

Chenhao Li | PhD

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Summary

An experienced computational biologist with strong passion for understanding biology through computational approaches. Proficient in mining, visualizing, interpreting and modelling high-throughput sequencing data. Interested in a broad range of biological problems, especially understanding the dynamics of microbial communities.

Education

PhD in Computer Science

National University of Singapore

Jan 2015–Apr 2019

Thesis: Modelling Approaches to Predicting Microbial Interactions

Supervisors: Niranjana Nagarajan, Limsoon Wong

- Award for outstanding achievement 2018 (GIS Graduate Student Prize)
- Award for excellence in teaching 2018 (Honor List of Student Tutors)

BSc (Hon.) in Computational Biology

National University of Singapore

Aug 2010–Jun 2014

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

- Best academic exercise in Computational Biology 2014 (Lijen Industrial Development Medal)
- Best student in Computer Science stream 2011 (Lim Soo Peng Book Prize)
- Dean's List (2011/2012 Semester II and 2013/2014 Semester I)
- Full scholarship for Chinese students awarded by the Ministry of Education 2009 (SM3)

Work Experience

Research Fellow

Xavier lab at Massachusetts General Hospital and Broad Institute

Dec 2020 – Present

- Analysis of single cell and spatial transcriptomics data of gut tissues
- Investigation of associations of gut microbiome and cardiovascular disease risks using multiomics data

Research Associate

Genome Institute of Singapore

Apr 2020 – Nov 2020

- Build and maintain bioinformatics infrastructure for COVID-19 sample analysis
- Lead bioinformatics analysis of skin metagenomics samples

Postdoctoral Fellow

Genome Institute of Singapore

Apr 2019 – Mar 2020

- Investigate antibiotics resistant bacteria in environmental samples
- Build and maintain data handling system for nanopore sequencing data for the institute
- Predict ecological interactions between microbial species

Bioinformatics specialist

Genome Institute of Singapore

Jul 2014 – Mar 2019

- Mine association between disease and human microbiome
- Predict ecological interactions between microbial species
- Design, optimise and maintain high-performance pipelines for sequencing data analysis
- Guide and train attachment students

Technical skills

Github page: <https://github.com/lch14forever>

- Programming languages: (advanced) R, Python and Linux bash scripting; (intermediate) Javascript, C, C++, MATLAB, JAVA, Perl, HTML, PHP and SCALA
- Bioinformatics: (advanced) workflow languages (Nextflow, Snakemake, Bpipe), next-generation sequencing data analysis (shotgun metagenomics, amplicon sequencing, RNA-Seq, whole genome sequencing, Single cell RNA-Seq and spatial transcriptomics)
- Scientific computing: high performance computing environments (cluster), cloud computing (AWS, GCP)
- Others: (advanced) git, docker

Software

1. BEEM-static - An R package for inferring microbial interactions based on Lotka-Volterra models from cross-sectional microbiome sequencing data. <https://github.com/lch14forever/BEEM-static>
2. BEEM - Estimating Lotka-Volterra models from time-course microbiome sequencing data. <https://github.com/lch14forever/BEEM>
3. shotgunmetagenomics-nf - A reference-based pipeline for shotgun metagenomics. <https://github.com/lch14forever/shotgunmetagenomics-nf>
4. MicrobiomeViz - An R package for visualising microbiome data. <https://github.com/lch14forever/microbiomeViz>

Publications (*: first author, #: correspondance author)

Under review.....

1. H. Hu*, Y. Tan*, **C. Li***, ..., L. Dai. StrainPanDA: linked reconstruction of strain composition and gene content profiles via pangenome-based decomposition of metagenomic data. **BioRxiv**. (2022).

Published.....

