



RTTAP: 基于短读长的全感染组分类学解决方案 赋能宏转录组数据分析

姜威¹, 廖和睿¹, 施莽², 陈良君^{3*}, 孙燕妮^{1*}

¹香港城市大学电机工程系

²中山大学医学院

³武汉大学中南医院医学检验科



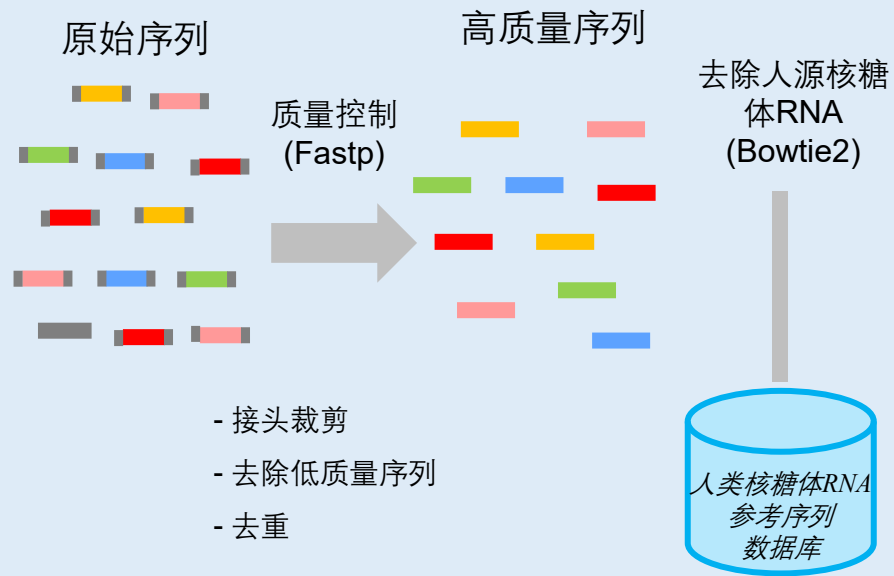
Wei Jiang, Herui Liao, Mang Shi, Liangjun Chen, Yanni Sun. 2025. RTTAP: Empowering metatranscriptomic data analysis with a read-based total-infectome taxonomic solution. *iMetaOmics* 2: e70044.

<https://doi.org/10.1002/imo2.70044>.

