https://tinyurl.com/CG-May2018

HL7 Clinical Genomics
WGM - May 2018, Cologne Germany

Mon Q3 1:45-3:00 PM

Mon Q4 3:30-5:00 PM

Tue Q1 9:00-10:30 AM

Tue Q2 11:00-12:30 PM

Tue Q3 1:45-3:00 PM

Tue Q4 3:30-5:00 PM

Wed Q1 9:00-10:30 AM

Wed Q2 11:00-12:30 PM

Wed Q3 1:45-3:00 PM

Wed Q4 3:30-5:00 PM

Agenda: https://tinyurl.com/CG-WGM-May2018-agenda

Mon Q3 1:45-3:00 PM

Co-chair - Gil Alterovitz

- Attendees
    - Bob Milius - NMDP/CIBMTR - bmilius@nmdp.org
    - Bob Freimuth - Mayo Clinic - freimuth.robert@mayo.edu
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Shennon Lu - NLM - shennon.lu@nih.gov
    - Lloyd McKenzie - Gevity - lmckenzie@gevityinc.com
    - Liz Amos - NLM - liz.amos@nih.gov
    - Clem McDonald - NLM - clemmcdonald@mail.nih.gov
    - Joel Schneider - NMDP/CIBMTR - jschneid@nmdp.org
    - Grant Wood - Intermountain Healthcare - grant.wood@imail.org
    - Dae-Soon Son - Samsung Genome Institute/S.Korea - ds3.son@samsung.com
    - Timo Kaskinen , HL7 Finland timo.kaskinen@salivirta.fi
    - Caterina Lasome - iON Informatics for the AFMS - cat@ioninformatics.com
    - Amnon Shabo (Shvo) - Philips - amnon.shabo@philips.com
    - Jane Millar - SNOMED International - jmi@snomed.org

- Connectathon summary
    - Bob M - Clinical Research track
    - Joel - Terminology
    - Amnon - Documents
    -
- International Affiliates Meeting on Sunday
    - discussion on having FHIR genomics reporting i separate IG vs in the spec
    - Issue: SNOMED and LOINC do not have agreement on genomics
        - some scandinavian countries use NPU (Nomenclature for Properties and Units) instead of LOINC
    - International affiliates (e.g. UK) have chosen not to implement LOINC
    - International vs US realm
        - LRI is US realm
    - restricting coding vs names?
    -
    - Lloyd: must have a fixed binding to a code for interoperability. Must have a open, available, free code system. Loinc fits those criteria. We need it if we are slicing on a code. We **cannot** slice on
        - example binding
        - text

        - coding.display
    - Gil - why is LRI US realm?
        - did we bring over the constraints from that to the CG IG?
        - LRI is US realm to meet US MU requirements.
    - Clem - asks for straw poll in the room
    - Lloyd - we can add guidance in the introduction to explain use of Loinc and why we're using it, and if you are in a jurisdiction that uses different systems, then here is what you can do (explain those things)
        - added gforge issue **#17151**
    - Amnon suggested to relax the strength of binding from ‘required’ to ‘preffered’, for example, in the binding to “Genetic analysis overall interpretation”, see here: http://hl7.org/fhir/uv/genomics-reporting/obs-overall.html
- Prep for Joint with FHIR
    -
- FHIR Reconciliation?
    -

Mon Q4 3:30-5:00 PM

Co-chair - Gil

- Attendees
    - Grant Wood - Intermountain Healthcare - grant.wood@imail.org
    - Bob Milius - CIBMTR/NMDP - bmilius@nmdp.org
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
    - Joel Schneider - CIBMTR/NMDP - jschneid@nmdp.org
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Bob Freimuth - Mayo Clinic - freimuth.robert@mayo.edu

