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Bioinformatics technology in clinical and public health microbiology applying computational methods

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The role of clinical genomics in infectious disease diagnostics and public health microbiology is the topic of discussion during a recent decade. Although much of this work is aimed at describing the structure of outbreak communities, the methodology works equally well to identify pathogens in clinical samples. Clinical genomics is the exploitation of genome sequence data for diagnostic, therapeutic and public health purposes. Central to this field is the high-throughput DNA sequencing of genomes and metagenomes. The key concept in using clinical genomics methodology is that detection of microbes is independent of culture and is not limited to targets used for in-depth PCR assays. Rather, it is a process of generating large-scale sequence datasets that adequately sample a specimen for microbial content and then of applying computational methods to resolve the sequences into individual species, genes, pathways, or other features.

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