HL7 Clinical Genomics Weekly Call - July 10, 2018 11:00 AM (US Eastern)

Minutes:
https://docs.google.com/document/d/12-uBrMmav71a3_c9h_FXQteJo_I5Kt72NEBYXZuwhFg/edit

Attending the meeting:
Join the online meeting (VoIP available with this):

- Online Meeting Link:
    - https://join.freeconferencecall.com/clingenomics
    - Meeting ID: clingenomics

Dial into the conference:

- Dial-in Number:
    - (515) 604-9708 - United States
    - Access Code: 289092
- International Dial-in Numbers:
    - https://www.freeconferencecall.com/wall/clingenomics/#international

Agenda

Attendees Sign-in

Minutes Approval

Topics to Review

- Agendas and Important Dates
- External efforts
- Subgroup reports

Topic 0: NIB vote

Topic 1: Genomics Reporting IG ballot reconciliation - Block Vote

Topic 2: Continued discussion re definitional resource for variant and/or sequence

Topic 3: Ballot discussion - “Variant Grouping”

Chat

Attendees Sign-in

(Presiding co-chair: Bob Milius - NMDP/CIBMTR - bmilius@nmdp.org)

1. Amnon Shabo (Shvo), Philips, amnon.shabo@philips.com
2. Dorina Bratfalean -CDISC- dbratfalean.external@cdisc.org
3. Scott Robertson - Kaiser Permanente - scott.m.robertson@kp.org
4. Patrick Werner - Molit Institute / Heilbronn University - patrick.werner@molit.eu
5. Lloyd McKenzie - Gevity - lmckenzie@gevityinc.com
6. Dora Finkeisen - Molit Institute - dora.finkeisen@molit.eu
7. Bob Dolin - Elimu Informatics - bdolin@elimu.io
8. Deepak Sharma - Mayo Clinic - sharma.deepak2@mayo.edu
9. Alex Mankovich - Philips - alex.mankovich@philips.com
10. Andrea Pitkus - apitkus@gmail.com
11. Joel Schneider - NMDP/CIBMTR - jschneid@nmdp.org
12. Ning Xie - BCH - ningxie2018@gmail.com
13. Amnon Ptashek - genptashek@gmail.com
14. Bret Heale - Intermountain Healthcare - bheale@gmail.com
15. Arthur Hermann - Kaiser Permanente - arthur.hermann@kp.org
16. Murat Sincan - Sanford Health - murat.sincan@sanfordhealth.org
17. Jamie Parker - Carradora Health - jamie.parker@carradora.com
18. Scott Robertson - Kaiser Permanente - scott.m.robertson@kp.org

Minutes Approval

- June 26
    - http://wiki.hl7.org/index.php?title=File:HL7_CG_20180626.pdf
    - motion/2nd to accept minutes - Patrick / Lloyd
    - discussion - none
    - Abstain / Nay / Yea:
        - 0 / 0 / 14
    - result - motion passes

Topics to Review

Agendas and Important Dates

Date	Co-Chair	Agenda	Important Dates
5/29/2018	Bob M	Review WGM minutes (note that Amnon Shabo edited the minutes regarding the sessions when his ballot comments were discussed)	
6/5/2018	Kevin	Ballot comments	Jun 6 - Deadline for connectathon proposals to FMG
6/12/2018	Kevin	Con call tech Connectathon 'Variant Grouping'	
6/19/2018	Kevin	Con call tech Connectathon Block Vote 'Variant Grouping'	
6/26/2018	Bob M		June 27 - Connectathon Proposals Due
7/3/2018			Jul 1 - Work groups notify the FMG whether they need to reballot normative packages (due to substantive change), STU resources (due to significant refactoring) or IGs during the Sept. cycle July 6 - Deadline to notify HG of additions/changes to co-chair opentings

7/10/2018	Bob M	IG block vote NIB vote	July 11 - Call for co-chair nominations July 15 - Notification of Intent to Ballot
7/17/2018	Bob M		
7/24/2018			July 23 - formation of consensus groups
7/31/2018			
8/7/2018	Bob M		Aug 5 - Reconciliation packages must be posted by this date at the absolute latest Aug 10: All substantive reconciliation applied. FHIR Core is frozen, limited QA process for content subject to ballot only Aug 10 - close to co-chair nominations
8/14/2018			Aug 17: Pre-ballot (and connectathon) content freeze. Publication process begins, including ensuring that content is appropriately flagged for ballot status and there are no last minute QA issues
8/21/2018			Aug 24 - ballot opens for voting
8/28/2018	Bob M		
9/4/2018			
9/11/2018			
9/18/2018	Bob M		
9/25/2018			
32nd Annual Plenary & Working Group Meeting Sep 29, 2018 to Oct 5, 2018 - Baltimore, MD			

