

李陈浩

博士后研究员

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教育背景

新加坡国立大学 (NUS)

博士, 计算机科学

2015 - 2019

- 论文: Modelling Approaches to Predicting Microbial Interactions

新加坡国立大学 (NUS)

学士, 计算生物学

2010 - 2014

- 学积分: 4.7/5.0 (一等荣誉学士)

工作经验

麻省综合医院及博德研究所 (Massachusetts General Hospital and Broad Institute)

博士后研究员

2021.12 - 至今

- 肠道微生物与心血管疾病关系研究
- 肠道单细胞测序及空间转录组数据分析

新加坡基因组研究所 (Genome Institute of Singapore)

博士后研究员 (II)

2020.4 - 至今

- 微生物组生态网络预测
- 牛津纳米孔测序数据分析

新加坡基因组研究所 (Genome Institute of Singapore)

博士后研究员 (I)

2019.4 - 2020.4

- 微生物组生态网络预测
- 医院微生物组项目生物信息分析
- 亚洲人体皮肤微生物计划生物信息分析

新加坡基因组研究所 (Genome Institute of Singapore)

生物信息分析师

2014.7 - 2019.3

- 宏基因组分析流程的搭建与维护
- 宏基因组数据分析和解读
- 数据统计建模分析、可视化及论文撰写

专业技能

- 精通 R, Python, Shell 脚本, 熟悉 Linux 环境, 应用过多种编程语言 (C/C++, Java, SCALA, Perl, PHP, Matlab)
- 熟悉宏基因组, 转录组, 牛津纳米孔 (Oxford Nanopore) 分析流程
- 精通生物信息软件容器 (Docker) 及版本控制 (git), 熟悉高性能计算 (SGE) 及云计算 (AWS) 环境
- 精通机器学习, 统计分析理论和应用
- 丰富生物信息流程开发经验 (Bpipe, Snakemake, Nextflow)

发表论文

发表

1. 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, IF2020: 4.5)
2. D. Danko, et al. A global metagenomic map of urban microbiomes and antimicrobial resistance. **Cell** (2021, IF2020: 42) (as MetaSUB consortium member)
3. A. S. L. Tay[#], C. Li[#], T. Nandi[#], ..., N. Nagarajan. Skin microbiome dermatotypes in atopic dermatitis are linked to host immunity and microbial virulence. **The Journal of Allergy and Clinical Immunology** (2021, IF2020: 11)
4. J. G. A. Aw, S. W. Lim, J. X. Wang, ..., C. Li, ..., N. Nagarajan, Y. Wan. Direct RNA sequencing reveals structural differences between transcript isoforms. **Nature Biotechnology** (2021, IF2020: 55)
5. Y. Tan, H. Hu, C. Li, X. Luo, Y. Tan, L. Dai. Research progress and applications of strain analysis based on metagenomic data. **生物工程学报** (2020)

6. T. Nandi, I. R. Lee, T. Ghosh, ..., **C. Li**, ..., N. Nagarajan. Gut microbiome recovery after antibiotic usage is mediated by specific bacterial species. **Nature Ecology and Evolution** (2020, IF2020: 15)
7. K. R. Chng[#], **C. Li**[#], D. Bertrand[#], ..., N. Nagarajan. Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. **Nature Medicine** (2020, IF2020: 53)
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, IF2019: 12)
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, IF2019: 37)
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** (2017, IF2017: 8.0)
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, IF2017: 3.7)
12. K. M. K. Lim, **C. Li**, K. R. Chng, N. Nagarajan. @MInter: Automated text-mining of microbial interactions. **Bioinformatics** (2016, IF2016: 5.5)
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, IF2016: 1.4)
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, IF2017: 14)
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 genomes simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. **Nature Methods** (2015) (as DREAM challenge participant)

[#]: (共同) 第一作者; [§]: (共同) 通讯作者

软件开发 (github: lch14forever)

1. BEEM-static - 对微生物组（横断面数据）成分数据拟合 Lotka-Volterra 模型的 R 包
2. BEEM - 对微生物组（时间序列）成分数据拟合 Lotka-Volterra 模型的 R 包
3. MicrobiomeViz - 微生物组可视化的 R 包
4. MinION watchdog - 实时分析 MinION 测序数据
5. INC-Seq - INC-Seq 滚环扩增建库方法的分析流程
6. Shotgun metagenomics pipeline - 基于 Nextflow 的宏基因组有参分析流程

获奖经历

- GIS 研究生突出成就奖, 2018 (GIS Graduate Student Prize)
- NUS 教学卓越奖, 2018 (Honor List of Student Tutors)
- 计算生物专业最佳毕业设计, 2014 (Lijen Industrial Development Medal)
- 理学院计算机方向最优学生, 2011 (Lim Soo Peng Book Prize)

同行评议

Bioinformatics, GigaScience, Nature Methods, PeerJ, Scientific Reports, PLOS Computational Biology, Microbiome 审稿人, iMeta 青年编委

受邀报告

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