HL7 Clinical Genomics WGM - January 2017, San Antonio

Mon Q3 1:45-3:00PM

Mon Q4 3:30-5:00PM

Tue Q1 9:00-10:30AM

Tue Q2 11:00-12:30AM

Tue Q3 1:45-3:00PM

Tue Q4 3:30-5:00PM

Wed Q1 9:00-10:30AM

Wed Q2 11:00-12:30AM

Wed Q3 1:45-3:00PM

Wed Q4 3:30-5:00PM

The HL7 CG WG has earned another gold star! Thanks to our WG chairs and members for helping to keep our WG vibrant.

Mon Q3 1:45-3:00PM

Co-chair - Gil

- Email from Lloyd:
  Hi everyone,

  This set of instructions applies to most work groups in HL7. If you're not sure if it applies to you, check to see if your work group is listed here. The primary target of this email is co-chairs and facilitators, but other work group members should pay attention as well. And if you're a "FHIR consumer", this will help give you an idea of how much work goes into prepping for a release. If you have a few spare cycles and would like to help work groups get ready, send me an email and I'll see if anyone can use your help. (And similarly, if your work group needs help, let me know what with and I'll see if I can match you with a volunteer or two.)

  The publication schedule is posted here. It is not expected to change, regardless of work group readiness. This email calls out key tasks, in order of priority, to be

completed this week and in the coming weeks to ensure work groups are prepared for publication.

1. Tracker issue clean-up ASAP!!!!

- Look for your email address in the Tracker Issues report
- The report is emailed out weekly, but you can look at a "current" (within the last hour or so) snapshot at any time
- If your email is on the report, it's because your gForge user id was responsible for the most recent change implicated in a gForge tracker rule violation
- If you understand or don't know how to fix the issue, email me
*- We **cannot** publish a reconciliation spreadsheet if this report isn't clean*
- Please try to be clean by afternoon of Jan 22nd
- If issues aren't cleaned, we may revoke your commit privileges
- Note that every time you update tracker items, you run the risk of creating new problems, so even if the report is clean, you're still responsible to check to see if your name appears in subsequent weeks.

2. Complete reconciliation for ballot items

- all balloted items must have a voted disposition (even if you voted to defer them in the STU 2 ballot) no later than Feb. 5
- you can find ballot items by searching the tracker. You can also see them in the tracker summary report
- If there's a "red" number in the Triaged or Waiting-for-input column for your work group in the FHIR Tracker summary, that indicates the number of non-reconciled ballot items for your work group
- Disposition can be voting to defer addressing the issue to FHIR Release 4
- Any issues not reconciled for core will be voted to be deferred to FHIR Release 4 by the FMG and may result in a reduction in FMM level of impacted artifacts.
- Any issues not reconciled for IGs may result in the IGs being excluded from the FHIR Release 4 publication timeline - the IGs can be published at some future time after STU 3 is published

3. Address warnings in the build so you can be non-draft

- QA rules in the build have changed. So even if you haven't changed anything, you may be at FMM 0 (draft) right now even if you were FMM 1 or higher (STU) last time
- This applies to almost everyone - see the CI build QA report
- If you don't think a warning should apply to your artifact, you can ask MnM to override. (Ask soon)
- Warnings should be gone no later than Feb 28th (sooner is better). If you want an override, ask for it no later than Feb 14th.
- If you don't clear your warnings or get them overridden, your artifact will be dropped to FMM0 (draft) and your implementers will be unhappy. So will the FMG . . . :>

4. Complete reconciliation for non-ballot tracker items that may result in substantive change

- Particularly critical for normative candidate resources/pages (see comments at the end)
- We don't want substantive changes for normative candidate content after this release if we can possibly avoid it
- Essentially, look at all your "triaged" and "waiting-for-input" tracker items - ballot or not

5. Scan deferred ballots for urgent/low hanging fruit

- Especially substantive changes for normative candidates
- Search in the tracker for items marked as "deferred" and assigned to your work group
- E.g. typos, "important" changes

