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Editorial: Methods in bioinformatic and predictive virology

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Editorial on the Research Topic
Methods in bioinformatic and predictive virology

Viruses were cast under the international spotlight due to the global COVID-19 pandemic in the early 2020s, renewing interests and applications in the field. With the pandemic still ongoing at the time of writing due to escape variants and subvariants, there is renewed interest in studying, developing, or applying predictive methods from other viruses unto SARS-CoV-2. There is much to cross-fertilize, especially when there are ongoing viral infections that continue to plaque the world apart from COVID-19.

Given the great resources to experimentally work on pathogenic viruses that few scientists have access to, such as access to samples, higher biosafety facilities, the tools and applications from bioinformatics was a great welcome, particularly in prediction.

Applications from ongoing viral pathogens, particularly ongoing old viral infections like the human immunodeficiency virus (HIV) (1) had provided a lot of transferable knowledge in the treatment of COVID-19 (2–5). Using HIV as a model, mutations have been studied experimentally (6) to allow computational modelling to study drug cross-resistances (7, 8), and viral fitness (9) towards the development of interventions (10–12).

Incorporating both experimental and computational methods, it is possible to build frameworks for future pandemic preparedness through the understanding of how mutations enable zoonotic transmissions from animal reservoirs as gleaned from H5N8 avian influenza (13). There is certainly much that methods in the computational analysis towards predicting zoonoses and cross-drug resistance can contribute to healthcare now and in the future.

Given the attention to COVID-19, there has been a large amount of literature on the virus released since year 2020. Within this topic of Methods in Bioinformatic and Predictive Virology, we have examples of the potential of such methods, both

computational and experimental towards the application in COVID-19. We have the building of OrthonaVirae Tree, an analysis software on the relatedness of Orthornavirae from the RNA-dependent RNA polymerase (RdRp) gene sequence (Cheng et al.) that allows the potential informing of viral relatedness and by extension, guide the possible cross-use of existing antivirals to newly discovered viruses.

Similarly, we have SARSNTdb, a database to study the conservation of regions in SARS-CoV (Orgera et al.) that can allow the identification of conserved target regions for long-lasting vaccines and interventions that not only is relevant to COVID-19, but future coronavirus-related infections.

Similarly, the ability to predict the activity of neutralizing antibodies to new mutations in the SARS-CoV-2 spike (Ford et al.) will shed light on how effective interventions would be in the appearances of novel mutations and new variants. The Research Topic covered important areas in tracing, targeting, and evaluation required in pandemic preparedness in years to come.

Author contributions

SG: Conceptualization, Funding acquisition, Investigation, Resources, Writing – original draft, Writing – review & editing. EK: Writing – original draft, Writing – review & editing.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

The author(s) SG, EK declared that they were editorial board members of Frontiers, at the time of submission. This had no impact on the peer review process and the final decision.

Publisher's note

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