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The role of high throughput bioanalysis tools ("OMICS") in alert and surveillance Keywords: genomics, metagenomics, transcriptomics, alert, surveillance

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The Covid-19 pandemic highlighted the risks associated with zoonotic reservoirs of human pathogens and the ease of spread of infectious diseases due to the increasing globalisation of population exchanges. In this context, high-throughput biological analysis tools ("OMICS") have demonstrated their full potential for understanding the epidemic. Genomics, through the massive sequencing of the genomes of SARS-Cov2 strains, has made it possible to understand the mechanisms of the virus' spread and to understand its evolution. To date, more than 11 million viral sequences have been produced worldwide. In parallel, highthroughput sequencing tools have been adapted to the characterisation of complex microbial flora by identifying any nucleic acid in a given sample (metagenomics). Initially reserved for the study of the microbiota, metagenomics was rapidly adapted to rapid diagnosis, making it possible to detect any type of microorganism in a clinical sample without any preconditions. Finally, metatranscriptomics, the purpose of which is to identify the genes transcribed by a given organism, now makes it possible to detect specific bacterial, viral or parasitic infection profiles, even going so far as to characterise the type of agent involved. In addition to their technological performance and the quantity of sequences produced, high-throughput sequencing techniques can be implemented very quickly, as a sequence reaction can be produced from any type of sample, in any type of environment, in less than 10 hours. These characteristics make OMICS particularly suitable for monitoring and warning of infectious risks.