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Microbial informatics: tools for microbial genome analysis

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ene finding can be broadly defined as a process of identification of genomic DNA regions encoding proteins. This is a J powerful technique that has vast applications in structural genomics, functional genomics and genome studies. While the genomes of several bacterial species have been sequenced over the last decade, transforming such raw sequence data into information pertaining to genes that identify the organisms and ascertain the organisms' virulence profile remains a key challenge. This is where microbial bioinformatics becomes a key tool, for microbial genome analysis. The GeneSeekr is one such powerful bioinformatics tool developed by researchers at the Canadian Food Inspection Agency (CFIA) to address this challenge. It does not work like the multitude of gene prediction programs available today; tools that look for open reading frames (ORFs), start/stop codons, gene density, ribosomal binding site (Shine-Dalgarno sequence), repetitive sequences etc. In sharp contrast, the GeneSeekr pattern searches through raw sequence data utilizing full length gene sequences to "seek" genes of interest; hence the name - GeneSeekr. This versatile tool has been applied to find genes of interest in a variety of bacterial species that include Escherichia coli, Bacillus, Salmonella, Listeria, Staphylococcus, Campylobacter etc. Existing gene targets (identification genes as well as virulence profile genes) from several compendium methods for a number of species have been transferred over to the GeneSeekr making an analysis available for researchers across CFIA whenever they sequence a pathogenic bacterial genome. For some techniques (E. coli verotoxin subtyping for example), the GeneSeekr offers a highly accurate and a far superior alternative for gene subtyping along with gene finding. Whole genome sequencing has been a game changer but it is the microbial bioinformatics that has shifted the paradigm and also opened many exciting possibilities for the

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