptome assembly with short RNA-Seq reads, ***Bioinformatics (IF: 6.93)***, 15(30):1660-6, 2014. (Citation: 879)
48. G. Zhang[*], X. Fang, X. Guo[*], L. Li, **R. Luo**[#], …, Ji. Wang, Y. Yin[*], Ju. Wang[*]. Oyster genome reveals stress adaptation and shell formation complexity. ***Nature (IF: 69.50)***, 490(7418):49-54, 2012. (Citation: 1870)
49. Y. Li, H. Zheng, **R. Luo**[#], H. Wu, H. Zhu, …, H. Yang, Ji. Wang[*], Ju. Wang[*]. Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome *de novo* assembly. ***Nature Biotechnology (IF: 68.16)***, 29(8):723-30, 2011. (Citation: 136)
50. R. Li, Y. Li, H. Zheng, **R. Luo**[#], H. Zhu, …, H. Yang, Ju. Wang[*], Ji. Wang[*]. Building the sequence map of the human pan-genome. ***Nature Biotechnology (IF: 68.16)***, 28(1):57-63, 2010. (Citation: 251)

Co-authored publications:

51. Rozowsky et al, The EN-TEx resource of multi-tissue personal epigenomes & variant-impact models. ***Cell***, 186(7), 1493-1511, 2023.

52. Zhou et al., Generalized radiograph representation learning via cross-supervision between images and free-text radiology reports. ***Nature Machine Intelligence (IF: 25.89)***, 4:32-40, 2022.
53. Rogrigo et al., Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer. ***JCO Precision Oncology (IF: 5.47)***, 6:e2100365, 2022.
54. Tsoi et al., Temporal Control of the WNT Signaling Pathway During Cardiac Differentiation Impacts Upon the Maturation State of Human Pluripotent Stem Cell Derived Cardiomyocytes. ***Frontiers in Molecular Biosciences (IF: 6.11)***, 9:714008, 2022.
55. Yan et al., Drug Repurposing for the Treatment of COVID-19: A Knowledge Graph Approach. ***Advanced Therapeutics (IF: 5.00)***, 4(7):2100055, 2021. (Citation: 8)
56. Zhang et al., Distinct disease severity between children and older adults with COVID-19: Impacts of ACE2 expression, distribution, and lung progenitor cells. ***Clinical Infectious Diseases (IF: 20.99)***, 73(11):e4154-65, 2021. (Citation: 25)
57. Zhang et al., Clinical analysis and pluripotent stem cells-based model reveal possible impacts of ACE2 and lung progenitor cells on infacts vulnerable to COVID-19. ***Theranostics (IF: 11.55)***, 11(5):2170-81, 2021. (Citation: 9)
58. Liu et al., High-quality bacterial genomes of a partial-nitritation/anammox system by an iterative hybrid assembly method. ***Microbiome (IF: 14.65)***, 8(1):155, 2020. (Citation: 11)
59. Chen et al., Identification of Cooperative Gene Regulation Among Transcription Factors, LncRNAs, and MicroRNAs in Diabetic Nephropathy Progression. ***Frontiers in Genetics (IF: 4.77)***, 11:1008, 2020. (Citation: 1)
60. Wu et al., Translocator: local realignment and global remapping enabling accurate translocation detection using single-molecule sequencing long reads. ***ACM conference on Bioinformatics, Computational Biology and Biomedicine***, 10.1145/3388440.3412457, 2020.
61. Li et al., MC-Explorer: Analyzing and Visualizing Motif-Cliques on Large Networks. ***International Conference of Data Engineering***, 10.1109/ICDE48307.2020.00154, 2020. (Citation: 4)
62. Mai et al., AC-DIAMOND v1: accelerating large-scale DNA-protein alignment, ***Bioinformatics (IF: 6.93)***, 34(21):3744-6, 2018. (Citation: 8)
63. Lee et al., Transcriptome Analysis of Acute Phase Liver Graft Injury in Liver Transplantation. ***Biomedicines (IF: 4.75)***, 6(2):41, 2018. (Citation: 6)

