

LI Chenhao | Resumé

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Date of Birth: 16/02/1991

Education

National University of Singapore

Doctor of Philosophy (Part-time),

January 2015–2019

Computer Science (Computational biology)

National University of Singapore

Bachelor of Science (Honours),

August 2010–June 2014

Major: Computational Biology

Cumulative Average Point: 4.7/5.0 (First Class Honours)

- Full scholarship sponsored by Development Bank of Singapore (SM3)
- Dean's List of AY2011/2012 Semester 2 & AY2013/2014 Semester 1
- Lim Soo Peng Book Prize 2011 (Best student in computer science stream)
- Lijen Industrial Development Medal (Best academic exercise/projects in the discipline)

National University of Singapore

English Bridging Course,

January 2010–June 2010

- Full scholarship sponsored by Development Bank of Singapore (SM3)

Shijiazhuang 2nd Middle School (Hebei, China)

A-level equivalent,

September 2006–June 2009

National College Entrance Examination (Hebei) 647/750

Experiences

Working

Genome Institute of Singapore

Singapore

Bioinformatics specialist

July 2014 – Present

Full-time job

- Metagenomics data analysis
- Nanopore data analysis
- ICGC-TCGA DREAM Somatic Mutation Calling Challenge

Teaching

National University of Singapore

Singapore

Teaching assistant for CS1010X (Programming Methodology)

January 2018 – June 2018

National University of Singapore

Singapore

Teaching assistant for LSM2241 (Introduction to Bioinformatics)

August 2013 – December 2013

Academic Services

- Reviewer for *Bioinformatics*, *GigaScience*, *Nature Methods*

Publications

- Bertrand, D., Shaw, J., Narayan, M., Ng, A. H. Q., Kumar, S., Li, C., *et al.* (2018). Nanopore sequencing enables high-resolution analysis of resistance determinants and mobile elements in the human gut microbiome. *bioRxiv* (preprint).
- Li, C., *et al.* (2018). System Biology Modeling with Compositional Microbiome Data Reveals Personalized Gut Microbial Dynamics and Keystone Species. *bioRxiv* (preprint).
- Bertrand, D., Drissler, S., Chia, B., Koh, J. Y., Li, C., *et al.* (2017). ConsensusDriver improves

upon individual algorithms for predicting driver alterations in different cancer types and individual patients — A Toolbox For Precision Oncology. *Cancer Research*.

- Lim, K. M. K., Li, C., Chng, K. R., Nagarajan, N. (2016). @MInter: Automated text-mining of microbial interactions. *Bioinformatics*.
- Chng, K. R., Chan, S. H., Ng, A. H. Q., Li, C., *et al.* (2016). Tissue microbiome profiling identifies an enrichment of specific enteric bacteria in *Opisthorchis viverrini* associated cholangiocarcinoma. *Ebiomedicine*.
- Chng, K. R., Tay, A. S. L., Li, C., *et al.* (2016). Whole metagenome profiling reveals skin microbiome dependent susceptibility to atopic dermatitis flares. *Nature Microbiology*.
- Li, C., *et al.* (2016). Predicting Microbial Interactions through Computational Approaches. *Methods*. (Review.)
- Li, C., *et al.* (2016). INC-Seq: Accurate single molecule reads using nanopore sequencing. *GigaScience*.
- Wu, G., Zhao, H., Li, C. *et al.* (2015). Genus-wide comparative genomics of *Malassezia* delineates its phylogeny, physiology, and niche adaptation on human skin. *PLOS Genetics*.
- Ewing, A. D., *et al.* (2015). Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. *Nature Methods*. (Consortium.)

Software

- BEEM-static - An R package for inferring microbial interactions based on Lotka-Volterra models
- BEEM - Estimating Lotka-Volterra models from time-course microbiome sequencing data
- MicrobiomeViz - An R package for visualising microbiome data.
- MinION watchdog - Utilities for MinION real-time analysis.
- INC-Seq - Analysis pipeline for accurate single molecule reads using nanopore sequencing (The INC-Seq protocol)
- Shotgun metagenomics pipeline - A reference-based pipeline for shotgun metagenomics. Github page: <https://github.com/lch14forever>

Talks

- System Biology Modeling with Compositional Microbiome Data Reveals Personalized Gut Microbial Dynamics and Keystone Species. IHMC2018.

Languages

English: Spoken & Written

Chinese: Spoken & Written

Relevant skills

Programming skills (working knowledge): Python, R, Unix bash scripting

Programming skills (basic knowledge): Scala, C, C++, MATLAB, JAVA, Perl, HTML, PHP

Bioinformatics:

- Substantial experience with software for analysing high-throughput sequencing data
- Extensive experience with data processing, modelling and visualization
- Experience in working with high performance computing environments (LSF, SGE)
- Familiar with bioinformatic pipeline frameworks (Snakemake, Nextflow), version control systems (git) and containers (docker)