2018-05-22 - SNOMED on FHIR Meeting (TB)

Date/Time

20:00 UTC on Tuesday 22 May 2018 - 90 minutes.

Meeting Details

Online: https://snomed.zoom.us/my/snomedhl7

Phone: See https://zoom.us/zoomconference for available phone numbers (meeting id **242-348-6949**)

Chat: https://chat.snomedtools.org/channel/snomed-fhir
(instructions and guide here - Getting Started with Rocket Chat)

Objectives

- Bindings to FHIR Clinical Resources (e.g. value set bindings)

Attendees

Rob Hausam, Peter G. Williams, Jeremy Rogers, Jane Millar, Linda Bird, Anne Randorff Højen, David Sperzel, Peter Jordan, Patrick Granvold, Yongsheng Gao

Apologies

Meeting Recording

https://snomed.zoom.us/recording/share/ay4aGTawb2k_7aPySU4yvd7b-HzLKvTMHeqmpy6cch2wIumekTziMw

Discussion items

Item	Description	Mins	Owner	Notes & Actions
1	Welcome and introductions	5	Peter G. Williams Rob Hausam	Recording + Notes.
2	Summary of previous week	5	Peter G. Williams Rob Hausam	Summary of previous week: - 2018-05-15 - SNOMED on FHIR Meeting (TS)
3	Update from HL7 Cologne	20	Rob Hausam	Discussions around use of SNOMED CT in FHIR and renewed possibilities of a "free set" of codes used in "required" bindings. Jane is waiting for update from Graham G. Terminfo project - original project will be retired, CDA guide has been published. Moving to collaborative effort with SNOMED International, with more official HL7 participation. Update next week on proposed changes to Terminology Services.
4	Condition Resource	60	Jeremy Rogers	Condition Resource ☐ All please review the above page. Discussion on https://www.hl7.org/fhir/v3/NullFlavor/cs.html and whether null type values (eg UK's "Unknown Severity") should have their use dictated. RH Said the FHIR approach was to not represent unknown data ie leave field blank. Note that the removals in the ECL for Condition.code were stated to avoid overlap with the Allergy resource ie to make the two valuesets disjoint. Issue with how to specify laterality if an implementer is not capable of doing post-coordination. ☑ Jeremy Rogers to supply material from the UK's work on this resource. Discussion on problem list for "code" element requested by suppliers. Would be helpful to have access to real data in order to "sanity check" problems reported against the suggested binding. For example, suggestion to remove "Allergic reaction to substance", "Pseudoallergy to substance" and "Allergic disposition" from << Clinical Finding rather than "Hypersensitivity condition" In terms of deliverable output going forward, we have a GitHub project that can contain profiles, for example these ones supplied by Daniel: https://github.com/IHTSDO/snomed-ig/tree/master/profiles/clinical/summary

5	Profile for Specimen Resouce	10	Jeremy Rogers	Specimen binding - follow up
				Suggestion from Jim Case that the type attribute would be better bound to (< Substance OR < Morphologic Abnormality OR < Physical Object (or selection thereof)) rather than Specimen as it avoids any potential conflict with the other attributes and is effectively opening up post coordination, rather than sticking to a inherently restricted set of pre-coordinated concepts.
				Similarly (Linda Bird), the method attribute is currently a selection of SNOMED CT concepts plus a V2 valueset.
				Two main options:
				1. Use Specimen hierarchy for "type" (*suggested new .code element*) and then constrain what can appear in the other fields (and how we deal with conflict!). This concept could also be a post coordinated expression in the "type" attribute (Jim Case noted that some aspects - like the shipping container - may not be characteristics intrinsic to the specimen). 2. Specify appropriate bindings for individual elements.
				Jim Case also suggested that using these decomposed fields would only be used outside of a SNOMED context. Otherwise could be achieved - (PWI: more safely due to MRCM) - with post coordinated. However (PWI notes): some members are some way off being able to use post-coordination and - at the same time - would experience restriction if limited to pre-coordinated content.
				☐ Rob Hausam Solicit opinion / Create tracker item to take forward the 3 suggested (see bold items) added to Specimen binding page. FOA HL7's Orders and observations group.
				☐ Suggested work to look through the V2 value set here to collect a set of SNOMED sub-hierarchies that would cover same. (NHS will get to this resource at some point!). Note that advertising provenance of each ValueSet would give some confidence the quality. Also document rational for inclusions.
				☐ Peter G. Williams 434711009 |Specimen container (physical object)| appears insufficient for binding to Specimen container. Investigate possibilities for development in this area to better support FHIR (Pathology working group? PALM). Also additives potentially more interesting.
				☐ Rob Hausam follow up that http://build.fhir.org/valueset-specimen-container-type.html contains not relevant information about Cholesterol.
				Suggestion (LB) for decomposition template that would describe the mapping from a post coordinated concepts into the various FHIR fields.
6	ValueSets	10		How do we produce and publish ValueSets?
				• Tools?
				☑ Question for Daniel Karlsson - Were you suggesting that we systematically replace HL7 ValueSets with SNOMED CT equivalents? Or are there places where ValueSets are required that aren't currently specified?
7	Next meeting	5		Tuesday 5 June 2018
				Next Resources to look at: Observation, Medication selected. Dion McMurtrie may have an interest here.

Meeting Files

File	Modified

No files shared here yet.

Previous Meetings

Title	Creator	Modified

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