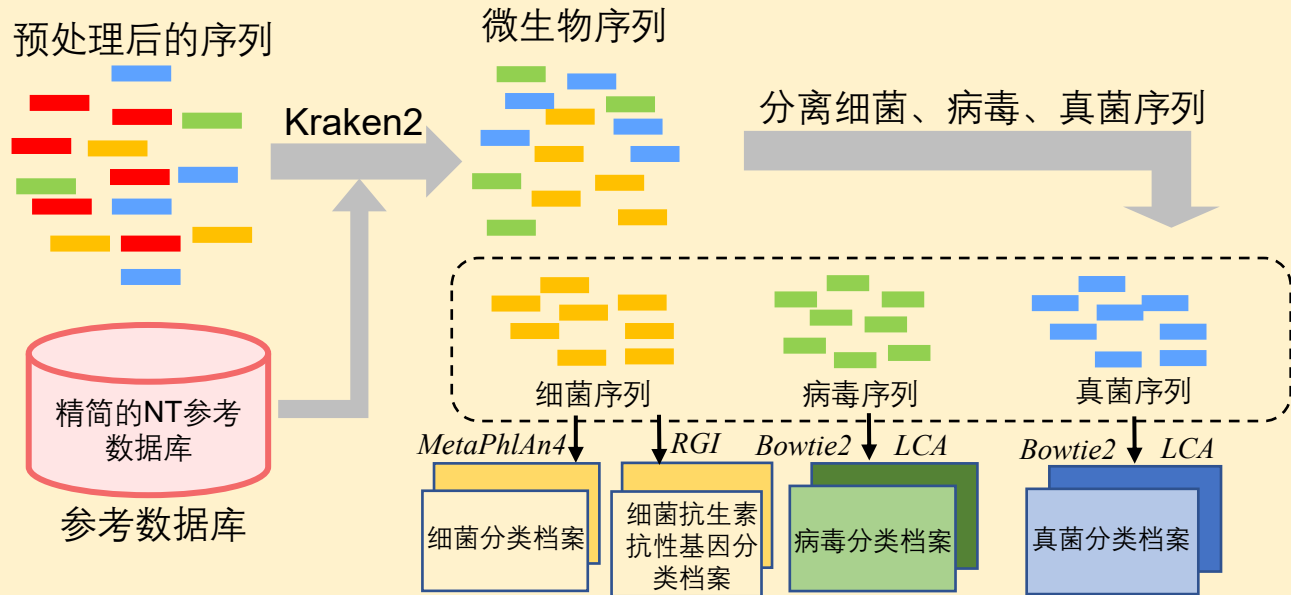


简介

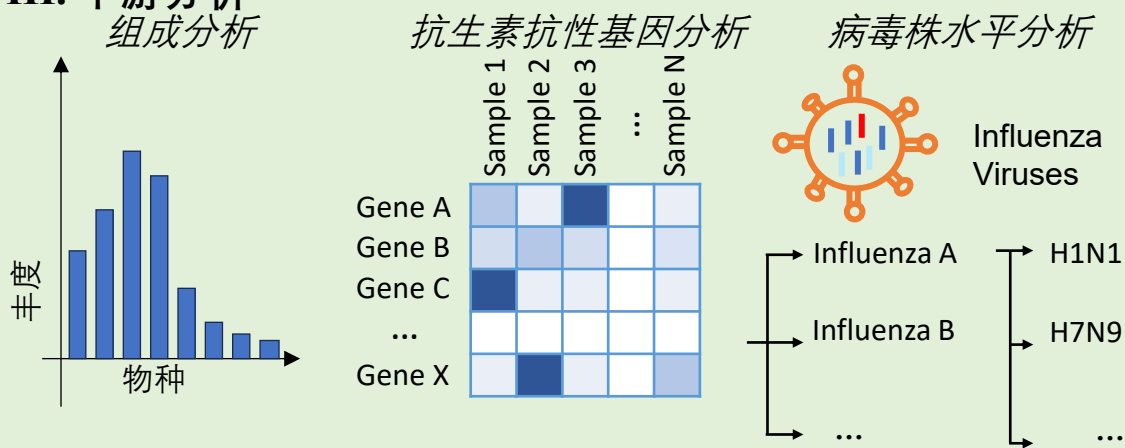
I. 预处理



II. 分类学分类



III. 下游分析



文档:

