

# 2020-09 CG WGM Agenda - Virtual

## Create Attendance

Create Minutes

- CG-2020-09 WGM Attendance (Clinical Genomics)

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Attendance Instructions:

- 1) Always be logged into Confluence
- 2) Only click "Check In" the first time to add your name
- 3) After that, click "Edit" by your name
- 4) If you have multiple rows, click delete on the extra rows.

### SESSIONS

Day	Date	Time	Event	Host	Joining	Chair	SCRIBE	Notes
Monday	September 21	12:00 PM - 1:45 PM (EDT) (UTC-5)	Session 1 Additional IG content/documentation Work on examples <a href="https://jira.hl7.org/browse/FHIR-28403">https://jira.hl7.org/browse/FHIR-28403</a> Monday Q2				Jamie	BF avail 2nd half only
Monday	September 21	2:00 PM - 3:45 PM (EDT) (UTC-5)	Session 2 1. S4G (first) 2. Family History (Grant)? 3. examples (cont) Monday Q3				Jamie	BF avail 1st half only <ul style="list-style-type: none"> <li><del>emerge</del> <ul style="list-style-type: none"> <li>no new updates</li> <li>might be worthwhile to review issues previously reported</li> </ul> </li> <li>(moved mCode to Wed Session 6)</li> </ul>
Monday	September 21	4:00 PM - 6:00 PM (EDT) (UTC-5)	CG-FHIR-I Joint session with FHIR-I 15 minute summary presentation and 15 minutes of discussion time on specific work group issues Monday Q4	FHIR-I		N/A	Jamie	<ul style="list-style-type: none"> <li>FHIR-I Points               <ul style="list-style-type: none"> <li>Improve FHIR build tooling (separate branch to main build)                   <ul style="list-style-type: none"> <li>R4B release</li> <li>R5 ballot</li> </ul> </li> <li>FMM levels for resources</li> <li>'Must Support' in IGs</li> </ul> </li> <li>CG Discussion points:               <ul style="list-style-type: none"> <li>MolecularSequence - alignment with IG / clean up</li> <li>IG - STU2 ballot in Jan 2021</li> <li>MolSeq + IG alignment with emerging IM model</li> <li>R4B request - cleanup of 'genomics guidance' page?</li> <li>Guidance for WGs that were maintaining IGs via spreadsheets?</li> <li>"Compare Profiles" - how to learn if an instance is compatible with multiple profiles. How to ensure that a profile can be compatible with multiple other profiles? Tooling seems broken.</li> <li>New Resources - Is this the process?                   <ul style="list-style-type: none"> <li>Resource Proposals</li> </ul> </li> </ul> </li> </ul> <ul style="list-style-type: none"> <li>CG members should relate FHIR issues that are important to resolve</li> <li>Could be a prelude to tooling discussion</li> <li>Can we confirm what time slot will we be presenting? - Jamie will try to find out</li> </ul>
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Tuesday	September 22	10:00 AM - 11:45 PM (EDT) (UTC-5)	Session 3 Tuesday Q1	Joint session with O&O	O & O	N/A	Patrick	<ul style="list-style-type: none"> <li>Diagnostic report...I think it is time for a cross-domain (AP, CG, etc.) IG. We need to take what we have on a test drive to see where the gaps are. <ul style="list-style-type: none"> <li><b>FHIR-20315</b> - Genomic Diagnostic reports should have better ability to reference another diagnostic report. <span>TRIAGED</span></li> </ul> </li> <li>Further discussion/plans on the use of "notes" or something else for extra information on genetic findings that we talked about a few months ago. <ul style="list-style-type: none"> <li>in particular, in place of eMERGE's 'Summary/InterpretationText' extension (<a href="https://emerge-fhir-spec.readthedocs.io/en/latest/artifacts/extensions.html">https://emerge-fhir-spec.readthedocs.io/en/latest/artifacts/extensions.html</a>)</li> <li>And Test Disclaimer: <a href="https://emerge-fhir-spec.readthedocs.io/en/latest/artifacts/extensions.html#x6-test-disclaimer">https://emerge-fhir-spec.readthedocs.io/en/latest/artifacts/extensions.html#x6-test-disclaimer</a></li> </ul> </li> <li><b>FHIR-20978</b> - Ability to include interpretation text/findings and recommendations to Observation <span>TRIAGED</span></li> <li><b>FHIR-26362</b> - What is an appropriate resource and element to include addendum text? <span>TRIAGED</span></li> <li><b>FHIR-25170</b> - relatedArtifact extension on Observation.component <span>TRIAGED</span></li> </ul> <ul style="list-style-type: none"> <li>Discuss the ability / guidance around delivering biomarker observations</li> <li>Merging DocRef/Media - updates on current status</li> <li>Alignment of Observation.category and DiagnosticReport.category valueSets?</li> <li>FYI update on OO/PA work on a new "task"-like resource to handle the movement of specimens and other procedural things</li> </ul>	
Tuesday	September 22	12:00 PM - 1:45 PM (EDT) (UTC-5)	Session 4 Tuesday Q2	Jira review			Kevin Patrick	<p>Liz / Rachel</p> <ul style="list-style-type: none"> <li><b>FHIR-27748</b> - Rename "Functional Annotation" Component to "Variant Consequence" <span>APPLIED</span></li> <li><b>FHIR-27747</b> - New Component for Functional Effect <span>TRIAGED</span></li> </ul> <p>Kevin (discuss what the 'genomics guidance' page should/should not contain)</p> <ul style="list-style-type: none"> <li><b>FHIR-27159</b> - Update Genomics Guidance page to more clearly point to our IG <span>RESOLVED - CHANGE REQUIRED</span></li> <li><b>FHIR-16402</b> - Add material from guidance document <span>RESOLVED - CHANGE REQUIRED</span></li> </ul> <ul style="list-style-type: none"> <li>Ready to Vote: <a href="https://jira.hl7.org/issues/?filter=13081">https://jira.hl7.org/issues/?filter=13081</a> <ul style="list-style-type: none"> <li>actually not quite ready to vote</li> <li>need to review comments</li> </ul> </li> <li>Not ready to vote - still needs discussion <ul style="list-style-type: none"> <li>Pending with a resolution: <a href="https://jira.hl7.org/issues/?filter=13016">https://jira.hl7.org/issues/?filter=13016</a></li> <li>Pending with no resolution: <a href="https://jira.hl7.org/issues/?filter=12414">https://jira.hl7.org/issues/?filter=12414</a></li> </ul> </li> </ul>	
Tuesday	September 22	2:00 PM - 3:45 PM (EDT) (UTC-5)	Session 5 Tuesday Q3	<ol style="list-style-type: none"> <li>mCode (May T)</li> <li>Tooling <ol style="list-style-type: none"> <li>IG creation/publishing</li> </ol> </li> </ol>			Kevin Jamie		
Day	Date	Time		Event	Host	Joining	Chair	SCRIBE	Notes
Wednesday	September 23	10:00 AM - 11:45 PM (EDT) (UTC-5)	Session 6 Wednesday Q1	1. Jira review (cont)			Patrick	Jamie	<ul style="list-style-type: none"> <li><b>FHIR-16402</b> - Add material from guidance document <span>RESOLVED - CHANGE REQUIRED</span></li> <li><b>FHIR-27864</b> - Update binding to LOINC Diagnostic codes value set <span>WAITING FOR INPUT</span></li> </ul> <ul style="list-style-type: none"> <li>LOINC / "TBD code" reconciliation</li> </ul>
Wednesday	September 23	12:00 PM - 1:45 PM (EDT) (UTC-5)	Session 7 Wednesday Q2	IM summary/work			Bob	Kevin	<ul style="list-style-type: none"> <li>overview of where we are</li> <li>update on recent modeling</li> <li>roadmap - priority <ul style="list-style-type: none"> <li>laundry list of what we can do</li> </ul> </li> <li>technical approach to implement into FHIR IG</li> <li>GA4GH alignment</li> </ul>
Wednesday	September 23	2:00 PM - 3:45 PM (EDT) (UTC-5)	Session 8 Wednesday Q3	<ol style="list-style-type: none"> <li>Wrap up</li> <li>Additional IG content/documentation</li> <li>Work on examples</li> </ol>			Jamie	Bob	KP avail 1st half only