64. Li et al., MegaGTA: a sensitive and accurate metagenomic gene-targeted assembler using iterative de Bruijn graphs. ***BMC Bioinformatics (IF: 3.32)***, 18(Suppl 12):408, 2017. (Citation: 13)
65. Gonzalez-Beltran et al., From Peer-Reviewed to Peer-Reproduced in Scholarly Publishing: The Complementary Roles of Data Models and Workflows in Bioinformatics, ***PLoS ONE (IF: 3.752)***, 10(7):e0127612, 2015. (Citation: 39)
66. The 1000 Genomes Project Consortium, A global reference for human genetic variation. ***Nature (IF: 69.50)***, 526(7571):68-74, 2015. (Citation: 10953)
67. Zhang et al., Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. ***Plant Cell (IF: 11.27)***, 27(6):1595-604, 2015. (Citation: 121)
68. Wang et al., FaSD-somatic: a fast and accurate somatic SNV detection algorithm for cancer genome sequencing data. ***Bioinformatics (IF: 6.93)***, 30(17):2498-500, 2014. (Citation: 22)
69. Bradnam et al., Assemblathon 2: evaluating *de novo* methods of genome assembly in three vertebrate species. ***GigaScience (IF: 7.65)***, 2(1):10, 2013. (Citation: 719)
70. Ho et al., Whole Genome Sequencing on Donor Cell Leukemia in a Patient with Multiple Myeloma Identified Gene Mutations That May Provide Insights to Leukemogenesis. ***Blood (IF: 9.53)***, 120(21):2414, 2012. (Citation: 5)
71. Liu et al., SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. ***Bioinformatics (IF: 6.93)***, 28(6):878-9, 2012. (Citation: 315)
72. The 1000 Genomes Project Consortium, An integrated map of genetic variation from 1,092 human genomes. ***Nature (IF: 69.50)***, 491(7422):56-65, 2012. (Citation: 2535)
73. Li et al., Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. ***BMC Genomics (IF: 3.96)***, 13:300, 2012. (Citation: 265)
74. Earl et al., Assemblathon 1: A competitive assessment of *de novo* short read assembly methods. ***Genome Research (IF: 9.04)***, 21(12):2224-41, 2011. (Citation: 578)
75. Mills et al., Mapping copy number variation by population-scale genome sequencing. ***Nature (IF: 69.50)***, 470(7332):59-65, 2011. (Citation: 1178)
76. The International Cancer Genome Consortium, International network of cancer genome projects. ***Nature (IF: 69.50)***, 464(7291): 993-998, 2011. (Citation: 2044)
77. Li et al., The DNA Methylome of Human Peripheral Blood Mononuclear Cells. ***PLoS Biology (IF: 8.96)***, 8(11):e1000533, 2010. (Citation: 370)

78. Yi et al., Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. ***Science (IF: 63.71)***, 329(5987):75-8, 2010. (Citation: 1455)

Major grants

As Principal Investigator (PI)

1. RGC GRF/ECS, 27204518, An Artificial Neural Network-based discriminator for validating clinically significant genomic variants. 2018.08.01 - 2021.07.31, 550k HKD, PI
2. RGC GRF/ECS, 17113721, Cancer mutation detection using Single Molecule Sequencing, 2022.01.01 - 2024.12.31, 564k HKD, PI
3. Shenzhen Science and Technology Innovation Committee, General Research Fund 202103243005095, 研发将单分子测序运用于癌症体细胞变异检测的实验方案与算法, 2021.10.28 - 2024.10.31, 600k CNY (720k HKD), PI
4. Industrial donation to support general research from Oxford Nanopore Technologies. 2022.02.01 - 2026.02.01, 260k GPB (2.7M HKD), PI

As Co-PI or Co-PC

5. ITC PRP, PRP/070/19FX, Cardiovascular risk prediction model for patients on lipid modifying drugs. 2020.12.1 - 2022.11.30, 3.18M HKD, Co-PC
6. ITC Research Talent Hub for ITF Projects (RTH-ITF)
   - PiH/361/21, 2021.09.01 - 2022.11.30, 502k HKD, Co-PC
   - PiH/119/21, 2021.05.03 - 2022.11.30, 634k HKD, Co-PC
7. RGC TRS, T21-705/20-N, Assess antibiotic resistome flows from pollution hotspots to environments and explore the control strategies. 2021.01.01 - 2025.12.31, 30M HKD, Co-PI

As Co-I:

8. ITC ITF ITSP Tier 2, ITS/255/20FP, Towards a Fully-Automated Karyotype Analysis for Detecting Chromosomal Abnormality via Intelligent Bioinformatics and Image Analysis, 2021.07.01 - 2023.06.30, 6.295M HKD, Co-I
9. RGC TRS, T12-703/19-R, Fighting Disease Recurrence and Promoting Tissue Repair after Liver Transplantation: Translating Basic Discoveries to Clinical Excellence. 2019.12.01-2024.11.30, 50M HKD, Co-I
10. ITC ITF ITSP Tier 2, PiH/160/18, Advanced 3GS-based bioinformatics algorithms and a complete bioinformatics solution for clinical genetics. 2018.11.01 - 2020.04.30, 6.03M HKD, Co-I

