

ADVANCED BIOINFORMATIC TECHNIQUES FOR MICROBIAL ANALYSIS AND DIAGNOSTICS

Dr. Michael B Hall



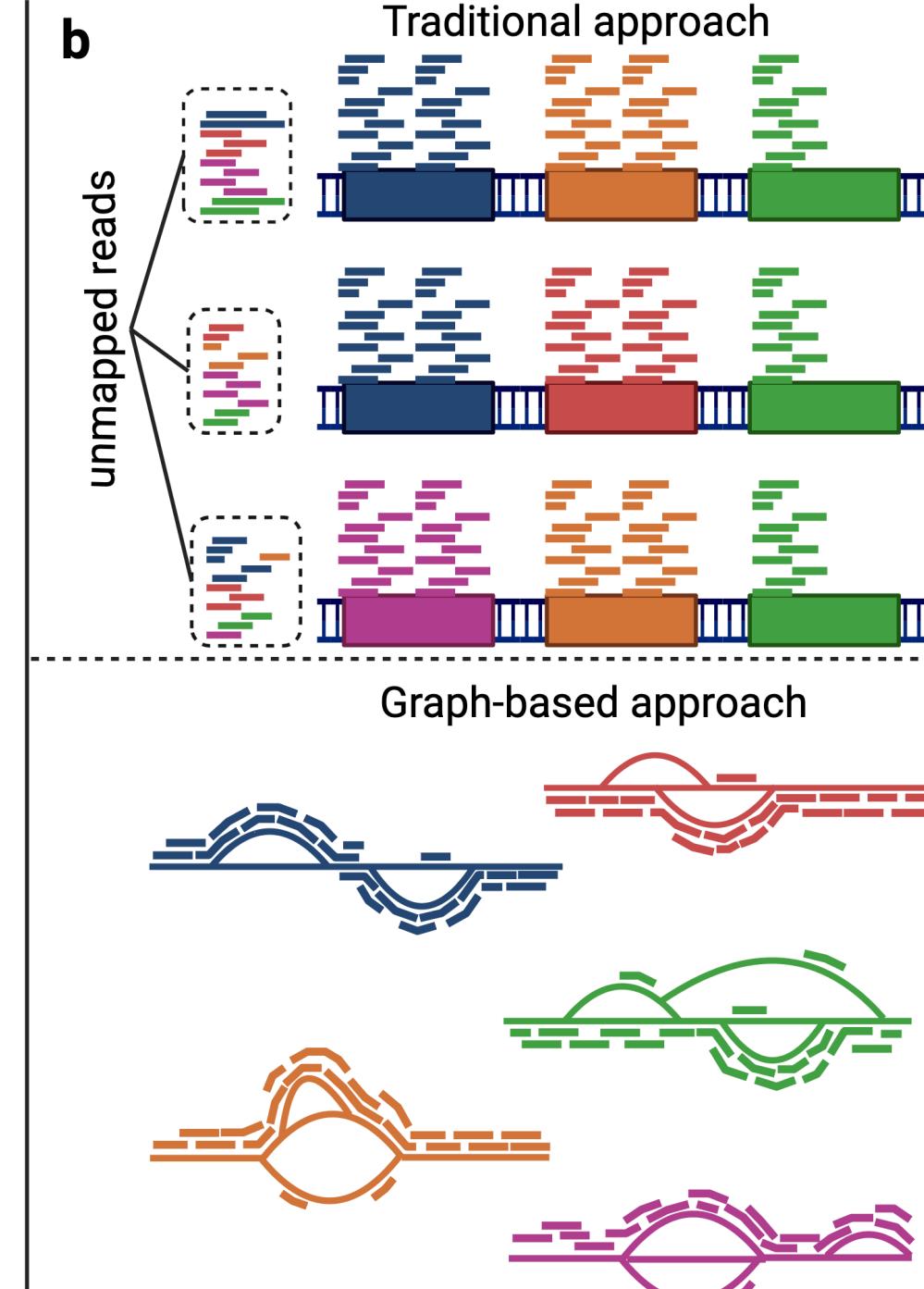
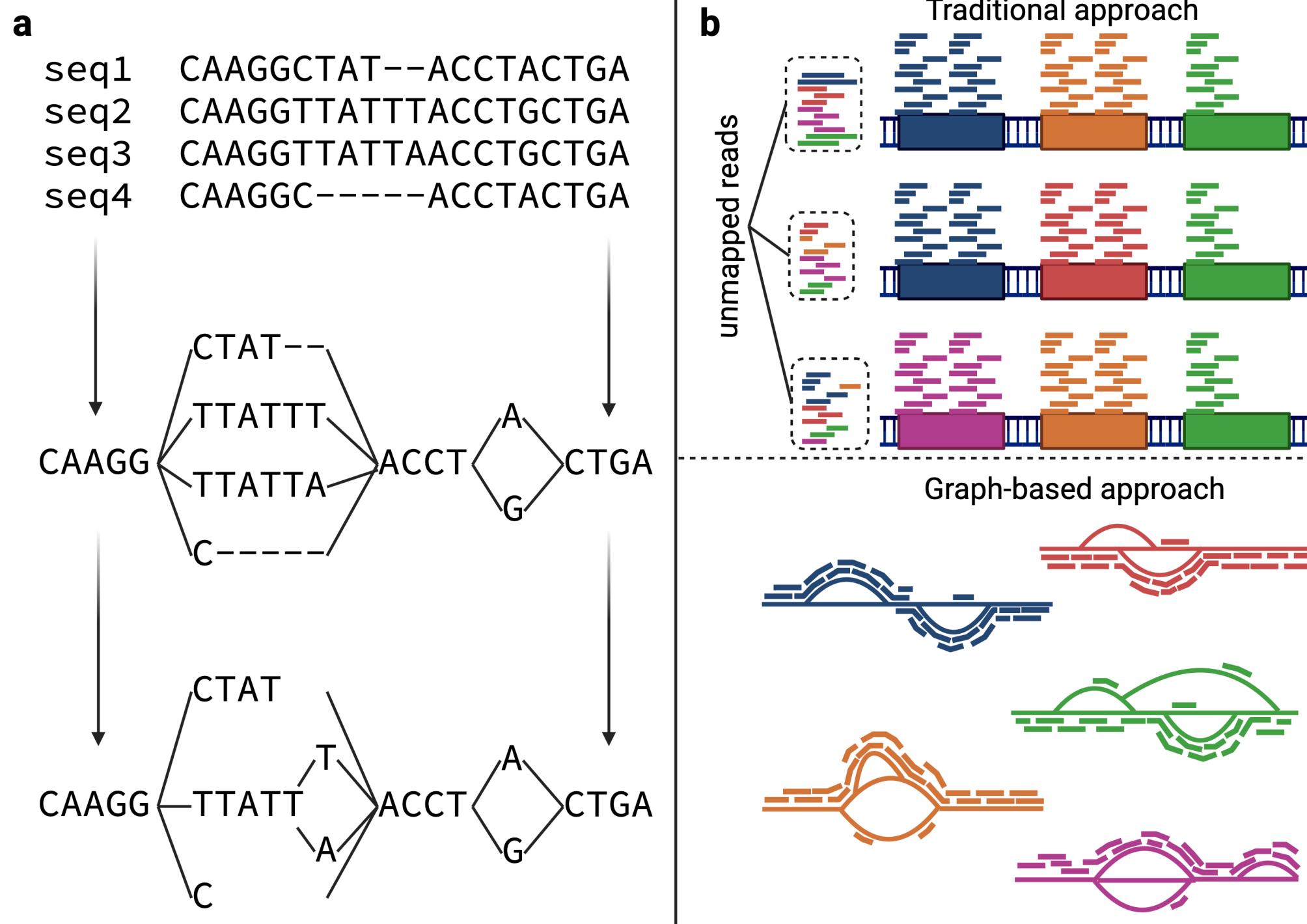
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GENOME GRAPHS



