EDITORIAL

Editorial: Cutting Covid no slack

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Published online: 20 May 2020 © European Society of Human Genetics 2020

Not only the public media, but also the scientific press is currently hit by a plethora of Covid-19 manuscripts. To contribute its part, but add some broader insight, the EJHG decided to devote space to several brief overview reports of a number of large international Covid-19 focused initiatives, which you can find in the POLICY section of this ESHG issue. On one hand, these are the responses of existing and well-established ESFRI infrastructures, aimed to channel their historic strengths to this new challenge. One is from ELIXIR, the proven and tried infrastructure established to organize the European research data arena with EBI as central hub, but connecting a large number of national nodes throughout Europe, and now gearing up to turn its longstanding expertise and model into maximizing the access to data and materials.

The second is from BBMRI-ERIC, the equally venerable infrastructure of the European biobanking field and its related biomolecular data, based in Graz but equally connecting an ever-growing number of national nodes. For BBMRI-ERIC, with their huge resource of on-stream biobanks and cohorts and their key role in the development of biobanking sample quality and safety procedures, the Covid19 crisis may become a cornerstone of their utility linking research and health care.

Then there is a newer development, VODAN IN, sprouting from the European Open Science Cloud and GO FAIR communities, aiming to assist science and health care in getting access to, and mining all types of data, but more fundamentally decentralized as, e.g., ELIXIR. Given the complexity of the Covid crisis and the extreme speed of its development, as well as the views on how to curb it and how to deal with the "privacy vs. progress" issue, time will tell if there is an optimal data access model, more

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centralized or less, and no one should be amazed if they will have complementary utilities and applications.

Last but not least, there is the international Covid-19 Host Genetics Initiative. A grassroots development of top genetic epidemiologists, clinicians and statisticians, originating in Finland, Italy and the US, notably the Broad Institute but now counting hundreds of participating institutions worldwide. It is aiming at the rapid elucidation of host genetic factors involving susceptibility to infection, and subsequent development of the disease course, by the instantaneous sharing of data, existing as well as newly discovered. Its cornerstone is the use of the Slack app, a sort of online, filtered email/WhatsApp tool, where people can float ad-hoc findings, viewpoints, discuss specific topics and subtopics. This Slack channel has several sub-streams like phenotypes, analysis, questionnaire development, bioinformatics, sex differences to name but a few, and one can participate in as many of these as one desires to contribute data or viewpoints. There have now been three well-organized ZOOM calls with from 200 to 500 participants (but strictly organized agenda's, successfully avoiding hour-long free-for-alls) and at the date of writing this editorial the first main paper of comprehensive meta-analysis is being compiled. It is impressive how this approach has taken off since its start in mid-March. Some idea of the thundering speed with which this initiative is proceeding:

31 March-first online partial UK Manhattan lot.

8 April—first Finnish Manhattan plot. No Genome-wide significant hits yet, but sufficient substructure, i.e. no flat "Sahara plot" but rather something on its way to a Manhattan plot(what I call an "Amsterdam plot").

15 April—a more or less complete analysis plan with several main questions.

17 April—first exchange of big biobank questionnaires.

17 April—the first indication of a lead variant I the local Finnish GWAS.

8 May-data submission deadline for the first main meta-analysis.

In short: to be continued, so keep tuned in to EJHG!

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