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Education

- Ph.D. in Computer Science** Sept 2019 – Present
The University of Hong Kong, Hong Kong
Supervisor: Ruibang Luo
- M. Eng. in Computer Science and Technology** Sept 2017 – Jun 2019
Harbin Institute of Technology, Harbin
Supervisor: Yadong Wang
- Exchange Student in Computer Science and Engineering** Sept 2015 – Jan 2016
National Chiao Tung University, Taiwan
- B. Eng. in Bioinformatics** Sept 2013 – Jun 2017
Harbin Institute of Technology, Harbin

Work Experience

- Teaching Assistant**, The University of Hong Kong Spring 2023
▪ COMP2501, Introduction to Data Science and Engineering, Undergraduate Course
- Teaching Assistant**, The University of Hong Kong Spring 2020, 2021, 2022
▪ CCST9047, The Age of Big Data, Undergraduate Course, Common Core
- Teaching Assistant**, Harbin Institute of Technology Fall 2018
▪ Bioinformatics, Undergraduate Course
- Bioinformatics Intern**, WeGene (ShenZhen) Summer 2016, 2017
▪ Topic: SNP applications development and data mining

Peer-reviewed Publications

Corresponding (*), first or co-first author (†):

1. 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*, 2022.
 - Built the state-of-the-art germline small variants caller for the Nanopore long-read data.
 - Over 110k downloads. Open source at: <https://github.com/HKU-BAL/Clair3>.
2. J. Su, Z. Zheng, 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*, 2022.
 - Improved family trio variant calling accuracy of over +10% F1-Score at the low coverage Nanopore long-read data.
 - Over 2.2k downloads. Open source at: <https://github.com/HKU-BAL/Clair3-Trio>.

3. **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*, 2021.
 - Extended relation extraction to full-text articles scope and mined all gene-disease relations from all open-access full-text articles (1.8M) with a large GPUs cluster.
 - Over 1.2k downloads. Open source at: <https://github.com/sujunhao/RENET2>.
4. **J. Su**, W. Lui, Y. Lee, Z. Zheng, ..., R. Luo*. Evaluation of *Mycobacterium tuberculosis* enrichment in metagenomic samples using ONT adaptive sequencing and amplicon sequencing for identification and variant calling. *Scientific Reports*, 2023.
 - Benchmarked adaptive sequencing performance at metagenomic samples and built a Nextflow pipeline for *Mycobacterium tuberculosis* data analysis.
 - Open source at: <https://github.com/HKU-BAL/ONT-TB-NF>.

Co-author:

1. Y. Liu, T. Jiang, **J. Su**, B. Liu*, T. Zang*, Y. Wang*. SKSV: ultrafast structural variation detection from circular consensus sequencing reads. *Bioinformatics*, 2021.

Presentations

Talk:

1. December 2022 – Presenter at HKU Bioinfo-seminars, The University of Hong Kong, Hong Kong
2. June 2023 – Presenter at TRS Symposium, The University of Hong Kong, Hong Kong

Poster:

1. April 2023 - ClusterV: Accurate Detection of HIV Quasispecies and Drug Resistance Mutations using ONT Sequencing Data. RECOMB-SEQ, Istanbul, Turkey

Professional Activities

- Reviewer for ISMB/ECCB, BMC Bioinformatics, Patterns, NeurIPS, ACM BCB.

References

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Associate Professor of Computer Science, The University of Hong Kong

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Tak-Wah Lam

PhD Co-supervisor

Professor of Computer Science, The University of Hong Kong

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Yadong Wang

Master Supervisor

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