External efforts

- GA4GH Genomic Knowledge Standards (GKS) (leads: Bob Freimuth, Andy Yates)
    - Variant Representation (formerly VMC)
        - no report
    - Variant Annotation
        - no report
- DIGITiZe (aka National Academies) (Grant Wood, JD Nolen)
    - no report
- ClinGen/ClinVar (Larry Babb, Bob Freimuth)
    - no report
- CDISC PGx (Dorina B.)
    - no reprot
- ONC Sync for Genes (Bob Freimuth)
    - Pilot sites are planning/implementing their respective use cases. ONC will be encouraging their participation in both the Sept 2018 and Jan 2019 FHIR Connectathons.
    - ONC 2nd Interoperability Forum (August 6th- 8th, 2018 in Washington, DC)
    - https://www.healthit.gov/news/events/oncs-2nd-interoperability-forum

Subgroup reports

- IM (Bob F)
    - https://docs.google.com/document/d/1azKiQdhAQKuHhxAznEp8141FLdFLACIu8MzF2LxADxg/edit#
        -
- FHIR (Gil)
    - https://docs.google.com/document/d/1FGCQRtxJKyHhnC1uB_t4sJZ9yXbLMGOqPXHPr5tSLLQ/edit#heading=h.nts1cfujf9t5

Topic 0: NIB vote

- Notice of Intent to Ballot Genomics Reporting IG for Sep 2018 ballot
    - http://www.hl7.org/Special/committees/tsc/ballotmanagement/EditNIB.cfm?ballot_document_sdo_id=953&Action=Edit
    - Universal vs US
    - STU vs Informative
    - Note: This is just a Notice of Intent. We aren't obligated to submit ballot content if we aren't ready.
        - we may not be able to reconcile current ballot comments in time to ballot again.
    -
- Motion/2nd :
    - Bob D / Bret
- Discussion:

    - none
- Abstain/Nay/Yea
    - 0 / 0 / 15
- Motion passes

Topic 1: Genomics Reporting IG ballot reconciliation - Block Vote

Comment Submitters

- Amnon Shabo
- Bob Milius
- Clement McDonald

Line Items

- 16823 Comment+to+consider+including+answer+lists+to+help+user+understand+what+variables+are+supposed+to+report+-+2018-May+Genomics+%2340 (Clement McDonald) Not Persuasive
- 16508 deconstruct+HLA+example+bundle (Bob Milius) Persuasive
- 16510 Need+more+examples (Bob Milius) Persuasive
- 16770 Remove+text+to+broaden+statement+-+2018-May+Genomics+%2326 (Clement McDonald) Persuasive
- 16873 Inconsistent+figures+with+attributes%2Fobjects+described+elsewhere+-+2018-May+Genomics+%2357 (Clement McDonald) Persuasive
- 16774 Add+RiskAssessment+resource+to+clarify+since+mutation+analysis+test+does+not+include+a+risk+assessment+-+2018-May+Genomics+%2327 (Clement McDonald) Persuasive with Mod
- 16879 Singling+out+age+when+it+is+already+part+of+Patient+resource+-+2018-May+Genomics+%2359 (Clement McDonald) Persuasive with Mod
- 16919 reflex+panels+-+2018-May+Genomics+%2372 (Amnon Shabo) **In Person** Persuasive with Mod

motion to accept block as proposed dispositions: Kevin P/ Clem
discussion: none
abstain: 0
nay: 0
yea: 14
motion passes

Topic 2: Continued discussion re definitional resource for variant and/or sequence

- see notes from http://tinyurl.com/fhirgenomics
- Lloyd - we don't want to have two diffrerent ways to report the same content
- Clem - heard that Larry wanted a conical variant identifier (eg Baylor has one, but not embrace by everyone, COSMIC might also be one). Wanted a statement about which code systems could be used.
- Patrick - we already have a way to link to a conical identifier, a variation code. Use the system of your choice.
- Clem - dbsnp only has location, not the variation
- Patrick - everything goes into variation code, slide the codeable concept to give examples of how to use specific codes
- Clem - I think we already have this
- Patrick - should have a more open description
- move discussion to FHIR call, perhaps for next ballot cycle/comments

Topic 3: Ballot discussion - “Variant Grouping”

- Several trackers logged around the various profiles we have defined for “Variant Grouping” - so our concepts like:
- Genotype
- Haplotype
- SequenceConfiguration

- Bob Dolin presented summary slide showing redundant groupings

See pages here:
http://build.fhir.org/ig/HL7/genomics-reporting/general.html#findings
http://build.fhir.org/ig/HL7/genomics-reporting/sequencing.html (see ComplexVariant)

ID	Summary	Details
16812	Comment on haplotype being identified absence info on variant - 2018-May Genomics #37	Submitted by: Clement McDonald (National Library of Medicine) Existing Wording: Figure 5: Variation (any type) --- Comment: Didn't think a haplotype can be identified in absence of any information on variant. --- Summary: Comment on haplotype being

