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284 ONEIDA-INNUENDO - A bioinformatic platform for the integration of genomics in surveillance and outbreak detection

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Background: Outbreak investigations and pathogen surveillance are crucial tasks to control transmission of infectious agents. The decreasing costs of high-throughput sequencing (HTS) are leading to the increasing use of HTS in typing for routine surveillance and outbreak investigations. However, lack of standardized bioinformatics infrastructures for data processing and integration, together with limited bioinformatics skills, continue to be major hurdles of HTS routine implementation. To overcome these limitations, we developed the ONEIDA-INNUENDO platform, a user-friendly infrastructure providing the required framework for data analysis, from raw data quality assurance to integration of epidemiological data and visualization of the final analyses, allowing the use of HTS in everyday surveillance and outbreak investigation activities.

Materials/methods: The ONEIDA-INNUENDO platform uses Docker containers to enhance portability. It includes the INNUca pipeline for processing from automatic QC of reads to draft genome assemblies, which ultimately aims at producing consistently high-quality and comparable contigs. The curated genome assemblies are then analyzed following a gene-by-gene typing based approach using the chewBBACA software for whole genome MLST (wgMLST) profile definition. The wgMLST profiles generated for each isolate can then be compared with profiles already stored in the platform's database. The wgMLST profiles of the isolates of interest, together with a selection of the closest ones in the database, can then be filtered to produce a core genome MLST (cgMLST) and the data sent to PHYLOViZ Online for the construction of a minimum spanning tree annotated with metadata, allowing the exploration of possible epidemiological scenarios. Other in-silico typing tools for the inference of important epidemiological traits, such as serotype or antimicrobial resistance, can also be included in the platform in an organism specific way.

Results: The ONEIDA-INNUENDO platform was developed with a modular design allowing the incorporation of different bioinformatic tools for the characterization of specific pathogens. Currently tools focusing on foodborne pathogens and streptococci are available.

Conclusions: Information on the installation requirements for each possible setup is available in the documentation (<https://innuendo.readthedocs.io/>) and source code is available at Github (https://github.com/B-UMMI/INNUENDO_REST_API and https://github.com/B-UMMI/INNUENDO_PROCESS_CONTROLLER). A Docker-compose version (https://github.com/B-UMMI/INNUENDO_docker) of the system is also available which greatly automates installation minimizing user intervention.

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