Q: The proper names are important. However, LOINC can use synonyms to guide LOINC users to the right code. For a test with a proper long name, having a synonym term that also leads to it (user friendly) would help adoption.

Q: Will "COVID-19" be included as a "related Names" field in the LOINC release file for searchability?
   A: We agree. All of the LOINC terms related to SARS-CoV-2 testing are linked to a variety of Related Names, including COVID-19, Wuhan coronavirus, and 2019 Novel Coronavirus. Users who search using any of these search strings will find the SARS-CoV-2 terms.

Q: What about tests that look for antibodies? Should they reference the disease name or the virus name?
   A: Tests that are looking for antibodies have the virus name in the LOINC Component, because the antibodies are to the virus, not the disease. However, these terms also have COVID-19, Wuhan coronavirus, and 2019 Novel Coronavirus as synonyms for searching.

Q: I think the ICTV discourages the use of acronyms for species names. To help clarify the meaning of SARS-related coronavirus as the species, is there value in spelling out the full name?
   A: We usually follow ICTV naming conventions, but in this case, we included the “SARS” acronym in the Component because 1) we want to be consistent with existing terms, and 2) most users will recognize the acronym rather than the full name. However, Severe Acute Respiratory Syndrome is included as a synonym for searching.

Q: Do you have any suspicion that the 2002-03 virus will be renamed "SARS-CoV-1"?
   A: We have seen a few references to the 2003 virus as SARS-CoV-1 in manufacturer’s literature and scientific publications, but there is no indication that the name of the virus will be formally changed by ICTV.

Q: My understanding is that there are differences between the CDC test kit and the WHO test kits. Will there be something in "related Names" that will allow us to differentiate between the two test kits?
   A: Per our current understanding, the WHO has not developed its own test kit but rather has information about other organizations’ assays on its website. Regardless, we will not be including references to assay names or manufacturers in the Related Names, because assays can evolve over time, and the characteristics of the test (analyte, specimen, etc.) should be used to determine the correct LOINC term for a specific test kit.

REQUESTS FOR NEW LOINCs

Q: Did you get any request from Italy or China or Korea? (or did LOINC reach to them just like it did to US CDC?)
   A: We have received requests from China as well as several other countries, reference laboratories, and IVD manufacturers.
Q: Are you getting requests to create codes for the various COVID-19 clinical trials’ testing?
   A: We have received requests for Research Use Only (RUO) lab tests, but have not received any other requests related to clinical trials.

Q: When you say LOINC users send in submissions - is that the manufacturer that sends a request about a LOINC code? Or how should it be understood?
   A: Requests can come from IVD manufacturers, commercial and reference labs, public health agencies, and other organizations. To request new codes, please see our website: https://loinc.org/submissions/request/

Q: Will you create new codes based on the Healthy People 2030 goals, scheduled to be published on 3/31/20?
   A: We have not received any requests specific to Healthy People 2030.

Q: Besides lab LOINC - Will LOINC consider temp codes for clinical-LOINC codes for COVID19.
   e.g. CDC form https://www.cdc.gov/coronavirus/2019-ncov/downloads/pui-form.pdf has:
   "Community contact with another lab-confirmed COVID-19 case-patient"
   "Exposure to a cluster of patients with severe acute lower respiratory distress of unknown etiology"
   "Household contact with another lab-confirmed COVID-19 case-patient"
   Or per SNOMED-LOINC agreement, SNOMED will do that. Here the coordination is crucial. What code turf is LOINC pursuing and what code turf is SNOMED pursuing. (or neither SDO is truly interested in detailed codes).
   A: LOINC will consider the creation of clinical terms related to COVID-19 and SARS coronavirus 2 where they are in the purview of the LOINC mission and there is a common need (like the laboratory terms have been). This includes clinical questions, survey documentation, and clinical document types. We are currently working with the CDC to create a LOINC panel to represent the CDC’s COVID-19 PUI and Case Report Form. Values such as the ones in your question will be assigned LOINC Answer (LA) codes. If SNOMED CT codes are assigned for these values, we will include the SNOMED CT mappings in the Answer list.

Q: SNOMED CT did an out of cycle release. When is LOINC planning to do the same so that LP codes are visible and also temp codes are fully in RELMA. Why is it not technically possible to do an April 10 release out of cycle LOINC release?
   A: The pre-release terms are evolving rapidly, and it is likely that there will be a large number of additions leading up to the next scheduled release, so having a single interim release on April 10 would not be sufficient. In addition, while technically possible, a formal release in its current form involves a time-consuming validation process, which would take resources away from urgent term creation. For these reasons, we are not planning an interim release at this time.