README

RTTAP

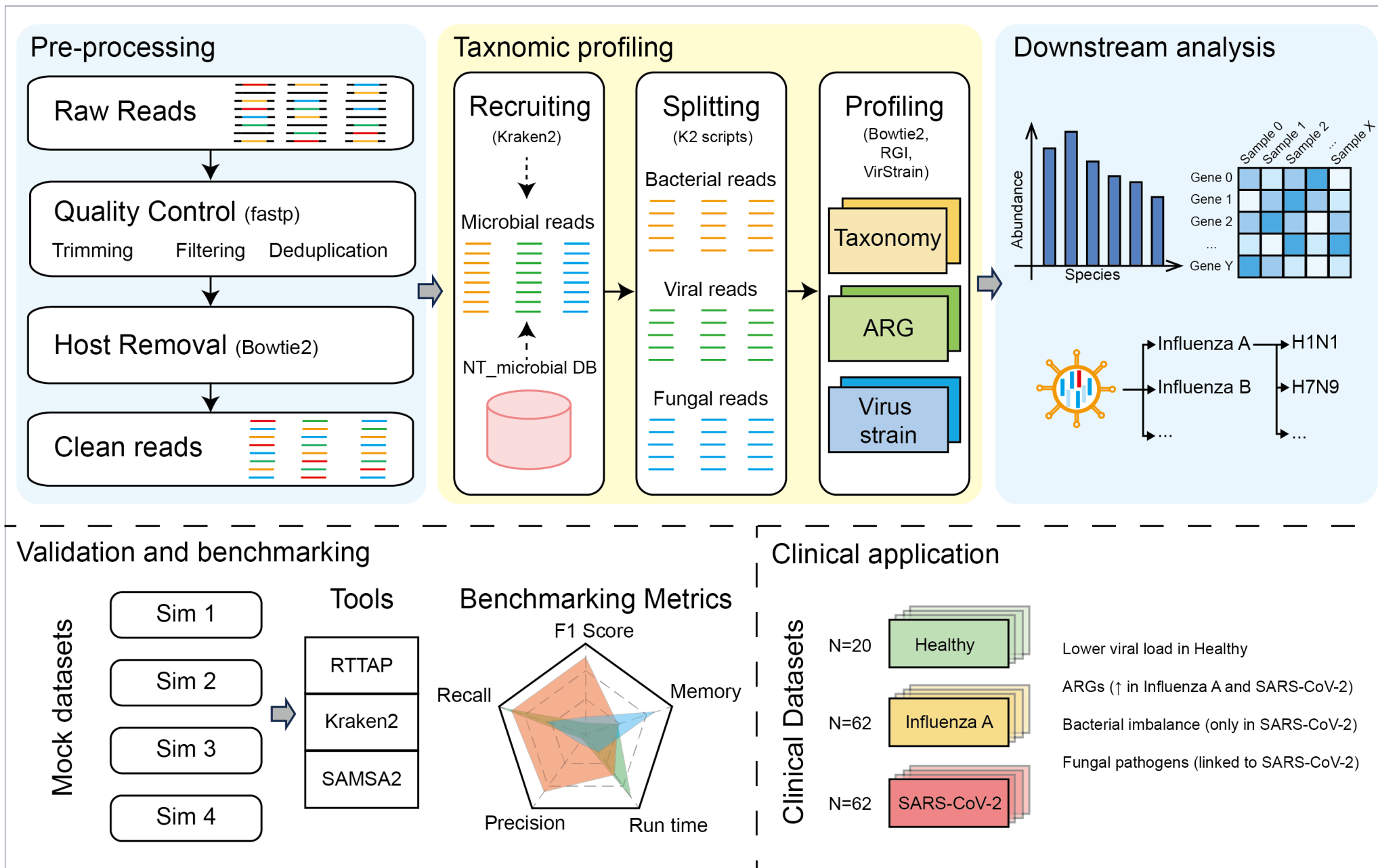
The Read-based Total-infectome Taxonomic Analysis Pipeline.

RTTAP (Read-based Total-infectome Taxonomic Analysis Pipeline) is a fast, accurate, and sensitive pipeline focusing analyses of the total-infectome of clinical metatranscriptomic data. It includes multiple useful functions to process and analyze raw sequencing reads: quality control, taxonomy profiling, ARG profiling, and virus strain-level profiling thus providing users comprehensive insights about the microbial composition in clinical samples. It is user friendly and easy-to-use, involving minimum human intervention: all its steps could be finished in a single run.

