

Title: Encoding microbiology *In Vitro* Diagnostics (IVD) tests results with SNOMED CT : assessment & road blockers

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Audience

Those involved in transmitting IVD tests results to LIS for further integration into EHR.

Objectives

This study has two objectives : (i) demonstrate feasibility of SNOMED CT to encode microbiology IVD tests results and (ii) identify road blockers preventing a full use of SNOMED CT in this use case.

Abstract

Each IVD systems transmits its tests descriptions (aka. Observations¹) and tests results (aka. Observation Values¹) to the LIS using its owns idiosyncratic vocabulary thus posing interoperability challenges.

Through its VITEK2® system running automated microbiology identification and antibiotic susceptibility testing, bioMérieux made a first step toward the current standards in health IT. Indeed the last version of this system implements HL7 - LAW profile together with LOINC codes^{1,2}.

We want to (i) know to which extend SNOMED CT allows to code microbiology IVD observation values, (ii) identify the technical road blockers for a global adoption of SNOMED CT to code microbiology IVD observation values and lastly (iii) propose options to circumvent those blockers.

We present our syntactic alignment results between the microorganism taxonomy managed at bioMérieux and the SNOMED CT 410607006 | Organism (organism) | and 404684003 | Clinical finding (finding) | hierarchies concepts. We focused on 2 IVD systems observation values (VITEK2®, VITEK MS®) representing 958 taxa. 88% of those correspond to consensual taxa (fully aligned onto the referenced publications such as ICSP, i.e. ‘International Committee on Systematics of Prokaryotes’) and 12% fit instruments analytic capabilities (i.e. variant, taxon groups and ‘x OR y’ organisms).

We are able to map to SNOMED CT 83% of VITEK2® and 95% VITEK MS® taxa. Coverage analysis by taxon rank shows that 94% of consensual taxa are mapped (100% of genus; 93% of species and subspecies) whereas most of non-consensual taxa as ‘x OR y’ taxa (58%) and variants (78%) are not. We also observed wide differences of alignment coverage between bacteria, yeasts and filamentous fungi.

The road blockers preventing a full SNOMED CT adoption to code microbiology IVD Observation values are (i) those unmapped taxa and (ii) ‘x OR y’ and ‘groups’ taxa spread between core and national extensions (US & Canadian ones where investigated). This work is being expended to all our IVD systems observation values as well as our full collection of taxonomy.

References

1. Understanding Observations and Observation Values ; <https://www.healthit.gov/isa/node/1096>
2. VITEK® 2 System connectivity enhanced with support for the ICC/IHE LAW Profile and LOINC® ; <http://ivdconnectivity.org/vitek-2-system-connectivity-enhanced-support-iccihe-law-profile-loinc/>