Q: So far, all that has been published online for the SARS CoV 2 LOINC codes are the FSNs [Fully Specified Name]. Is there a resource that contains all of the different names for these? i.e. long common name, short name, etc.
A: We updated the prerelease details pages for the Special use terms during the first week of April to include the Long Common Name, Short Name, and Display Name, as well as term descriptions, Answer lists, Related names, and example UCUM units of measure.

Q: PLEASE add CSV download option on this pre-release page. (even left right scrolling is implemented no well. Why not display more columns without scrolling?)
A: We do not provide a formal download file for many of the same reasons that we are not planning to publish an interim release. While users are free to copy and paste from the prerelease page, if we provide a download file, we would have to determine versioning, packaging, validation, etc. Due to the rapid evolution of these terms, we prefer users to consult the prerelease page directly for the most up-to-date information.

Q: To confirm, SARS coronavirus 2 LOINC codes will not be released until June?
A: Correct, they will remain in a prerelease state until the official LOINC release in June.

Q: Will we get an automated email when new vendors agree to have their LOINCs posted on SARS interest page, or is that only when new LOINCs are posted on the pre-release?
A: The automated email is only sent when Special Use codes are updated or new Special Use codes are added to the prerelease page.

TERMINOLOGY/MAPPING

Q: Can you verify the LOINC code for the SARS-CoV-2 Egene for qualitative to be 94315.9? What is the qualitative LOINC code for the SARS-CoV-c ORF1Lab Region?
A: There are multiple codes for qualitative SARS-CoV-2 E gene and ORF1ab region testing depending on the specimen type. Please see our prerelease or FAQ page to find the appropriate terms.

Q: Which pre-existing LOINC codes do you recommend we use for COV2 testing? We have chosen not to report with the pre-release codes until formal
A: There are no existing LOINC terms that are specific for SARS-CoV-2, so our recommendation is to use the prerelease codes that are created specifically for SARS-CoV-2 testing. As the prerelease codes are subject to change, they must be re-imported with the full LOINC release in June 2020 to ensure that all of the changes are included.

Q: There are available multiple COVID-19 Diagnostic Tests for the virus and ab responses that will have different positive and negative predictive values (sensitivity and specificity). If the codes of these different test kits are not captured in the EHRs, we will be totally unable to make these important assessments.
A: We highly recommend that information about the specific test kit that was used be stored and communicated with the test result, along with granular information about the specimen and any other information that is not sufficiently captured by the LOINC term. As you know, positive and negative predictive values (PPV and NPV, respectively) are a function not only of the test, but also the population being tested. For example, the same test would have a lower PPV in a population with low prevalence of disease. As a result, it is difficult to encode those distinctions in the lab terminology. That being said, if there are identifiable methods that clearly and reliably show different sensitivity or specificity, LOINC will differentiate those by method. At this point, there are hundreds of kits currently in use or being developed for SARS coronavirus 2, and
LOINC will not attempt to distinguish between various kits that use similar methodology unless there are established comparative data. It is understood that comparative assessment of individual test kits that are otherwise identical by the 6 primary LOINC axes will sometimes need to be made (Common in laboratory medicine practice).

Q: It’s amazing the work that has been accomplished in such a short time. From a molecular biological standpoint, are every entrant’s sequence ensured to be 100% unique and separate from an all known DNA sequences? Are the LOINC codes being created all based on location from a specific standard point such as the +1 replication starting position? Will this point be part of the probe.amp.1 or .1234, this will make it easier for users to know the specific region being amplified?
   A: One of the major objectives of LOINC is to facilitate interoperability of clinical results. This question gets to how specific LOINC codes should be to make appropriate clinical distinctions between tests, yet not be so specific that interoperability is compromised. At this time, LOINC will distinguish tests to the level of gene target, but not to the specific position, primer, or probe.

Q: The PUI request of data elements was a general request? not specific to SARS-CoV-2, correct?
   A: We are working with the CDC to represent the CDC SARS-CoV-2 PUI and Case Report form.

Q: If assay can pick up IgA (i.e. completely isotype nonspecific can pick up IgA or IgM or IgG) can we use the LOINC code IgG+IgM?
   A: The LOINC IgG+IgM code should ONLY be used for tests that can detect both IgG and IgM but not differentiate between them. For a test that detects all antibody classes, it is advisable to use a general “Ab” term. Similarly, the IgG+IgM code should not be used for tests that only detect IgG, or IgM.