详情请见: <https://github.com/weijiang34/RTTAP>



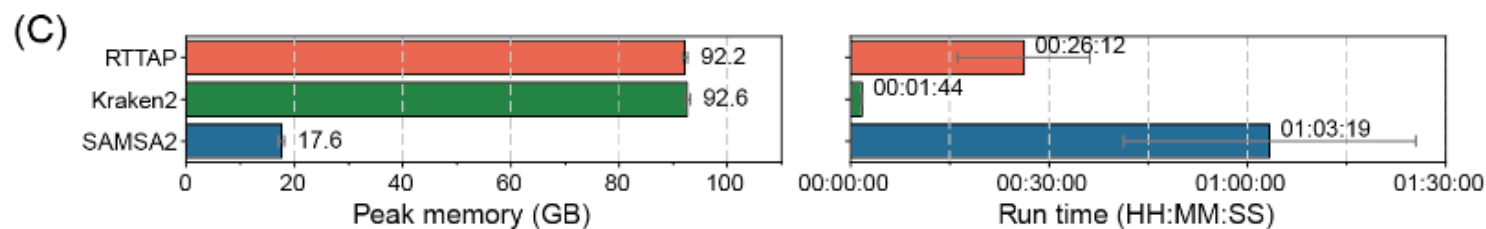
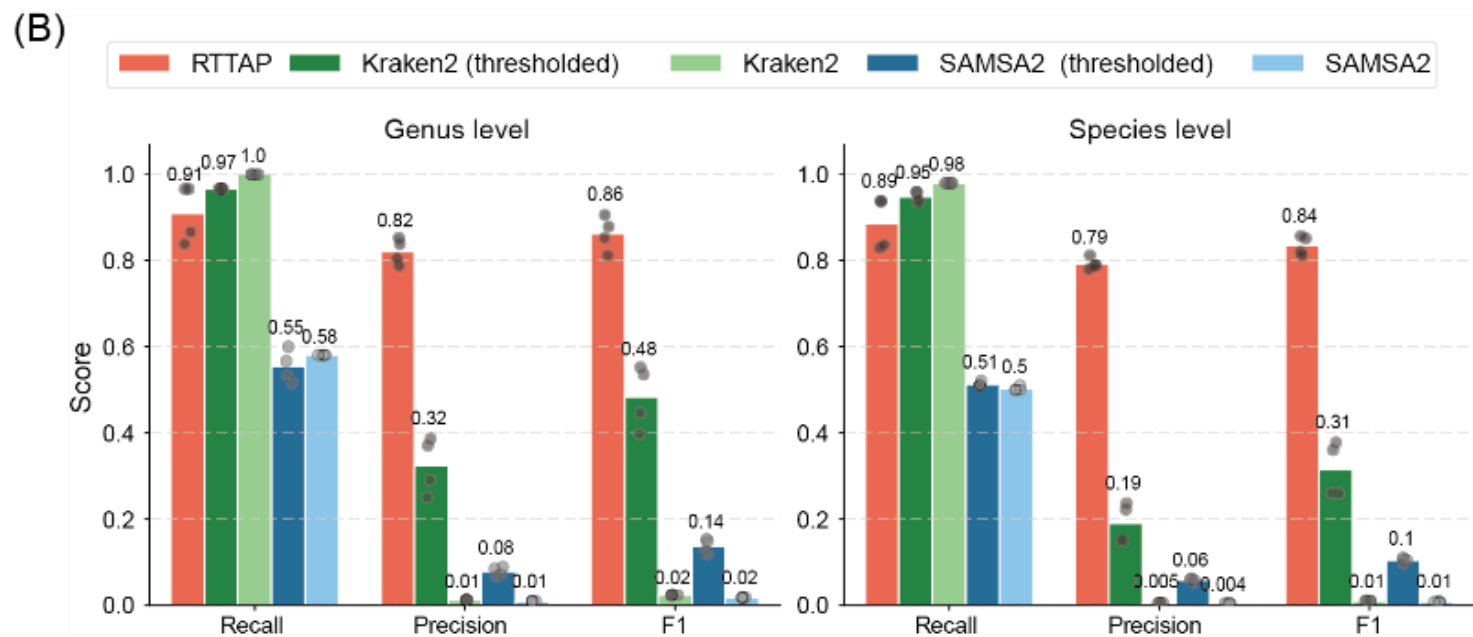
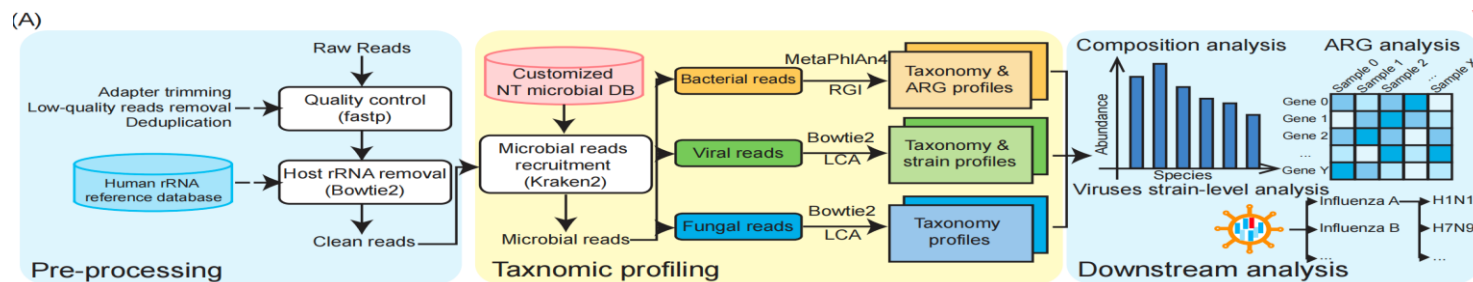
亮点





