

# Chenhao Li | PhD

✉ lichenhao.sg@gmail.com

## Summary

---

An experienced computational biologist with strong passion for understanding biology through computational approaches. Proficient in mining, visualising, 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*

*Dec 2020 – Present*

- affiliated with the Broad Institute and Harvard Medical School
- 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>

- Proficient in R, Python and Linux bash scripting; experience with C, C++, MATLAB, JAVA, Perl, HTML, PHP and SCALA
- Extensive experience with bioinformatic pipeline frameworks (Nextflow, Snakemake, Bpipe), high performance computing environments (cluster, AWS), version control systems (git) and containers (docker)
- Experience with next-generation sequencing data (Shotgun metagenomics, amplicon sequencing, RNA-Seq, whole genome sequencing)

## 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>
5. INC-Seq - Analysis pipeline for accurate single molecule reads using nanopore sequencing. <https://github.com/CSB5/INC-Seq>

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

---

1. C. Li<sup>\*#</sup>, T. V. Av-Shalom, J. W. G. Tan, J. S. Kwah, K. R. Chng, N. Nagarajan<sup>#</sup>. BEEM-Static: Accurate inference of ecological interactions from cross-sectional metagenomic data. **PLOS Computational Biology**. (2021).
2. A global metagenomic map of urban microbiomes and antimicrobial resistance. **Cell**. (2021). (MetaSUB consortium).
3. 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).
4. A. S. L. Tay<sup>\*</sup>, C. Li<sup>\*</sup>, T. Nandi<sup>\*</sup>, ..., 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)
5. 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).
6. K. R. Chng<sup>\*</sup>, C. Li<sup>\*</sup>, D. Bertrand<sup>\*</sup>, ..., N. Nagarajan. A cartography of opportunistic pathogens and antibiotic-resistance genes in a tertiary hospital environment. **Nature Medicine**. (2020).
7. C. Li<sup>\*</sup>, K. R. Chng, T. V. Av-Shalom, ..., N. Nagarajan. An expectation-maximization algorithm enables accurate ecological modeling using longitudinal microbiome sequencing data. **Microbiome**. (2019).
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. C. Li\*, K. R. Chng, K. M. K. Lim, N. Nagarajan. Predicting Microbial Interactions through Computational Approaches. **Methods**. (2016).
  15. C. Li\*, K. R. Chng\*, E. J. H. Boey, ..., N. Nagarajan. INC-Seq: Accurate single molecule reads using nanopore sequencing. **GigaScience**. (2016).
  16. 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).
  17. 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*

## References

---

### Niranjan Nagarajan

[nagarajann@gis.a-star.edu.sg](mailto:nagarajann@gis.a-star.edu.sg)

Associate Director and Senior Group Leader, Genome Institute of Singapore

### Limsoon Wong

[limsoon@nus.edu.sg](mailto:limsoon@nus.edu.sg)

Kwan-Im-Thong-Hood-Cho-Temple Chair Professor of Computer Science, National University of Singapore

**Greg Tucker-Kellogg**

*dbsgtk@nus.edu.sg*

Professor in Practice, Department of Biological Sciences, National University of Singapore