- Joint with FHIR-I
    - Josh Mandel representing FHIR Infrastructure
    - started with Bob M's gforge issues
    - [#16467] Summary: repeated terminology bindings
        - e.g., http://hl7.org/fhir/uv/genomics-reporting/2018May/obs-described-variant.html
        - Josh entered a gforge issue:
            - [#17159] Summary: When multiple components are profiled, the bindings table is very hard to interpret
    - [#16472] Summary: clarify allelic-phase
        - *The definition of Observation.component(allelic-phase) is listed as "The period of stage of an allele."*
        - *I have no idea what this means.*
        - *Please provide a practical example of how this used.*
        - Need input from Lloyd
    - [#16492] Summary: coordinate system and HGVS usage
        - agreed that more language is needed to require 1-based coordinate system if HGVS is used.
        - may use FHIRPath expression to enforce?
    - [#16496] Summary: phase set of sequences (not variants)
        - similar in concept to haplotype, but then would need to have haplotype of haplotypes
        - Bob F: ComplexVariant is composed of DescribedVariants - this implies cis
            - Clem - don't think so, can have complex variant that are trans
            - need to verify
        - current http://build.fhir.org/extension-observation-geneticsphaseset.html does this
        - SequenceConfiguration similar - has cardinality of 0..2; can we have 0..* just for cis?
        - need discussion with Lloyd
    - [#16506] Summary: Definitional Sequence elements
        - will combine this discussion with Bob Dolin's ballot comments
    - [#16508] Summary: deconstruct HLA example bundle

        - Bob M will created individual resources from this bundle to be included as examples for the individual observation profiles
    - [#16510] Summary: Need more examples
        - Bob: need at least one meaningful example for profile
        - Clem: has examples from LRI that Lloyd can use to create examples
        - Gil: can we take existing examples and re-write for IG profiles?
    -

Tue Q1 9:00-10:30 AM

Co-chair – Bob Milius

- Attendees
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Amnon Shabo (Shvo) - Philips - amnon.shabo@philips.com
    - Shennon Lu - NLM - shennon.lu@nih.gov
    - Liz Amos - NLM - liz.amos@nih.gov
    - Clem McDonald - NLM - clemmcdonald@mail.nih.gov
    - Attila Farkas - Canada - afarkas@infoway.ca
    - Joel Schneider - CIBMTR/NMDP - jschneid@nmdp.org
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Bob Freimuth - Mayo Clinic - freimuth.robert@mayo.edu
    -

- Review Agenda
- Review of Clinical Genomics activities for newcomers

- FHIR ballot reconciliation
    - Amnon's comments (gforge IDs to be mapped later)
        - Issue #xxxx
          See slide 2 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
            - Guide section 1.2 (guiding principles), existing statement re: guide avoids pre-coordination
            - Amnon would like to include a balancing statement that says post-coordination should be preferred, not only at the terminology level, rather at any structure level, e.g., biomarker single code is an example of pre-coordination of some biological phenomenon and a marked phenotype of that phenomenon, and thus should be structured in a post-coordination fashion, i.e., separating the biological phenomenon and the phenotype and associate them explicitly
            - Significant discussion about need to support pre-coordinated terms within the clinical genomics domain vs. informatics principles
        - Issue #xxxx
          See slide 3 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
            - Re: profile "Genetics diagnostic report"
            - Proposal: rename profile to "Genomics (Test) Report"
            - Genomics tests are not necessarily diagnostic, e.g, HLA, carrier, etc.

        - Significant discussion about use of the word “diagnostic” within the profile name (not all uses of this profile would be diagnostic in nature)
        - Disagreement about use of genomics vs. genetics
        - Disagreement about need to address the use of “diagnostic”
- Issue #xxxx
  See slide 4 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
    - Observation should not include downstream analysis
    - FHIR observation defined as “measurements and simple assertions”
    - Do genomics observations analysis results meet this definition? Need a different or new resource to capture the analysis results (e.g., interpretations, impacts, clinical relevance, etc.)
    - Proposal: explore the use of the GuidanceResponse resource instead
    - The use of observation to capture interpretation of a genomics observation creates another issue which is how and if to use the Observation.interpretation attribute - should it be populated, ignored, left to the implementer discretion?
    - Should an interpretation of an observation be another observation as it is in the May 2018 ballot of FHIR CG?
    - Observations of observations?

