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Machine Learning, COVID-19 (2019-nCoV), and multi-OMICS

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THE primary plan of my editorial for this month was to highlight and comment on the special issue of this month: "Machine Learning for Single Cell Data". I wish to emphasize and thank the Guest Editors of this special issue, Yvan Saeys and Greg Finak, for their outstanding success and hard work to assemble excellent manuscripts for this issue. I am referring to their guest editorial giving you more details on aims and scopes and elaborating on specific articles.

I started drafting this editorial while attending the annual Photonics West conference in San Francisco, presumably the largest showcase on photonics technologies and instrumentation. Scientifically, the sub-conference BIOS demonstrated the broadness and vividness of photonics technologies in life sciences and particularly in single cell analysis. When searching for relevant literature for this editorial, I was also tracking the actual global developments. This brought me to change my focus and comment on some issues that are relevant to our field and somewhat related to that of the special issue.

First of all, Nature Methods announced their Method of the Year 2019 (1). It is: "Single-cell multimodal omics" and acknowledges (among others) the important contribution of highly multiplexed flow cytometry and cell sorting to the increased understanding of single cell biology and cell systems. This is motivating and confirms that cytometry is receiving the focus of attention.

Concurrently, in the last weeks the relevance of the recent COVID-19 (2019-nCoV) outbreak and its effects started to become evident as everybody was monitoring the number of cases registered globally (2). As conference chairs, we were facing the fact that many of our speakers and colleagues became unavailable. Not only that, but the eeriness of the infection (it is transmissible already during its asymptomatic latency period of up to two weeks, recent results indicate even longer) gave many attendees an uneasy feeling.

This brings me to two points worth discussing. (a) Are large scale conferences with global attendance still state of the art or should they be rethought; and (b) to what extent can cytometry support global efforts in various fields of epidemic outbreaks of infectious diseases? In the past one to two decades the world faced several outbreaks of different viral infections that were luckily not as disastrous as initially anticipated but still claimed victims. These were coronaviruses such as the Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) in 2002/2003, the Middle East Respiratory Syndrome coronavirus (MERS-CoV) with occasional outbreaks since 2012 or influenza viruses like the H1N1 pandemic in 2009/2010. It is only a matter of time until other pandemics follow.

Global travel for work and leisure supports viral spread and can transport the infection to nearly all places of the globe within days. Global conferences contribute to such a rapid spread and one should reconsider this model of scientific exchange from time to time and scrutinize potential alternatives. Models for sustainable international conferences are under testing and combine venues in close proximity to institutions with a substantial expertise on the focus area of the conference with virtual participation and contribution by internet for participants on more distant places. Although personal meetings are essential for optimal information exchange, a reduction in travel would not only reduce the risk of dissemination of disease but, as a side effect, could result in

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budgetary savings, reduce travel-related emissions (in the wake of Greta), and eliminate jetlag.

Now, what can Cytometry do for help in pandemics? Cytometry has already supported several achievements as a quick and non-representative literature search shows. Image cytometry methods (3) and bead-based flow cytometry methods (4) are at hand to enable for screening and detecting antibody virus interactions and detect viral antigens. Airway memory T-cells and viral E protein mutations have been identified in CoV infections as potential targets for vaccine strategies (5,6). Immune responses seem to be indicative of disease severity (6,7) but more studies are needed to have a practical assay for decision making at hand.

In fact, easy to use and rapid assays derived from Cytomics or multi-OMICS approaches are needed to rapidly distinguish severe from mild cases and identify future critically ill individuals before symptom onset. Such a test would clearly take the pressure off of the clinicians because only those with high probability to becoming critically ill would receive intensive care early. Hopefully we will see more related studies in this journal in the near future.

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