6. Apply all artifact changes

- Substantive changes for core must be applied by Feb. 19
- Non-substantive and IG changes (if you want to publish at the same time as core) by Feb. 26
- Look at the Resolved, Unapplied column in the Tracker item report
- If ballot-related changes aren't applied in time, the FMG may drop the artifact from STU down to draft

7. Fill out the FMM spreadsheet to reflect your resource's status

- The spreadsheet is here
- The details of the QA criteria are here
- Complete no later than Feb. 28

8. If you want to be FMM 3, you need to get rid of "information" messages in the build too

- http://build.fhir.org/qa.html
- Can ask MnM to override on or before Feb. 14
- Complete no later than Feb. 28

9. Add mappings to the workflow patterns if your resource is listed on the workflow page

- Add a column called Workflow Mapping
- Add mappings to the appropriate pattern as listed in the workflow page
- See Task as an example

10. What will your QA processes be for your resources?

- QA period is Feb 27-Mar 13
- Need all resources reviewed for grammar, graphic layout, spelling, etc.

Also, at the WGM and post-March:

What are your plans for next release?
- What artifacts are candidates for normative?
- How will you move your artifacts up the publication curve?
- Are there artifacts implementers aren't using? Why?
- What does the community want you to focus on?

Normative candidates include infrastructure pages, infrastructure resources, some administrative resources and possibly a limited number of clinical resources (e.g. Observation).

***Lloyd McKenzie**, P.Eng.*

- Gil presentation
    - Intro - FHIR Genomics: Building and Ecosystem for Precision Medicine
        - Meaningful Use 3 - patients can view, download, and transmit data using API's apps.
    - Where we are
        - Clinical Sequencing DAM
        - FMM - FHIR Maturity Model
            - http://wiki.hl7.org/index.php?title=FHIR_Maturity_Model
            - we voted for FMM 1 for Sequence resource on Dec 20, 2017
            - creating a spreadsheet to record data elements and usage (for FMM 2)
        - STU 3 Pilots
            - complete implementation materials (eg IG)
            - build out
                - tools
                - testing platforms
                - open source software
            - Get feedback
        - Start of STU 4
            - produce content based on clinical genomics DAM?
            - produce content based on clinical genomics IM?
    - Question for FHIR-I
        - Workflow and clia for labs - how to be sure FHIR supports it well
        - How to think about and test examples with patient clinically identifiably info beyond connectathon testing?
        - Best way to think about doing CDA in FHIR - have version of CDA?
        - Process has been via FHIR subgroup to deal with tracking issues as they come up?

Mon Q4 3:30-5:00PM

Co-chair - Gil

- Joint with FHIR-I
- Grahame
    - principle activity - STU3, last week March publication
    - after, work toward STU4, what is in 4? what are priorities, what do want to kill? what do we accelerate?
    - release Normative?
        - april/may in 2017
        - pick 2 sections (eg infrastructure and patient) to be normative
            - one publication, but 3 ballots.
        - Profiles can be normative in the future
        - IG are candidates for normative, but if it depends on a resource that isn't it can't.
- Questions for FHIR-I
    - workflow and CLIA for labs - how to be sure FHIR supports it well
        - comment: show full stack examples for implementation guide satisfying CLIA requirements
        - out of scope for FHIR-I
        - can talk about personal experience in Australia
            - suggest we talk to OO and US Realm
            - understand intent of rules vs how rules are stated
            - as product director Grahame can talk to ONC
            - Eric Haas working on technical details on LRI for FHIR, Hans would be the process info
    - How do we think about and test examples with patient clinically identifiable information - beyond connectathon testing?
        - common question about quality of data.
        - connectathon focused on apis
        - connect with Mitre on creating synthetic data with genetic data
    - Best way to thinking about CDA in FHIR
        - The Clinical Genomics Work Group developed and published a version of structured document/CDA called Genetic Testing Report
        - three ways
            - encapsulated
                - good for short term for learning fhir
                - bad in long term, (athletes bound to concrete block)
                - not a standards solution, but an implementation solution
            - composition using existing resources

