2016-06-08 - SLPG Meeting

Date & Time
Wednesday 8th June 2016, 20:00 UTC

GoToMeeting Details
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Click here to see GoToMeeting recordings

Goals
- To finalize the ECL v1.1 updates
- To briefly mention MRCM development work
- To continue work on SNOMED CT Templates

Attendees
- Chair: Linda Bird
- Project Group: Ed Cheetham, Michael Lawley, Daniel Karlsson, Harold Solbrig, Rob Hausam
- Linda Bird
- Michael Lawley
- Ed Cheetham
- Daniel Karlsson
- Harold Solbrig
- Rob Hausam

Apologies
- Alejandro Lopez Osornio, Brian Carlsen

Observers

Agenda and Meeting Notes

<table>
<thead>
<tr>
<th>Item</th>
<th>Description</th>
<th>Owner</th>
<th>Notes</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Welcome, introductions and apologies</td>
<td>Linda Bird</td>
<td>Apologies from Alejandro and Brian</td>
<td>Check attendance details and apologies</td>
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<tr>
<td>2</td>
<td>Agenda review</td>
<td>Linda Bird</td>
<td>Review agenda for today's meeting</td>
<td>Review agenda</td>
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<td>3</td>
<td>ECL</td>
<td>Linda Bird</td>
<td>Discuss finalization of Expression Constraint Language</td>
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<td></td>
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<td></td>
<td>Correct childOf, parentOf symbols to “&lt;!” and “&gt;!” respectively.</td>
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<td>3</td>
<td>MRCM</td>
<td>Linda Bird</td>
<td>A brief look at how we plan to use Expression Constraints and Expression Template in the MRCM.</td>
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<td>Example attribute rule:</td>
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<td></td>
<td></td>
<td></td>
<td>(&lt;&lt; 404684003 (Clinical finding (finding)) OR &lt;&lt; 272379006 (Event (event))):</td>
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<td></td>
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<td></td>
<td>[0..<em>] { [0..</em>] 255234002 (After (attribute)) = (&lt;&lt; 404684003 (Clinical finding (finding)) OR &lt;&lt; 71388002 (Procedure (procedure))) }</td>
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<tr>
<td>4</td>
<td>Template Syntax - FHIR Examples</td>
<td>Linda Bird</td>
<td>Condition</td>
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<td></td>
<td></td>
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<td>([1..1]@findingWithExplicitContext):</td>
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<td></td>
<td></td>
<td></td>
<td>[1..2]@RG1 { 246090004 (Associated finding) = [0..1]@associatedFinding ];</td>
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<td></td>
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<td></td>
<td>[0..1]@RG2 { 246112005 (Severity) = [0..1]@severity},</td>
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<td></td>
<td></td>
<td></td>
<td>363698007 (Finding site) = [0..1]@findingSite )</td>
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<td></td>
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<td>408732007 (Subject relationship context) = 410604004 (Subject of record),</td>
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<td>408731000 (Temporal context) = [1..1]@temporalContext ],</td>
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<td>408729009 (Finding context) = [1..1]@findingContext ] )</td>
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<td>AllergyIntolerance</td>
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<td>([1..1]@findingWithExplicitContext[]):</td>
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<td>[0..2]@RG1 { 246090004 (Associated finding) = [1..1]@associatedFinding ];</td>
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<td>370135000 (Pathological process) = [0..1]@pathologicalProcess ],</td>
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<td>[0..1]@RG2 { 255234002 (After) = [0..1]@after },</td>
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<td>246075003 (Causative agent) = [1..1]@causalAgent ];</td>
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<td>408732007 (Subject relationship context) = 410604004 (Subject of record),</td>
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<td>408731000 (Temporal context) = [1..1]@temporalContext ],</td>
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<td></td>
<td>408729009 (Finding context) = [1..1]@findingContext ] )</td>
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<td>Procedure</td>
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<td>129125009 (Procedure with explicit context):</td>
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<td>[1..1]@RG1 { 363589002 (Associated procedure) = [1..1]@associatedProcedure ];</td>
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<td>363704007 (Procedure site) = [0..1]@procedureSite ],</td>
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<td>363699004 (Direct device) = [0..1]@directDevice ],</td>
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<td>424361007 (Using substance) = [0..1]@usingSubstance ];</td>
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<td>424226004 (Using device) = [0..1]@usingDevice ] )</td>
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<td></td>
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<td>408732007 (Subject relationship context) = 410604004 (Subject of record),</td>
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<td></td>
<td></td>
<td>408731000 (Temporal context) = 410512000 (Current or specified time),</td>
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<td></td>
<td>408729004 (Procedure context) = [0..1]@procedureContext ] )</td>
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Review discussion on optionality and populating attribute groups:

1. Scope and purpose of syntax
   a. Extract/disentangle SNOMED CT (and SNOMED CT-relevant) content from a FHIR Condition resource (i) into a free-standing and 'recognisable' SNOMED CT expression, whilst (ii) 'leaving nothing behind' which may be of relevance to further processing.
   b. Specify mappings from FHIR value sets (e.g. Condition.clinicalStatus) into SNOMED CT
   c. Transform the extracted expression into an ‘optimally-processable’ SNOMED CT expression (in particular grouping body site values with morphology)
   d. Specify constraints on what the extracted/disentangled SNOMED CT expression could or couldn’t contain (by e.g. cardinality instructions).

2. Cardinality - How to specify cardinality of (i) an attribute, (ii) an attribute group, (iii) a focus concept?
   3. Do we need to be able to name the role groups to refer to them in the Mapping/Transformation code?
   4. What will the mapping/Transformation code look like? What dependencies does it have on the Template?