JUNHAO SU

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Education

Ph.D. in Computer Science   Sept 2019 – Oct 2023
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; Spring 2018
- Topic: SNP applications development and data mining

Peer-reviewed Publications

Corresponding (*), first or co-first author (†):
1. **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.
2. 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.
3. 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.

4. L. Chen †, **J. Su†**, Z,Zheng, T. Lam, and R. Luo. Large-scale Dataset and Effective Model for Variant-Disease Associations Extraction. In Proceedings of the 14th **ACM International Conference on Bioinformatics**, Computational Biology, and Health Informatics, 2023.
5. **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.
6. 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.
7. **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.

Co-author:
1. C., Lei, **J. Su,** T. Lam, and R. Luo. Exploring Pair-Aware Triangular Attention for Biomedical Relation Extraction. In Proceedings of the 14th **ACM International Conference on Bioinformatics**, Computational Biology, and Health Informatics, 2023.
2. S. Li, B. Yan, B. Wu, **J. Su**, J. Lu, T. Lam, ..., and R. Luo. Integrated modeling framework reveals co-regulation of transcription factors, miRNAs and lncRNAs on cardiac developmental dynamics. **Stem Cell Research & Therapy** (2023).
3. 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

1. Talk: December 2022 – Presenter at HKU Bioinfo-seminars, The University of Hong Kong, Hong Kong
2. Talk: June 2023 – Presenter at Theme-based Research Scheme (Budget 34M HKD), The University of Hong Kong, Hong Kong
3. Poster: 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.