Exported to PDF April 5, 2016

HL7 Clinical Genomics Weekly Call - Wed Mar 29, 2016

Attendees

1. Amnon Shabo (Shvo) - Philips - amnon.shvo@gmail.com
2. Jonathan Holt (SeqTechDx) jholt@seqtechdx.com
3. Bob Freimuth - Mayo Clinic - freimuth . robert at mayo . edu
4. David Kreda - david.kreda@gmail.com
5. Gaston Fiore - BCH - gaston.fiore@gmail.com
6. Siew Lam - Intermountain Healthcare - siew.lam@imail.org
7. Mollie Ullman-Cullere - mollie.ullmancullere@gmail.com
8. Jeremy Warner - Vanderbilt University - jeremy.warner@vanderbilt.edu
9. Joseph Kane - Epic - jkane@epic.com
10. Kevin Power - Cerner - kpower@cerner.com
11. Andrea Pitkus - IMO - apitkus@imo-online.com
12. Bret Heale - Intermountain Healthcare/ University Utah - bheale@gmail.com
13. Jennifer Brush - ESAC (SDC Project Manager) - jennifer.brush@esacinc.com
14. Vijay Shah - JBS (SDC Technical Lead) - vshah@jbsinternational.com
15. Perri Smith - Accenture (SDC) perri.smith@accenturefederal.com
16. Perry Mar - Partners HealthCare System - pmar@partners.org
17. Joey Yang- HFUT -jiaoyun@hfut.edu.cn
18. Ning An - HFUT - ning.g.an@acm.org
19. Anwaruddin Mohammad - Oracle - anwaruddin.mohammad@oracle.com
20. Terry McDonnell - Syapse - terrym@syapse.com
21. Brett johnson - icanbrj@gmail.com
22. Larry Babb - lbabb@geneinsight.com

Discussion -

- Minutes approval (Mar 15 and Mar 29)
  - http://wiki.hl7.org/index.php?title=File:HL7_CG_20160315.pdf
  - Recorded audio at http://www.hl7.org/documentcenter/public/wg/clingenomics/minutes/HL7%20CG%20call%2020150315.mp3
  - Motion to approve
    - motion= / Bob F. second= Melinda Owens
    - Yea/Nay-0/Abstain- Perry Mar, VJ, Mollie, Perri Smith, Gil, Jenny = 7 Nay and 9 approval

- Updates from external efforts (GA4GH, ClinGen/ClinVar, IOM, etc)
  - ClinGen - helping Stanford team model variant assessment

- Additional information for clinicians tracking knowledge of pathogenicity independent of patient data and how this would be mapped into ClinVar
- Stanford - Gene Curation App & Variant Curation App - open for ClinGen groups - unsure about broader release likely requires additional work
- Clem commented that this is still early e.g. unsure about what id's to grab etc.. allelles can be simple (single variant) or complex in the current vision of the ClinGen Allele registry
- Larry commented trying to work on content as well as structure e.g. deciding if the Monarch initiative's ontology should be used for expression(ontology for description see here for more information - https://monarchinitiative.org/)

- GA4GH
  - Gil - Genetics/Genomics
    - Conference end of April in Washington and May 17 as connectathon
    - Interested in getting involved - mappings and integrations with FHIR
    - Clem - confirmation not to have GA4GH not be a field name as in a spec, but has all the elements needed to access as well as access any public repositories - yes this was confirmed by Gil
    - Need to make sure NCBI, EBI, and COSMIC work as well - make sure we aren't narrowing scope to one actor
  - Grant - Family History
    - extending to family history - writing requirements for a patient consent management system for patient to define sharing of family history data
    - Kevin Hughes/Brett J- converter to translate pedigree model in v3 into FHIR and into format to go into Intermountain FH tool (as first pass file) with goal to test data flow of FHIR message to integrate into agnostic EHR
    - Also capable of working with Risk Analysis web service for algorithmic processing and triage of patients - making sure everything works and no loss of information
    - Clem - Kevin confirmed keeping modular format
- FHIR connectathon
  - No one currently signed up for Family History - Grant considering Intermountain
  - To sign-up edit wiki site or contact Gil and he'll edit wiki site accordingly
    - Log-in required so Gil can edit for you