1. F. Meyer, A. Fritz, ..., **C. Li**, ..., A. C. McHardy. Critical Assessment of Metagenome Interpretation - the second round of challenges. **Nature Methods**. (2022).
2. **C. Li*#**, T. V. Av-Shalom, J. W. G. Tan, J. S. Kwah, K. R. Chng, N. Nagarajan#. BEEM-Static: Accurate inference of ecological interactions from cross-sectional metagenomic data. **PLOS Computational Biology**. (2021).
3. A global metagenomic map of urban microbiomes and antimicrobial resistance. **Cell**. (2021). (MetaSUB consortium).
4. J. G. A. Aw, S. W. Lim, J. X. Wang, ..., **C. Li**, ..., N. Nagarajan, Y. Wan. Determination of isoform-specific RNA structure with nanopore long reads. **Nature Biotechnology**. (2021).
5. A. S. L. Tay*, **C. Li***, T. Nandi*, ..., N. Nagarajan, J. Common. Atopic dermatitis microbiomes stratify into ecological dermatotypes enabling microbial virulence and disease severity. **The Journal of Allergy and Clinical Immunology**. (2021)
6. K. R. Chng, T. Ghosh, Y. H. Tan, T. Nandi, ..., **C. Li**, ..., N. Nagarajan. Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. **Nature Ecology and Evolution**. (2020).
7. K. R. Chng*, **C. Li***, D. Bertrand*, ..., N. Nagarajan. A cartography of opportunistic pathogens and antibiotic-resistance genes in a tertiary hospital environment. **Nature Medicine**. (2020).
8. **C. Li***, K. R. Chng, T. V. Av-Shalom, ..., N. Nagarajan. An expectation-maximization algorithm enables accurate ecological modeling using longitudinal microbiome sequencing data. **Microbiome**. (2019).
9. D. Bertrand, J. Shaw, M. Narayan, A. H. Q. Ng, ..., **C. Li**, ..., N. Nagarajan. Nanopore sequencing enables high-resolution analysis of resistance determinants and mobile elements in the human gut microbiome. **Nature Biotechnology**. (2019).
10. D. Bertrand, S. Drissler, B. Chia, ..., **C. Li**, ..., N. Nagarajan. ConsensusDriver improves upon individual algorithms for predicting driver alterations in different cancer types and individual patients — A Toolbox For Precision Oncology. **Cancer Research**. (2018).
11. Y. O. Zhu, P. P. K. Aw, P. F. de Sessions, ..., **C. Li**, ..., M. Hibberd. Single-virion

- sequencing of lamivudine-treated HBV populations reveal population evolution dynamics and demographic history. **BMC Genomics**. (2017).
12. K. M. K. Lim, **C. Li**, K. R. Chng, N. Nagarajan. @MInter: Automated text-mining of microbial interactions. **Bioinformatics**. (2016).
 13. K. R. Chng, S. H. Chan, ..., **C. Li**, ..., N. Nagarajan. Tissue microbiome profiling identifies an enrichment of specific enteric bacteria in *Opisthorchis viverrini* associated cholangiocarcinoma. **EBioMedicine**. (2016).
 14. K. R. Chng, A. S. L. Tay, **C. Li**, ..., N. Nagarajan. Whole metagenome profiling reveals skin microbiome dependent susceptibility to atopic dermatitis flares. **Nature Microbiology**. (2016).
 15. **C. Li**^{*}, K. R. Chng, K. M. K. Lim, N. Nagarajan. Predicting Microbial Interactions through Computational Approaches. **Methods**. (2016).
 16. **C. Li**^{*}, K. R. Chng^{*}, E. J. H. Boey, ..., N. Nagarajan. INC-Seq: Accurate single molecule reads using nanopore sequencing. **GigaScience**. (2016).
 17. G. Wu, H. Zhao, **C. Li**, ..., N. Nagarajan. Genus-wide comparative genomics of *Malassezia* delineates its phylogeny, physiology, and niche adaptation on human skin. **PLOS Genetics**. (2015).
 18. A. D. Ewing, *et al.* Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. **Nature Methods**. (2015). (DREAM Challenge team Lofreq).

Teaching experience

Teaching assistant for CS1010X (Programming Methodology)

National University of Singapore

Jan 2018 – Jun 2018

Teaching assistant for LSM2241 (Introduction to Bioinformatics)

National University of Singapore

Aug 2013 – Dec 2013

Talks

- System Biology Modeling with Compositional Microbiome Data Reveals Personalized Gut Microbial Dynamics and Keystone Species. International Human Microbiome Congress 2018, Ireland.

Academic Service

- *Ad hoc* reviewer for *Bioinformatics*, *GigaScience*, *Nature Methods*, *PeerJ*, *Scientific Reports*, *Microbiome*, *Journal of Genetics and Genomics*