

A multi-viral genome reconstruction pipeline for the integrated genomic surveillance at the Robert Koch Institute (RKI), Germany's Public Health institute

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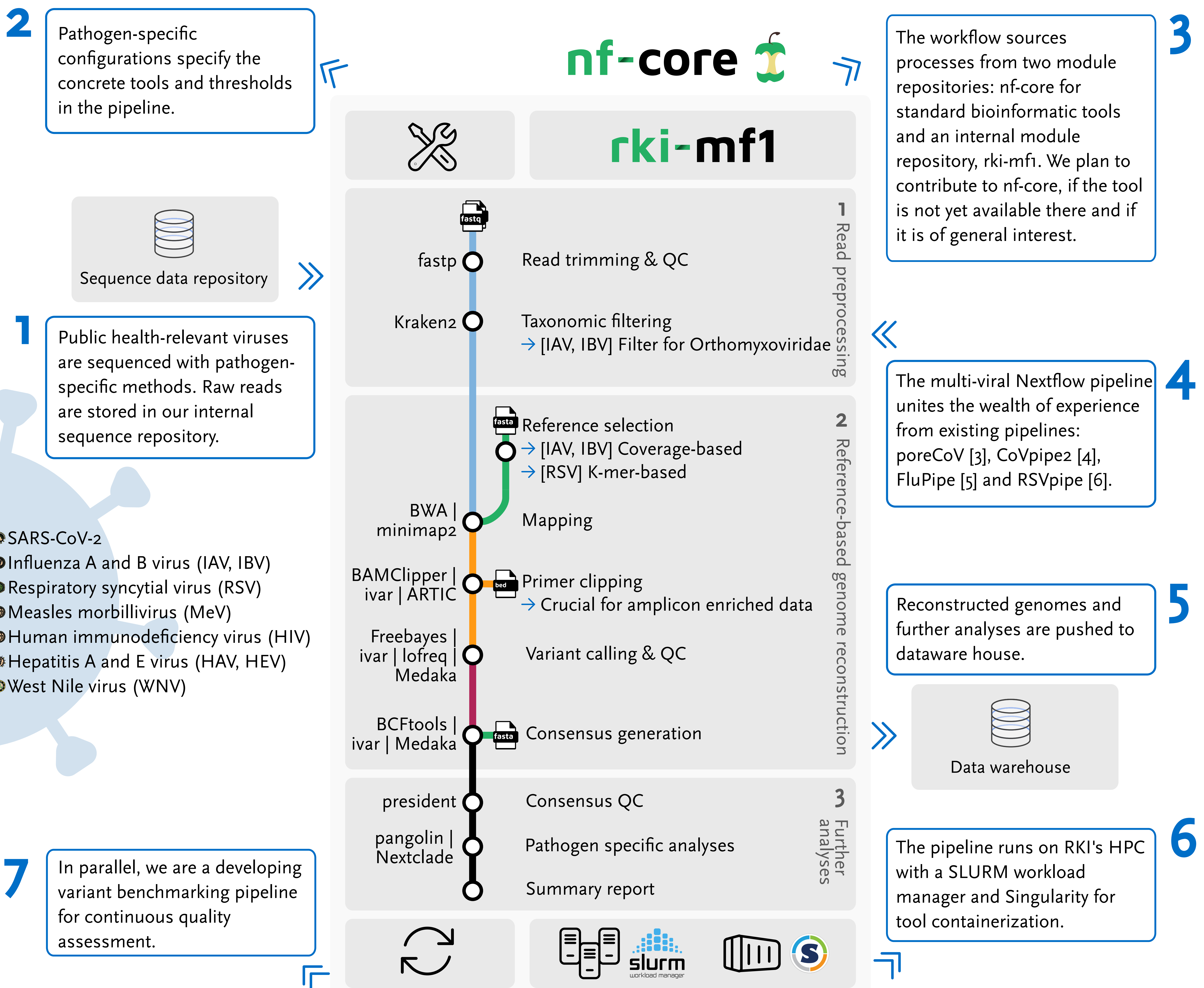
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Integrated genomic surveillance relies on high quality genome sequences

Integrated genomic surveillance (IGS) is crucial for monitoring pathogens of public health significance and focuses on the rapid detection of changes in the pathogens' genome sequences. Such changes include the identification of new mutations, new viral variants, as well as concerning accumulations and spread of pathogens.

The timely detection of such patterns and dynamics enables rapid detection of outbreaks and resistance developments, and reveals variants with acquired higher transmissibility or virulence. The COVID-19 pandemic has clearly demonstrated that surveillance relies heavily on quality genome sequences of high and in-depth nucleotide resolution [1,2].

Schema for a multi-viral genome reconstruction pipeline embedded in RKI's infrastructure



[1] Oh, Djin Ye, et al. "Advancing precision vaccinology by molecular and genomic surveillance of severe acute respiratory syndrome coronavirus 2 in Germany, 2021." Clinical infectious diseases 75, Supplement_1 (2022): S110-S120.

[2] Salzberger, Bernd, et al. "An appeal for strengthening genomic pathogen surveillance to improve pandemic preparedness and infection prevention: the German perspective." Infection (2023): 1-7.

[3] <https://github.com/replikation/poreCov>

[4] Lataretu, Marie, et al. "Lessons learned: overcoming common challenges in reconstructing the SARS-CoV-2 genome from short-read sequencing data via CoVpipe2." F1000Research 12 (2023): 1091. <https://github.com/rki-mf1/CoVpipe2>

[5] <https://github.com/rki-mf1/FluPipe>

[6] https://gitlab.com/rki_bioinformatics/next-rsv-seq

