COVID-19 Evidence Accelerator Collaborative

Diagnostics Evidence Accelerator #48

Thursday, June 16, 2022, 12-1 PM ET

Call Summary

Introduction to Diagnostics Evidence Accelerator Meeting #48

This week's Diagnostics Evidence Accelerator meeting consisted of 2 presentation:

1. Real-world assessment of diagnostic and serologic testing of SARS-CoV-2 (Drs. Garrett Jenkinson and Benjamin Pollock, Yale-Mayo Clinic CERSI)
2. Steps Towards Laboratory Interoperability for RWD/RWE (Dr. Andrea Pitkus, University of Wisconsin-Madison)

Real-world assessment of diagnostic and serologic testing of SARS-CoV-2 (Drs. Garrett Jenkinson and Benjamin Pollock, Yale-Mayo Clinic CERSI)

Mayo Clinic, along with Yale University, through the Center for Excellence in Regulatory Science and Innovation (CERSI) program, identified patients who were diagnosed with COVID-19 at three Mayo Clinic sites and Yale University. These data were collected via the Mayo Clinic Laboratory Information System (LIS) (Figure 1) which is well integrated. However, with the different COVID-19 tests that were rolled out at the beginning of the pandemic, he LIS required significant IT staff efforts to keep up with all the tests administered and the constantly evolving testing landscape.

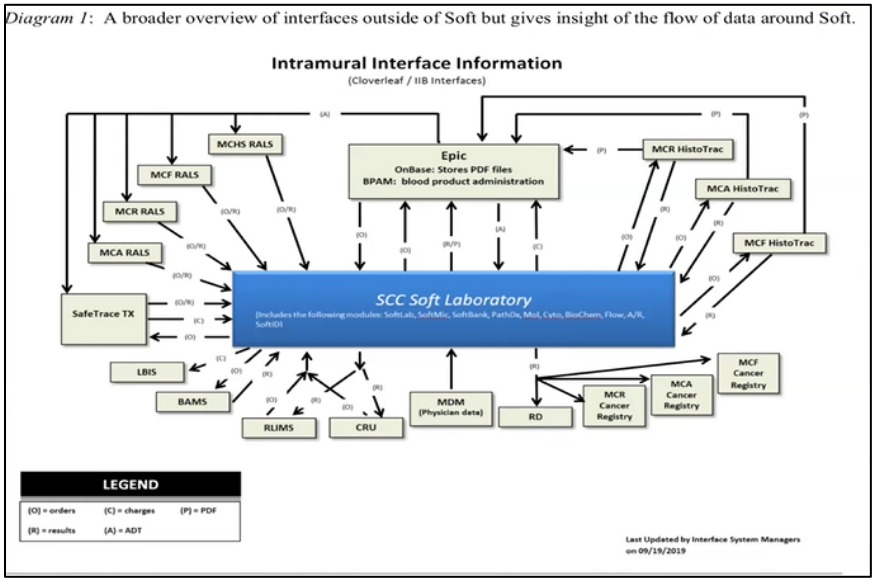

Figure 1: Mayo Clinic Laboratory Information System.

To summarize the findings from the study, the team has published a paper titled *A multicenter evaluation of computable phenotyping approaches for SARS-CoV-2 infection and COVID-19 hospitalizations* to discuss their COVID-19 patient cohort. They analyzed what real-world data (RWD) they had in terms of informatics data via testing and diagnostics on patients. The results showed that 55% of patients had a PCR/antigen positive test and a principal diagnosis. 19% of patients had only the principal diagnosis and 12% of patients only had a PCR/antigen positive test. The authors displayed the data across the different Mayo Clinic sites also to show how the COVID-19 cohorts were documented. The clinical site at Arizona captured both the diagnosis code and test results, however in Minnesota and Florida, there were more PCR/antigen test results due to more outpatient clinical sites. Sometimes, these test results do not make it into the electronic health record (EHR) for documentation. The second part of the study discussed diagnosis codes for hospitalized patients. The authors found that if COVID-19 is the secondary diagnosis, there was higher observed mortality compared to COVID-19 as the primary diagnosis. The overall findings showed that "In two large, integrated health systems with multiple care delivery networks and associated outpatient clinics, COVID-19 diagnosis codes alone were frequently not consistent with case identification and epidemiological surveillance of SARS-CoV-2 infection based on antigen/PCR testing, with significant variation across two major health systems."

In the second study, Mayo Clinic, along with Yale University, looked at informatics driven real-world analysis of SARS-CoV-2 serologic response and in-vitro diagnostic accuracy. The results from this study provided valuable information from a real-world data set to better understand serologic results. Additionally, the team will be able to provide feedback on the use of real-world data to assess the accuracy of diagnostic tests, and gain valuable insights on the accuracy of commercial serologic assays. The study design took the target cohort (from study 1) and then separated them out into the outcome's cohort (antibody positive and antibody negative).

