

Department of Computer Science
Faculty of Engineering, The University of Hong Kong
Rm307, Haking Wong Bldg
HKU, Pokfulam Rd., Hong Kong

+852-564-33-527
jhsu@connect.hku.hk
<https://sujunhao.github.io>

Education

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

Work Experience

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

Peer-reviewed Publications

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

1. H. Yu[†], Z. Zheng[†], **J. Su***, T. Lam*, and R. Luo*. Boosting variant-calling performance with multi-platform sequencing data using Clair3-MP. *BMC Bioinformatics*, 2023.
 - Open source at: <https://github.com/HKU-BAL/Clair3-MP>.
2. **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.
 - Open source at: <https://github.com/HKU-BAL/ONT-TB-NF>.
3. T. Ng[†], **J. Su†**, et al. Long-Read Sequencing with Hierarchical Clustering for Antiretroviral Resistance Profiling of Mixed Human Immunodeficiency Virus Quasispecies. *Clinical Chemistry*, 2023.
 - Open source at: <https://github.com/HKU-BAL/ClusterV>.

4. **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.
 - Over 2.2k downloads. Open source at: <https://github.com/HKU-BAL/Clair3-Trio>.
5. 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.
 - Over 110k downloads. Open source at: <https://github.com/HKU-BAL/Clair3>.
6. **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.
 - Over 1.2k downloads. Open source at: <https://github.com/sujunhao/RENET2>.

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 Theme-based Research Scheme (Budget 34M HKD), 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

Ruibang Luo

PhD Supervisor, Associate Professor of Computer Science, The University of Hong Kong

rbluo@cs.hku.hk

Tak-Wah Lam

PhD Co-supervisor, Professor of Computer Science, The University of Hong Kong

twlam@cs.hku.hk

Yadong Wang

Master Supervisor, Professor of Computer Science and Technology, Harbin Institute of Technology

ydwang@hit.edu.cn