**Orders & Observations Conference Call**

**August 30, 2017**

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**WebURL: https://join.me/vernetzt.us**

**Attendees:**

|  |  |  |
| --- | --- | --- |
|  | Name | Organization |
| 1 | Sandy Jones | CDC |
| 2 | Kathy Walsh | LabCorp |
| 3 | Riki Merrick | Vernetzt, LLC / APHL |
| 4 | Ted Klein | Klein Consulting |
| 5 | JD Nolen |  |
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 Regrets:

**Co-Chair**: Riki Merrick

**Scribe:** Riki Merrick

Agenda/Minutes:

1. Agenda Review
2. Approve minutes = postpone till later
	1. from March 22, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20170322_ConCall.docx>
	2. From May 3, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20170503_ConCall.docx>
	3. From May 17, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20170517_ConCall.docx>
	4. From June7, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20170607_ConCall.docx>
	5. From June 14, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_201706014_ConCall.docx>
	6. From June 21, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_201706021ConCall.docx>
	7. From June 28, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_201706028_ConCall.docx>
	8. No quorum July 5, 2017
	9. From July 12, 2017: [http://wiki.hl7.org/index.php?title=File:SPM\_Minutes\_20170712\_ConCall.docx](http://wiki.hl7.org/index.php?title=File:SPM_Minutes_201706028_ConCall.docx)
	10. No quorum July 19, 2017
	11. From July 26, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20170726_ConCall.docx>
	12. From August 2, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20170802_ConCall.docx>
	13. No Call August 8, 2017
	14. From August 2, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20170802_ConCall.docx>
	15. From August 23, 2017: <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_201708023_ConCall.docx>
3. Specimen DAM ballot reconciliation

Specimen ID handling etc

NAACCR **draft document** to set the stage (DO NOT DISTRIBUTE): 

Pathologist collects samples at the lab, sometimes samples, like skin scrapes or stamps are collected at dermatologist office and sent to the first lab

Each lab assigns a specimen ID – some labs do not assign their own IDs – depends if they do testing on the sample or just forward to a reference lab sometimes.

Sent to internal lab as well as one or more external labs

Specimen IDs on orders could be barcoded, handwritten, phone orders as well as electronic

Each lab in turn assigns their own ID – and captures only the ID of the lab that sends to them directly, not all the prior IDs.

Cancer registry is expected to get 1 report with consolidated results, but they could come in multiple messages – example: CA requires each testing lab to report; in CA they are ONLY allowing use of NPI for ordering provider - at least that is covered as a standard ID

Patient ID may or may not be the same on these reports and also may not be unique across the state, there is currently no master patient index – so hard to match reports on different samples to the same patient sometimes

Example is TN lab that does biomarker testing sends their results directly to CA cancer registry – often before the final consolidated report gets sent – deduplication is needed here

Suggestion to use SPM-29 (Specimen Child Role, CWE) – not a good fit and not the intent of the field

CA registry is using v2.5.1 HL7 ORU^R01 messages - there is resistance to pre-adopt SPM-30 (Accession number, CX) and SPM-31 (other specimen ID, CX)

The community does not support proper HL7 batch files – though often they send concatenated HL7 message files without the proper segments – sent daily or weekly; no ACKs either, so that errors need to be handled manually

In addition to knowing the specimen IDs from all prior labs do we also need to provide information on original vs current sample type (SPM-4 – SPM-10 type attributes) = that is currently sent in narrative text – not separately LOINC coded as part of the entire pathology report

There are a few that send the more structured report, where at least the different narrative sections are labeled and provided in a standard order, and then there are very few that support fully structured synoptic reports based on the CAP electronic Cancer Checklists (eCC)

In synoptic report we have type = tissue, then the location is fully described, including laterality, clock wise positions, margin descriptions and relationship of sample to them; these are also encoded using SCT, TNM CAP codes – that so far only used in 12 facilities in Canada (Ontario and Manitoba) – in CA mostly narrative reports

There is also overlap with the reporting of biomarkers between AP and CP lab reports, as well as the lab report requirements from Meaningful Use: discrete data reporting for Healthcare Acquired Infections (HAI) in AP samples

Have done a formal comparison to LRI and the current NAACCR guide – goal is to harmonize as part of the 2010 update

Registries currently ONLY consume ORU messages, not OML messages

The cancer registries would like a structured consolidated case report for each patient from a single source

How to best pass on a case ID through all the orders – issue is also that not all are electronic – most are paper or verbal – also results often are still faxed or paper

Accession ID is describing different things in different organizations – sometimes the sample, sometimes the order, sometimes the case – not reliable for use

Do we also need to convey the related block and slide ID of a derived sample? So far the lowest level that should be reported is block ID, but need to have information about the relationship of said sample to tumor margins

In CA regulation now requires use of HL7 message – no longer emailing of reports – but those are still sent as blobs in OBX-5 in most cases – or as ED even

Second page: describes the different type of AP reports – only 1 synoptic report has been implemented so far – and it’s not the full eCC defiend yet – SDC is working on migrating eCC into FHIR

All reports, regardless of format used can have these types:
supplements / can be corrected or amended or appended / or can have additional reports associated with them – e.g. biomarker studies, radiological studies etc.

The IDs that are assigned are dependent on the workflow used for each of the samples

Require support for SPM-3 for ALL samples, so at least you get the immediate parent

The specimen DAM covers: specimen ID, parent specimen IDs, accession ID

Require the assigning authority – for example the OID of the Lab or its LIS as the root of all specimen IDs to ensure global uniqueness – there was some discussion on the research side of things how to work with masking (opaque ID required)

How is the linkage between send-out lab and submitter handled?

Specimen ID is assigned and printed on label and entered in LIS, then sent to lab#2 – the receiving system keeps the placer ID and assigns its own ID to the sample

Lab 2 makes blocks, each with their own ID, BUT they have to look up information about the parent as part of the workflow

There was some discussion about potentially concatenating all IDs into a single ID that gets passed on to each consecutive lab, but that will blow out the barcode limits pretty fast – so not an option

RULES:

In the upstream report ALWAYS INCLUDE:

* Ensure ALL IDs are 2 parts = assigning authority (root) and ID (extension)
* SPM-3 (Parent Specimen ID, EIP = placer parent and filler parent ID)
* SPM-31 (additional Specimen IDs, CX) – require use of typecode in addition to ID and assigning authority, so that you can also cover block and slide IDs, if needed

**NEXT CALL 9/6/2017 4 – 5 PM EDT =** FHIM comparison to DAM and SPM-13 and the pooled vs grouped samples

Call adjourned 5:02 PM EDT

1. Resources:
	1. Link to Specimen DAM: <http://wiki.hl7.org/index.php?title=Specimen>