**Specimen Project Conference Call**

**7 March 2013**

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**Attendees:**

|  |  |
| --- | --- |
| Name | Organization |
| Lorraine Constable | Constable Consulting |
| Riki Merrick | IConnect |
| Ron van Duyne | CDC |
| Margaret Marshburn | CDC |
| Jim Case | NLM |
| Diane Vaughan | Kaiser Permanente |
| Dmytro Rud |  |
| Lori Dieterle | Kaiser Permanente |

**Co-Chair**: Lorraine Constable

**Scribe:** Riki Merrick

**Minutes**

Approve Meeting minutes from 1/31/ and 2/14 – approve as distributed

Motion by Riki Merrick, Ron van Duyne, No further discussion,

Against: 0, Abstain:1, In Favour: 6

**Model Review**

Reviewed current state of modeling effort:

* Last discussed specimen container – would be good to review with Lori
* Looking at v2.x fields mapping
* Updated model was posted to the wiki

Diane Vaughan was lead on specimen tracking project

Lorraine gave overview of project – starting with the HL7 OO wiki page

* Model is in gForge
* Started from NCI LSDAM logical model
* Building conceptual level model with attributes at the higher level

In the model:

* First use case was on genomic specimen handling and processing requirement
* Specimen collection is performed on subject
* Which can be a living subject or a material – could just change to non-human living subject to cover plants
* Currently have specimenID on specimen, but also have ID on container [0..\*] = lab automation, container ID, Specimen ID
* Related project is AP specimenID project – need to harmonize
* Still not fleshed out the container - carrier – storage equipment – which attributes we need on what type
* We decided to have the container = closest to the specimen
* Carrier would be a rack, slide books, tray – this is recursive
* Need to still work on the definitions for all of the attributes – so far only have drafts, or stubs…

Discussion on model classes:

Diane: Specimen container carrier is that referring to the original block it’s being put on?

* Main specimen is the top point to which the children refer to
* Aliquots are also contained in a container
* In many spaces – automated lab – separately IDs the container, and that is what is tracked – need to be tracking both
* Do we need to a container ID attribute to separate container ID, specimenID, lab automation ID

Why create a separate class for biological specimen list, just move them all into specimen, but make them RE, that way can cover both biologic and environmental types

nameCode is CD datatype – would need to define the concept domains for the codes – not necessarily the value set – is the name the specimen type?

* What is the difference between nameCode and typeCode?
* TypeCode used to be the same as classCode in HL7 – it assists in creating the concept domain for the subtypes
* What is the value of typeCode, subtypeCode and nameCode – hierarchical representation of the same concept – may not need all three, especially if binding to hierarchical terminology like SNOMED
* Specimen name = description
* Origin – duplicative of typeCode (as defined in HL7), so make origin an alias of type code and copy definition over.

If it is a derived specimen it has a parent identifier

Still need to build out the attributes for material and non-human living subject

formCode is also in material class and biologic specimen – if we can generalize, then should be in specimen class

functiontypeCode definition is confusing – no reference to function in specimen in universal CMET – should we remove it for now, unless a use case needs it

add description to specimen attributes and effective range, then delete biologic specimen

out of sequence call this week, so next call back to the original schedule:3/14/2013

Next call look at the HL7 v2.x fields