Tue Q2 11:00-12:30 PM

Co-chair – Gil

- Attendees
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Bob Freimuth - Mayo Clinic - freimuth.robert@mayo.edu
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Shennon Lu - NLM - shennon.lu@nih.gov
    - Liz Amos - NLM - liz.amos@nih.gov
    - Clem McDonald - NLM - clemmcdonald@mail.nih.gov
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Joel Schneider - CIBMTR / NMDP - jschneid@nmdp.org
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        -

- FHIR ballot reconciliation
    - Amnon's comments (gforge IDs to be mapped later)
        - Issue #xxxx
          See slide 5 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
            - Ontology of phenotype-related concepts
                - Currently, there are quite a few concepts such as Interpretation, assessment, significance, relevance, impaction, annotation, etc. that need to be put on the 'same page', e.g., via an ontology/concept map
            - Distinction between interpretation and impact is unclear
            - Next step: improve definition and use of these terms
            - Resolution: consider this comment for future work
        - Issue #xxxx
          See slide 7 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
            - DiagnosticReport.risk (extension)
            - Proposal: IG should state that this approach SHOULD (not MAY) be used for recording risk, not putting risk data in any of the other phenotype-related concepts (see previous issue)
        - Issue #xxxx
          See slide 8 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
            - Test panels
            - Proposal: delete the indicated statement from the IG

        - Discussion: this reflects FHIR approach of being able to interpret each instance from a resource independently
        - Example: panels and subpanels where each subpanels is performed based on results of the previous testing, thus constitute context that is important to preserve
        - Do we need to capture the internal business logic of the lab?
        - Resolution: persuasive with mod (clarify wording related to “interpreted”)
- Issue #xxxx
  See slide 9 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
    - (Genetic) finding
        - This term is ambiguous, needs better definition
    - Separate issue submitted as part of FHIR ballot to define “finding”
    - Passionate discussion ensued.
    - Amnon will provide suggested wording
- Issue #xxxx
  See slide 10 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
    - Interpretation CAN be derived from vs. Impact MUST be derived from genetic observations
    - Proposal: both should be SHOULD because (1) there is no point making a distinction between the two and (2) ideally it has to be SHALL, but realistically - let’s go with SHIULD as guidance for ‘best practice’
- Issue #xxxx
  See slide 11 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
    - Descriptive vs computable
    - Standardization is about designing computable infromation structures, so it’s not unique to CG structures and thus is not worthwhile highlighting it in contrast to the descriptive; the latter should be included with the structured data serving as the source data being structured
    - Proposal: remove Descriptive Genetic Finding, add “text” attribute to Computable Genetic Finding
    - Need to clarify the definitions of these classes
- Issue #xxxx
  See slide 12 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
    - Conveying knowledge (structured data from publications)
    - No action needed - just something to keep in mind as we expand our scope

- Issue #xxxx
  See slide 13 in the ballot comments overview slides deck (available from the HL7 CG WG main page), and also slides 14-17 describing the document layer (discussed in detail on Wednesday)
    - Overall interpretation needs a better definition and should be used only at the level of a “genomics study”
    - Passionate discussion about the level of granularity of overall interpretation, the philosophy of what should constitute the scope of reporting-out (study → panel → test → observation)
-

Tue Q3 1:45-3:00 PM

Co-chair - Gil

- Attendees
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Amnon Shabo (Shvo) - Philips - amnon.shabo@philips.com
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
    - Bob Milius - NMDP/CIBMTR - bmilius@nmdp.org
    - Joel Schneider - NMDP/CIBMTR - jschneid@nmdp.org
    - Grant Wood - Intermountain Healthcare - grant.wood@imail.org
    - Scott Robertson - Kaiser Permanente - scott.m.robertson@kp.org
    - Bob Freimuth - Mayo Clinic - freimuth.robert@mayo.edu

