

HL7 Clinical Genomics Weekly Call - Dec 6, 2016

Attendees

1. Bob Milius - NMDP - bmilius@nmdp.org (presiding co-chair)
2. Jonathan Holt - SeqTechDx jholt@seqtechdx.com (half listening, abstaining from voting)
3. JD Nolen - Cerner johndavid.nolen@cerner.com
4. Perry Mar - Partners HealthCare System - pmar@partners.org
5. Xin Liu - BCH - xinliu215@gmail.com
6. Joseph Kane - Epic - jkane@epic.com
7. Shannon Lu - NLM - shannon.lu@nih.gov
8. Yi Wang - USTC - panzer.wy@gmail.com
9. Joel Schneider - NMDP - jschneid@nmdp.org
10. Xiao Luo - USTC - I.xander.233@gmail.com
11. Tianlong Chen - USTC - wijp619@gmail.com
12. Clem McDonald - NLM - ClemMcDonald@mail.nih.gov
13. David Kreda - HMS - david.kreda@gmail.com
14. Andrea Pitkus- IMO- apitkus@imo-online.com
15. Bret Heale - Intermountain Healthcare - bheale@gmail.com
16. Scott Bolte - Trailhead Clinical Strategies - Scott.Bolte@gmail.com
17. Kevin Power - Cerner
18. Gil Alterovitz - BCH
19. Joey Yang
20. Eric Whitebay

Discussion

- **Minutes approval**
 - http://wiki.hl7.org/index.php?title=File:HL7_CG_20161129.pdf
 - motion to approve - Joseph
 - second - JD
 - discussion -
 - abstains - Jonathan, Andrea,
 - nays - 0
 - yeas - 18
 - motion - passes
- **Brief reports from external efforts (discussion only if needed)**
 - GA4GH -
 -
 - National Academies
 - Nothing new to report (JD)
 - Clingen/Clinvar
 -
 - GA4GH Variant Modeling Collaborative (VMC)
 -
 - NHGRI
- **Deadlines**
 - 2016-12-08: Last day to sign up for Ballot Consensus Group (aka Ballot Pool)
 - need to sign up if you want to submit a ballot comment on LRI/V2 Lite

- 2016-12-09: Provisional ballot opening
- 2016-12-16: Deadline to post CG WGM agenda on the [WGM information](#) page (WG Health metric)
- **Upcoming calls through next WGM in San Antonio**
 - Dec 13 - Amnon presenting his FHIR proposal
 - Dec 20 - Deadline for DAM poll results; vote to accept FHIR subgroup recommendations
 - Dec 27 - (cancel?)
 - Jan 3 -
 - Jan 10 -
- **DAM**
 - <https://docs.google.com/document/d/1BrpqPbgUCvtrPvRdf-oikK0pHiKUxo5QdZahxX9Z7dU/edit>
 - Dec 6 - Truly quick review (20 min) of new Clinical Sequencing DAM document by Gil or David with a google or doodle poll released opens after meeting to vote yes/no to publish and stays open until Dec 20 (per below) as the document is long!
DAM document will be delivered in two formats: markup in view-only Google doc and clean version in PDF, the actual candidate.
 - David K - presented the document
 - Clem - suggested that the title be altered with a clarifying subtitle
 - members encouraged to submit possible subtitles to co-chairs
 - Clem - can we make changes/edits?
 - Bob M - we had several weeks for changes and edits; this should be a vote for the document as is; workgroup should read and submit vote with commits
 - David K - this doesn't have to be perfect; we need to publish the DAM and continue to work on the next version. It's a valuable document and should be shared.
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- **FHIR Ballot reconciliation update**
 - FHIR reconciliation spreadsheet
 - Short url - <http://bit.ly/2gaglig>
 - Long url - <https://docs.google.com/spreadsheets/d/17fqBTWKrlvPysZXIhLhLX4proKpv95inFQGVNO54axk/edit#gid=0>
 - FHIR Subgroup Meeting minutes:
 - Short url - <http://bit.ly/2gvRSbq>
 - Long url: https://docs.google.com/document/d/1FGCQRtxJKyHhnC1uB_t4sJZ9yXbLMGOqPXHP5tSLLQ/edit?pref=2&pli=1#heading=h.ntntuef6iwzkDAM
 - See <http://build.fhir.org/> for current build.
 - Motion by David Kreda, second by Clem
 - *We (a) approve the reconciliation by the CGWG FHIR subgroup of the STU3 genomic profiles/resources (voted on Nov 17 to upload to gforge), which include 6 specifications in total;*

- ~~(b) deem that reconciled specification to have achieved a Level 1 Maturity in terms of the FHIR Maturity Model. (b) to be submitted to subgroup~~
 - discussion
 - tabled for two weeks (to voted on Dec 20)
 -
 - Upcoming deadlines based on email from Lloyd about FHIR workflow:
 - Timelines for the revised cycle are as follows:
 - ~~Sun. Nov. 27~~ - Ballot substantive resource freeze (prioritize resources that IGs will be based on)
 - ~~Sun. Dec. 4~~ - Ballot total freeze
 - **Sun. Dec. 9** (or a day or two earlier) - Freeze released - all changes allowed
 - **Sun. Feb. 5** - Ballot reconciliation deadline - All ballot comments must be reconciled, tracker issue report must be clean
 - **Sun. Feb. 19** - Publication substantive resource freeze
 - **Sun. Feb 26** - Publication total freeze
 - **Mon. Feb 27** - QA period opens
 - **Tue. Feb 28** - [FMM QA spreadsheet](#) updated for all WG resources
 - **Sun. Mar. 13** - QA period closes
 - **Sun. Mar. 20** - All QA applied
 - "following week" STU 3 is published
- **V2 "Lite" / LRI**
 - LRI PSS update
 - Weekly V2 Lite sub-group meeting
 - Mondays, at 12:00-1:00PM ET
 - day/time based on respondents to doodle poll sent out last month
 - First meeting yesterday
 - http://wiki.hl7.org/images/a/a9/HL7_CG_V2_20161205.pdf
 - Triaged a block of Negative votes, to be sent to larger group for block vote.
- **Decision Making Processes**
 - http://www.hl7.org/documentcenter/public/wg/clingenomics/HL7_WG_DMP_v3.0_CG_v2_09172014%20final.doc
- **San Antonio WGM - Agenda**
 - http://wiki.hl7.org/index.php?title=File:HL7_WGM_Jan2017_-_Clinical_Genomics_Agenda.docx
- **Other**
 -
- **Chat**
 - from Kevin M. Power (internal) to Everyone:
 - Hi everyone - I have started the WebEx, but won't be joining the audio today (in case someone tries to ask me something). Have a good meeting.
 - from Andrea Pitkus to Everyone:

- This looks great David! It captures many of the different use cases where genetic testing is valuable for patient care.
- from Bret Heale to Everyone:
 - looking forward to reading it...how about just removing 'Sequencing'and replace with 'Genomics in Practice'
- from Bret Heale to Everyone:
 - or just Genomics
- from Bob Milius to Everyone:
 - @Bret, because it's focussed on a sequencing workflow. It doesn't cover other kinds of methods, like FISH

Bret: makes sense, thx. after the discussion, the idea of somehow communicating that this document is a 'living' document which will be versioned as new knowledge is brought to bear seems worthwhile to me.