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Pandora: nucleotide-resolution bacterial pan-genomics with reference graphs

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Genome Biology 22, Article number: 267 (2021) | [Cite this article](#)

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MICROBIAL GENOMICS

Volume 9, Issue 8

Research Article | Open Access

Drug resistance prediction for *Mycobacterium tuberculosis* with reference graphs

Michael B. Hall^{1,2} , Leandro Lima¹ , Lachlan J. M. Coin²  and Zamin Iqbal¹ 

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Published: 08 August 2023 | <https://doi.org/10.1099/mgen.0.001081>



NANOPORE SEQUENCING

Research Article

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Freshwater monitoring by nanopore sequencing

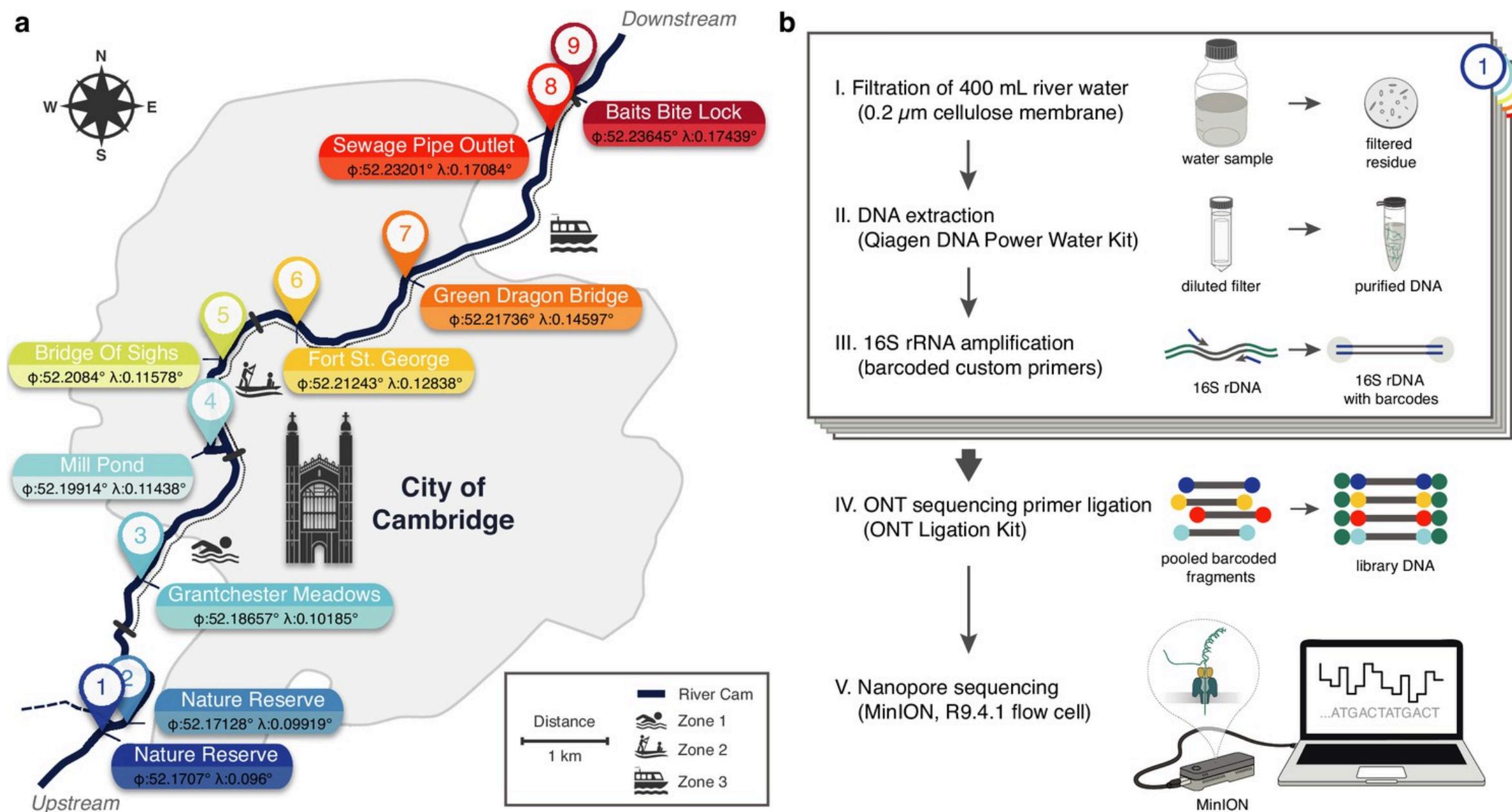
Lara Urban , Andre Holzer , J Jotautas Baronas, Michael B Hall, Philipp Braeuninger-Weimer, Michael J Scherm, Daniel J Kunz, Surangi N Perera, Daniel E Martin-Herranz ... Maximilian R Stammnitz  [see all »](#)

