Using Genomics to Track Global Antimicrobial Resistance

The recent advancements in rapid and affordable DNA sequencing technologies have revolutionized diagnostic microbiology and microbial surveillance. The availability of bioinformatics tools and online accessible databases has been a prerequisite for this. We conducted a scientific literature review and here we present a description of examples of available tools and databases for antimicrobial resistance (AMR) detection and provide future perspectives and recommendations. At least 47 freely accessible bioinformatics resources for detection of AMR determinants in DNA or amino acid sequence data have been developed to date. These include, among others but not limited to, ARG-ANNOT, CARD, SRST2, MEGARes, GeneFinder, ARIBA, KmerResistance, AMRFinder, and ResFinder. Bioinformatics resources differ for several parameters including type of accepted input data, presence/absence of software for search within a database of AMR determinants that can be specific to a tool or cloned from other resources, and for the search approach employed, which can be based on mapping or on alignment. As a consequence, each tool has strengths and limitations in sensitivity and specificity of detection of AMR determinants and in application, which for some of the tools have been highlighted in benchmarking exercises and scientific articles. The identified tools are either available at public genome data centers, from GitHub or can be run locally. NCBI and European Nucleotide Archive (ENA) provide possibilities for online submission of both sequencing and accompanying phenotypic antimicrobial susceptibility data, allowing for other researchers to further analyze data, and develop and test new tools. The advancement in whole genome sequencing and the application of online tools for real-time detection of AMR determinants are essential to identify control and prevention strategies to combat the increasing threat of AMR. Accessible tools and DNA sequence data are expanding, which will allow establishing global pathogen surveillance and AMR tracking based on genomics. There is however, a need for standardization of pipelines and databases as well as phenotypic predictions based on the data.