RTTAP流程的验证与表现

基于在四个模拟样本上的基准测试结果，RTTAP流程具有高准确率的同时也兼顾灵敏性，表现出较高的F1分数。

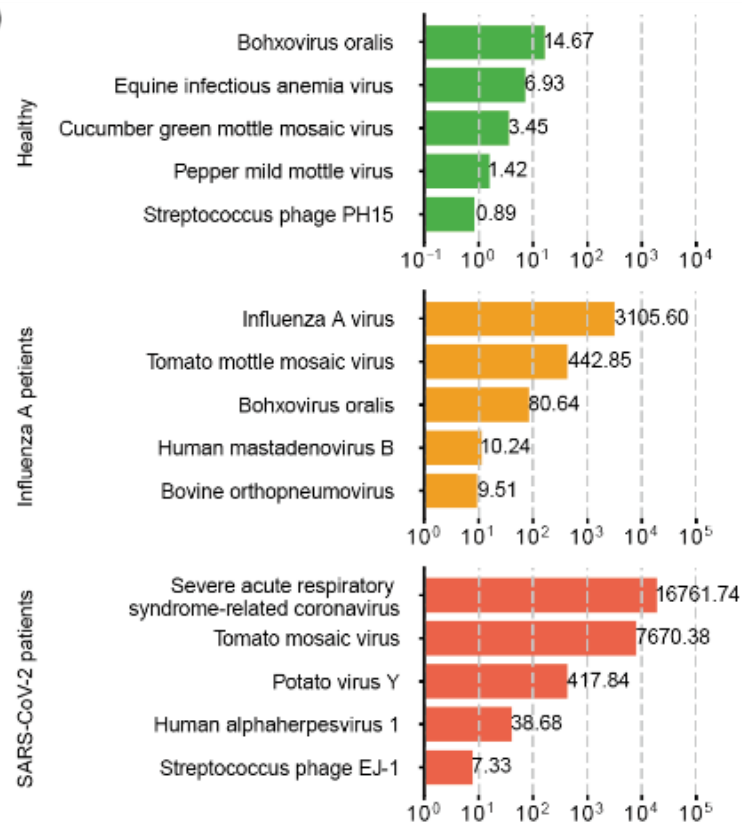




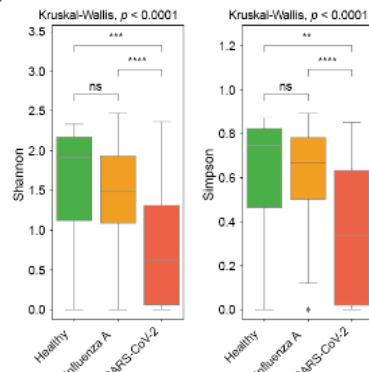
临床样本上的应用

通过在144个临床样本上的测试，RTTAP流程表现出准确的检出和分类能力，同时能够给出丰富的信息供下游分析使用。