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Jan 19, 2021 • <https://doi.org/10.7554/eLife.61504>  



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ARTICLES · Volume 4, Issue 2, E84-E92, February 2023 · Open Access

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Evaluation of Nanopore sequencing for *Mycobacterium tuberculosis* drug susceptibility testing and outbreak investigation: a genomic analysis

Michael B Hall, PhD^a · Marie Sylvianne Rabodoarivelo, PhD^{b,c} · Anastasia Koch, PhD^{d,g} ·
Anzaan Dippenaar, PhD^{h,i} · Sophie George, MSc^j · Melanie Grobbelaar, PhD^h. et al. Show more

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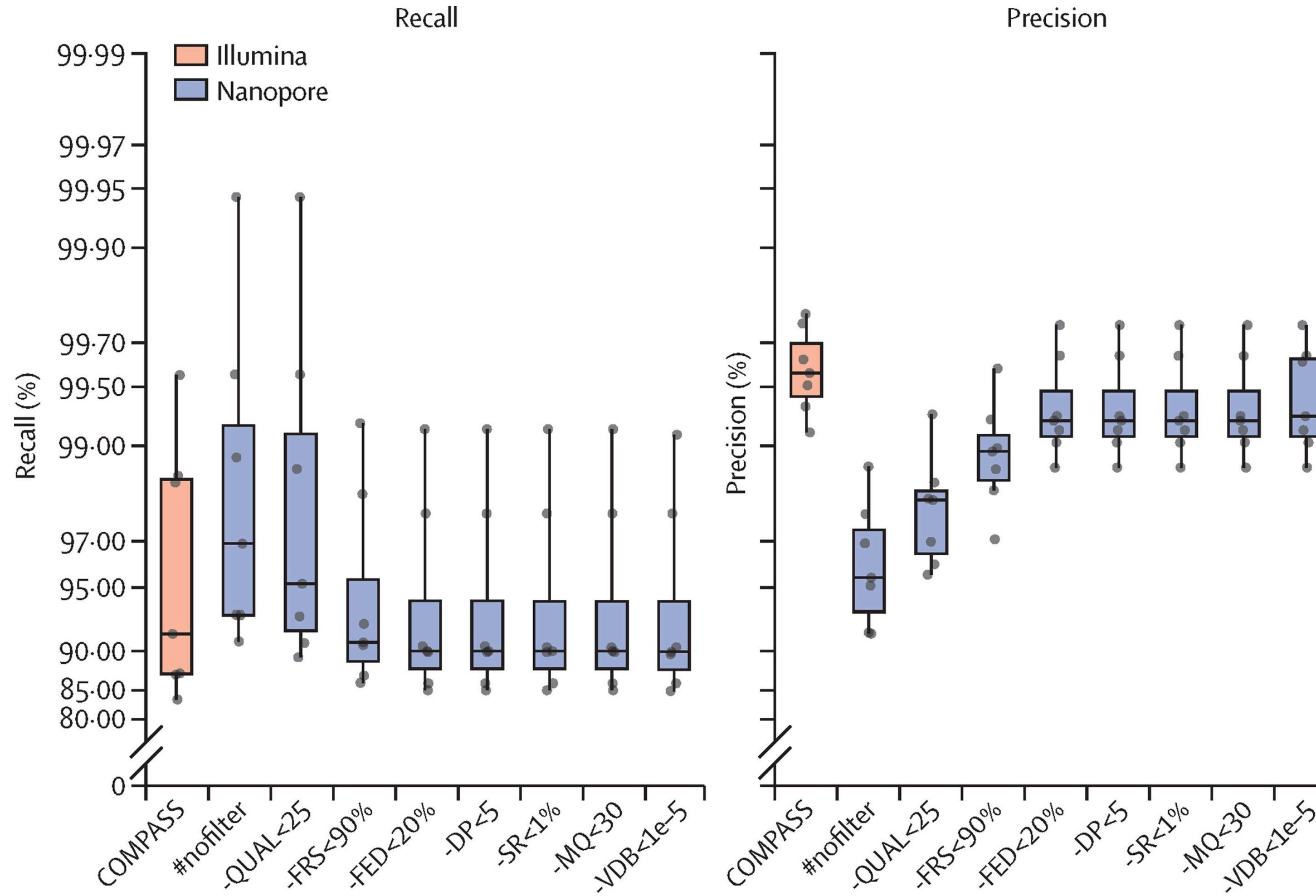
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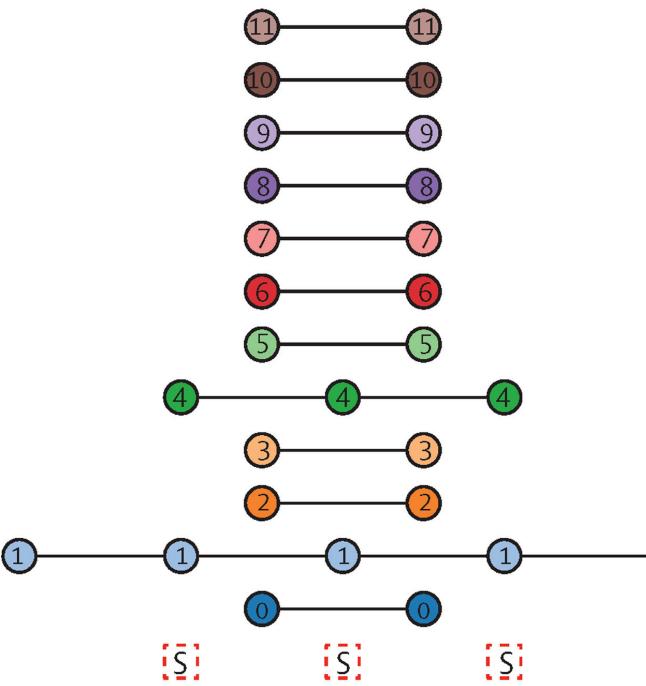


