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201917 Integrating the SNOMED CT and AMT drug models, revisited

Michael Lawley , AEHRC, CSIRO (Australia)

Summary

We review the new International drug model and AMT V3 to understand their possible alignment. We describe the use of GCIs to manage variations in the drug strength models. We describe a heuristic approach to aligning the two substance hierarchies and detail issues found following classification.

Audience

Technical , Research/academic

Learning Objectives

1. Understanding of the International drug model and AMT V3 and their differences.
2. An introduction to the potential of GCIs for integrating drug models.
3. Insight into a range of specific and general issues relating to integrating a national drug model with the international model

Abstract

The SNOMED CT drug model is intended to be useful as a common generic model from which various national drug models can extend. In this way, national drug models represent the specific brands and packaging available on the local market, while the international model provides a common abstract layer that supports shared knowledge artifacts such as drug-drug interaction models and drug-condition contra-indications.

The Australian Medicines Terminology (AMT) V3 was released in June 2014 as a SNOMED CT extension which fully modelled drug concepts using concrete domains for strength information. Due to limitations and ambiguities in the SNOMED CT substance hierarchy that make it unsuitable for fully-defining drug concepts, AMT uses its own disjoint substance hierarchy. The consequence of this is that the AMT model is effectively disjoint from the rest of SNOMED CT, and in particular the drug class concepts and the Clinical Finding concepts that reference said drug classes.

Previous work on integrating these models focused on the older AMT V2 model where all AMT drugs were primitive, and strengths were not modelled as well as the then International drug model. It used a purely lexical-match based approach to develop a substance-to-substance map as the basis for integrating the two models. This work uses the

AMT V3 model, the latest, revised, International drug model that is based on IDMP, and seeks to make use of newly supported description logic features such as GCIs and concrete domains.

Our new approach to integration makes use of GCIs to resolve differences in the modelling representations of strengths. Furthermore, instead of using the ADHA's AU-substance to INT-substanxce map directly, we use several heuristics to identifiy those hierarchical relationships between base and salt-form substances in the International model that violate the expectations and requirements of the AMT drug model. These relationships are then re-targetted for the purposes of the integration.

By classifying the resulting integrated model and inspecting the results, we are able to evaluate aspects of the suitability of the International model for its intended role as a common integration layer as well as identify some existing modelling errors and limitations in both models.