    - this and next are related
    - good if existing resources exist
- create new resources/profiles that match requirements of a CDA document
    - lose integrity when looking at each individually
- Process has been via FHIR subgroup to deal with tracking issues as they come up.
    - Options
        - up to group
        - 1 everything happens in main group
        - 2 everything happens in subgroup and then brought to main group
        - 3 subgroup has delegated everything to subgroup and only bring to main group if necessary
        - 4 main group delegates to subgroups (sarcasm)
-
- Is it possible to do a branch in FHIR? Is there a mechanism to do a bake-off?
    - Resources are weighted based being tested by one or more connectathons. The more it is vetted the more established it becomes
    - Bake off is possible, but needs to be between milestones and vetted in connectathons
    - Gil - we should work on incrementing gforge issues into current build.
    - Clem - find a middle ground, the structural change is too big to do. Agrees with a part of Amnon's proposal, but the whole thing is too much. Need to downsize our ambitions.
    - Kevin - need the plan for STU4 and see if it satisfies stakeholders
    - Amnon - the example Grahame gave on having at some point Goal1 & Goal2 is inadequate in our case, because the alternatives are in fact ‘models’, each interrelates resources and profiles in a different way using different constituents; is that a FHIR ‘module’, ‘implementation’?; how the implementation guidance relates to those resources?
    - Need consensus if we need a bake-off or not.
- How to integrate with payers (which groups to work with)?
    - implementation question rather than a standards question
    - talk to payers forum
    - talk to Wayne
    -

-

Tue Q1 9:00-10:30AM

Co-chair – Bob M

- Review Agenda
- Review of Clinical Genomics activities for newcomers
- Review of external efforts
    - National Academies - JD
        - Digitize - review history (http://www.nationalacademies.org/hmd/Activities/Research/GenomicBasedResearch/Innovation-Collaboratives/EHR.aspx)
            - not a standards group, more of a project mgmt group
            - creating IGs
            - working on pilots
            - including FHIR implementations
    - GA4GH - tomorrow
    - VMC - tomorrow
- Review and Planning of Roadmap for CG Workgroup
    - from last WGM:
    - *Amnon - comment from CTO at co-chair dinner, we need a migration path from one standard to another (eg V2 <--> FHIR), in the long run all standards will merge*
    - *Grant - would like get a roadmap from this group that we can share*
        - *Bob and Grant will work on this*
- Presentation from Structured Data Capture (SDC)
    - Amnon: how SDC questionnaires are aligned with base structures of the hosting standards, e.g., how a diagnosis captured by SDC is aligned with FHIR Condition if attributes are misaligned, etc.?
- Precision Medicine with FHIR - Diego, who was sub for Gil who usually teaches tutorial (but was returning from Asia then).
    - https://goo.gl/GZsPsV
    - comments from Diego:
      1) You use in the guidance, and in the Sequence and Observation resources a lot of words and acronyms that normal people do not understand. We had 70% of people in the tutorial that had not previous experience with the domain. THere should be a small thesaurus with the difficult words defined.
      2) The workflow part in the DAM should be complemented in the guidance with some information on how to implement the workflow (WITH WHICH SPECIFIC RESOURCES, and how to combine them)
      3) The required SEARCHES should be defined in the profile: Which fields should be searched and which combinations are allowed

4) The FamilyMemberHistory profile is not included in the Guidance. Should be included

- Provided thesaurus of terms needed to be better defined (Bob M will provide link)

Tue Q2 11:00-12:30AM

minutes recorded here : http://tinyurl.com/HL7CGJan2017

Co-chair - Gil

- Domain Analysis Model (DAM) update
- History
    - strong baseline document
    - issues
        - small technical flaws
        - scope creep
        - too many chapters, problems in ordering
        - need more diagrams, workflow for CLIA
        - some chapters could be merged
            - e.g., 5 & 6 could be merged (use cases)
    - Scope
        - One DAM?
            - + strong unified treatment
            - - needs constant harmonization
                - Bob M - both scenarios (one DAM or many) need to continually harmonized
            - - needs careful organization
            - - benefits fro more cross-referencing
            -
        - Many DAMs?
            - + quick focused efforts
            - + easier to write
            - - harder to get big picture
            - - coverage is un-synchronize
        -
        - <debate regarding the definition of “omics” and the appropriate scope of the DAM>
            - Current DAM contains valuable use cases but not a formal model. This fits HL7’s strict definition of a “DAM” but may lack content that readers may expect.

