Ontology-based knowledge management for clinical data and pharmaceutical modelling: applying the RICORDO and ApiNATOMY toolkits for drug development

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This presentation outlines tangible interoperability challenges in bridging clinical trial data to related pharmacometric models, as well as relevant solutions, applied by the Drug and Disease Modeling Resource (ddmore.eu). DDMoRe is an Innovative Medicines Initiative project, involving ten global pharmaceutical companies and a number of academic centres, that aims to develop an interoperability framework for modeling in drug development.

Semantic interoperability solutions being tested by the DDMoRe effort involve the combined use of the ontology-based RICORDO semantic metadata framework (ricordo.eu) and the ApiNATOMY toolkit for ontology visualization (apinatomy.org).

The RICORDO framework is based on formal knowledge representation methods, including the use of ontologies, and associated tools. This approach uses the explicit representation of anatomical and medical knowledge in the management of data and model resource (DMR) annotation. These annotations, which constitute the resource metadata, are statements mapping ontology term identifiers onto resource element identifiers. Ontologies facilitate machine processing, standardisation of resource metadata, as well as reasoning. The resulting method allows the navigation and querying of annotation repositories using biomedical knowledge.

The ontology visualization approach central to ApiNATOMY is the depiction of ontology terms as tiles within a treemap (Fig. 1), where child terms of a parent term as shown as child tiles nested within the corresponding parent tile. A second key feature of ApiNATOMY treemaps is the representation of metadata related to a particular ontology term as a symbolic icon embedded within the boundaries of the corresponding term tile.

Although, as the name suggests, ApiNATOMY treemaps are particularly useful in the graphical depiction of treemap schematics representing anatomical structure, in practice ApiNATOMY can be applied to the consistent layout of any ontology. However, for the purposes of this presentation, the use of ApiNATOMY in the automatic generation of anatomy schematics will be described in the context of the visualization of modeling-related RICORDO metadata in drug development.
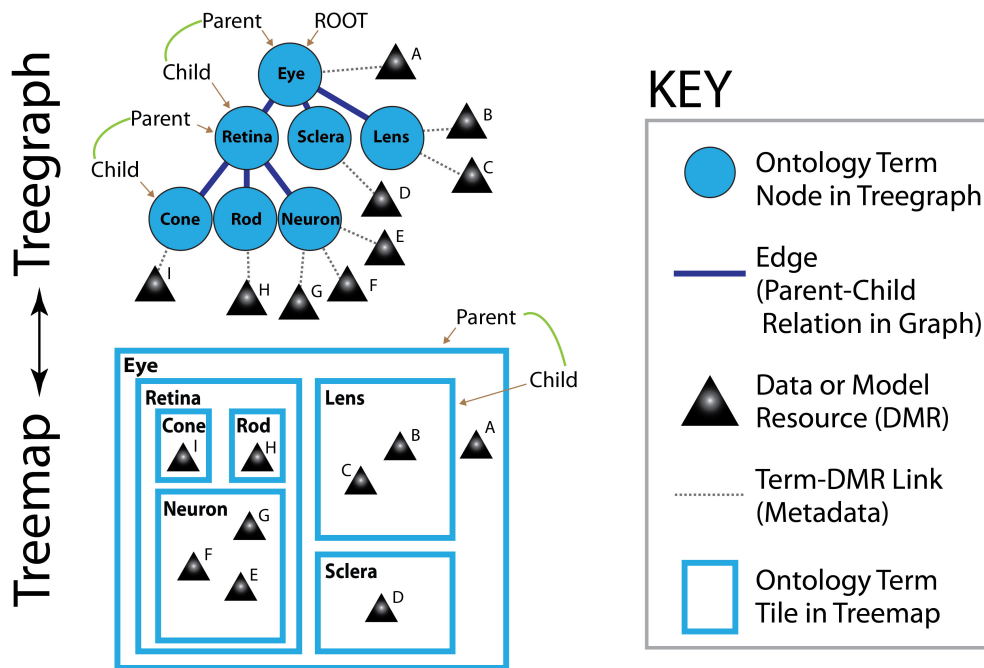
FIGURE 1. A graph representing a simple ontology of eye anatomy is shown in two configurations – in treegraph (top) and topologically-equivalent treemap form (bottom). Ontology terms are depicted as nodes in the treegraph and as tiles in the treemap. An ontology relation is shown as a graph edge (a blue line) that links two nodes in the treegraph, while the same relation is depicted as the location of one tile within another in the treemap (known as 'nesting') – the type of relation is not specified. Data and model resources (DMRs) linked to ontology terms via metadata are represented in triangular form.