香港浸會大學
HONG KONG BAPTIST UNIVERSITY

DEPARTMENT OF
COMPUTER SCIENCE
計算機科學系

A computational framework to prioritize disease-associated low frequency variants from Identity-By-Descent regions

PI : **Dr. Zhang Lu**

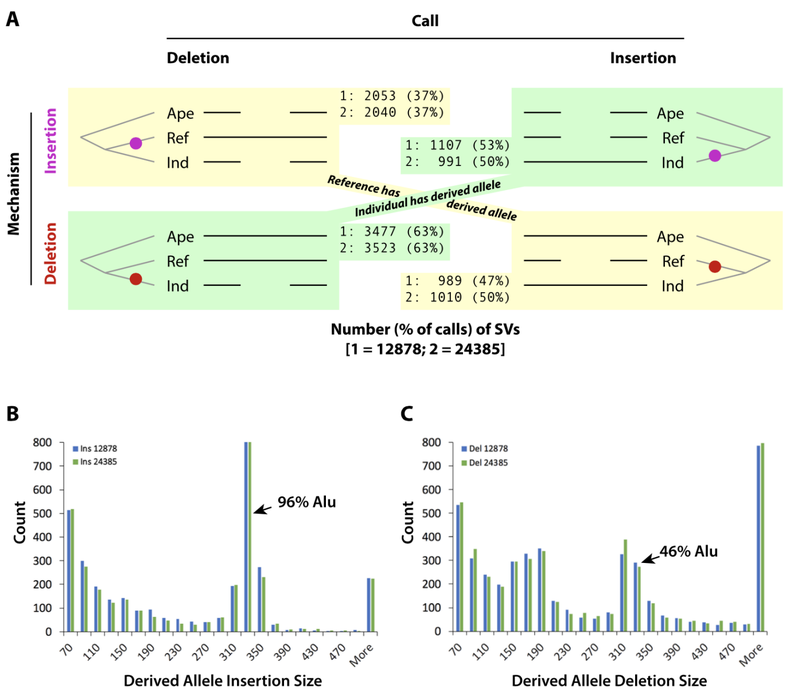
Funding Scheme: **Early Career Scheme**
Project Ref. No.: **22201419**
Amount Awarded (to HKBU): **HK$ 651,769**
Project Period: **Sept 2019 - Aug 2022**

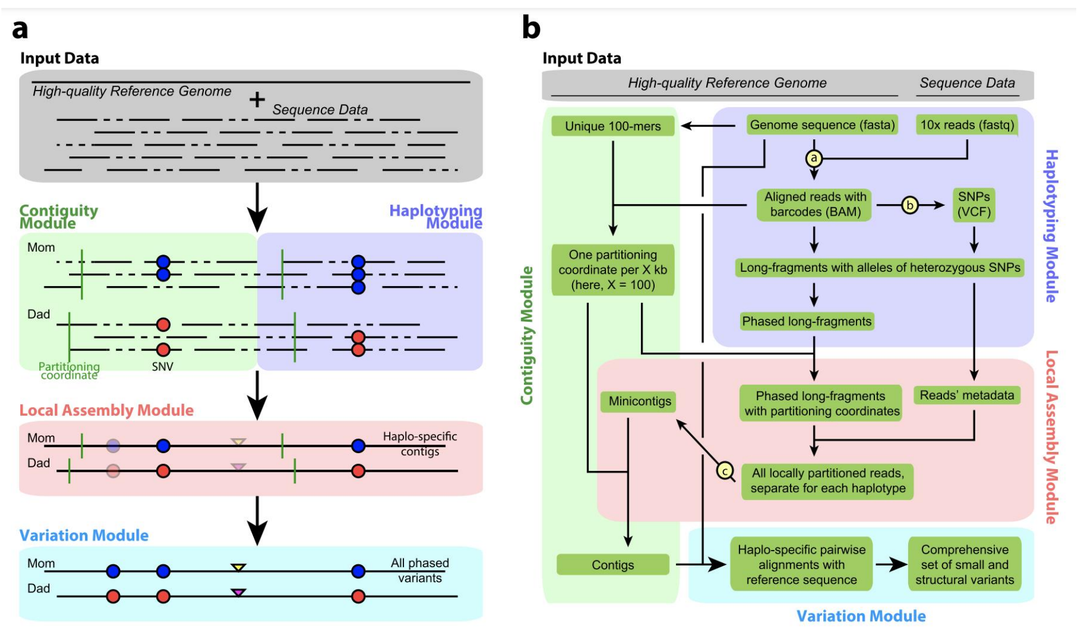
OBJECTIVES

1. To detect full spectrum genomic variants by *de novo* assembly.
2. To identify the identity-by-descent regions using low allele frequency single nucleotide variants.
3. To explore the patient subclusters using multi-omic data.