- update final publication of Domain Analysis Model (DAM) after ballot reconciliation
    - Recently ballot the DAM - Jan 2018
        - passed - reconciled ballot comments
        - for publication need link to reconciliation update
    - Future items list: https://docs.google.com/document/d/10Aw3ttQjcbpqLB9w3iFAvIbHYv9KZ8eMmmMRg01VdVQ/edit
    -
    - Grant - pull data from Direct To Consumer products,
        - e.g.:
            - 23andme
            - Illumina: know your genome
            - Personal genome project
        - Gene-orosity (Intermountain) program where patients give genomics to patient record
            - genomics family history
            - clinical record
        - in discussion at DOD
        - German law restricts access to genomic data, must have a genetics counselor to interpret.
        - China has a something similar to 23andme
    - Workflow with LIMS and genomic pipelines
    - Differential Expression, Enrichment Analysis,

- Epigenetic and metagenomics (microbiome)
    - Grant - definitely need this, labs are now reporting this
    - diagnosing infectious disease - can more quickly identify pathogen by sequencing microbiome
    - Clem would like to follow-up on this, sounds very interesting
        - what is the sample? gut/stool? blood?
    - Grant knows prof at UofUtah developing tool that does this analysis
- Biocompute Object
    - way of submitting the process of doing the genetic test, understand quality metrics, etc
    - developed George Washington University
    - from wikipedia: The **BioCompute Object (BCO) Project** is a community-driven initiative to build a framework for standardizing and sharing computations and analyses generated from High-throughput sequencing (HTS), also referred to as next-generation sequencing (NGS) or massively parallel sequencing (MPS)
    - https://en.wikipedia.org/wiki/BioCompute_Object

- Need SMEs for each of these
- Bob M - DAM is list of uses cases, we are adding to the wishlist; We also need to provide solutions for these use cases.
- Bob M - must remind ourselves of our promise to merge DAM and Information Model into single document.
- Grant - we need to share this, dissemination
    - Bob M : we had press release of the 1st version; next press release should be an announcement that it's been updated and this is the added content
    - Bob F - Share at the GA4GH meeting in Toronto; work on developing strategic roadmap
    - Bob M - Two levels of dissemination
        - broad to everyone
        - targeted to specific group with aim of development strategic engagement
    - grant - what European groups should we engage?
        - GA4GH
        - HL7 Europe
    - Need transparency regarding the state of our work, how many of these do we have solutions? Can we mark some as having

solutions (eg V2, FHIR), and others that we don't yet have solutions for?
        - Grant - we know we can't do it all ourselves, Send preamble describing we are seeking SMEs to help work on this.
        - Bob F - envisioning a work document that is not a word document, must be a useable tool, get oriented to the material, how to find material, how to find V2 solutions, how to find FHIR solutions, etc
        - Bob M - first thing that comes to mind is a wiki
        -
- FHIR reconciliation
    - did not address any others

Tue Q4 3:30-5:00 PM

Co-chair – Amnon

- Attendees
    - Bob Milius - NMDP/CIBTMR - bmilius@nmdp.org
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
    - Amnon Shabo (Shvo) - Philips - amnon.shabo@philips.com
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Scott Robertson - Kaiser Permanente - scott.m.robertson@kp.org
    - Joel Schneider - NMDP/CIBMTR - jschneid@nmdp.org
    - Grant Wood - Intermountain Healthcare -
    - Bob Freimuth - Mayo Clinic - freimuth.robert@mayo.edu

- Information Modeling - Overview of work - Bob Freimuth
    - Shared slides of Cologne Cathedral
    - Background - summary of last 4 mos of work
    - Technology agnostic
    - Conceptual information model
    - Not trying to boil the ocean
    - Promote harmonization and inter-artifact consistency among all CG WG standards
    - Modeling interplays - informing each other
        - DAM is actually a DA (Domain Analysis) - no model in it
    - Started with concept Sequence - pickin up on work from GA4GH and VMC
        - Biological definition vs computational definition
    - Sequence ---> 0..* SequenceRepresentations (abstract class represents the many different ways a molecular sequence could be represented.)
        - Simple sequence (string)
            - Encoding alphabet, eg IUPAC symbols
        - FormattedSequence
            - Predefined file format
            - Eg FASTA - file.contentType = text/x-fasta
        - ResolvableSequence
            - URI that can be resolved, can point to another system
            - Can include format
    - How to derive one sequence from another