		identified absence info on variant clem withdraws
16808	Complex variants distinguish cis from trans - 2018-May Genomics #36	Submitted by: Clement McDonald (National Library of Medicine) Existing Wording: Figure 5: Cis or Trans --- Comment: Unclear - I don't recall discussion plus the complex variants distinguish this (I think). --- Summary: Complex variants distinguish cis from trans clem - postpone to next week
16789	Discussion needed on change from display names on 84413-4 - 2018-May Genomics #31	Submitted by: Clement McDonald (National Library of Medicine) Existing Wording: Figure 5: Genotype 84413-4 Proposed Wording: Genotype Display Name 84413-4 --- Comment: I understand why you want to shorten, but the change could mislead. These are not solid codes for genotype or haplotype. Would like to find a way to link from the figure (or content below them) to the LOINC code, description and answer list. Have linked to the answer list in the change document but these early tables are a bit more digestable. Lets talk. --- Summary: Discussion needed on change from display names on 84413-4
16793	Discussion needed on change from display names on 84414-2 - 2018-May Genomics #32	Submitted by: Clement McDonald (National Library of Medicine) Existing Wording: Figure 5 Haplotype 84414-2 Proposed Wording: Haplotype Name 84414-2 --- Comment: Name in V2 --- Summary: Discussion needed on change from display names on 84414-2
16496	phase set of sequences (not variants)	http://www.hl7.org/fhir/2018May/extension-observation-geneticsphaseset.html easily describes how a set of sequences (not necessarily variants) can be grouped according to being in chromosomal phase with one another (cis, on the same molecule). This is useful for my use case. I don't see how this can be done in the current IG. allele-phase in described variant doesn't do it as far as I can tell. If it can, I need to see an example. Calling the phase-set a haplotype of sequences is technically correct, but seems awkward, especially since our domain talks about haplotypes in a whole gene level (eg describing whether two gene level alleles are on the same molecule. Is it possible to describe haplotypes of haplotypes? In the end, I need to see examples of this.
16173	Clarify usage of Genotype/Haplotype/SequenceConfiguration or remove for now	The Genotype/Haplotype/Sequence Configuration profiles involve groupings for various purposes. I do not believe our documentation for these is clear enough to ensure consistent usage. As an example - Sequence Configuration has basically no documentation in the IG. While these concepts are important, I am concerned that we do not have enough consensus to represent in our first draft of this IG. We need to either remove them for now or spend time creating additional documentation in order to be very clear how each should be used. As a starting point, does everyone feel that the usage of Genotype/Haplotype in the PGx example is correct? http://hl7.org/fhir/uv/genomics-reporting/pharmacogenomics.html#examples It is also used in HLA examples. http://hl7.org/fhir/uv/genomics-reporting/transplants.html I am concerned that Genotype/Haplotype are not being used consistently even in our own initial examples.

16325	"haplotype" in medical genetics	Input from one of our physician/geneticists, Dr. Leslie Manace. Unfortunately, I do not have a specific url/location/resource to point this comment to. I believe the WG will be able to consider this generally and apply as appropriate. Fortunately, Kevin Power was able to provide inital feedback, which I have included below. Dr Manace: Genetic Assertions - "haplotype" is essentially never relevant in medical genetics. This is part of what gives me pause about the MD representation in this group Kevin Power: There are use cases in HLA (and even some in Pharmacogenomics) where haplotype is relevant. So, this is another case of ‘when you need haplotype, structure it like this – but skip it if you don’t need it’
16820	More explanation needed to describe genotype definition - 2018-May Genomics #39	Submitted by: Clement McDonald (National Library of Medicine) Existing Wording: Genotypes&#65533;describe combinations of genetic variations that together are associated with a particular phenotype - i.e. a specific physical, behavioral or risk-associated difference associated with the organism whose specimen was tested. --- Comment: This may not be true. I have understood that the genotype is everything you know about the individual genetics including all the normals as well as possibly multiple things that might be described as separate phenotypes. (Will need the experts to weigh in) --- Summary: More explanation needed to describe genotype definition
15885	Should consider how the PhaseSet match to the IG strucuture	The elements in the Observation-geneticsPhaseSet are different from the Allele Phase information the IG currently have. Need to think about if it should be a part of elements in Haplotype (it seems to be similar with Haplotype feature). May need a clear documentation about how to use the phaseSet element and the LOINC Allele Phase in the IG. Fan: Move the Phaseset to HaploType. And is it suitable for deleting PhaseSet ID, which is no mapping to coding system (LOINC) and unuseful
16512	Sequence Configuration cardinality	Sequence Configuration has a obs-focus with a cardinality of 2..2. I assume this for the case when trans is value. But if the value is cis, then the cardinality could be 2..* Not sure how, but It would be nice to be able to do this. Then I could effectively have a set of sequences in a phase-set. Practically speaking, I think most labs report if they have evidence of sequences being cis, but not for trans. Evidence for trans is usually inferred from lack of evidence them being in cis.

Chat

Clinical Genomics Docs

- SWOT
    - https://docs.google.com/document/d/1zFUzRYLfCmrnThBU8xXVS_JiScDACBi13tzFJep751k/edit
    - Review complete as of Aug 1, 2017
    - Approved in Sep 2017 WGM in San Diego
- Decision Making Process
    - https://docs.google.com/document/d/18ZxNAjMukUKXxbNPRtRdjytMCvnRns4srlDe0EBs0FI/edit
    - Review complete as of Aug 15, 2017
    - Approved in Sep 2017 WGM in San Diego
- DAM
    - http://tinyurl.com/damcgdoc