        - Suggestion: have a “core” DAM and then separate documents for extensions?
        - https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2442266/
        -
- Publication
    - The DAM has not yet been published - we need to submit a formal publication request to HL7
        - Add link to ONC document, available from wayback machine: https://web.archive.org/web/20111017131028/http://www.hhs.gov/healthit/usecases/documents/PHCDetailed.pdf
        - (Can we archive this on the WG site so it doesn’t disappear someday?)
        -
- Future: Next iteration of DAM?
    - Workflow?
    - See notes taken separately
        - Gil - please copy the list from the slide to this document:
        - Clinical focus:
        -
        - Related to genomics:
        -
        - Cytogenetics
        -
        - SNP chip, PCR/exome, etc
        - NICU- trios with exomes. Diagnose newborns. (look at edit/adding)
        -
        - Epigenomics parts- histone modifications, etc- U Utah (ask Grant Wood)
        -
        - Population genetics/CDC?. PHER/O&O joint. “Population health” (not just infectious disease)
        - Public health reporting on resistance. (check existing doc)- bacteria.
        - interpretive guidance- how to get that into the EHR in codified way.
        -
        -
        - Gene Expression
        -
        -
        - Population genetics- tumor genetics- look in detail
        -
        - Genomics
        -
        - RNA- rnaseq
        -
        - Protein structures
        -
        -
        - Later?:

        -
        - Functional
        -
        -
        - Epigenomics?- rest
        - Proteomics?
        - Metabolomics?
        - Microbiome?

    - Amnon: the ‘use case’ Grant Wood brought up, i.e., interpretation of genomics for clinical use, is common to all types of use cases described in the DAM, and should be the focus of Clinical Genomics, that is, harmonizing the modeling of interpretation, significance, relevance, annotation - and phenotype in general - of any type of omics data, rather than focusing on modeling the omics data on the one hand or the phenotypic data on the other hands - each being modeled already in bio and clinical informatics respectively

Tue Q3 1:45-3:00PM

Co-chair Bob

- LRI/V2 lite – Clem leading discussion
- LRI Ballot Reconciliation Started
- comments
    - # 8 - Swapna Abhyankar
        - Section 5.1.2 discusses the dot notation in OBX-4 and says "this approach conforms to the preferences of the Laboratory Results Interfacing (LRI) Implementation Guide". However, section 8.11.2 of the IG discusses adoption of the OG-01 data type in OBX-4, as do the eDOS and LOI IGs. After reviewing the OG-01 syntax, I think it includes the necessary complexity to fit your use case, and having a single model across domains would simplify implementation for users.
        - disposition: address later , this is similar to several other, e.g., #9 (Swapna)
    - #60 - Hans Buitendijk
        - Section 5.5 onwards (up through 5.11) should not be in the Use Case chapter, rather further in. Options: after 8.11.2 or after 10 (while moving current 11 to further down).
        - disposition:
    - #68 - David Burgess
        - Current wording indicates reference to a specific panel. It appears this may be meant to be more generic. Please clarify.
        - disposition: persuasive
    - #70 - David Burgess