        - Need to convey location
            - 1- vs 0-based (interval) coordinate system
            - Describe interval
        - ApproximateInterval - Fuzziness
            - Start range
            - End range
        - Cytoband location
            - arm, region, band, subBand
            - cytobandInterval
                - Chromosome
                - Cytoband start
                - Cytoband end
        - Relative Sequence
            - Reference
            - Series of edits
        - Action item - add example for indel
        - Clem prefers Alt to Replacement
    - Discussion around process/protocols for sequence analysis from specimen
        - Capture information around device (software and hardware) include settings and variables, and workflow.

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Wed Q1 9:00-10:30 AM

Co-chair – Bob M

- Attendees
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Shennon Lu - NLM - shennon.lu@nih.gov
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Joel Schneider - NMDP/CIBMTR - jschneid@nmdp.org
    - Bob Freimuth - Mayo Clinic - freimuth.robert@mayo.edu
    - Clem McDonald - NLM - clemmcdonald@mail.nih.gov
    - Grant Wood - Intermountain Healthcare - grant.wood@imail.org
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    -

- Brief Updates (attempted to limit to 30 min total, Grant/Bob F failed miserably)
    - Grant -
        - HL7 Genomics and AI Conference
            - Policy issues
            - Guiding principles on how AI is applied to genomics
                - AI should augment provider and patient, not replace
                - avoid over reliance
                - demonstrate that AI is understandable and reliable
                - etc
            - Research and clinical genomics applications
            - Use of FHIR Genomics standards
            - Critical data sets
            - Patient and Healthcare consumer applications
            - Global genomics, public health and implementations
            - Genomics and AI action agenda: Key components and collaborations
        - Genomic AI Coalition (GACT)
        - GA4GH (will be covered by Bob F)
            - Grant co-chair of subgroup #2

        - workshop of current users of FHIR within GA4GH to gan an undersatnding of the current patterns of use of FHIR resourece in describing and exchange cliniical phenotype informations
        - 15 driver projects around the world
        - no results yet
    - Phenopackets Hackathon - Toronto Canada
        - tutorial on Phenopackets
        - overview of FHIR resource (Alejandro)
        - review of Hapi server, ClinFhir, etc possible tools for people to use
        - Activity/challenge - try to alighn FHIR and Phenopackets; describe a patient, and see if we can describe that patient in both systems, and translate between the two systems
- Genomic medicine implementation in low resource settings
    - 4th meeting
- Marc Abramowicz - prof and head of Hopitaux Universitarires de Geneve
    - Phenomics
    - add genomics
    - infer paitent outcome fro the genomic cata + phenomic data + …
- NIH Family HIstory
    - NIH Clinical Center to integrate genetic pedigrees into EMR workflow
    - Nurse trained to take family history including pedigree
    - Family history risen to level to importance
- 13 European countries have signed a declaration to share genetic data
-
- Bob F -
    - Slides found in CG Document Center
        - External activities update - GA4GH and S4G
    - GA4GH
        - VMC
    - Sync4Genes

- FHIR - IG ballot reconciliation
    - Ballot
        - 34 Affirmative (need 26 to pass)
        - 9 Negative
        - 95 Abstain
        - 23 No Vote
    - gForge Issues
        - 198 total (152 ballot comments)
        - 64 Affirmative
        - 88 Negative
        - 46 None (gForge issue submitted, but not a ballot spreadsheet; doesn't count)
    - [#16683] Summary: Overall comments on 1.1 and 1.2 re: organization - 2018-May Genomics #1
        - comments in gforge, repeated here
        - Word document uploaded with ballot spreadsheet, we need to review it with group
        - It contains proposal for additional text to clarify
        - In introduction, explain how to do "standard", "easy" genetics, then look at "this"
        - We could instead add another section with a simple recipe for most common genetic report; a 'quick-start' guide to avoid complexity
        - will summarize with word doc to be distributed to group for vote in either FHIR call or Group call.
        - word document uploaded to CG Document Center
            - http://www.hl7.org/documentcenter/public/wg/clingenomics/2018%2005%2007%20More%20edits%20for%20the%20FHIR%20ballot.docx
            -