## Other Proposed Topics

- Build Examples
  - Arthur - look at whole IG, examples, identify what needs to be updated
    - focusing on variant right now
    - standard genetic test data
    - interested in retrospective reports
    - will provide examples of their needs
  - Anand (Clinical Architecture) - wholehearted agreement in need for examples
  - Bret - can we work through an example during one session?
  - Jamie - can put through an example of something that has been figured out
  - Arthur - review v2 LRI genetics examples - can we convert each to FHIR without losing information?
- May - work through what's already there (Jamie's work with spreadsheet)
  - Jamie agrees
  - Preparation needed - Jamie will lead, topic for Mondays
  - Anand - wants to be involved
  - JD Nolan - would like this to be on Monday of the WGM
- \* Existing JIRA review
  - Kevin (from zulip) - I know the meeting is going on, but while I am on my conflict call, but for WGM topics, don't forget we can/should do a review of pending JIRAs. Discuss resolution, and perhaps even vote on some
  - Jamie - finish work on implication (current Jira tickets)
- \* External Efforts
  - Jamie - have a session on mCode or another external effort?
  - \*Arthur - update on eMerge?
  - Jamie - Sync 4 Genes?
- \* Modeling
  - Arthur - need a session on IM at WGM and implications on the IG
- \* Additional IG topics
  - May - continue discussion with Swapna( with LOINC - need to contact for availability
    - Clem - need proposed changes to submit to LOINC
    - May - need to create the proposal
    - Need to have it ready before WGM as strawman proposal to vote on or change
    - Clem - Swapna has no opinion on what should be proposed
    - perhaps use a call between now and WGM to work on proposal
    - Clem - need loinc codes and answer lists, if new loinc codes then we need definitions
    - Patrick - need some kind of preparation of WGM
      - chat
      - summarize current state
      - identify gaps, and decisions that are needed
  - Patrick - interested in order entry, what does it mean to order a panel. Need examples. Need guidance.
    - Bob - need to provide specific guidance around ServiceRequest codes and DR codes.
- Tooling
  - May - revisit tooling, delve into IG authoring tool options
    - right now we're editing SDs
- Additional content / documentation
  - Bret - can we record the intro session?
  - Jamie - can create more slides for intro/teaching. We created some for DevDays
  - Patrick - need to update those slides