- IOM Updates
  - Grant - still putting teams together currently 20 people from 5-6 EHR vendors/labs to hear presentation and form pilot teams
- CQF (clinical quality framework) - FHIR (http://hl7-fhir.github.io/cqif/cqif.html)
  - Considering a pilot of the IOM high-level guide to CDS pharmacogenomics
    - Published in Dec
    - Ken Kawamoto HL7 co-chair of CDS participates
    - Desire to work with the IOM group to "quickly" pilot any future CDS IGs in FHIR using CQF.
  - Profile on current build for managing knowledge for CDS
  - CG's should consider this broader approach
    - Define use cases and start tackling

- Can we discuss the proposal that I sent via email regarding 1..* for referenceSeqId before the code freeze? (Jonathan)
  - **Current:**
    - { "referenceSeq": [{ "chromosome": { "coding": [{ "code": "7" }] }, "genomeBuild": "GRCh37", "windowStart": 55227970, "windowEnd": 55227980 }] }

rather, we should use a versioned codeable concept for chromosome:

- Example - #1:
  - { "referenceSeq": [{ "referenceSeqId": { "coding": [{ "code": "NC_000007.14" , "system" : "2.16.840.1.113883.6.280" }] }, "windowStart": 55227970, "windowEnd": 55227980 }] }

  - Example #2: why not just use both: - move to this
    { "referenceSeqId": [{ "chromosome": { "codingDisplay": [{ "code": "7" }] }, "genomeBuildDisplay": "GRCh37", "coding": [{ "code": "NC_000007.14" , "system" : "2.16.840.1.113883.6.280" }] , "windowStart": 55227970, "windowEnd": 55227980, }] }

Creating an Array

{ "referenceSeq": [{ "chromosome": { "coding": [{ "code": "7" }] }, "genomeBuild": "GRCh37", "windowStart": 55227970, "windowEnd": 55227980 }] }

Motion = "I move that we constrain referenceSeqId to be 1..1 under the referenceSeq FHIR sequence resource". (Jonathan)

Second Motion - Mollie
Nah's -
Abstain - Clem, VJ, Perri Smith, Perry Mar, Jenny, Gaston, Andrea Pitkus Brett J,
Yah's - Jonathan H, Bret H, Larry Babb, Gil, Joseph K, Mollie, Kevin P,
Passes

- Vote on proposal - will go in current build and may make cut for code freeze, if delaying snapshot (freeze date was 3/28/2016)

    - Is this useful? (from https://www.hl7.org/fhir/valueset-data-types.html)
        - "Code The code (used as the code in the resource instance)
          Display The display (used in the display element of a Coding). If there is no display, implementers should not simply display the code, but map the concept into their application"
    - Concerned raised on 0 based or 1 based numbering - will add to next week's agenda - this issue will not be addressed here as it is separate

- Forming a DIM subgroup
- Presentation from SDC Team: Update on SDC Profile (11:30AM ET). Following is the update from the SDC Team. Should there be any questions, or if this group would like to discuss any items in detail, the SDC team is happy to attend a future call.
    - SDC Overview
        - The S&I SDC Initiative defines the necessary requirements (including metadata) to facilitate the collection of supplemental EHR-derived data.
        - Defines a structured form definition model (e.g. a template that can be used for creating forms for different domains making them interoperable)
        - Guidance for structured Data Element definition model (note: SDC is not creating new Data Elements, however it defines structure (provides template) to create / edit Data Elements)
    - SDC and HL7 FHIR
        - SDC makes use of the following FHIR Resources: FHIR Data Element Resource, FHIR Questionnaire Resource, FHIR QuestionnaireAnswer Resource, FHIR ValueSet Resource
    - Recent Activities - FHIR SDC Profile
        - FHIR Connectathon Participation – January 2016: Currently addressing issues identified during the connectathon in our weekly FHIR Coordination meetings; status and resolutions are documented in the FHIR GForge project.
        - FHIR SDC Pilots will kick off in Spring of 2016

