HL7 Clinical Genomics Call: FHIR IG publishing discussion - 24 Sep 2019 11:00 AM (US Eastern)

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

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(Presiding co-chair: Kevin Power - kpower@cerner.com)

1. James Jones - BCH - james.jones.bch@gmail.com
2. Liz Amos - NLM - liz.amos@nih.gov
3. Bob Dolin - Elimu Informatics - bdolin@elimu.io
4. Patrick Werner - MOLIT Institut - pw@molit.eu
5. Joel Schneider - NMDP/CIBMTR - jschneid@nmdp.org
6. Nephi Walton - Geisinger - nawalton@geisinger.edu
7. Darren Johnson - Geisinger - dkjohnson3@geisinger.edu
8. Bob Milius - NMDP/CIBMTR - bmilius@nmdp.org
9.

Notes

BLOCKER

AFTER_Publication

- Review of WGM outcomes
  - Notes: https://docs.google.com/document/d/1dPlTu4yqqJRD4nO_8Chk3G4S1jkIDetIcTGNdOueAdk/edit#
- (blocking) todos before publishing

- Must-support & cardinalities
  - Just remove all must-supports? Reassess must supports as they are inherited by profiles
  - Review cardinalities
    - Replace with WARNING/Error → Invariant
    - Remove Observation.interpretation 0..0 (need tracker) https://gforge.hl7.org/gf/project/fhir/tracker/?action=TrackerItemEdit&tracker_item_id=24879
- Resolve build errors
  - Anchor links are the only build errors as of now
  - New Icon build error?
  - Broken links should be fixed soon but can be ignored
- Getting validation errors resolved

many examples do not validate against an IG profile using the FHIR Validator (voted/approved)

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  - Tx server errors should be resolved next update of Tx server
  - Matching multiple error class should go away after Tx server fix
- CodeSystems
  - Updated uri's (technical correction)
  - Write letter to HGNC
  - Create 2 new CodeSystems Genes and Gene Families in HGNC
- Align Haplotype with Variant
  - Add note: we aware that these profiles aren't inconsistent will be addressed in a future version. Do the alignment after publication.
- Applying changes of "resolved - change required" (9 trackers)
  - All change required ballot comments need to be addressed unless retracted by submitter
    - Update from Clem: "I'll take em out if I have to"
  - Committee-requested changes not specifically stating inclusion before the next release have more lee-way, can be voted on in committee under due process.
  - Need to send out the 9 trackers, call out the submitter, and ask if they wish to withdraw / defer to next ballot. If not, we should plan to apply, and need someone to assign to each one.
- Names and headings
  - Spreadsheet can capture Title and Computable names
- Add Glossary
- Update Queries
  - Bret H did work at Connectathon?

Additional request:

- Add variant component for Allele origin (could bind to https://dataexchange.clinicalgenome.org/interpretation/terminologies/AlleleOriginValueSet.html)

24853	need data element for Variant Inherited From

    - Can currently send as locally defined component, haven't been able to fully vet use case for it yet
        - looking for relevant LOINC code