        - This is an incomplete sentence and needs to more explanation. It does not appear to be related to Section 5.9 in the preceding sentence.
        - disposition:
    - #166 - Erin Holt Coyne TN Dept of Health
        - I believe OBX-5 in the existing wording should really be OBX-3.
        - disposition:
    - #184 - Austin Kreisler Leidos, Inc.
        - This section outlines an algorithm for populating OBX-4 using a dot notation that is intended as an alternate mechanism in place of utilizing parent/child result linking. Unfortunately, because of the adoption of the new 2.8.2 OG data type for OBX-4, the algorithm is outdated since it is based on the assumption that OBX-4 is only a string, which is no longer the case. The algorithm needs to be updated to reflect the new data structure used by the OG data type and reconcile dot notation with the now required group, sequence and identifier components of the OG data type.
        - disposition:
    - #185 - Austin Kreisler Leidos, Inc.
        - With the introduction of an alternate mechanism to linking parent/child results, the IG now needs a clear mechanism for identifying which mechanism is in use in a particular message. I believe new profiles need to be introduced that allow message senders to declare which style is being used so message processors can predictably process these messages. A specific profile should be added for the dot notation, with clear rules on use and appropriate message/segment/data type constraints, along with a separate profile for the existing parent/child linking detailed in a similar fashion. This will enable implementers to clearly declare and understand which approach they are using.
        - disposition:
    - #227 - Ulrike Merrick Vernetzt, LLC
        - In v2 message the Code system name in CWE.3 or CWE.6 is supposed to be drawn from HL70396 - can that be added to the table or create a new datatype to use CWE.14 instead of CWE.3 and CWE.17 instead of CWE.6 respectively. (Can pre-adopt the definition of CWE from v2.8.2)
        - disposition:
    - #228 - Ulrike Merrick Vernetzt, LLC
        - Need to for sure create a CWE datatype flavor specific for LRI_CG_Component to accommodate this.
        - disposition:
    - #239 - Ulrike Merrick Vernetzt, LLC
        - "Per Table 5-1 the expected datatype is either Ed or FT, so change to FT here and in all other examples where this LOINC is used

OBX-5 does not repeat, so cannot use '~' as line feed; suggest to use FT as datatype and use \.br\ for line feeds
Applies to ALL examples where ~ are used"
        - disposition:
    - #240 - Ulrike Merrick Vernetzt, LLC
        - "Need to create separate OG datatype flavor to support use of the ST datatype for CG AND update the examples to support the rest of the OG datatype components that are required in LRI base (or us OG_00 n base and make each profile define which OG to use)
Applies to ALL examples "
        - disposition:
    - #242 - Ulrike Merrick Vernetzt, LLC
        - Fix example - IF the code system uses a delimiter like '^' it would need to be escaped '\S\' in the code as well as in the description, else we have different sub-components populated - please review and fix examples, where needed
        - disposition:
    - #244 - Ulrike Merrick Vernetzt, LLC
        - This should be in this table at all, since it does NOT appear in OBX-3, but in OBR-4 - may be write as text before the table?
        - disposition:
    - #245 - Ulrike Merrick Vernetzt, LLC
        - "Should add text to the Term description that this code does not appear in the HL7 message
or put in Example values, as is done for 81297-4 - Table 5-3 first row"
        - disposition:
    - #247 - Ulrike Merrick Vernetzt, LLC
        - "Should add text to the Term description that this code does not appear in the HL7 message
or put in Example values, as is done for 81297-4 - Table 5-3 first row"
        - disposition:
    - #248 - Ulrike Merrick Vernetzt, LLC
        - ID is not an allowed datatype in OBX-5 by the base standard, suggest to either go to CWE if code system should be identified or ST, if not important what the code system is
        - disposition:
    - #249 - Ulrike Merrick Vernetzt, LLC
        - "Should add text to the Term description that this code does not appear in the HL7 message
or put in Example values, as is done for 81297-4 - Table 5-3 first row"
        - disposition:
    - #250 - Ulrike Merrick Vernetzt, LLC

