




A metagenomics pipeline reveals insertion sequence-driven evolution of the microbiota











































Joshua M. Kirsch • Andrew J. Hryckowian • Breck A. Duerkop  ⁴  • [Show footnotes](#)Published: April 01, 2024 • DOI: <https://doi.org/10.1016/j.chom.2024.03.005> •  Check for updates

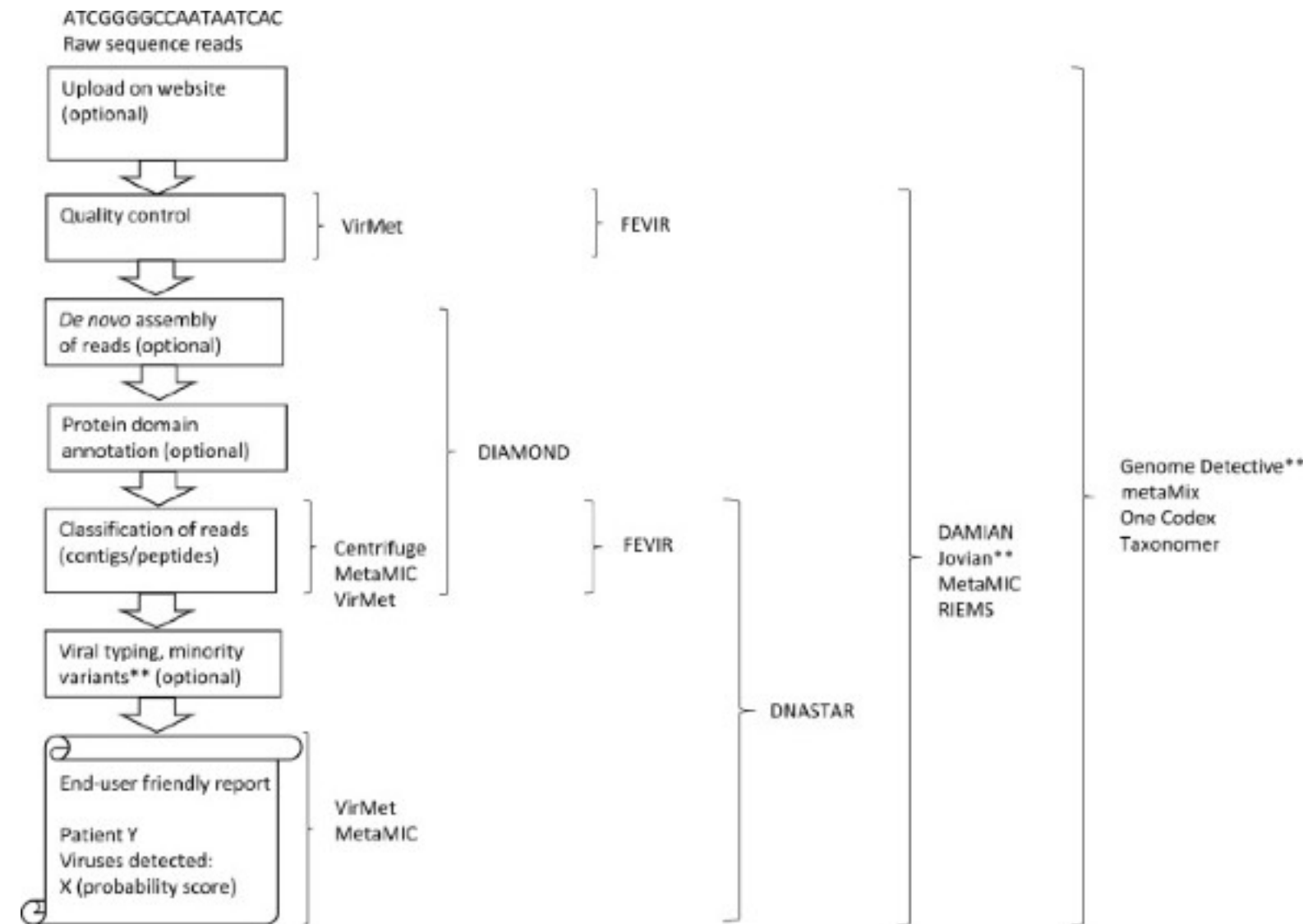

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Benchmark of thirteen bioinformatic pipelines for metagenomic virus diagnostics using datasets from clinical samples


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[Aubrey R. Odom](#), [Tyler Faits](#), [Eduardo Castro-Nallar](#), [Keith A. Crandall](#) & [W. Evan Johnson](#) [Scientific Reports](#) **13**, Article number: 13957 (2023) | [Cite this article](#)29k Accesses | 14 Citations | 116 Altmetric | [Metrics](#)

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Code


alessia Updated containers, bumped version
 9a844a7 · last year
🕒 49 Commits

📁 assets	Added test data, demo data, and asset data	3 years ago
📁 bin	Small edits and typos	3 years ago
📁 conf	Improved testing	last year
📁 data/test_data	Added test data, demo data, and asset data	3 years ago
📁 modules	Update to DSL2	last year
📄 LICENSE	Initial commit	7 years ago
📄 README.md	Updated containers, bumped version	last year
📄 YAMP.nf	Update to DSL2	last year
📄 nextflow.config	Updated containers, bumped version	last year

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Yet Another Metagenomic Pipeline (YAMP)

Thanks to the increased cost-effectiveness of high-throughput technologies, the number of studies focusing on microorganisms (bacteria, archaea, microbial eukaryotes, fungi, and viruses) and their connections with human health and diseases has surged, and, consequently, a plethora of approaches and software has been made available for their study, making it difficult to select the best methods and tools.

Here we present Yet Another Metagenomic Pipeline (YAMP) that, starting from the raw sequencing data and having a strong focus on quality control, allows, within hours, the data processing up to the functional annotation (please refer to the YAMP [wiki](#) for more information).