Supervised students and research staff

Graduated / Thesis submitted:

Primary supervisor:

- M.Phil.:
  1. LUI, Wai Wang (2022). "Accurate bioinformatic software for metagenomic sequencing"
  2. MA, Wen (2020). "Restricted Boltzmann Machine for Missing Data Imputation in Biomedical Datasets"
- Ph.D.:
  3. LI, Shumin (2022). "New methods for studying massive and complex biological data: from ultra-low depth sequence to high resolution structure"
  4. LI, Qiuhui (2022). "Identification and analysis of novel genomic and transcriptomic sequences"
  5. ZHENG, Zhenxian (2023). "Nanopore long-read variant calling"
  6. SU, Junhao (2023). "Computational methods to bridge genomics data with medical applications"

Co-supervisor:

- M.Phil.:
  7. LIU, Yibing (2022). "Identifying prognostically relevant transcription factor activity in breast cancer"
  8. LU, Jianliang (2021). "A Restricted Boltzmann Machine-based method for efficient processing of large biomedical datasets"
- Ph.D.:
  9. YU, Huijing (2023). "Detection of genomic variations with data from multiple sequencing platforms"

Post-doc alumni:

1. LEUNG, Henry C. Now works as a Senior Research Office at Hong Kong Sanatorium and Hospital
2. LEUNG, Amy W. Now works as a Research Officer at Hong Kong Sanatorium and Hospital

MSc dissertation:

1. Mishty, Negi. "Methylation Identification and its Automation using Single Molecule Sequencing"

2. Wang, Yi. "Understanding Financial Reports with NLP"
3. Gao, Chenyu. "Improve Traditional Alpha Using Sentiment Analysis on Financial News in A Share Market"

Teaching

Course designed:

1. COMP3353 Bioinformatics. Class size 50. Started in 2017
2. Real-life Data Science. Class size 120. Starting in 2023

Teaching duties:

1. ENGG1340/COMP2113 Computer programming II. 2018-22
2. COMP3353 Bioinformatics. 2018-21,22-24
3. STAT1005 Essential skills for undergraduates: Foundations of Data Science. 2021-22
4. COMP2501 Introduction to Data Science and Engineering. 2022-24

Award winning Final Year Projects:

1. Angel Chung Yu Woo, Snow Xue Wu, and Kwanyoung Lee
   - Computer Science, Faculty of Engineering
   - Title: "Building a code and data repository for teaching algorithmic trading"
   - **Won The Champion award in the FYP final competition in 2021**
2. Tarun Sudhams & Saripalli Varun Vamsi
   - Computer Science, Faculty of Engineering
   - Title: "Understanding Financial Reports using Natural Language Processing"
   - **Won the 1st runner-up award in the FYP final competition in 2019**

Patents

1. VARIANT CALLING IN SINGLE MOLECULE SEQUENCING USING A CONVOLUTIONAL NEURAL NETWORK (2023)
   - US patent 11,842,794. Ruibang Luo, Tak-Wah Lam, Chi-Man Liu
2. METHODS AND SYSTEMS FOR DETECTING GENOMIC STRUCTURE VARIATIONS (2010)
   - CN patent no. CN201080068345; Ruibang Luo; Haojing Shao; Haoxiang Lin

3. METHOD AND SYSTEM FOR DETECTING POLYMORPHIC LOCUS IN TARGETED GENOMIC REGION (2010)
    - CN patent no. CN201010270464; Yingrui Li; Chang Yu; Ruibang Luo; Fan Zhang

Services / Administration

Service to international professional organizations:

- Grant reviewer for "Natural Sciences and Engineering Research Council of Canada", and "European Bioinformatics Institute"
- PC member of prestigious bioinformatics conferences from 2017 to present including ISMB, RECOMB, RECOMB-Seq, IEEE BIBM, ACM-BCB, AICoB, and GIW/ABACBS
- Reviewer for journals including *Nature*, *Nature Method*, *Nature Biotechnology*, *Nature Communication*, *Nature Machine Intelligence*, *Genome Medicine*, *Genome Biology*, *Bioinformatics*, *BMC Bioinformatics*, *PLoS Computational Biology*, *PLoS ONE*, *Genome Research* and *GigaScience*

Service to local professional organizations

- Served the Technology Review Panel for Hong Kong Applied Science and Technology Research Institute Company Limited (ASTRI) since 2022