From: **Marc Salit -- Coronavirus Standards WG** msalit@stanford.edu
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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 are here. My slides that include a proposal for work to do are here.

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?

Shared, widely available genome reference samples	Authoritative Characterization	Open Data	Reference Pipeline	Benchmarking Tool
• Establish a library of reference samples representing strains of interest • use strain library from BEI	• Integrate results from multiple sequencing platforms • distinguish between variation and sequencing artifacts	• Make available raw data from characterization • multiple technologies • data support methods development	• Make available full analysis for characterization • offer prototype analysis pipeline for field use	• Enable field use of reference samples to evaluate performance of... • wet lab • dry lab

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-

hosted platform derived from precisionFDA would be straightforward.

Our meeting recording is here, and our website 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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