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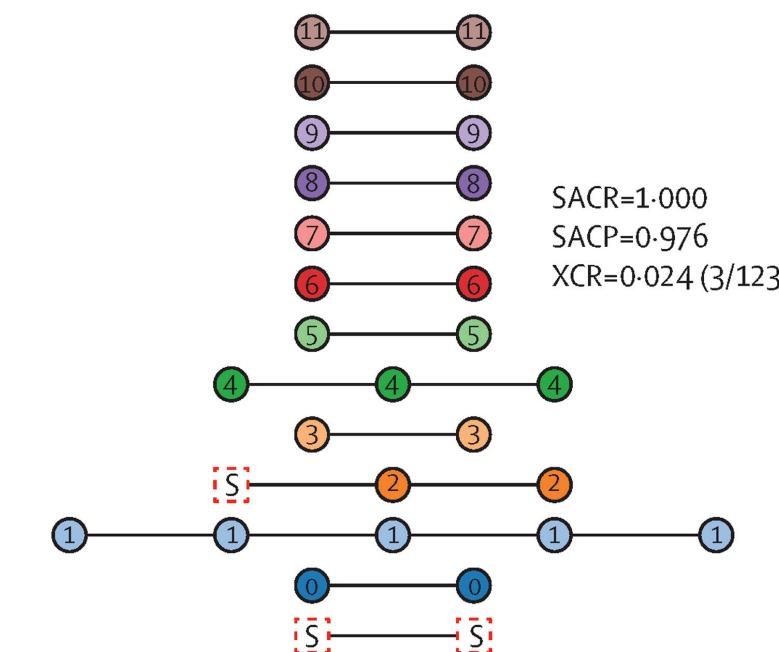


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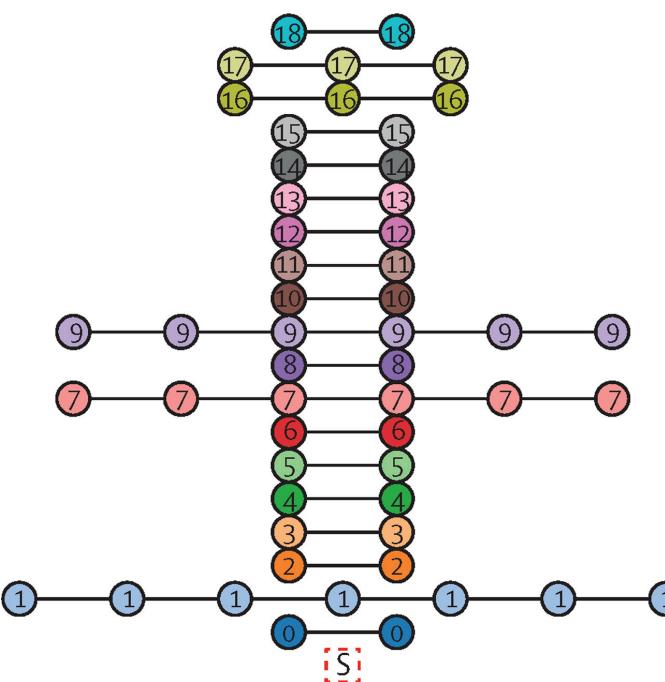
A Illumina threshold=5



