**User-friendly web tool for typing and characterization of ESKAPEE pathogens**

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Multidrug resistant bacteria pose a significant threat in hospital environments, particularly pathogens from the so-called ESKAPEE group. Identifying and characterizing individual strains of a given species is crucial for tracking the spread of infections within hospital units and for selecting appropriate treatments. Multilocus sequence typing (MLST) differentiates strains by comparing selected housekeeping gene sequences with existing allelic profiles to assign a sequence type, while also enabling prediction of associated resistance and virulence factors. Although tools exist for these analyses, their use typically requires bioinformatics expertise to run analyses and interpret results coherently.

Here, we present a comprehensive web-based tool for rapid bacterial typing and characterization using MLST, designed for use by hospital personnel without programming skills. The sequence type of a pathogen is determined either from assembled contigs using BLAST or directly from raw reads using KMA, referencing allelic profiles in PubMLST database. In addition, the presence of virulence genes is predicted using hits from the BIGSdb-Pasteur and PubMLST databases, while antibiotic resistance genes and single nucleotide polymorphisms are identified using ResFinder tool. The tool was developed as a web application using Python Flask framework, offering submission of input data, selection of requested analysis and providing comprehensive result summaries in the form of tables and heatmaps to visualize similarities with the local result database and assist in tracking of possible outbreaks.

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