

8 MAY 2020 CSWG SC MEETING SUMMARY

NEXT MEETING 15 MAY 2020 0800 PDT

Thank you as always for everyone's engagement at Friday's Steering Committee meeting. This summary is an open document — please share this with any who might be interested, and please continue to reach out to relevant partners and stakeholders inside and outside of your organizations. This document and the slide decks from the presentations at the meeting are available in our Slack workspace (#steering-committee channel) and on the JIMB website at <https://jimb.stanford.edu/covid-19-standards>. All meeting summaries and slide decks are archived there as well.

Sarah Wait Zaranek took meeting notes at our meeting this week — this summary is based in large part on those notes — thanks to Sarah!

This week's highlights were progress on the Minimum Information About a Viral Control (MIAViC) draft standard (with great help from Pete Vallone and Jim Huggett) and, an online database of viral controls that (roughly) correspond to our draft MIAViC (thanks Patrick Chain and Po-e Li), and progress on the manuscript, with the figures in near-final design and annotation (thanks Tim Mercer!).

We had a presentation from Patrick Chain of Los Alamos National Lab on the molecular assay bioinformatics platform created in his group, and a proposal for a CSWG-led study from Russell Garlick of LGC SeraCare Life Sciences.

STEERING COMMITTEE MEETING

MANUSCRIPT AND STANDARDS UPDATE

The DRAFT MIAViC standard is described in this google doc:
<https://docs.google.com/document/d/1gnxMVx9ooMnV1bs-cgfRzRQrPE-UoTV0VnwfbSvjmbk/edit>

The online database of controls is here: https://poeli.gitlab.io/collated_vendor_info/

Our latest figures are in the Slack in the #figures channel, with harmonized designs for the measurement process of both molecular and serological.

EDGE BIOINFORMATICS COVID-19 GENOME ANALYSIS

Patrick Chain from Los Alamos National Lab presented and demonstrated the [EDGE Bioinformatics COVID-19 Genome Analysis](#) platform, which does *in silico* modeling of molecular assay performance across all SARS-CoV-2 genome sequences reported. Patrick demonstrated the platform, which is continually updated as new

genomes accrue. This platform was developed as a product of the DOE National Virtual Biotechnology Laboratory, which is also supporting some of the operation of this WG.

Patrick's slides are available on the Slack steering-committee channel, and the website is live here: <https://covid19.edgebioinformatics.org/#/home>

STUDY & STANDARDS DEVELOPMENT PROPOSAL

Russell Garlick of LGC SeraCare Life Sciences presented a proposal to the working group: “**Advancing SARS-CoV-2 Virus Testing During the Global Emergency**”

Russell proposed that we establish a set of reference samples and use these as a basis for a coordinated multilab study. One form of the study would invite all manufacturers of EUA tests and EUA LDTs to measure the same reference sample set. This multilab study might be an authoritative comparison of performance, and we could establish the reference sample set as a shared benchmark.

There was strong interest and assent to fleshing out the proposal, and an open meeting of interested WG members will be convened to discuss this further. **We will try to meet during the week of 11 May, and have a brief update at our next SC meeting on Friday 15 May,**

This proposal is consistent with objectives and plans as the WG was being formed, and a reference sample set, study design, and analysis could be a way to harmonize good performance across the population of assays and labs, enabling enduring and repeated benchmarking.