        - "Should add text to the Term description that this code does not appear in the HL7 message
          or put in Example values, as is done for 81297-4 - Table 5-3 first row"
        - disposition:
    - #251 - Ulrike Merrick Vernetzt, LLC
        - "Should add text to the Term description that this code does not appear in the HL7 message
          or put in Example values, as is done for 81297-4 - Table 5-3 first row"
        - disposition:
    - #252 - Ulrike Merrick Vernetzt, LLC
        - disposition:
    - #253 - Ulrike Merrick Vernetzt, LLC
        - disposition:
    - #254 - Ulrike Merrick Vernetzt, LLC
        - disposition:
    - #255 - Ulrike Merrick Vernetzt, LLC
        -
        - disposition:
    - #256 - Ulrike Merrick Vernetzt, LLC
        -
        - disposition:
    - #432 - Bob Yencha
        - The requirements are not represented in the Message, Segment, or Data Type tables or in conformance statements.
        - disposition:
    - #436 - Bob Yencha
        - Align concept to use OG DT and/or adjust OG use rules to accommodate hierarchy req's
        - disposition:
    - #437 - Bob Yencha
        - missing info, the sentence is incomplete
        - disposition:
    - #440 - Bob Yencha
        - Delete the phrase in red, adjust the text to align with the CWE display rules
        - disposition:
    - #42 - Ruth Berge GE Healthcare Digital
        - The absence of a user story or any diagrams of the messaging means that this is problematic to put into place. I don't even know which system is expected to receive the message. Since the acknowledgements are cited differently in the other two use cases, I have no idea what type of acknowledgement is presumed here. This section needs to have the same sub sections to help the reader and explain the messaging.

        - disposition:
    - #469 - Lori Dieterle Kaiser Permanente
        - What is listed under Existing Wording is the full content of the second paragraph. This needs to be made into a sentence that makes sense.
        - disposition:
    - #508 - Lori Dieterle Kaiser Permanente
        - "All of the CWE flavors defined require CWE.3 to be populated if CWE.1 is populated. this recommendation would fail ... a default value for CWE.3 needs to be defined.

          Also, this is not very clear. Row B.6 is a HGVS entry, possibly meant to refer to B.4? Might be better not to refer to Table 5.2 at all. Just bring up the concept of Transcript Reference Sequence in a local system."
        - disposition: defer

Summary: We reviewed all the Negative comments, and pulled: 8, 9, 184, 185, 42, 508, all of Riki's comments (227, 228, 239, 240, 242, 244-45, 247-55), and Bob Yencha's comments (some of which require in-person resolution - 432, 436, 440). Voted 9-0-0 (For, Abstain, Again) for the dispositions. (Clem was mover, Brett was seconder).

Tue Q4 3:30-5:00PM

Co-chair Bob

- V2
    - More ballot reconciliation
    - Discussion of Need to able to have revision of genetic results
    - Do need a Next version LRI/V2 -
- Continued discussions
- (concurrent with Joint Meeting hosted by Patient Care - negation modeling)

Reviewed all A-S and A-C comments. We pulled Comment 201 (A-S) vote. For everything else, we voted to accept the dispositions. For all A-S comments, we voted 9-0-0 (Kevin moved, Elizabeth seconded). For all A-C comments, we voted 9-0-0 (Kevin moved, J.D. seconded).

Wed Q1 9:00-10:30AM

Co-chair Bob

- Pedigree standard – time to re-ballot
    - Kevin Hughes uses this in their commercial
    - Motion - Grant
        - re-affirm Pedigree and re-ballot, and to add addendum to IG to describe FHIR work
        - 2nd - Kevin

        - abstain - 0
        - nay - 0
        - yea - 12
    Grant - will do this
- Related external activities - Grant
    - Bob Wilden - NHGRI
        - NLM Jan 2017 hack-a-thon using My Family Health Portrait - status unknown
    - National Family Health History Group discusses issues of implementation
    - GA4GH
        - FHH consent project. Looking at engaging an Informatics student for Master Thesis
        - 5-year planning
            - vision for 2022
            - Bob F - need to establish formal relationship between HL7 and GA4GH if it doesn't exist already so that the APIs in their vision can be standardized
    - HIMSS 2017 HL7 booth presentations
    - FHIR implementations around country
    - FHIR-based Predictive Analytics: A Breast Cancer Pilot (document)
    - Intermountain efforts: Project idea approved by Stan Huff - FHH- FHIR based iCentra Implementation
    -
- Prep for Clinical connectathon
    -
- Madrid
    - Possible joint with WHO
    - One full day
    - focussed on LMICs (low-to-middle income countries)
    - better identify clinical, educational, technical, and informational needs related to genomics
    - discuss how to create relevant patient-centric genomics resources

Wed Q2 11:00-12:30AM

Co-chair

- continued discussion
- (concurrent with Joint meeting hosted by OO)