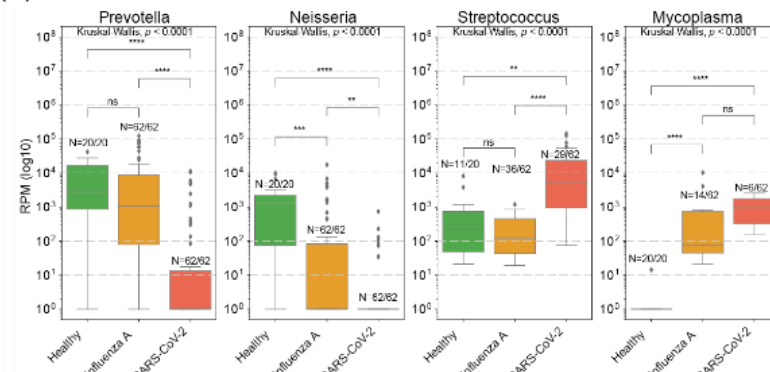
(D)



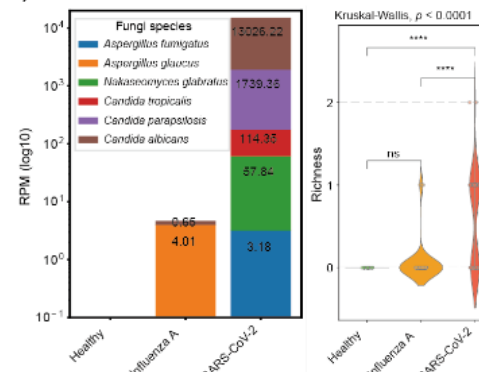
(E)



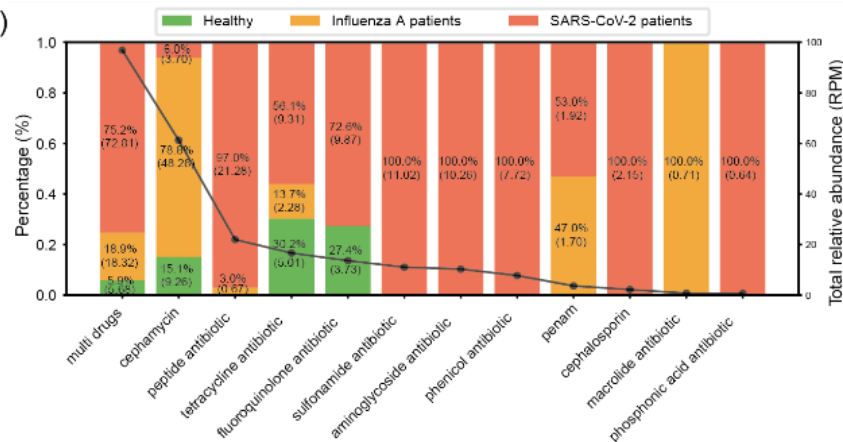
(F)



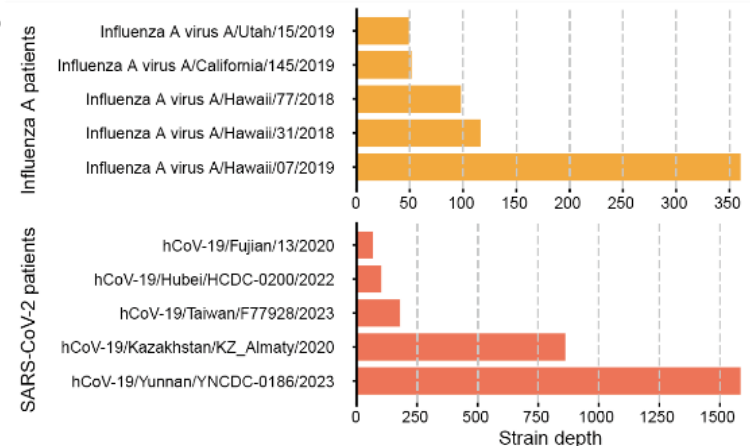
(G)



(H)



(I)

