**Orders & Observations Conference Call**

**July 12, 2017**

**+1 770 657 9270, Passcode: 398652#**

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

**Attendees:**

|  |  |  |
| --- | --- | --- |
|  | Name | Organization |
| 1 | Kathy Walsh | LabCorp |
| 2 | Riki Merrick | Vernetzt, LCC / APHL |
| 3 | Mike Martin |  |
| 4 | JD Nolen | TBD |
| 5 | Ron van Duyne | CDC |
| 6 | Raj Dash | Duke / CAP |
| 7 |  |  |
| 8 |  |  |
| 9 |  |  |
| 10 |  |  |
| 11 |  |  |
| 12 |  |  |

 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
3. Specimen DAM ballot reconciliation – see spreadsheet: <http://wiki.hl7.org/index.php?title=File:Ballotcomments_V3_DAM_SPECIMEN_R2_I1_2017MAY_Consolidated.xlsx>

#45: Update definition for dimensions - Motion to find persuasive with mod - change definition for horizontal dimension to: "The point on the horizontal dimension (width) of the defined object." Change the name horizontal dimension (x) to "width (x)", change the name vertical dimension (y) to "depth (y)", change the name vertical dimension (z) to "height (z)" and make similar definitions for depth (y) and height (z). – Kathy, JD, no further discussion, against: 0, abstain:0, in favor: 5

#65: handling of herds – email from Mike Martin (7/10/2017): There are two scenarios that apply.

1. A number of specimens are taken from members of a herd or flock and pooled for testing. In that case each individual is a Subject but that would be dealt with via parent specimens – pooled specimen relationships.

2. A number of samples are taken from anonymous members of a herd (flock usually) and pooled “in the field.” The way we have dealt with that is to treat the flock as if it was “THE subject.” That includes using flock identifiers as “patient identifiers” and so on. The one issue that comes up is annotating somewhere the number of individuals in the pool (important statistically).

For #1, if you address pooling from parent specimens, there shouldn’t be an issue. For #2 the question would be whether treating a herd as a single subject is really right or a kluge that should be fixed. The key facts for us would be the size of the herd (somehow incorporated into non-human living subject) and number in the sample (which would I guess have to be in the Specimen somewhere).

I’m so used to the “herd as subject” view that I guess I would like to see herd size as an attribute of non-human living subject and number of individuals represented in sample in Specimen. But that might drive most folks crazy.

Discussion: For scenario #2 need to know how many individuals were in the herd, when not all individuals are tracked – where would we carry that?

Motion to find not persuasive - verified per email above; we can with the existing elements in DAM cover the scenarios described above - for the purpose of the DAM a non-human living subject could be a herd - as that is treated as 1 in the herd sampling case, where individuals are not captured. allowing for a count of individuals included in the pool using Specimen.SpecimenGroupCount in the DAM. Kathy, Mike, no further discussion, against: 0, abstain:0, in favor: 5

POST CALL EMAIL FROM Mike Martin: 7.4.3.13 SPM-13 Grouped Specimen Count (NM) 01763 Definition: This field refers to the number of individual specimens of a particular type represented by this instance of a specimen. The use of this field is restricted to specimens upon which all specimen related attributes are identical. This field would only be valued if the specimen role attribute has the value "G". - Specimen.SpecimenGroupCount is mapped to SPM-13; the IHE profile uses SPM-13, so we may need to revisit there, too!

#19: The barcodes are actual genetic sequences that are specific for each patient (A/C/G/T in 8 base pairs), so they show up in the results and you have a linkage between the barcode sequence and the subject – each sample is placed in its own well, so not really a pooled sample, more of a run in clin chemistry – Raj will do more research before we vote

#12: Per JD’s homework the Specimen DAM, we are lacking spots for device identifier, serial number, and donation identification number (page 1). So ballot-wise I say we are good, but we might want to ponder those other fields and how we could tackle them (either formally or via an IG).

These IDs are important in the donation tracking scenario – maybe we need to add that as a use case to the DAM for chain of custody – event tracking? Use case would be an implanted hip joint is taken back out – that would essentially create 2 subjects – the patient and the hip joint? OR is the hip joint the specimen? If that is the case we can use speicmenID for serial and model number

POSTCALL EMAIL FROM HANS: Just a quick note to use http://www.hl7.org/documentcenter/public/wg/orders/Harmonization\_Pattern\_for\_Unique\_Device\_Identifiers\_R3\_20160314.docx for the Harmonization pattern

**Next call – 7/19/2017**

1. Resources:
	1. Link to BRIDG model: <http://bridgmodel.nci.nih.gov/files/BRIDG_Model_4.0_html/index.htm> - chose VIEW:BSP - biospecimen
	2. Link to Specimen DAM: <http://wiki.hl7.org/index.php?title=Specimen> – scroll to bottom for image