Coronavirus Standards Working Group Meeting Summary

Dear Colleagues —

It was great to share the outcomes and possible next steps from the community convening on a Standards Architecture for Pathogen Genomic Surveillance on Friday morning. We spent a few minutes after that presentation and discussion on some next steps for the RNA Harmonization Study. Our working group slide deck is linked here, and the Pathogen Genomic Surveillance slides are linked here. The recording and transcript are linked here.

Pathogen Genomic Surveillance Standards Architecture
Arend Sidow and I developed a "Standards Architecture" for pathogen genomics surveillance. This work was sponsored by The Rockefeller Foundation, and conducted by Viridae, Inc. The strawperson was considered in a convening workshop with 5 sessions in June, 2021. You can see the strawperson and the slides from the workshop closing plenary at this link. Thanks for the good discussion at our meeting -- there are likely developments to follow-up on.

**Harmonization Study Development**
We had a brief discussion of the Harmonization Study analysis and development -- it's been suggested we conduct a small (3-ish labs) experiment to demonstrate the utility of harmonized calibration materials. The sketch of this would be to share archived clinical samples (8 each of low, medium, and high abundance) and use several different types of (inactivated virus, recombinant virus, recombinant bacteriophage) calibration materials from our study to run at multiple labs. The objective would be to test the hypothesis that reference samples harmonized to the International Standard can be used to measure clinical samples with comparable results reported in the International Unit (IU).

We'll be discussing this in September.

I've made a couple of changes in the dashboard to help identify biases in the harmonization results. This includes putting all the material analysis box plots on a common scale (+/- 1 log -- 100-fold from bottom to top) and adding a box plot ordered by lab:target. I also shared a graph I made to examine deviations from the population medians, see below. There are a couple of subtle effects upon cursory examination, mostly that particular samples seem to share bias at a given lab for multiple targets (see biodesix for the Microbiologics sample, Western for the NIBSC sample, LANL for Asuragen). Such patterns might hint at a sample-handling effect due to dilution or extraction.

Deviations from median by Lab:Target
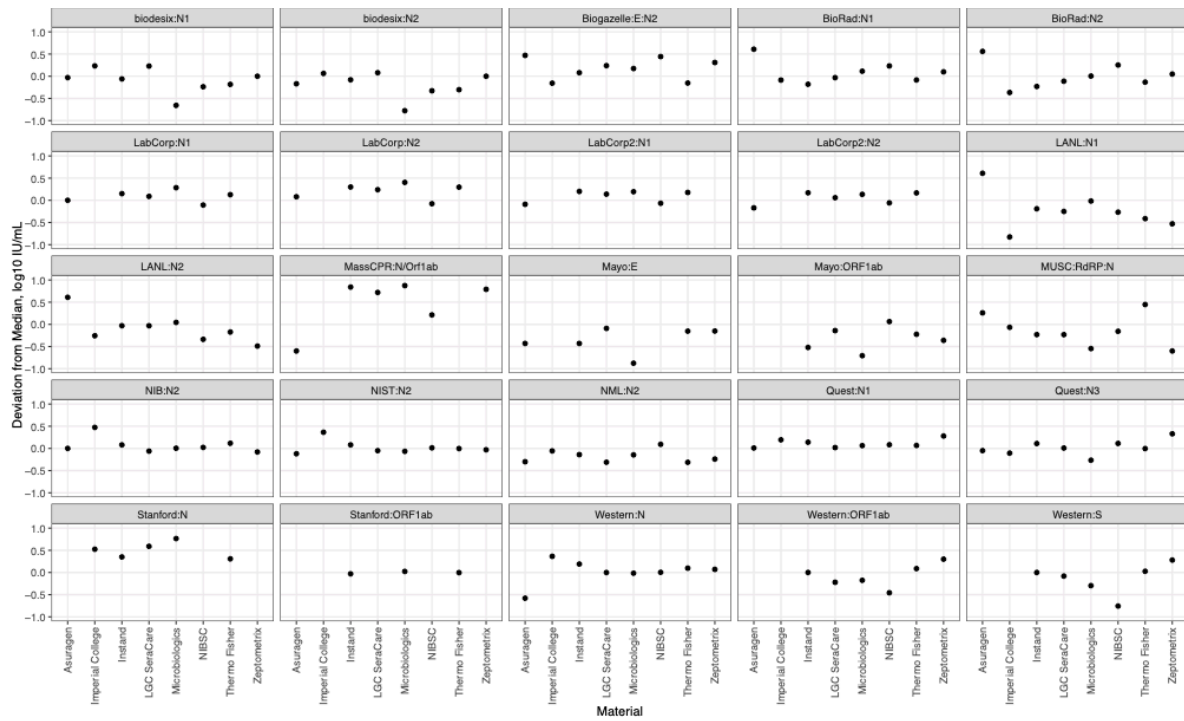
Cheers and stay safe!
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