Coronavirus Standards Working Group Meeting Summary

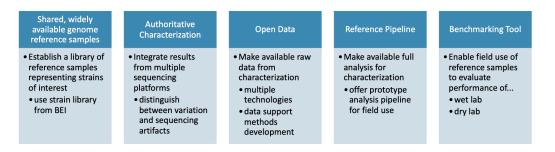
Dear Colleagues -

Thanks to all for our meeting this morning Friday 19 March — this is a brief summary to get the materials and links in everyone's hands quickly. Thanks to Jack Collins of the Frederick National Lab (an NCI FFRDC) for starting a conversation about standards needs for genomic surveillance. Jack's slides <u>are here</u>. My slides that include a proposal for work to do <u>are here</u>.

The architecture of what I'm proposing is pictured here -- I suggest we (1) establish a library of viral RNA genomes (~16) from the BEI resources, (2) characterize those and (3) make available all data. We should (4) provide access to a family of informatics analysis pipelines, with guidance on use and performance, and (5) develop and deploy a benchmarking tool that would permit field users to evaluate the performance of their lab.

What can we do to support community to understand & report sequencing data quality?

What can we do to be confident in genomic surveillance?



Deliver technology-agnostic standards for Wet Lab -> Dry Lab -> Public Health

There are details of implementation, but a clear message from the meeting today was to focus on delivering a 'good enough' solution rapidly. "Six months is too long!"

Rapid response is a reasonable and urgent design principle; using existing samples and analysis tools is imperative. We can use currently available reference strains from BEI and other already- or near-term available materials. There are several analysis pipelines/tools already available. The "invention" required will be a benchmarking tool. Integration of the "dry-lab" elements into a cloud-

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hosted platform derived from precisionFDA would be straightforward.

Our <u>meeting recording is here</u>, and our <u>website</u> will be updated to include the slides and this meeting summary.

Your thoughts are very welcome on this critical topic -- more to come!

Cheers and stay safe! Marc

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