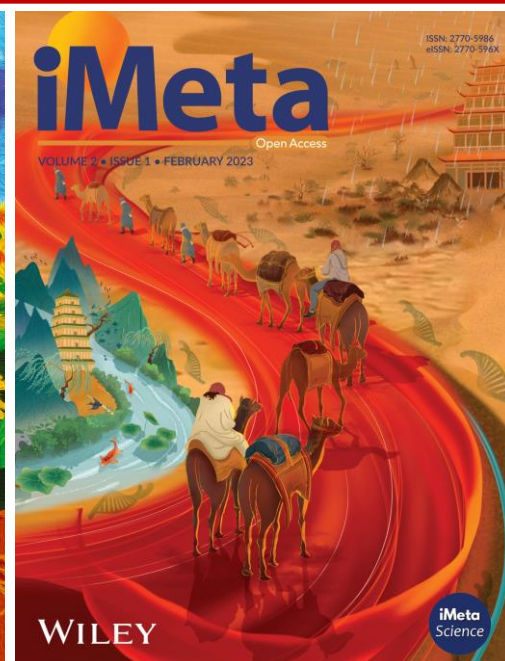
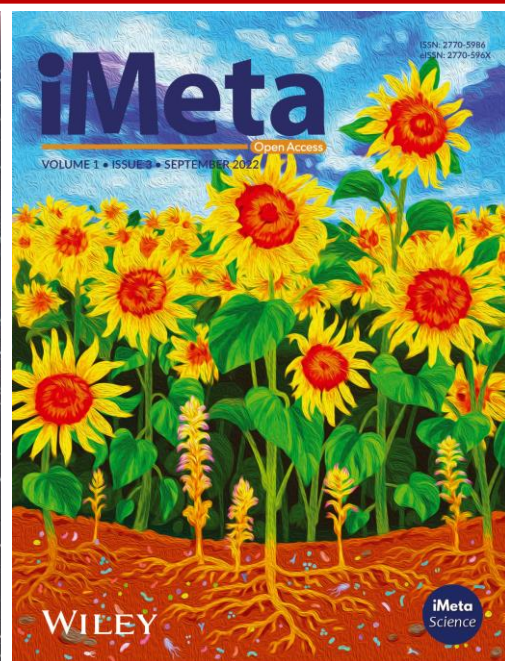




总结

- ❑ RTTAP是一种高效且灵敏的分类学分析流程，专门针对包括病毒、细菌和真菌在内的宏转录组感染分析进行了优化；
- ❑ 详尽的基于模拟数据以及临床数据的验证和测试确保了RTTAP具备可靠的分析性能；
- ❑ 其用户友好型设计兼顾常规分析的简单需求和复杂使用场景中的自定义需求，确保了具有不同背景的研究人员都能无障碍使用；
- ❑ RTTAP流程地址：<https://github.com/weijiang34/RTTAP>

Wei Jiang, Herui Liao, Mang Shi, Liangjun Chen, Yanni Sun. 2025. RTTAP: Empowering metatranscriptomic data analysis with a read-based total-infectome taxonomic solution. *iMetaOmics* 2: e70044.
<https://doi.org/10.1002/imo2.70044>.



iMeta期刊(影响因子**23.8**)由宏科学、千名华人科学家和威立出版, 主编刘双江和傅静远教授。目标为生物/医学/环境综合期刊群(对标Cell/Nature/Science), 任何高影响力的研究、方法和综述均欢迎投稿, 重点关注技术、信息和组学等前沿交叉学科, 已被**SCIE**、**PubMed**等收录, IF 23.8位列全球SCI期刊前千分之五, 微生物学研究类全球第一, 中科院生物学双1区Top; 外审平均21天, 投稿至发表中位数57天。
子刊**iMetaOmics**(主编赵方庆和于君教授)、**iMetaMed** 定位IF>10和15的综合、医学期刊, 欢迎投稿!



主页: <http://www.imeta.science>

出版社: <https://wileyonlinelibrary.com/journal/imeta>

iMeta: <https://wiley.atyponrex.com/journal/IMT2>

投稿: iMetaOmics: <https://wiley.atyponrex.com/journal/IMO2>

iMetaMed: <https://wiley.atyponrex.com/journal/IMM3>



office@imeta.science

imetaomics@imeta.science



宣传片



iMeta



更新日期
2025/5/21