

Encoding microbiology *In Vitro* Diagnostics (IVD) tests results with SNOMED-CT : assessment and road blocks

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INTRODUCTION

Automated *in vitro* diagnostic (IVD) systems transmit observations and observation values to the LIS using their own vocabulary, which raises interoperability challenges.

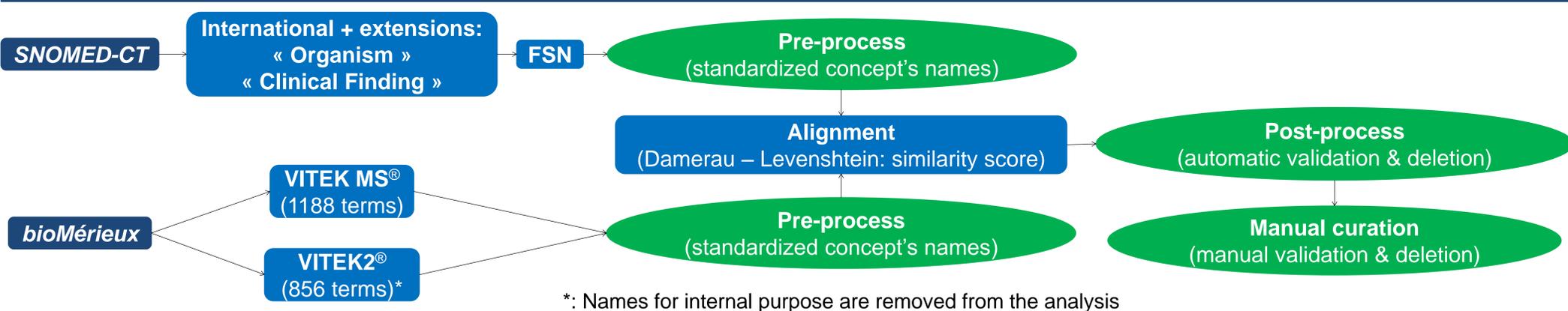
bioMérieux made a first step toward the use of standardized interoperability interface in the last version of its VITEK2[®] system (running automated microbiology identification, ID, and antibiotics-susceptibility testing, AST): implementation of HL7 – LAW profile and use of LOINC to code ‘observations’.

We present our syntactic alignment between ‘observation values’ from two such ID and AST systems (VITEK2[®] and VITEK MS[®]) and SNOMED-CT.

OBJECTIVES

This study aims at (i) investigating the capability of SNOMED-CT to encode microbiology IVD observation values, (ii) identifying the technical road blocks for a global adoption of SNOMED-CT to code microbiology IVD observation values and lastly (iii) proposing options to circumvent those blockers.

METHODS



RESULTS

Figure 1 shows the alignment status after post-process and manual curation steps.

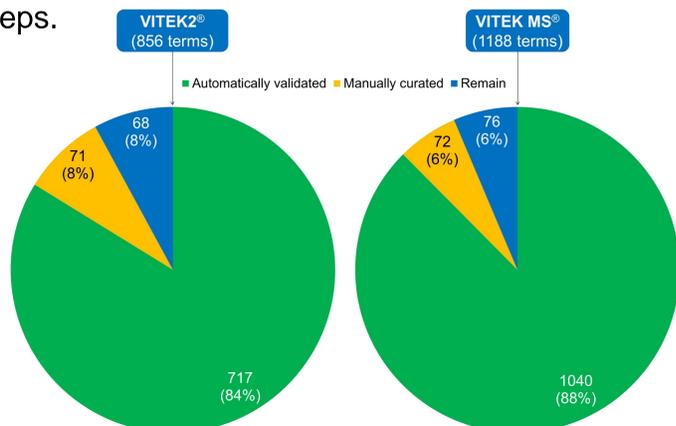


Figure 1: Distribution of VITEK2[®] and VITEK MS[®] terms

We removed terms used on internal process and concentrated on customers facing terms. Figure 2 shows remaining terms by taxon level.

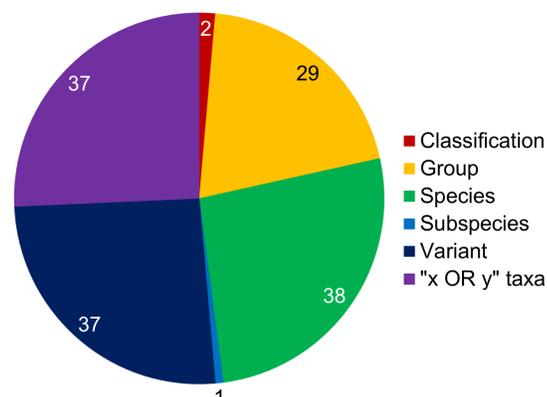


Figure 2: Distribution of VITEK2[®] and VITEK MS[®] filtered remaining terms

Figures 1 and 2 show that non-aligned terms are mainly no consensual taxa (Groups, Variants and ‘x OR y’ taxa). These differ according to the laboratory and are one of the road blocks of our syntactic alignment. Examples of remaining terms are presented in table 1.

In addition **25%** of the remaining consensual taxa (Classification, Species and Subspecies) are **yeast or filamentous fungi**. This is the second road block : Yeast and Fungi taxonomy and nomenclature used to vary according to their different sexual states (pleomorphism and teleomorphism). This is currently subject to revision.

Terms	Taxon level
Cronobacter dublinensis ssp lactaridi	Subspecies
Aspergillus lentulus	Species
Bacillus cytotoxicus	
Actinobacillus equuli or Actinobacillus suis	"x or y" taxa
Nocardia nova or Nocardia africana	
Clostridium group	Group
Fusarium solani complex	
Escherichia coli 1	Variant
Streptococcus suis I	

Table 1: Few examples of VITEK2[®] and VITEK MS[®] remaining terms

A way to fill these gaps is to look on national extensions which may contain new microorganism terms. But last SNOMED-CT Release (2017/07/31), as well as, Canadian, US and UK extension did not improve this situation.

CONCLUSION

Although this study shows that SNOMED-CT is able to code **93% of our terms** (92% for VITEK2[®] and 94% for VITEK MS[®]) it appears that 144 taxa names are not matched. We identify the following road blocks:

- No consensual taxa
- Filamentous fungi and Yeast

These use case warn us to be cautious with National extensions content.

We have a **complete list of SNOMED-CT missing terms** for those 2 products terms. We now look forward to collaborate with SNOMED-CT to fill these gap in the international core, thus allowing world wide usage. The work presented in this study is being expended to all our IVD systems observation values as well as our complete taxonomy.