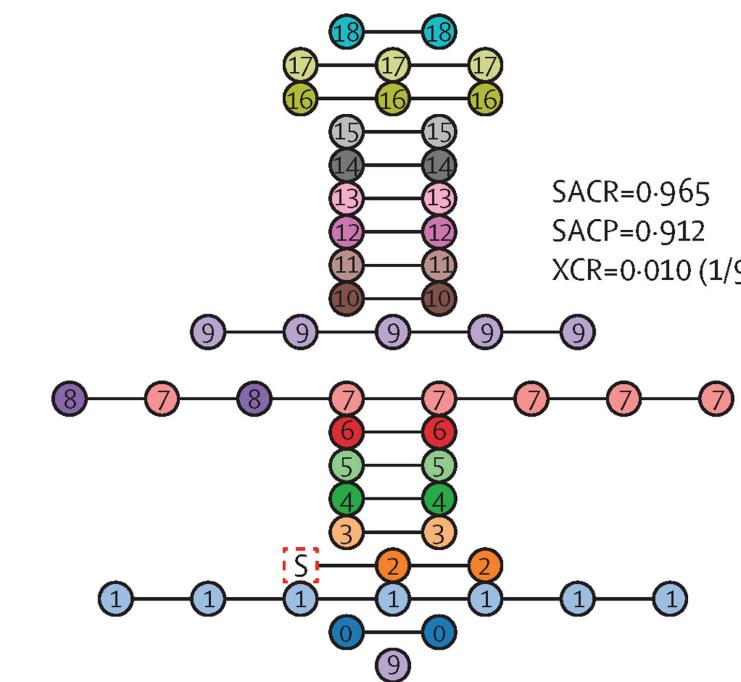
Nanopore threshold=6



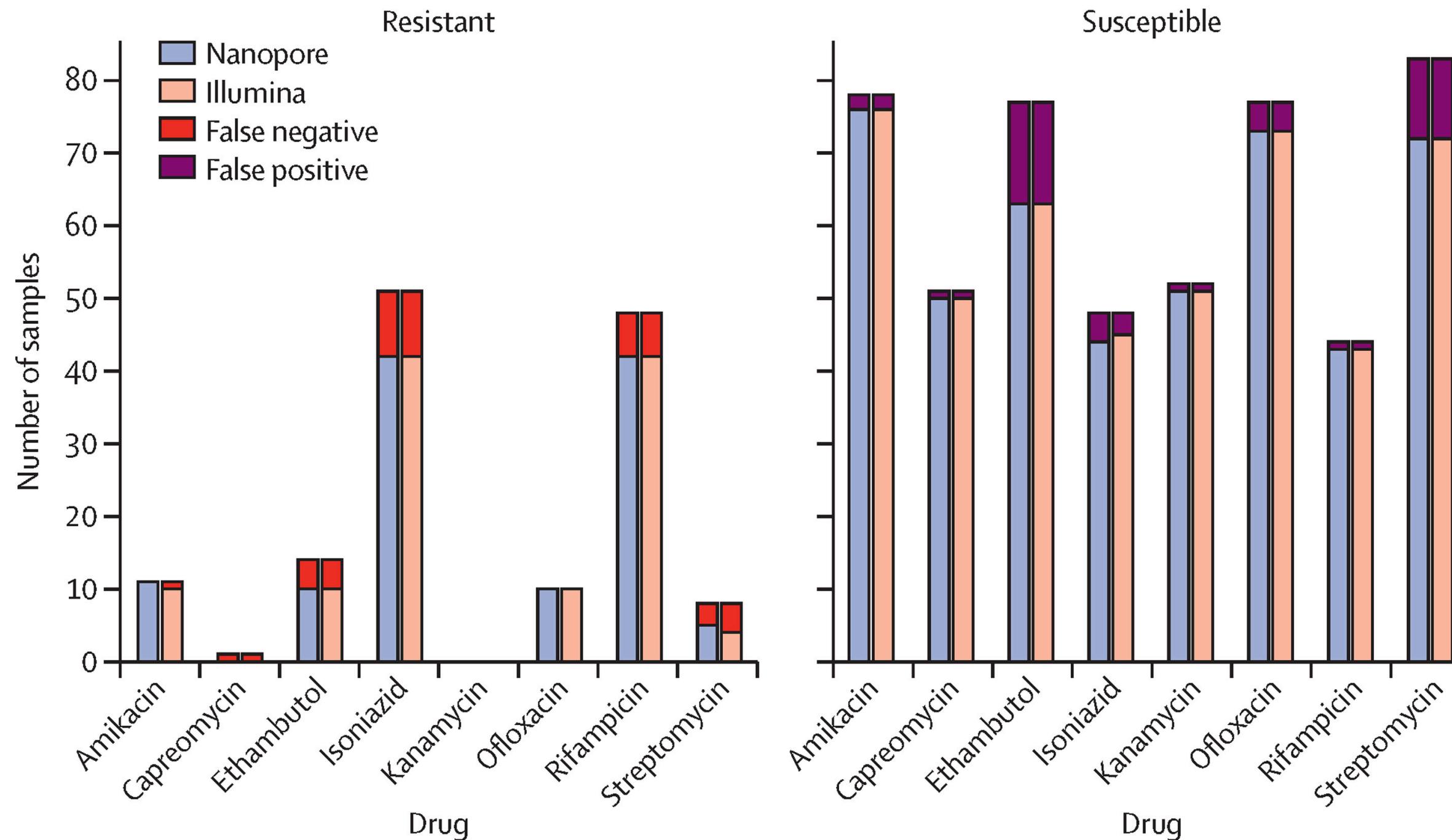
B Illumina threshold=12



Nanopore threshold=12



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Research Article

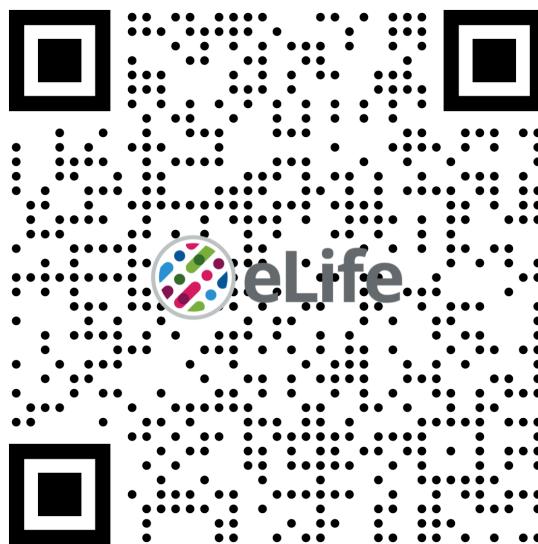
Computational and Systems Biology, Microbiology and Infectious Disease

Benchmarking reveals superiority of deep learning variant callers on bacterial nanopore sequence data