Wed Q3 1:45-3:00PM

Co-chair – Amnon

- Agenda:
    - Bob F will help lead discussion
    - Information Modeling – overview of work;

        - Update group with subgroup work – model
        - Talk about PSS for IM
    - VMC – variant model collaborative review
- Notes:
    - Amnon presented the history of domain modeling in HL7 Clinical Genomics
    - Bob Freimuth led the discussion
    - Bob F. - Proposed changes to the DIM PSS, publishing draft models for comments, with first ballot a year from now
    - Bob M. PSS title should perhaps be Conceptual Information Modeling
    - Amnon - Perhaps we need to expand it to “Domain Modeling” and include the CG DAM and the conceptual modeling, both handled in the IM Subgroup
    - Bob F - reviews the discussions held in the IM weekly calls
    - ‘Outsourced’ the variant representation to VMC
        - Glossary development effort, e.g., define an allele
        - Data types, etc.
        - Getting to logical and physical models (e.g., XML and json)
        - Led by Reece who gave a presentation on a recent CG weekly call
    - Collaboration is kicked off - CG IM with CDISC
        - CDISC SDTM for PGx
    - Lauren (CDISC)
        - FDA and PMDA require the use of CDISC standards
        - Standards cover protocol-driven research
        - STDM
            - Showed an overview of domains
            - STDM IG PGx 1.0 Domain Details
            - BRIDG & STDM IG PGx
        - Proposal to CGWG
            - Compare STDM to CG DAM
            - Map the two models
            - Create a collaboration scope
        - Bob F. - we should be modeling ‘by reference’ and avoid remodeling because it’s ‘not invented here’
        - Bret - how all of this is going to be useful in clinical practice?
        - Amnon - perhaps through the HL7 SPL = Structured Product Label, the medication insert as a dynamic knowledge source
    - Bob F - roadmap
        - Results and their provenance, interpretations and phenotypes
        - Observed versus derived findings

Wed Q4 3:30-5:00PM

Co-chair – Bob

- Deadlines
    - Rooms for next WGM - ??? 2017
        - repeat same schedule for May 2017?
        - Joint with WHO

        - Joint with PC, OO, SD, EHR?
        - Mon q3&4 - fhir
        - Tue - WHO
        - Wed - CG mtgs
        - Update - HL7 Leadership wants to attend but our original schedule conflict with their meetings. So we will have the Joint with WHO on Wednesday, all day.
    - Must submit PSS to PMO and Steering Division - Sunday, Jan 29, 2017
        - Pedigree
    - Submit Notice of Intent to Ballot - Sunday Feb 19, 2017
        - Pedigree
    - Final Content - Sunday, March 26, 2017
        - Pedigree
    - Ballot opens for voting - March 31, 2017
        - Pedigree
    - FHIR
        - STU3
        - Publishing goal is end of March
    - LRI
        - Sunday, March 12 - All reconciliation activities must be complete
    - WG docs
        - DMP
            -
            - open process and transparency for all projects and artifacts in development
            - addendum with figures about subgroup workflows
                - bob will send out ppt for comments/changes
            - Add language: subgroups shall operate according to CG WG practices
                - Bob M to add cheat sheet listing steps to be taken to comply with DMP (e.g., sending agendas x days before the meeting, posting minutes, approving minutes, announcing when voting will occur and when relevant materials need to be circulated for those votes, etc)
            - Transparency (and advance notice) when WG members are presenting HL7 CG projects to external groups
            - Joel: requesting clarification on 2 things: 1) whether the advance notification requirement applies to meetings only, or also to “binding decision” voting, and 2) definition of “binding decision”, i.e. does that term apply to internal meeting and group decisions such as assigning action items to group members or ending a meeting early, or does it apply only to decisions having some long-lasting effect outside of the meeting
        - SWOT

- WGM Review
    - for future agendas
        - Grant - future connectathons - use WG to produce better scenarios/teaching tools?
        - become aware of other connectathons outside of HL7
        - put links in agenda to products/documents inside of agenda
        -
- Leftover topics
- WG business and planning