The results showed:

- Results correlated well between Mayo Clinic and Yale, with the primary variation being the relationship between symptoms and comorbidities with serologic result
- Phenotype selection can impact "accuracy" of downstream serological results
- As demonstrated in other studies, serologic specimens taken soon after first PCR positive test have higher likelihood of being negative
- Increased comorbidity burden was associated with higher likelihood of negative serology result (but only significant in Yale cohort)
- Symptomatic patients more likely to have a subsequent positive serology test (but only significant in Yale cohort)
- Different assay manufacturers were associated with increased or decreased likelihood of a positive serologic assay, but difficult to attribute to 'real-world performance' based on temporal variations in testing patterns

The research team is also looked at data from COVID-19 vaccine. In summary, there were a variety of EHR, testing (PCR & serology), and vaccination data is likely available most institutions. The research team were able to descriptively share real-world results of these testing/diagnostic data, NLP data showed potential. The major limitations of the data set were linkage, completeness, and reasons for testing.

Steps Towards Laboratory Interoperability for RWD/RWE (Dr. Andrea Pitkus, University of Wisconsin-Madison)

The current landscape of laboratory interoperability consists of laboratory data exchanged with IVD test systems, Laboratory Information System (LIS), electronic health record (EHR), public health LIMS/ NHSN, federal agencies and other information systems.. Figure 2 summarizes the current landscape of the laboratory interoperability.

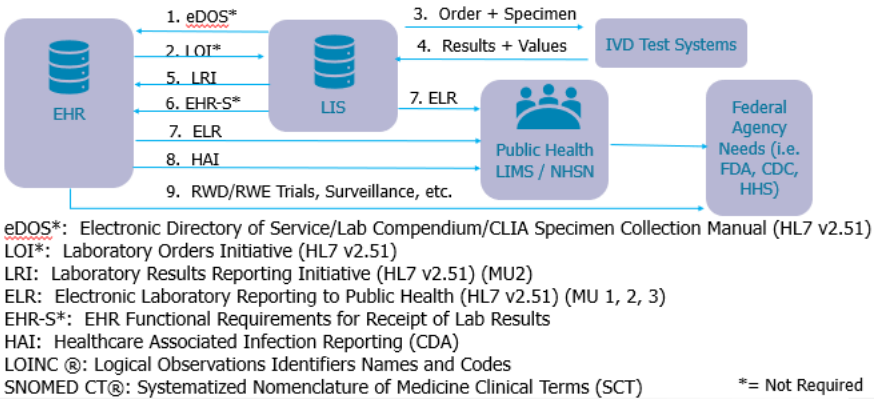

Figure 2: Current landscape of laboratory interoperability.

Additionally, there are many HL7 guides available for reference and implementaters. However, due to different implementation requirements, guidance may vary across information systems.. LIS is considered a "hub of lab data". Receivers of LIS lab data include hospital EHRs, clinic EHRs, other lab LISs & reference labs, research data warehouses (RWD/RWE), nursing homes/rehab (SNF/LTC), community testing sites, HIEs, and Public Health.

A food analogy comparing laboratory interoperability to a cheeseburger was shared during the presentation. For example, someone at a burger restaurant will not be able to order tacos because tacos are not on the menu and the restaurant will not have the materials to make it. This is similar to a physician only being able to order tests that are on a specific laboratory's 'test menu'. Additionally, if someone wants a cheeseburger, their menu options may vary based on the restaurant's choices of ingredients. This is similar to differences in how tests are performed amongst different IVD test vendor systems. For example, different laboratories may map to different LOINC codes for a test, reflecting the IVD differences. .

Additionally, there might be different perspectives of how and where the lab data is used. Depending on the different view (e.g., IVD vendor, regulatory, provider, laboratory, or public health), the lab data may be structured in different ways. Therefore, the goal is to have computer actionable data that is interoperable with complete meaning. In order for the data to be usable, the data needs to be

1. Electronic;
2. Discretely Modeled. PDF/Text Blob reports are human readable, but not very computer processable;
3. Encoded with standard code systems like LOINC for lab orders and results and SNOMED CT for qualitative result values, organisms, specimen types, specimen sources, etc.;
4. Messaged with proper HL7 message structure and interfaces connecting systems; and
5. Maintained with test updates, coding updates, new message functionality, etc.

If the data is able to accomplish the above, then computers can utilize lab data better in queries, reports, etc. Additionally, the data will be available in downstream systems. This will enable physicians to view usable results. Also, encoding and structuring lab data at its point of origin reduces manual mapping outside the lab, and allows data to flow to downstream systems reducing potential for errors to be introduced later (a patient safety and data quality issue). Finally, the data will be available for RWD/RWE, trial, research, etc.

Next Steps

- Continue making data connections through the Evidence Accelerator and through www.EvidenceAccelerator.org.

Next Meeting: Thursday, July 21, 2022 12-1 pm ET