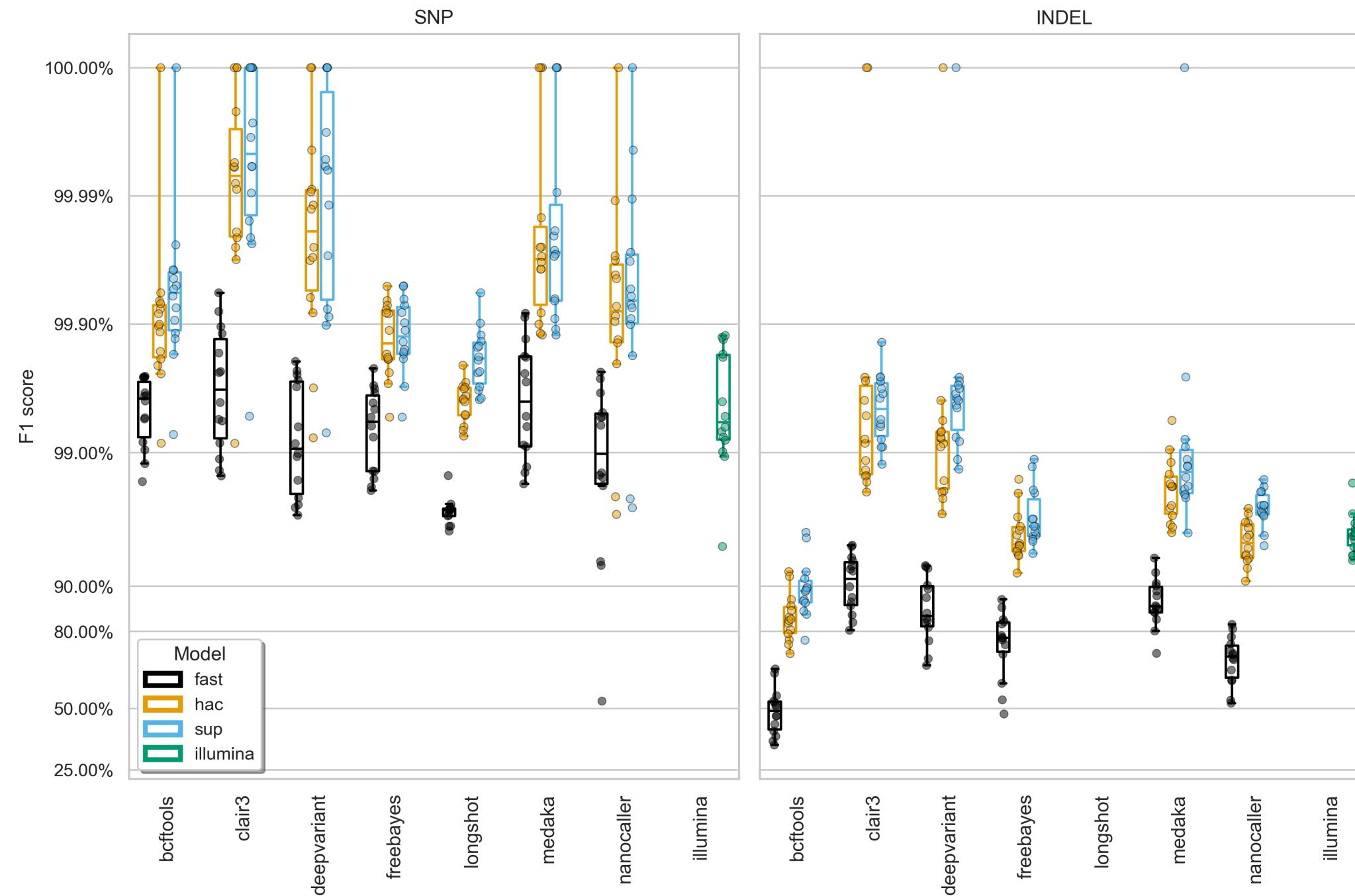
Michael B Hall , Ryan R Wick, Louise M Judd, An N Nguyen, Eike J Steinig, Ouli Xie, Mark Davies, Torsten Seemann, Timothy P Stinear, Lachlan Coin

Department of Microbiology and Immunology, The University of Melbourne, at the Peter Doherty Institute for Infection and Immunity, Australia; Centre for Pathogen Genomics, The University of Melbourne, Australia; Department of Infectious Diseases, The University of Melbourne, at the Peter Doherty Institute for Infection and Immunity, Australia; Monash Infectious Diseases, Monash Health, Australia

