



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

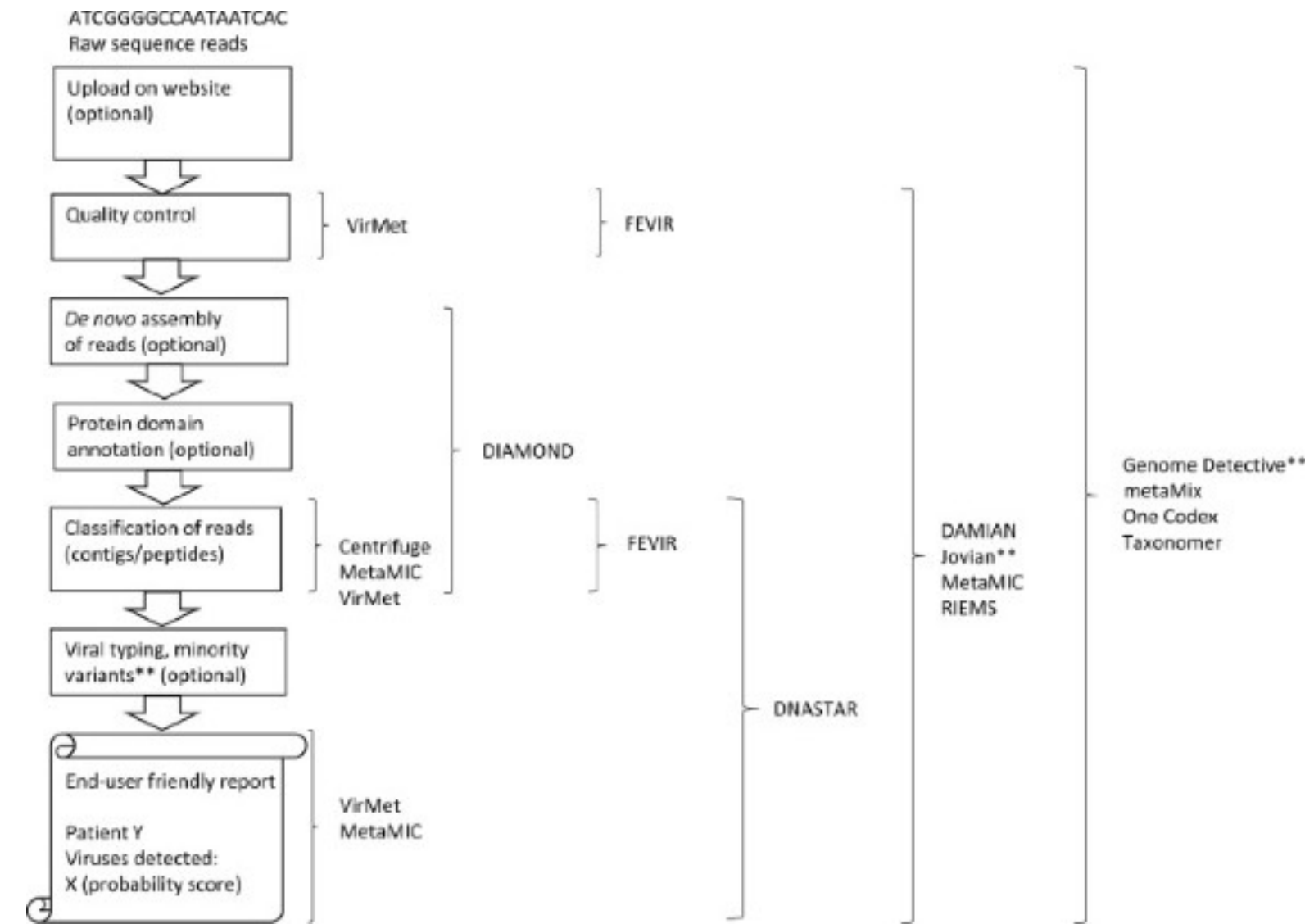
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Benchmark of thirteen bioinformatic pipelines for metagenomic virus diagnostics using datasets from clinical samples


Jutte J.C. de Vries ^a  , Julianne R. Brown ^b  , Nicole Fischer ^d  , Igor A. Sidorov ^a  ,
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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).