Wed Q2 11:00-12:30 PM

Co-chair – Bob F

- Attendees
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Grant Wood - Intermountain Healthcare - grant.wood@imail.org
    - Joel Schneider - NMDP/CIBMTR - jschneid@nmdp.org
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Amnon
    -

- Genomics Documents - Past and future - Amnon Shvo
    - See slides 13-17 in the ballot comments overview slides deck (available from the HL7 CG WG main page)
    - Adding a genomics document layer in FHIR
    - Overall interpretation
        - Current definition is ambiguous
        - Need an overall summary section at the “study” level?
        - Need a “genomics study document” that wraps “study summary section”, “test reports section”, and “test recommendations section”?
        - Example: hearing loss study (tests panel - see in the slides deck enclosed with the ballot spreadsheet, available off the HL7 CG WG main page)
        - Proposal: each test in a panel should be a separate instance of diagnostic report (genomics test report, similar to the current specification, except for the name change as proposed in another ballot comment)
        - Proposal: use merely “interpretation” rather than “test interpretation” or “overall interpretation” etc. and then the type of interpretation can be determined by the context in which the interpretation is placed, so for example if the interpretation is placed in the document summary section, then it should be understood as the ‘overall interpretation’
        - Action item: Amnon to create a draft profile that describes this idea, with a mocked up example to show its usage

            - Also side-by-side comparison of this structure vs. Imaging Study
            - Is this a generalizable pattern that can be used elsewhere?
        - Question for FHIR: why can't a diagnostic report be based on another diagnostic report?
            - Bob M - I saw this question while in the OO meeting, so I asked them. They are not absolutely firm in that. Other areas such as imaging have complex nesting of interpretations that may use this. OO requests a specific use case demonstrating how this would be used. They would then analyze it and discuss it with CG and come back either with an agreement to the change, or offer an alternative pattern in FHIR to do the same thing.
            - The need for nesting diagnostic reports is not instead of the document layer, rather to accommodate complex test that in turn are performed as subpanels
- CDA Genetic Testing Report - Informative Ballot - Amnon Shvo
    - See ballot xlsx in the file (including proposed predispositions) "CDAR2_IG_GENTESTRPT_R1_I1_2018JAN_PROPOSED_DISPOSITIONS" uploaded to the HL7 CG WG main page on Jan 31, 2018
    - Scanned briefly the main types of comments, as was done already in a CG session of the HL7 WGM January 2018 dedicated to this ballot
    - Ballot comments 1-14 complete
    - Motion: Amnon: Will circulate the ballot xlsx with proposed dispositions to WG list, for e-vote to accept resolutions
        - Julian: seconded
    - Votes: 0 abstain / 0 negative / 6 affirmative

Wed Q3 1:45-3:00 PM

Co-chair – Bob F

- Attendees
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu
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    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Jane Millar - SNOMED International - jmi@snomed.org
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Shennon Lu - NLM - shennon.lu@nih.gov
    - Clem
    - Grant