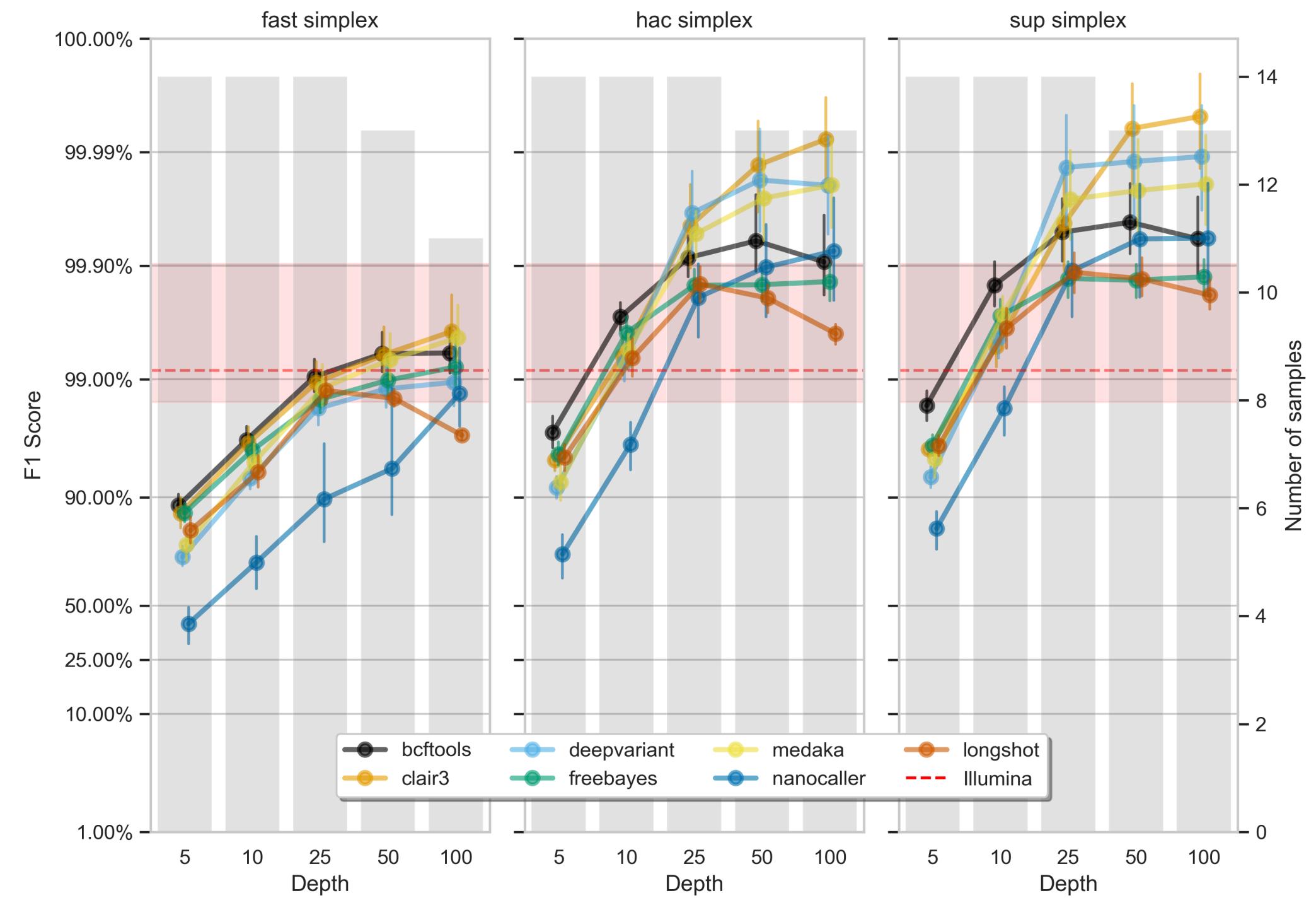
Oct 10, 2024 • <https://doi.org/10.7554/eLife.98300.3> 



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METAGENOMICS

**Pangenome databases improve host removal
and mycobacteria classification from clinical
metagenomic data** 

Michael B Hall , Lachlan J M Coin

GigaScience, Volume 13, 2024, giae010, <https://doi.org/10.1093/gigascience/giae010>

Published: 04 April 2024 **Article history** ▾



github.com/mbhall88/nohuman

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Genome size estimation from long read overlaps

