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Education

Ph.D. in Computer Science

Sept 2011 – Aug 2015

The University of Hong Kong, Hong Kong

Dissertation: An all-purpose genome assembler for next-generation sequencing reads

Supervisor: Professor Tak-Wah Lam

B. Eng. in Bioengineering

Sept 2007 – Jun 2010

South China University of Technology, Guangzhou

Professional Experience

Assistant Professor, The University of Hong Kong

Jan 2018 - Present

Postdoctoral Fellow, Johns Hopkins University

Sept 2016 – Dec 2017

Peer-reviewed Publications

Corresponding, first or co-first author:

- Li et al., Building the sequence map of the human pan-genome. *Nature Biotechnology*, 2010.
- Li et al., Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome *de novo* assembly. *Nature Biotechnology*, 2011.
- Luo et al., SOAPdenovo2: An empirically improved memory-efficient short-read *de novo* assembler. *BMC GigaScience*, 2012.
- Liu et al., COPE: an accurate k-mer-based pair-end reads connection tool to facilitate genome assembly. *Bioinformatics*, 2012.
- Zhang et al., Oyster genome reveals stress adaptation and shell formation complexity. *Nature*, 2012.
- Luo et al., SOAP3-dp: Fast, Accurate and Sensitive GPU-based Short Read Aligner, *PLoS ONE*, 2013.
- Xie et al., SOAPdenovo-Trans: *de novo* transcriptome assembly with short RNA-Seq reads, *Bioinformatics*, 2014.(cited 194 times)
- Liu et al., GPU-Accelerated BWT Construction for Large Collection of Short Reads, *Arxiv*, 2014
- Luo et al., BALSAs: integrated secondary analysis for whole-genome and whole-exome sequencing, accelerated by GPU. *PeerJ*, 2014.
- Ramos et al., Exome sequencing of tumor cell lines: Optimizing for cancer variants. *Cancer Research*, 2014.
- Cao et al., *De novo* assembly of a haplotype-resolved human genome. *Nature Biotechnology*, 2015.
- Ou et al., database.bio: a web application for interpreting human variations. *Bioinformatics*, 2015.
- Li et al., MEGAHIT: An ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph. *Bioinformatics*, 2015.
- Luo et al., MICA: A fast short-read aligner that takes full advantage of Intel Many Integrated Core Architecture (MIC). *BMC Bioinformatics*, 2015.

- Lee et al., Serine peptidase inhibitor, Kazal type 1 (SPINK1) as a novel downstream effector of the tumorigenic cadherin-17/ β -catenin axis in hepatocellular carcinoma. *Cellular Oncology*, 2017.
- Luo et al., 16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. *GigaScience*, 2017.
- Luo et al., LRSim: a Linked Reads Simulator generating insights for better genome partitioning. *Computational and Structural Biotechnology*, 2017.
- Luo et al., Restricted Boltzmann Machine and its Potential to Better Predict Cancer Survival. *Biomed J Sci & Tech Res*, 2018.
- Luo et al., Clairvoyante: a multi-task convolutional deep neural network for variant calling in Single Molecule Sequencing. *In press*, 2018.
- Luo et al., Skyhawk: An Artificial Neural Network-based discriminator for reviewing clinically significant genomic variants. *In press*, 2018.

Co-author:

- Li et al., The DNA Methylome of Human Peripheral Blood Mononuclear Cells. *PLoS Biology*, 2010.
- Yi et al., Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. *Science*, 2010.
- Mills et al., Mapping copy number variation by population-scale genome sequencing. *Nature*, 2011.
- Earl et al., Assemblathon 1: A competitive assessment of *de novo* short read assembly methods. *Genome Research*, 2011.
- 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*, 2012.
- Altshuler et al., An integrated map of genetic variation from 1,092 human genomes. *Nature*, 2012.
- Bradnam et al., Assemblathon 2: evaluating *de novo* methods of genome assembly in three vertebrate species. *BMC GigaScience*, 2013.
- 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. *American Society of Hematology*, 2013.
- Zhang et al., Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. *Plant Cell*, 2015.
- Li et al., MegaGTA: a sensitive and accurate metagenomic gene-targeted assembler using iterative de Bruijn graphs. *BMC Bioinformatics*, 2017.
- Lee et al., Transcriptome Analysis of Acute Phase Liver Graft Injury in Liver Transplantation. *Biomedicines*, 2018.

Awards

- Forbes 30 Under 30 Asia 2017: Healthcare and Science

Patents

- METHODS AND SYSTEMS FOR DETECTING GENOMIC STRUCTURE VARIATIONS
CN201080068345
Ruibang Luo; Haojing Shao; Haoxiang Lin
- METHOD AND SYSTEM FOR DETECTING POLYMORPHIC LOCUS IN TARGETED GENOMIC REGION
CN201010270464
Yingrui Li; Chang Yu; Ruibang Luo; Fan Zhang

Professional Activities

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- The Asian Young Researchers Conference on Computational and Omics Biology (AYRCOB), Organizer, 2011-2014
 - Biotechnology and Bioinformatics Symposium, Program Committee, 2012-2016
 - IEEE International Conference on Bioinformatics and Biomedicine, Accelerator-Enabled Algorithms and Applications in Bioinformatics, Program Committee, 2016
 - Reviewer for Nature Biotechnology, Genome Medicine, Genome Biology, Bioinformatics, BMC Bioinformatics, PLoS Computational Biology, PLoS ONE, Genome Research, GigaScience

Other Qualifications

- Advanced Open Water Diver, 2016, issued by Professional Association of Diving Instructors (PADI)
- Automobile Sports Competition License Level E, 2016, issued by Federation of Automobile Sports of the People's Republic of China (FASC)
- Private Pilot License, 2017, issued by Federal Aviation Administration (FAA)

References

Steven L. Salzberg

JHU Postdoc Advisor

Bloomberg Distinguished Professor of Biomedical Engineering, Computer Science and Biostatistics
School of Medicine, Johns Hopkins University

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Michael C. Schatz

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