- Gold Stars
- Next WGM
    - Sept 29 – Oct 5, 2018
    - Baltimore, MD
    - Room reservation – same schedule? (Mon Q3 – Wed Q4)
        - Amnon: Move newcomer's session to Mon Q3? Acknowledge limitation on schedule for FHIR experts
- Reaffirm tues time slot for calls
    - 5 pm Europe time works well (normal time)
- WG health – status of wg docs
    - No review needed at this time
- Meeting minutes
    - Main and subgroup calls - slightly different mechanisms for tracking minutes
    - Monday and Thursday use a ‘running’ google document (all days in the same document) whereas Tuesday saves a PDF snapshot after every meeting. While the running document is nice, I think the snapshot approach is better. Thoughts?
        - Amnon: subgroups don't develop the specs, which are brought back to the main group, so current approach is fine
        - Grant: agree with Amnon
        - I don’t know if the Monday and Thursday notes are ever saved to the HL7 Wiki. If they are not, they probably should be?
        - Yes – post pdf to wiki (on trimester schedule)

    - Some teams have moved their notes to the new Wiki site. Should we do the same?
        - Bob M – confluence? Want snapshot but also want it to be searchable.
        - Confluence can index pdf files, we need to ensure HL7's instance is configured as such
- Meeting schedule
    - Tuesday and Thursday calls are listed on the HL7 Calls page, but Monday is not. Seems like we should list all of our meetings there for visibility outside of just our group, so I suggest we add Monday to the calls page.
        - Agreed (via email) - Gil to add
- Meeting conference
    - Tuesday and Thursday use FCC, Monday uses Zoom. I suggest we switch the Monday call to FCC.
    - Discussion, comments/questions on FCC and Zoom
        - No problems with FCC
        - Muting/unmuting on FCC is a little cumbersome (but manageable)
        - FCC isn't as feature-rich
        - FCC won't utilize external speakers without additional configuration, must use headphones
        - Calls would be easier if all calls used same platform, dial-in number, etc
        - Zoom requires monthly subscription
        - Zoom UI takes time to get used to
    - Hand vote: 100% had no opinion on which platform to use
- Vocab facilitator for CG WG
    - Grant thinks Bret Heale would be good in this role
    - Joel is willing to serve in this role, has been engaged with vocab WG for a while
- Engagement plan for external groups
    - Grant – we need a process/consensus for how we're going to do this (e.g., MOU?)
        - Action item: follow up as agenda item on Tues call
- Vocabulary discussion (V2) - Clem
    - Explanation of use of coding systems (for variant IDs) in v2 LRI
    - dbVar may be deprecated
    - Clinical Table search service (at NLM)
        - API access, can query with terms to find codes
        - What is the relationship between this and UMLS?
            - Clem: none. UMLS is vocabs only, not coding systems

- Owners of coding systems have agreed to include their content here
    -

Wed Q4 3:30-5:00 PM

Co-chair – Bob Milius

- Attendees
    - Dora Finkeisen - Molit Institut - dora.finkeisen@molit.eu
    - Bob Freimuth - Mayo Clinic - freimuth.robert@mayo.edu
    - Joel Schneider - NMDP/CIBMTR - jschneid@nmdp.org
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Jane Millar - SNOMED International - jmi@snomed.org
    - Lloyd McKenzie - Gevity - lmckenzie@gevityinc.com
    - Julian Sass - Niederrhein University - julian.sass@hsnr.de
    - Shennon Lu - NLM - shennon.lu@nih.gov
    - Clem McDonald
    - Liz - NLM - liz.amos@nih.gov
    - Caterina Lasome - iON Informatics for AFMS - cat@ioninformatics.com
    - Patrick Werner - Molit Institut - patrick.werner@molit.eu

- Vocabulary - Clem (cont)
    - clinicaltables.nlm.nih.gov
    - Lhcforms.nlm.nih.gov
    - Action item: Sync list of coding systems in v2 LRI with FHIR terminology page
- Gforge issues (ballot)
    - 16689: persuasive with mod (fix typos in proposed wording) - pending block vote
    - 16723: withdrawn
    - 16727: persuasive - pending block vote
    - 16731: persuasive with mod (change proposed change from “units of analysis” to “residues”) - pending block vote
    - 16736: persuasive with mod (change proposed change from “units of analysis” to “residues”) - pending block vote
    - 16740: need to improve wording, can propose a mass change to the entire paragraph (tabled for future)
    - 16512: discussed; Bob M will mock up some examples to illustrate the issue