

EDITORIAL

Special issue on computational biology and bioinformatic applications to the COVID-19 pandemic

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The COVID-19 pandemic has caused a global crisis that prompted the scientific community to tackle new, extraordinary challenges. The urge to make informed decisions with dramatic impact on public health, wealth and society as a whole has pushed the scientific community to produce knowledge and tools at an unprecedented pace. This massive effort resulted in a deep understanding of the SARS-CoV-2 infection, spread and pathogenetic mechanisms, together with the assessment of non-pharmaceutical interventions (NPIs), and the development of therapies and vaccines. We argue that a remarkable contribution to the fight against the pandemic has been provided by the availability of computational biology and bioinformatics tools, which contributed to boost the research process in any possible application area and better cope with the urgent needs determined by the pandemic.

In this special issue of *Quantitative Biology* we collected seven studies that nicely exemplify such contribution. We believe that the methodology through which we selected the researchers to invite is worth mentioning by itself. Using our automated tools [1] to download, categorize and rank COVID-19 related scientific articles, we were able to filter relevant authors based on a predicted quality threshold automatically assigned to articles published on preprint servers. Starting from this shortlist, we then manually evaluated the most promising articles and sent out invitations. This application is part of our broader approach to cope with the extraordinary pace of publication during global emergencies such as the present pandemic. In the case of this special issue, it helped to quickly reach the right authors and make sure to cover the most relevant topics.

In particular, we believe that this collection properly reflects two of the major directions that the computational biology and bioinformatics efforts have been devoted to, *i.e.*, epidemiological modeling and automatic diagnostic tools. The former combines machine-learning with mathematical models to better understand the pandemic evolution and countermeasures. The latter takes advantage of the latest developments in machine-learning based image analysis and classification techniques to support clinical decisions.

Concerning epidemiological modeling tools, this special issue includes an interesting selection of alternative approaches. Jo *et al.*, for example, used a pure machine learning approach based on recurrent neural networks to predict daily deaths at the country level. On the other hand, Barmparis *et al.* combined machine learning with an SIR (susceptible-infected-removed) model to analyze the first wave of infections and perform short-term predictions. The remaining studies present different mathematical modeling approaches. Tang *et al.* used functional data analysis to assess the impact of NPIs, the correlation of confirmed cases and deaths, and to predict confirmed cases. Mourad *et al.* presented a discrete spread

model that interestingly includes social structure parameters like contact tracing and family groups. Finally, Grinchuk *et al.* showed an approach to model the spread of COVID-19 taking into account nonuniform population density, which is typical of large geographical areas.

Concerning diagnostic tools, Panday *et al.* proposed a survey of the published methods. The study highlights the role that such tools could have in emergency situations, when the availability of regular tests is limited or an overwhelming number of cases challenges the health system testing capacity. The authors of the survey analyzed 98 articles covering the entire analysis pipeline from the collection of X-ray and CT scan images to their preprocessing, classification and visualization stages. On the other hand, Abbasi *et al.* showed how a number of different machine learning methods can accurately predict SARS-CoV-2 infection and disease severity after training with chest X-ray scans.

We hope that this collection will be of interest to the readers of *Quantitative Biology* by providing interesting hints on some of the enormous efforts produced by the community of researchers to the fight against COVID-19 in diverse computational analysis areas.

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