# 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 gut microbial communities and their interaction with the host.

Key words: `metagenomics, spatial transcriptomics, single-cell transcriptomics`

## Education and academic training

**Instructor of Medicine**

*Xavier lab at Massachusetts General Hospital and Broad Institute*          *Mar 2024 – Present*

**Research Fellow**

*Xavier lab at Massachusetts General Hospital and Broad Institute*          *Dec 2020 – Feb 2024*

**Research Associate**

*Genome Institute of Singapore*          *Apr 2020 – Nov 2020*

**Postdoctoral Fellow**

*Genome Institute of Singapore*          *Apr 2019 – Mar 2020*

**PhD in Computer Science**

*National University of Singapore*          *Jan 2015–Apr 2019*

**Bioinformatics specialist (concurrent with PhD)**

*Genome Institute of Singapore*          *Jul 2014 – Mar 2019*

**BSc (First Class Honours) in Computational Biology**

*National University of Singapore*          *Aug 2010–Jun 2014*

## Awards

- Harvard Chinese Life Science Annual Distinguished Research Award 2024
- GIS Graduate Student Prize 2018 (Award for outstanding achievement)
- Honor List of Student Tutors 2018 (Award for excellence in teaching)
- Lijen Industrial Development Medal 2014 (Best academic exercise)
- Lim Soo Peng Book Prize 2011 (Best student in Computer Science stream)

- Dean's List 2011/2012 Semester II and 2013/2014 Semester I
- Scholarship for Chinese students awarded by the Ministry of Education 2009-2014 (SM3)

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

H-index: 17, Citations: 3,216 (2025-07-21)

## Selected publications

1. T. Mayassi*, **C. Li**\*, ..., R. Xavier. Spatial restricted immune and microbiota-driven adaptation of the gut. **Nature** (2024).

2. **C. Li**\*, M. Stražar*, ..., R. Xavier. Gut microbiome and metabolome profiling in Framingham Heart Study reveals cholesterol-metabolizing bacteria linked with lower cardiovascular risk. **Cell** (2024).

3. **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).

4. A. S. L. Tay*, **C. Li**\*, T. Nandi*, ..., N. Nagarajan, J. Common. Atopic dermatitis microbiomes stratify into ecological dermotypes enabling microbial virulence and disease severity. **The Journal of Allergy and Clinical Immunology** (2021).

5. 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).

6. **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).

7. **C. Li**\*, K. R. Chng, K. M. K. Lim, N. Nagarajan. Predicting Microbial Interactions through Computational Approaches. **Methods** (2016). *Review paper.*

8. **C. Li**\*, K. R. Chng*, E. J. H. Boey, ..., N. Nagarajan. INC-Seq: Accurate single molecule reads using nanopore sequencing. **GigaScience** (2016).

## Other publications

1. A. Ravikrishnan, I. Wijaya, ..., **C. Li**, ..., N. Nagarajan. Gut metagenomes of Asian octogenarians reveal a metabolic shift and distinct microbial species associated with aging phenotypes. **Nature Communication** (2024).

2. T. Nakata, **C. Li**, ..., D. Graham, R. Xavier. Genetic vulnerability to healing reveals a spatially resolved epithelial restitution program. **Science Translational Medicine** (2023).

3. F. Meyer, A. Fritz, ..., **C. Li**, ..., A. C. McHardy. Critical Assessment of Metagenome

Interpretation - the second round of challenges. **Nature Methods** (2022).

4. 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. **iMeta** (2022).

5. A global metagenomic map of urban microbiomes and antimicrobial resistance. **Cell** (2021). *As a member of the MetaSUB consortium.*

6. 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).

7. 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).

8. 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).

9. 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).

10. 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).

11. K. M. K. Lim, **C. Li**, K. R. Chng, N. Nagarajan. @MInter: Automated text-mining of microbial interactions. **Bioinformatics** (2016).

12. 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).

13. 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).

14. 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).

15. A. D. Ewing, *et al.* Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. **Nature Methods** (2015). *As a member of DREAM Challenge team Lofreq.*

## Invited talks

- Gut Microbiome and Metabolome Characterization Reveals Cholesterol-metabolizing Bacteria Associated with Lower Cardiovascular Risk. Gut Microbiota for Health World Summit, 2025, Washington, D. C.
- System Biology Modeling with Compositional Microbiome Data Reveals Personalized Gut Microbial Dynamics and Keystone Species. International Human Microbiome Congress 2018, Ireland.

## Mentorship

1. Kumar Thurimella, 2023, PhD student at University of Cambridge. Currently a MD student at University of Colorado.
2. Licheng Xu, 2019, Undergraduate intern at SUTD. Currently a software engineer.
3. Gerald Tan, 2019, Undergraduate intern at NUS. Currently a data scientist.
4. Tamar Av-Shalmon, 2018, Undergraduate intern at UBC. Currently a PhD student at University of Toronto.
5. Kenneth Lim, 2015, Undergraduate intern at NUS. Currently a software engineer.

## Teaching experience

**Teaching assistant for Programming Methodology/CS1010X**

*National University of Singapore*                                          *Jan 2018 – Jun 2018*

**Teaching assistant for Introduction to Bioinformatics/LSM2241**

*National University of Singapore*                                          *Aug 2013 – Dec 2013*