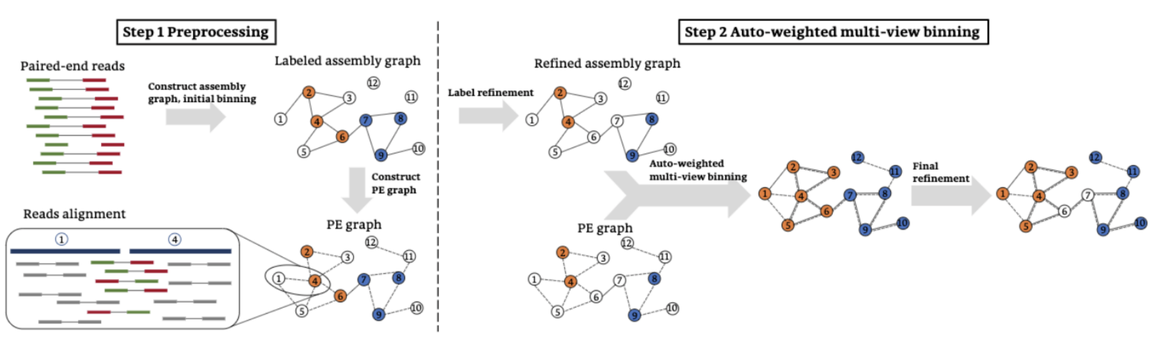
HIGHLIGHTS

1. Detect full spectrum genomic variants using genome assembly on linked-read sequencing [1,2,3]

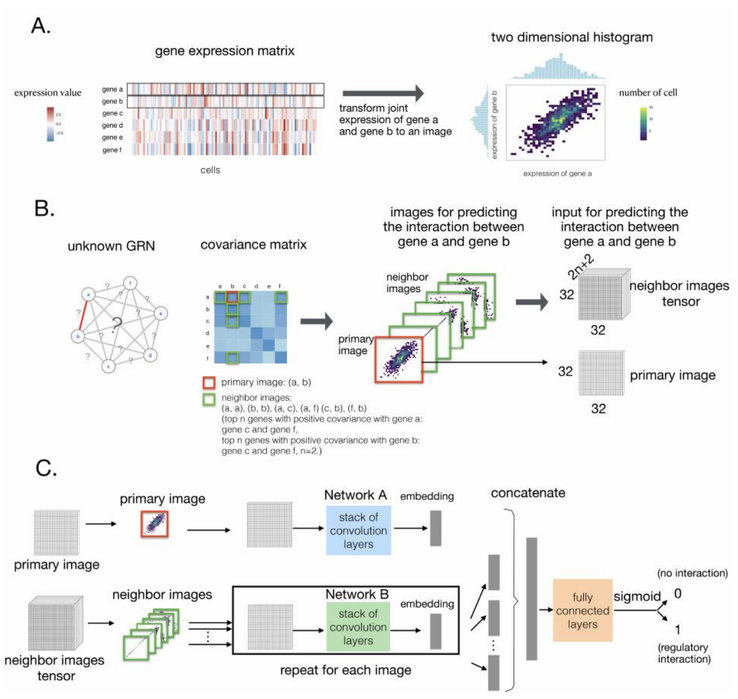




2. Decipher patients' gut microbiome by graph theory [4,5]



3. Identify the patients' cellular heterogeneity based on the gene regulatory networks from scRNA-seq [6]



SELECTED PUBLICATIONS

1. Lu Zhang, Xin Zhou, Ziming Weng, Arend Sidow. Assessment of human diploid genome assembly with 10x Linked-Reads data. **GigaScience** doi: 10.1093/gigascience/giz141
2. Lu Zhang, Xin Zhou, Ziming Weng, Arend Sidow. De novo diploid genome assembly for genome-wide structural variant detection. **NAR Genomics and Bioinformatics** doi: 10.1093/nargab/lqz018
3. 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** doi.org/10.1038/s41467-021-21395-x
4. Zhenmiao Zhang, Lu Zhang. METAMVGL: a multi-view graph-based metagenomic contig binning algorithm by integrating assembly and paired-end graphs. **APBC2021**
5. Lu Zhang, Xiaodong Fang et al. A Comprehensive Investigation of Metagenome Assembly by Linked-Read Sequencing. **Microbiome** doi: 10.1186/s40168-020-00929-3
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. **BioRxiv** doi.org/10.1101/2021.02.03.429484