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Sommario/riassunto	Since the late 1800s, the discovery of new viruses was a gradual process. Viruses were described one by one using a suite of techniques such as (electron) microscopy and viral culture. Investigators were usually interested in a disease state within an organism, and expeditions in viral ecology were rare. The advent of metagenomics using high-throughput sequencing has revolutionized not only the rate of virus discovery, but also the nature of the discoveries. For example, the viral ecology and etiology of many human diseases are being characterized, non-pathogenic viral commensals are ubiquitous, and the description of environmental viromes is making progress. This Frontiers in Virology Research Topic showcases how metagenomic and bioinformatic approaches have been combined to discover, classify and characterize novel viruses.