PathoFact: A pipeline for the prediction of virulence factors and antimicrobial resistance genes

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Abstract

Most of the microorganisms in the human microbiome are commensals, contributing essential functions to their hosts, while in contrast, pathogenic microorganisms cause disease by invading, colonizing, and damaging their hosts. Virulence factors, including bacterial toxins, contribute to their pathogenicity, and antimicrobial resistance (AMR) genes allow them to evade otherwise curative treatments. A new tool seeks to improve our understanding of virulence factors and antimicrobial resistance genes. PathoFact is a tool for the contextualized prediction of virulence factors, bacterial toxins, and AMR genes. In an evaluation with simulated metagenomic datasets, PathoFact outperformed two other existing analysis workflows, and in a test with three case-control datasets representing infection and chronic disease, PathoFact identified virulence factors that were either secreted or not secreted. The new tool also helped to identify virulence factors and AMR genes that differed between the case and control groups, revealing novel gene associations for the diseases. An easy-to-use, modular, and reproducible pipeline for identifying virulence factors, bacterial toxins, and AMR genes in metagenomic data, PathoFact is a flexible and versatile tool to provide further depth to metagenomic analysis of the microbiome. PathoFact and its models and databases are available at <https://pathofact.lcsb.uni.lu>.