Q: Are actual critical reagents also getting codes i.e. oligos used for detection in PCR?
   A: Reagents such as specific oligonucleotide primers are not typically assigned LOINC codes.

Q: Why are you creating codes with respiratory system when you strongly recommend upper and lower respiratory codes in the past? Thank you
   A: At the current time, the tests we have been coding as respiratory can be used for both upper and lower respiratory specimens. LOINC prefers to code specifically to upper or lower respiratory when there is a demonstrable clinical distinction between results based on those specimens. When and if that becomes clear in the case of SARS coronavirus 2, we would want to make that distinction as well.

Q: Is there any suggestion to use LOINC codes to codify sections? or documents?
   A: There has been some discussion about creating LOINC terms for COVID19 - specific documents. We are currently assessing what the needs and consensus would be for these document types. The section codes used inside these documents would likely be most of the same codes as those used in existing document types.

Q: When it is [sic] appropriate to use the special SARS email routing to LOINC vs the routine emails/submission process to get new assay information to the team?
   A: SARS email routing should be used for questions and comments related to SARS coronavirus 2 LOINC terms. The routine submission process should be used for all new LOINC term requests.

LOINC GROUPS AND FHIR TERMINOLOGY SERVICES
Q: Please talk about the special use value set more. Where are they? When are they used? Are they in FHIR?
What is the use of these value sets? What is the intent of these value sets?

A: We are considering making a FHIR ValueSet containing all of the prerelease Special Use codes that would be available prior to the June release. This is not available yet, but would be used by anyone wanting to access the Special Use prerelease codes using LOINC FHIR terminology services rather than from the prerelease page.

Q: When will the FHIR LG code be issued for SARS-CoV-2?

A: SARS-CoV-2 Groups will be included in the official LOINC release in June 2020. We will likely have one Group that includes all SARS-CoV-2 terms (including molecular, antigen, and antibody), as well as smaller groups that vary by the Component, Method, etc.

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**COLLABORATION WITH OTHER ORGANIZATIONS**

Q: It is unclear to me what exactly is the coordination boundaries agreed. (and coordinated)
The statement at [http://www.snomed.org/news-and-events/articles/snomed-loinc-coronavirus-collaboration](http://www.snomed.org/news-and-events/articles/snomed-loinc-coronavirus-collaboration) is missing crucial details. Term for COVID19 diseases (as Loinc Part) is in both LOINC and SNOMED CT. (duplication)

A: We are currently working on a new agreement with SNOMED International, the details of which have not been finalized. In general, LOINC terms are defined by specific combinations of LOINC Parts, and cannot be defined without the existence of LOINC Parts. Therefore, there will always be some overlap between LOINC Parts and SNOMED CT concepts, such as for SARS coronavírus 2. SNOMED CT has a concept for the virus in the organism hierarchy, and LOINC has a Component Part for the same. We will provide a mapping from one to the other in the Part file in the June 2020 LOINC release. However, LOINC Parts are not meant to be used apart from LOINC terms, except to help organize and facilitate the use of LOINC terms. Although some LOINC Parts may be able to stand on their own, others are ambiguous without the context of the LOINC term. SNOMED CT concepts are individually defined. We do not have a LOINC Part for COVID-19.

Q: Is there any discussion planned for public health using the eICR/eCR standard to push new reportable LOINC codes quickly and facilitate fast electronic resulting?

A: (from Andrea Pitkus) The best contact is Laura Conn of CDC who is a member of the PHER workgroup and helped create the eCR specification.

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**QUESTIONS FOR GUEST SPEAKERS**

Q: Is APHL coordinating test results propagation directly to patients, or will it always come through EHRs. Some initial test results were just delivered by a phone call. Not all tests may originate from health care provider.
A: We have sent this question to Riki with APHL and are awaiting her response. We will update this information as soon as we have it available.

Q: How does AIMS handle identity? Assume there is still Personally Identifiable Information (PII) info attached. Is this suitable to rapid results delivery to patients?
   A: We have sent this question to Riki with APHL and are awaiting her response. We will update this information as soon as we have it available.

Q: For SNOMED, is there a need to reconcile COVID-19 concepts between international edition and the national extensions and if so when might that work take place? (The reasons I ask is because I think I saw some national extension concepts being published out on the FHIR ZUPLIP chat.)
   A: (from Jim Case) SNOMED International has solicited COVID_19 related content from national extensions and is reviewing submissions for international relevance and potential addition to the SNOMED CT International release July 2020. A number of new concepts have already been added and it is expected all internationally relevant concepts will be available in July.

