RUIBANG LUO

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Career Statement

As a researcher with both a bio-engineering and a computer science background, I have worked on bioinformatics software development and biological, clinical and pharmaceutical projects. My interdisciplinary research results have been published in peer-reviewed journals such as *Nature*, *Nature Biotechnology* and *Bioinformatics*. My ongoing target is to become a world-class scientist, building models and developing software with my students and other collaborators with the aim of better understanding the origins of life and developing cures for cancer.

Education

Ph.D. in Computer Science Sept 2011 – Oct 2012 (Full-time)
Nov 2012 – Aug 2015 (Part-time)

The University of Hong Kong, Hong Kong
Dissertation: An all-purpose genome assembler for next-generation sequencing reads
Supervisor: Tak-Wah Lam

B. Eng. in Bioengineering Sept 2007 – Jun 2010

South China University of Technology, Guangzhou
Graduated one year early

Professional Experience

Postdoctoral Fellow, Johns Hopkins University Sept 2016 – Present
Joint post with the Center for Computational Biology, the School of Medicine, and the Department of Computer Science, Whiting School of Engineering

Peer-reviewed Publications *(Number of citations from Google Scholar, as of November 23, 2016)*

Corresponding, first or co-first author:

- Li et al., Building the sequence map of the human pan-genome. ***Nature Biotechnology***, 2010. (cited 130 times)
- Li et al., Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome *de novo* assembly. ***Nature Biotechnology***, 2011. (cited 87 times)
- Luo et al., SOAPdenovo2**:** An empirically improved memory-efficient short-read *de novo* assembler. ***BMC GigaScience***, 2012. (cited 938 times)
- Liu et al., COPE**:** an accurate k-mer-based pair-end reads connection tool to facilitate genome assembly. ***Bioinformatics***, 2012. (cited 59 times)

- Zhang et al., Oyster genome reveals stress adaptation and shell formation complexity. ***Nature***, 2012. (cited 676 times)
- Luo et al., SOAP3-dp: Fast, Accurate and Sensitive GPU-based Short Read Aligner, ***PLoS ONE***, 2013. (cited 66 times)
- 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 (cited 12 times)
- Luo et al., BALSA**:** integrated secondary analysis for whole-genome and whole-exome sequencing, accelerated by GPU. ***PeerJ***, 2014. (cited 6 times)
- 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. (cited 15 times)
- 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. (cited 59 times)
- Luo et al., MICA: A fast short-read aligner that takes full advantage of Intel Many Integrated Core Architecture (MIC). ***BMC Bioinformatics***, 2015. (cited 20 times)
- Lee et al., Serine peptidase inhibitor, Kazal type 1 (SPINK1) as a novel downstream effector of the tumorigenic cadherin-17/ß-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. ***Genome Biology***, 2017, in press.
- Luo et al., First Draft Genome Sequence of the Pathogenic Fungus Lomentospora prolificans (formerly Scedosporium prolificans). ***Nature Microbiology***, 2017, in press.

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, accepted.
- Daya et al., Genome-wide association study of asthma in individuals of African ancestry reveals novel asthma susceptibility loci. ***Nature Genetics***, 2017, in press.

Awards

- Forbes 30 Under 30 Asia 2017: Healthcare and Science

Patent Applications

- METHOD AND SYSTEM FOR ASSEMBLY OF GENOME
  WO2012171213 (Pending)
  Jun Wang; Ruibang Luo; Yinlong Xie; Yunjie Liu

- METHODS AND SYSTEMS FOR DETECTING GENOMIC STRUCTURE VARIATIONS
  WO2012034251 (Pending), CN201080068345 (Approved)
  Ruibang Luo; Haojing Shao; Haoxiang Lin

- METHOD AND SYSTEM FOR DETECTING POLYMORPHIC LOCUS IN TARGETED GENOMIC REGION
  WO2012027958 (Pending), CN201010270464 (Approved)
  Yingrui Li; Chang Yu; Ruibang Luo; Fan Zhang

Presentations

Talk:

- January 2010 - Invited speaker at Plant and Animal Genome Conference XVII, San Diego, CA
- November 2010 - Invited speaker at the 5th International Conference on Genomics Conference (ICG-5), Shenzhen, China
- October 2012 - Keynote speaker at Biotechnology and Bioinformatics Symposium 2012, Provo, UT
- November 2012 – Speaker at International Society of Molecular Biology Conference (ISMB) 2012, Long Beach, CA
- November 2012 - Invited speaker at the 7th International Conference on Genomics Conference (ICG-7), Hong Kong, China
- April 2015 – Invited speaker at the 1st Intel Bio-IT Forum, Beijing, China
- September 2015 - Invited speaker at the 4th Young Bioinformatics PI meeting, Wuhan, China

Lecture:

- November 2015 - Invited lecturer at Huazhong University of Science and Technology, Wuhan, China
- January 2016 – Invited lecturer at School of Life Sciences, Tsinghua University, Beijing, China

Poster:

- November 2012 - SOAP3-dp: Fast, Accurate and Sensitive GPU-based Short Read Aligner. International Society of Molecular Biology, Long Beach, CA
- October 2016 - Simultaneous detection of SNPs and Indels using a 16-genotype probabilistic model. Biological Data Science Meeting, Cold Spring Harbor, NY

Professional Activities

- 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 and Genome Research, GigaScience

Other Skills and Qualifications

- Stanford Genetics and Genomics Certificate, 2016, issued by the Stanford Center for Professional Development, Stanford University
- 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 Student, 2017, issued by Federal Aviation Administration (FAA)

References

Steven L. Salzberg
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