



New Insights in Viral Diseases and Computational Biology

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Message from the Guest Editor

Humanity and animality are facing threats from various viruses, including RNA viruses such as SARS-CoV-2, the influenza virus, the respiratory syncytial virus (RSV), and the Ebola virus. SARS-CoV-2, influenza virus, and respiratory syncytial virus all cause acute respiratory viral infections. As of August 2023, the World Health Organization (WHO) had reported over 769 million confirmed cases of COVID-19 and approximately 6.95 million confirmed deaths. The overlap of SARS-CoV-2 with seasonal epidemics of RSV and influenza viruses has also resulted in significant morbidity and mortality among young children worldwide [1]. Although Ebola virus outbreaks have been mainly restricted to Africa, they have resulted in much higher fatality rates, with an average of around 50%.

Bioinformatics approaches, employing vast new technologies, have been widely used to address research questions regarding virus evolution and host responses. Second- and third-generation sequencing have provided large amounts of resource data for bioinformatics analysis, aiding in the understanding of the biology of both the virus and its infected host.





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Message from the Editor-in-Chief

The worldwide impact of infectious disease is incalculable. The consequences for human health in terms of morbidity and mortality are obvious and vast but, when infections of animals and plants are also taken into account, it is hard to imagine any other disease that has such a significant impact on our lives—on healthcare systems, on agriculture and on world economics. *Pathogens* is proud to continue to serve the international community by publishing high quality studies that further our understanding of infection and have meaningful consequences for disease intervention.

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