        - Have provided updates to all of our HL7 sponsoring WG's the last two weeks (O&O, Vocab, Patient Care, CIC, HSI, and Clinical Genomics)
        - Planning a release of the updated FHIR SDC Profile in conjunction with the next release of FHIR CORE.
    - SDC Links
        - SDC Wiki Page: http://wiki.siframework.org/Structured+Data+Capture+Initiative
    - SDC Contact Information
        - Initiative Coordinator: Dr. Ed Hammond (william.hammond@duke.edu)
        - Project Manager: Jenny Brush (jenny.brush@esacinc.com)
        - Technical and Harmonization Lead: Vijay Shah (vshah@jbsinternational.com)
        - Harmonization Support: Perri Smith (perri.smith@accenturefederal.com)
        - CDE Subject Matter Expert: Robert Hausam (rrhausam@gmail.com)
        - FHIR Subject Matter Expert: Lloyd McKenzie (lloyd@lmckenzie.com)

Next week's agenda

- 0 vs. 1 based nucleotide numbering - continued discussion

More about referenceSeqId from above (Jonathan) also emailed :

OK, I believe this is an updated, properly formatted, JSON object to more clearly represent my proposal today.

"Cardinality should be 1..1 for referenceSeqId in the referenceSeq object to unambiguously represent the reference sequence. "

Included are the optional attributes ("chromosome" and "genomeBuild"). As I mentioned, these are nice to haves, but not need to haves. This information is intrinsic in the fully qualified code (i.e. "NC_000007.14"). Including it again is for convenience.

The codeable concept "text" attribute is for human readability and the chosen text is at the discretion of the implementer.

The "referenceSeqString" is also optional, but included for convenience, but notably all text string SHALL NOT exceed 1MB in size.

example 1 for genomic coordinates and array-based structural variants comparisons

```
{  "referenceSeq" :
          [
                    {
                    "referenceSeqId":
                              { "coding": [
                                        { "code":  "NC_000007.14" , "system" : "urn:oid:2.16.840.1.113883.6.280" ,
"display" : "Homo sapiens chromosome 7, GRCh38.p2 Primary Assembly" , "userSelected" : true  }
                                        ] ,
                              "text" : “Human chromosome 7"
                              },
                    "chromosome" :
                       { "coding" : [
                         { "code" : "7", "system" : "http://hl7.org/fhir/ValueSet/chromosome-human" , "display" :
"chromosome 7" }
                                        ],
                          "text" : "chromosome 7"
                              },
                    "genomeBuild" : "GRCh38",
                    "windowStart" : 140719326 ,
                    "windowEnd"   : 140719336 ,
                    "referenceSeqString" : "TGAAGACTTC"
            }
  ]
}
```

example 2 for gene-based variant comparisons.
notably absent are the chromosome and genomeBuild as they are not included from the transcript level detail for the transcript.
Asserting the chromosome has the unintended consequence that this transcript was observed on the patient’s chromosome 7, which can’t necessarily be known.

```
{  "referenceSeq" :
          [
                    {
                    "referenceSeqId":
                              { "coding": [
                                        { "code":  "NM_004333.4" , "system" : "urn:oid:2.16.840.1.113883.6.280" ,
"display" : "Homo sapiens B-Raf proto-oncogene, serine/threonine kinase (BRAF), mRNA" , "userSelected" : true  }
                                        ] ,
                              "text" : “Human B-Raf proto-oncogene, serine/threonine kinase (BRAF)"
                              },
                    "windowStart" : 600 ,
                    "windowEnd"   : 610 ,
                    "referenceSeqString" : "TCTAAAGAAA"
            }
```

```
  ]
}
```

Now, what is still missing: since this model still allows for 0..* “referenceSeq", we still need to discern which particular “referenceSeq" the “variant" is being compared to.