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TITLE: IMG/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes

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ABSTRACT:

The Integrated Microbial Genome/Virus (IMG/VR) system v.2.0 (https://img.jgi.doe.gov/vr/) is the largest publicly available data management and analysis platform dedicated to viral genomics. Since the last report published in the 2016, NAR Database Issue, the data has tripled in size and currently contains genomes of 8389 cultivated reference viruses, 12 498 previously published curated prophages derived from cultivated microbial isolates, and 735 112 viral genomic fragments computationally predicted from assembled shotgun metagenomes. Nearly 60% of the viral genomes and genome fragments are clustered into 110 384 viral Operational Taxonomic Units (vOTUs) with two or more members. To improve data quality and predictions of host specificity, IMG/VR v.2.0 now separates prokaryotic and eukaryotic viruses, utilizes known prophage sequences to improve taxonomic assignments, and provides viral genome quality scores based on the estimated genome completeness. New features also include enhanced BLAST search capabilities for external queries. Finally, geographic map visualization to locate user-selected viral genomes or genome fragments has been implemented and download options have been extended. All of these features make IMG/VR v.2.0 a key resource for the study of viruses.

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