



# Pathogen diagnostics for the masses

Rapid identification of pathogens from patient samples is vital for the accurate diagnosis and treatment of infectious diseases. A new bioinformatics tool that analyses and visualizes metagenomics data promises to speed up this process to a matter of minutes.

Next-generation sequencing has transformed microbial research and clinical diagnostics by facilitating the unbiased, hypothesis-free detection of vast numbers of common and rare pathogens, obviating the need to first grow these in culture. However, large-scale metagenomics studies require bioinformatics expertise and computational resources that are often absent in traditional diagnostics laboratories.

A team led by Robert Schlaberg and Mark Yandell at the University of Utah has now developed the publicly available, web-based metagenomic sequence analysis software Taxonomer. This tool enables the rapid detection and discovery of pathogens, including bacteria, viruses and fungi, from both DNA and RNA sequencing (RNA-seq) data, as well as from short reads and longer contigs assembled from metagenomics data sets. In addition, it allows for the simultaneous profiling of host gene

expression, which could be used, for example, for monitoring antimicrobial treatment success.

Taxonomer comprises four main modules: the 'Binner' module compares each read to several reference databases in parallel and categorizes ('bins') reads into broad taxonomic groups. Microbial and host gene expression is then profiled at the nucleotide ('Classifier' module) or at the amino acid level ('Protonomer' and 'Afterburner' modules). Protein-based classification aids the identification of genetically diverse and novel organisms.

Benchmark analyses revealed that Taxonomer has a high tolerance for sequencing errors, and is more sensitive, more accurate and faster than comparable tools, all while enabling the simultaneous profiling of host mRNA expression. "Often, the clinician is left to treat empirically," explains Schlaberg. "Profiling the host's mRNA expression response may be able to differentiate true infections from non-infectious mimics, and bacterial infections that need to be treated with antibiotics from non-bacterial infections, therefore helping to limit antibiotic overuse."

To simulate viral detection and discovery in public health emergencies, the researchers tested their tool on published RNA-seq data

from three different patient samples: serum from a patient with haemorrhagic fever caused by a novel rhabdovirus, a throat swab from a patient with avian influenza and plasma from a patient with Ebola virus. Even after removing all viral target-protein sequences from the reference database, to simulate the discovery of unknown pathogens, all three viruses or close relatives were identified by Taxonomer, showcasing the tool's utility for the detection and prevention of emerging epidemics.

Through its easy-to-use web-based interface, Taxonomer enables the upload and rapid analysis of sequencing data from patient samples using personal computers and mobile devices. This should help to remove barriers for the adoption of metagenomics in academic and clinical settings, and will hopefully translate to faster public health responses during infectious disease outbreaks.

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**WEB SITE**

<https://taxonomer.com>

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