







**SNOMED CT** 

**Concept ID** 

122551003

**Description ID** 

180796014

peripheral

blood

specimen

1123193014

muestra de

sangre

periférica

## Basis for establishment of the subset of the SNOMED CT terms related to biobanking activity.

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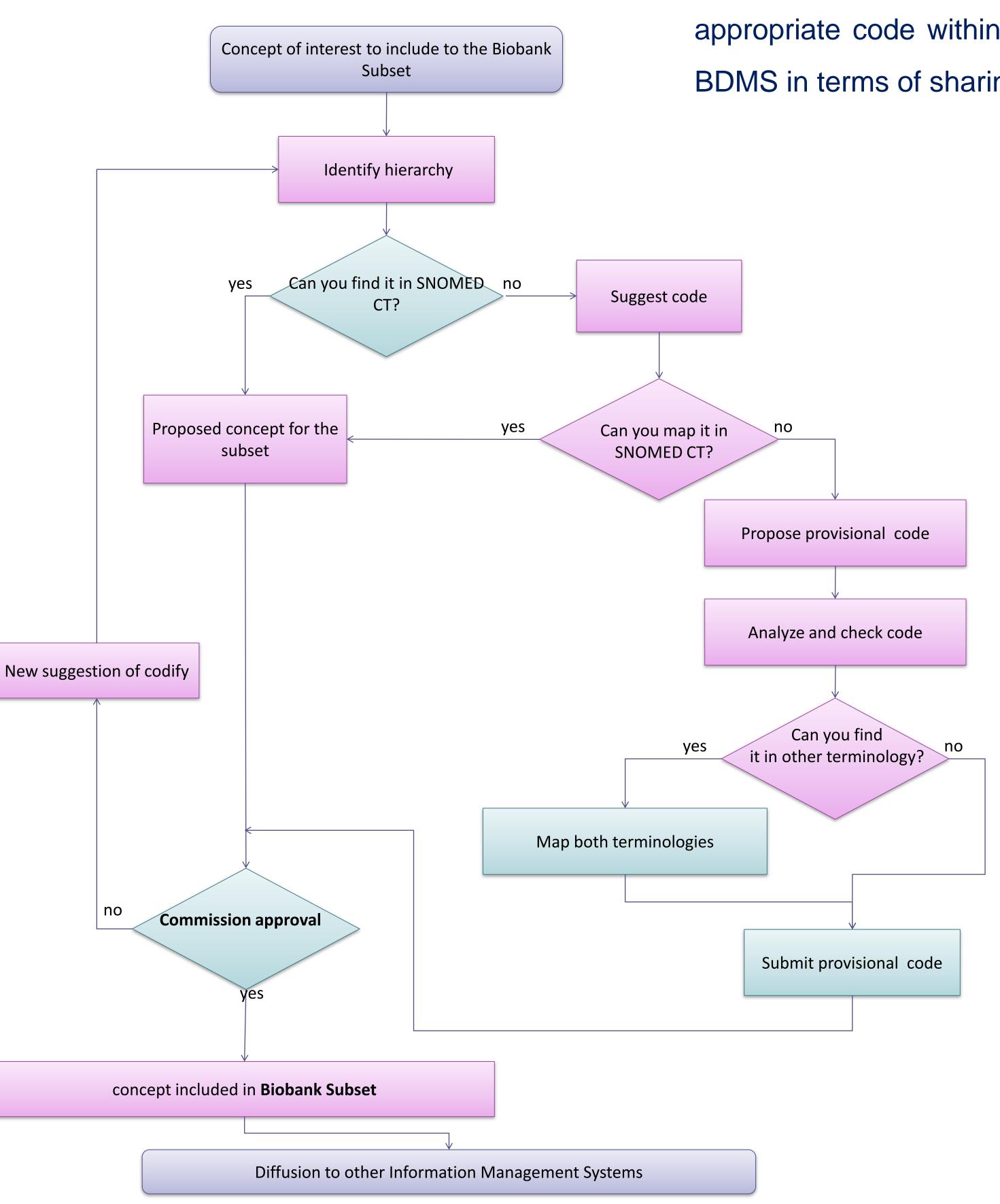
The Valencian Biobank Network (VBN) have unified the coding skills in order to attend to the necessities of integration of its own Biobank Data Management System (BDMS). This work shows the definition of the **subset of terms** referring to the activity **of biobanks**.

Since the beginning of the implementation of this BDMS there was a consensus about the necessity of using standard terminology reference.

The main problems during the implementation of the VBN-BDMS were:

- 1. the different sources of information systems from different areas, with very heterogeneous information;
- 2. the non-coded terminologies, representing a loss of data performance.

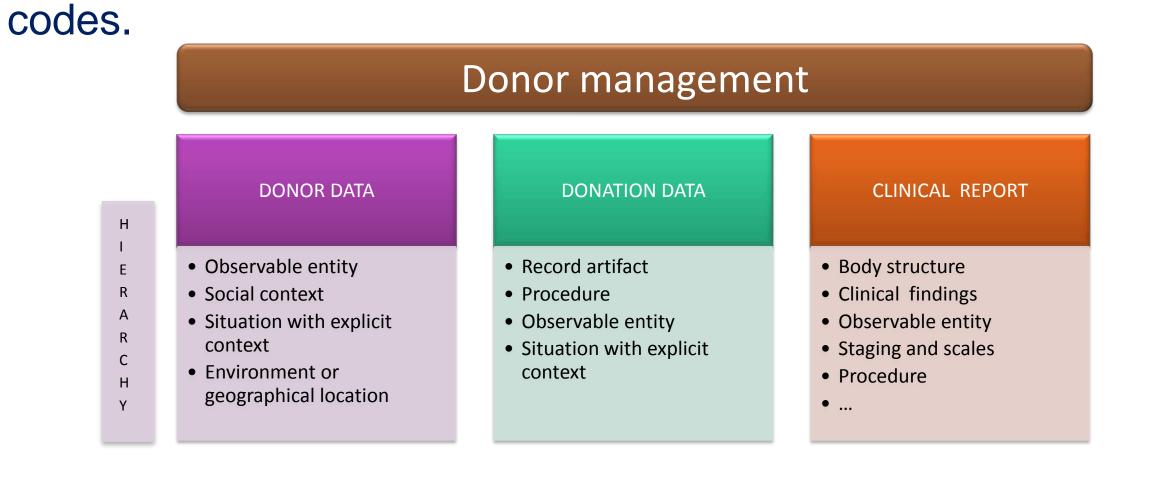
Furthermore, other problem that we find during the BDMS implementation is the absence of the appropriate code within the selected coding system. All together conditions the successful of the BDMS in terms of sharing information in a secure way.



Currently, the VBN is still working on the generation of a list of terms of **biobanking activity** within the context of SNOMED CT criteria. In addition, the functionality of such a subset of terms is being examined for **semantic interoperability** with different information management systems devoted to the mental health, reference population and pathological fields.

The first steps we performed were based on the SNOMED CT codification of the preanalytical variables defined by the SPREC code terminology. The SNOMED CT codification guarantees the decodification and interpretation of the SPREC codes which do not become compromised by the limitations found in the system. Once these objectives were reached, and based on the necessities of interoperability of our BDMS, we also coded terms related to the legal-administrative field and to the associated sample information. As expected, the mapping of the variables based on SNOMED CT was not always possible. For these cases we have

designed a series of algorithms in order to generate a local extension of



BIOBANK SUBSET
of SNOMED CT