Q: I've been hearing clinical decision support developers use vetted value sets like NLM's curated VSAC and to a lesser extent CDC's PHIN VADS. CDS templates have to be approved by local review boards, and they often look to these levels for pre-vetted information. There has been a notable lag during this pandemic to see a steward upload value sets, probably no fault for everyone who's trying to deal with other matters. Does ONC have the authority/governance to help improve this portion of communication in the future?
   A: One of the members on the ONC team has been able to help upload/update some of the VSAC value sets. If you would like to send the information to ONC, they can help upload/update the information. Please continue to send information that you find needs updated, and they will work to get that completed as soon as possible.

Q: In order to know how many negatives there are to create Stan's display, are ALL tests being reported to public health?
   A: All major labs used in Utah are reporting to the Utah Department of Health. They report all results, both positive and negative. There are a few small private labs that are not reporting results to the State.

Q: What would other institutions have to do to be able to pull together the same type of information that Intermountain has? I assume more than a parsing of LOINC and SNOMED-CT codes.
   A: The integrated dashboard depends on a lot of other systems besides lab testing systems - those that track beds, respirators, and several others. If you would like more information, Dr. Huff can route the question to the creators of the data for a more detailed answer.

Q: Why are you using a LOINC, rather than a SNOMED, for the specimen source?
   A: Specimen information can be sent many different ways, including in the HL7 v2 SPM segment, the FHIR Specimen resource, or as a separate observation. When sending as a separate observations, LOINC 31208-2 Specimen source (https://loinc.org/31208-2) and LOINC 66746-9 Specimen type (https://loinc.org/66746-9/) are used for the observations, e.g., in HL7 v2 OBX-3. The observation results should be coded using SNOMED CT when possible, regardless of whether it is being transmitted in SPM, the FHIR Specimen resource, or as separate observations.
Andrea Pitkus
International IVD vendors have requested LOINCs

Andrea Pitkus
Biomerieux advertises on their Italian page, the availability of their diagnostic tests for SARS-CoV-2: https://www.biomerieux.it/first-3-diagnostic-tests-sars-cov-2-coronavirus-available-biomerieux. Some IVD LOINCs are listed here: https://loinc.org/sars-coronavirus-2/

Andrea Pitkus
Preferably an IVD vendor/manufacturer should work with Regenstrief as they know how their test is performed. However, many laboratories may develop their own testing (known as Laboratory Developed Tests in US) and should also request, especially if they have modified an IVD test (perhaps for different specimens), so LOINCs are available for these distinctions.

Pam Banning
I'm learning some research labs are reflexing positive RNA detection onto full sequencing, to be able to record any newer mutations as it has reached the US. Will work further to see about getting them to submit; I imagine this is valuable epidemiologic information

Andrea Pitkus
Notification of pos results may be coming from the patient's provider or the jurisdictional health dept (state, county, etc.) in the US. Sometimes it's both, but rather get multiple notifications, than none.

Andrea Pitkus
As a reminder, anyone collecting specimens for COVID-19 testing, needs to provide the performing laboratory with patient demographics and contact information with the order, so it can be provided to the public health jurisdictions for positive cases reported via ELR. Public Health needs these details for patient follow up. Delays are resulting when this is not received by the performing lab and included in ELR reporting. It's critical to get this message to all specimen collection entities including drive up testing.

Pam Banning
General comment; the model of 31208-2 for a specimen source field in OBX3 and an XXX LOINC in a separate field is very very common. We are changing recommendations to IVD vendors we encounter to only provide specimen specific LOINCs. This is in response to conversations from Ana and Mike at FDA. There is overlap in systems of NASPH and respiratory.upper LOINCs for non-SARS-CoV-2 measurements. We aren't suggesting the "roll up" respiratory.upper systems to IVD. In the past few decades, 3M hasn't asked a client to change their LIS set up. LOINC accommodates multiple models. However, in 2020 with IVD mapping being the "headwaters" for the assay, it becomes a recommendation on how to build the LIS. In time, we'll see the model shift.

Andrea Pitkus
To add what Pam wrote, LOINC is used for the question on specimen source, but it's correct that the specimen type (i.e. swab) would be in the SPM 4 field mapped to a SCT specimen hierarchy code, while
the Specimen Source would be in the SPM 8 field (i.e. nasopharyngeal, left nares) and mapped to the SCT Anatomic Site hierarchy term. Complete details for ELR reporting in the ELR guide.