 Michael B Hall,  Lachlan J M Coin

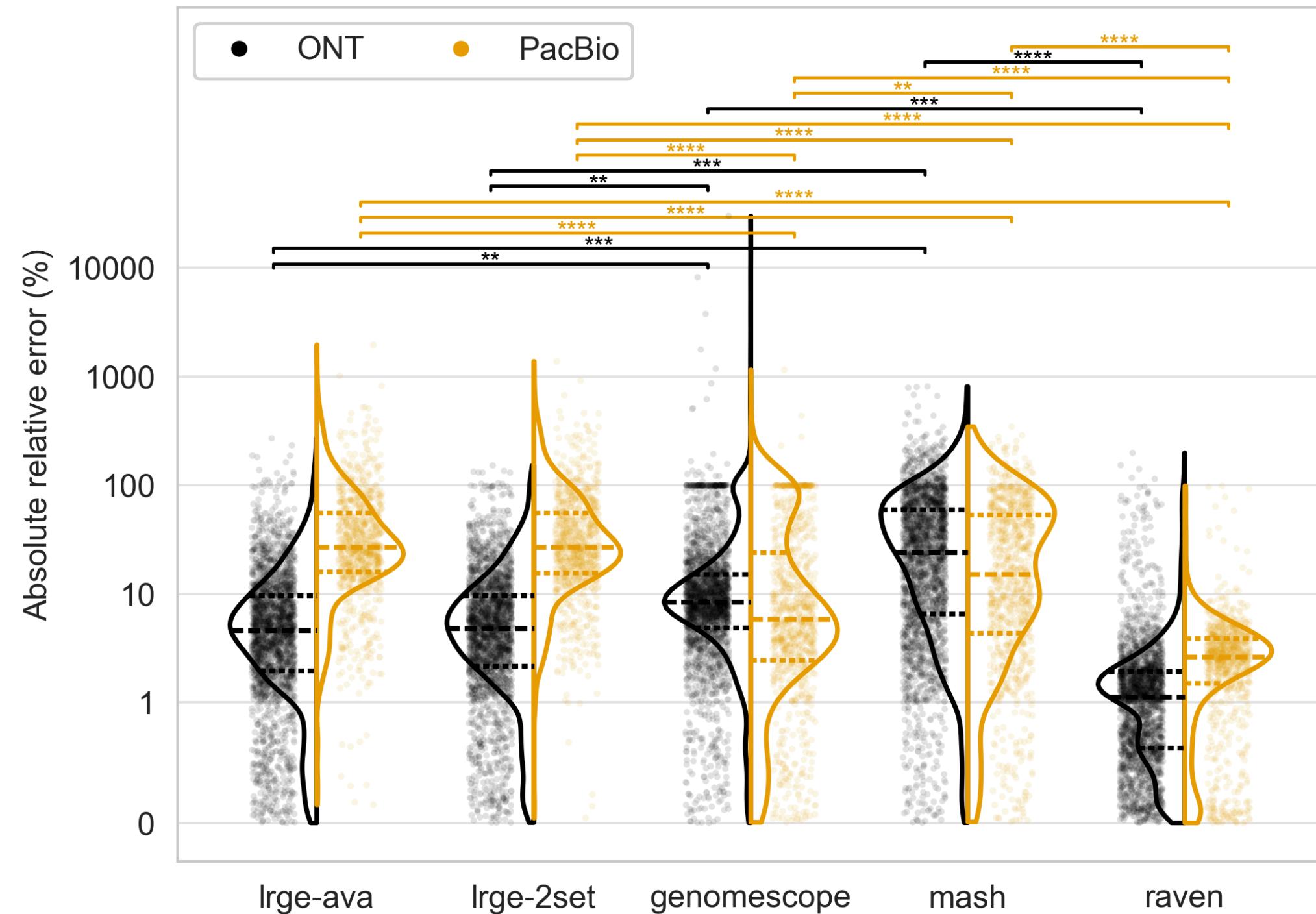
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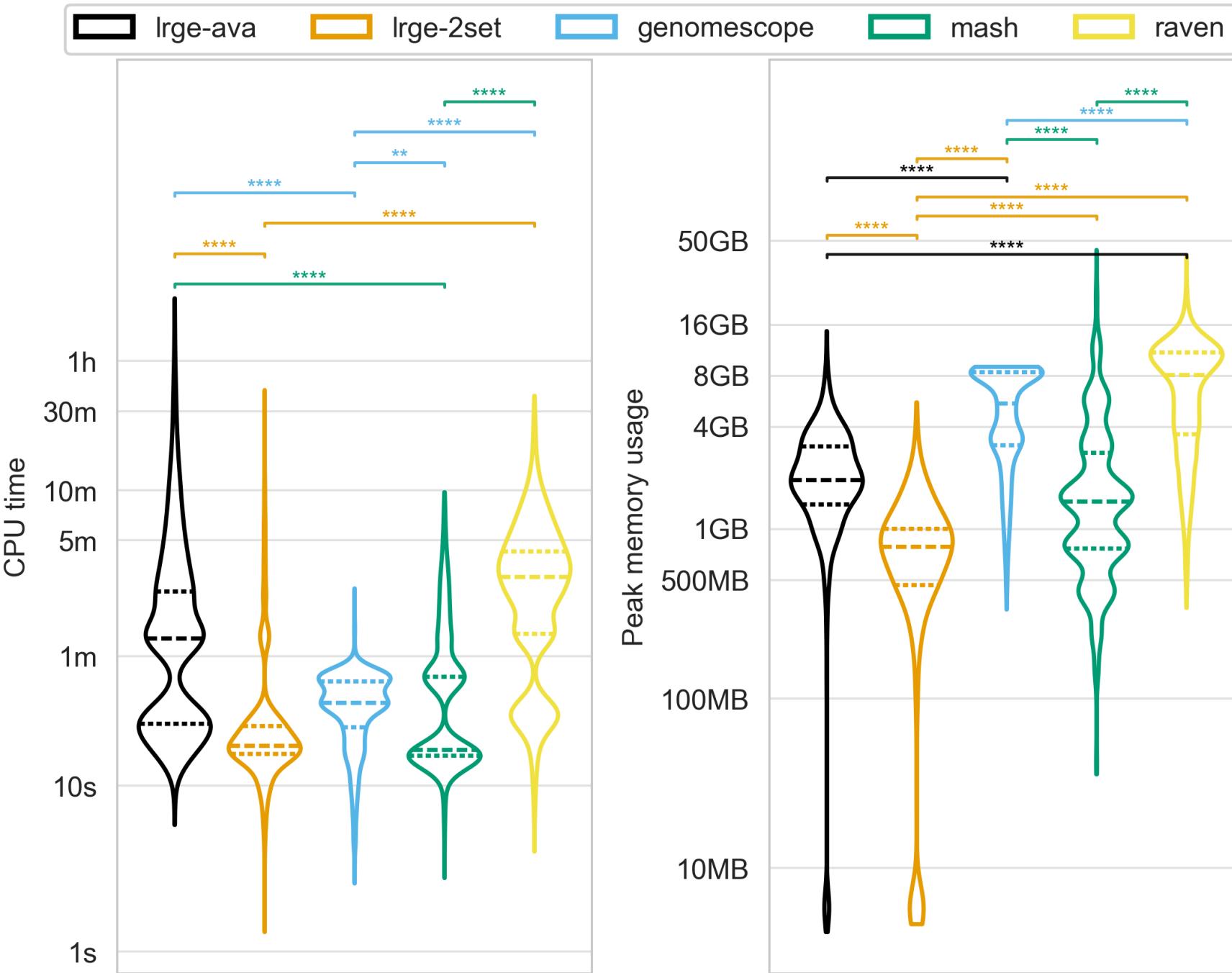


github.com/mbhall88/lrge

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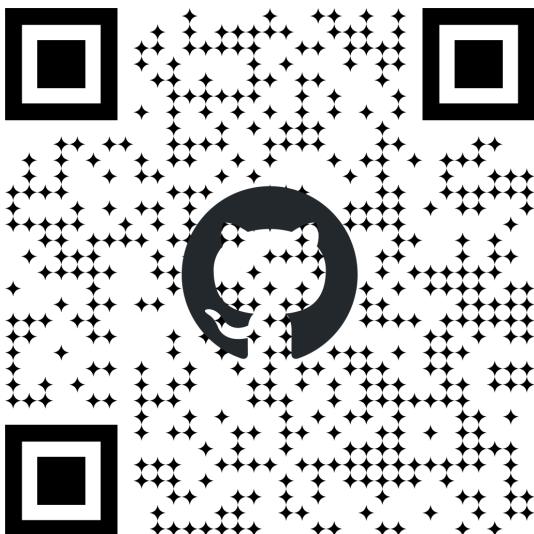
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