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Opinion Article

Insaflu-Televir: Empowering Genomic Surveillance and Viral Metagenomics

Veivnk Nerve*

Department of Virology, Istanbul University, Istanbul, Turkey

DESCRIPTION

Due to a lack of bioinformatics tools and/or experience, implementing clinical metagenomics and pathogen genomic monitoring might be particularly difficult. To address this issue, we have already created a free web-based bioinformatics tool called INSaFLU for the study of viral next-generation sequencing data. Here, we created a new module televir for metagenomic viral detection and significantly increased the genomic monitoring component of it. New workflows and functionalities were added to strengthen the routine genomic surveillance component. These included: i) An automated SARS-CoV-2 lineage classification pipeline using reference-based genome assembly for Oxford Nanopore Technologies (ONT) data; ii) Nextclade analysis; iii) Nextstrain phylogeographic and temporal analysis (SARS-CoV-2, human and avian influenza, monkeypox, respiratory syncytial virus). (RSV A/B), coupled with a "generic" construct for more viruses; and, iv) algn2pheno, which is used to screen for relevant mutations. An INSaFLU snakemake version was published, and both of the INSaFLU pipelines for reference-based consensus generation (Illumina and ONT) were benchmarked against widely used command line bioinformatics workflows for SARS-CoV-2. Concurrently, a novel module televir for viral identification was created, according to current guidelines and standards in the area and including thorough benchmarking of cutting-edge metagenomics software. TELEVIR enables the execution of intricate processes that encompass multiple iterations (e.g., incorporating or excluding viral enrichment or host depletion), classification tools (e.g., Kaiju, Kraken2, Centrifuge, FastViromeExplorer), and databases (e.g., Virosaurus, RefSeq viral genome), ultimately producing reports that are focused on the user and diagnosis. Lastly, we created find ONT to enhance real-time virus detection during ONT runs. An instrument designed to lower expenses and shorten the latency period between sample acquisition and diagnosis. It is anticipated that the usability, adaptability, and functionality of INSaFLU-televir will provide researchers and public and animal health laboratories with a user-friendly, pan-viral bioinformatics framework that supports regular genomics surveillance and more effective and timely viral metagenomic detection. The ongoing rise

rise of viral risks, as seen by the SARS-CoV-2 and MPXV outbreaks, highlights the critical need for early virus identification, characterisation, and monitoring on a worldwide scale. In this regard, we expanded upon an already-existing INSaFLU procedure on behalf of the EU-funded televir project, in addition to developing wet-lab methods for viral metagenomic identification utilising ONT sequencing and its research process for further study. Platform to implement the enhanced INSaFLU-televir platform as a publicly available and user-friendly "start-to-end" bioinformatics framework for regular genomic monitoring and viral metagenomic detection. In this report, we describe: i) The creation, testing, and deployment of a novel virus detection module televir, which identifies both DNA and RNA viruses based on reads and quality control; ii) The enhancement and modification of the "surveillance-oriented" platform components to handle "multi-technology" sequence data (ONT, Illumina, and Ion Torrent) of "any" virus, based on reads, quality control, consensus generation, alignments, genotyping (using Nextclade and pangolin), "genotype-phenotype" screening (by incorporating and releasing "algn2pheno" for mutation screening), phylogenetics, integrative phylogeographical analysis, and temporal analysis (by incorporating Nextstrain). Despite the fact that creating this piece in the final platform functionalities benefited from real-time software and data sharing at an international level, leading to the integration of cutting-edge and state-of-the-art bioinformatics features and resources in the context of a pandemic and a research field in continuous technological evolution (microbial genomics and metagenomics). Furthermore, it is noteworthy to emphasize that the data analysis and reporting workflows developed by televir, along with the tutorial and guidance offered in the comprehensive online documentation, were heavily influenced by state-of-the-art recommendations for the introduction of metagenomic next-generation sequencing in clinical virology. Therefore, the module does not aim to add another algorithmic method to the metagenomics classification area, which is currently overflowing with them. Instead, televir concentrates on using the variety of current methods in the final user's interest. First off, the architecture that is being suggested provides many databases and the previously indicated approaches to the non-technical user.

Correspondence to: Veivnk Nerve, Department of Virology, Istanbul University, Istanbul, Turkey, E-mail: venerve.anatomy@gmail.com