Bridging Computational Modelling and Clinical Information using openEHR and Semantic Web

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Background

Linking clinical information to computational physiology will enable real-world model validation as well as pave the way for personalised and population level predictive decision support tools. Electronic health records (EHR) embody quantifiable manifestations of genomic and environmental aspects that impact on biological systems. However data quality and semantic interoperability remains a major challenge in the world of EHRs. In the computational physiology domain recent attempts to enable semantic interoperability heavily rely on Semantic Web technologies and utilise ontology-based annotations (e.g. RICORDO[1]) but a wealth of useful information and knowledge sits in EHRs where Semantic Web technologies have very limited use. openEHR[2] provides a set of an open engineering specifications that provides a canonical health record architecture and open source tooling to support data collection and integration. Core openEHR specifications have also been adopted by ISO and CEN making it a full international standard which underpins many national programs and vendor implementations worldwide[3]. We describe how to use openEHR to normalise, annotate and link clinical data with biophysical models.

Method

At the heart of the openEHR formalism is the *Archetypes* which are constraint based models of health information based on stable technical building blocks (*Reference Model*) that define data structures, types and value sets etc. While the Reference Model provides syntactic interoperability reusable Archetypes define granular clinical concepts like blood pressure measurement, lab results or clinical diagnoses and enable semantic interoperability in healthcare. openEHR provides the means to annotate whole or parts of the information model by a mechanism called *terminology binding*.

A concrete example would be to link the anatomical location to both clinical terminology (e.g. SNOMED CT) and bio-ontology (FMA).
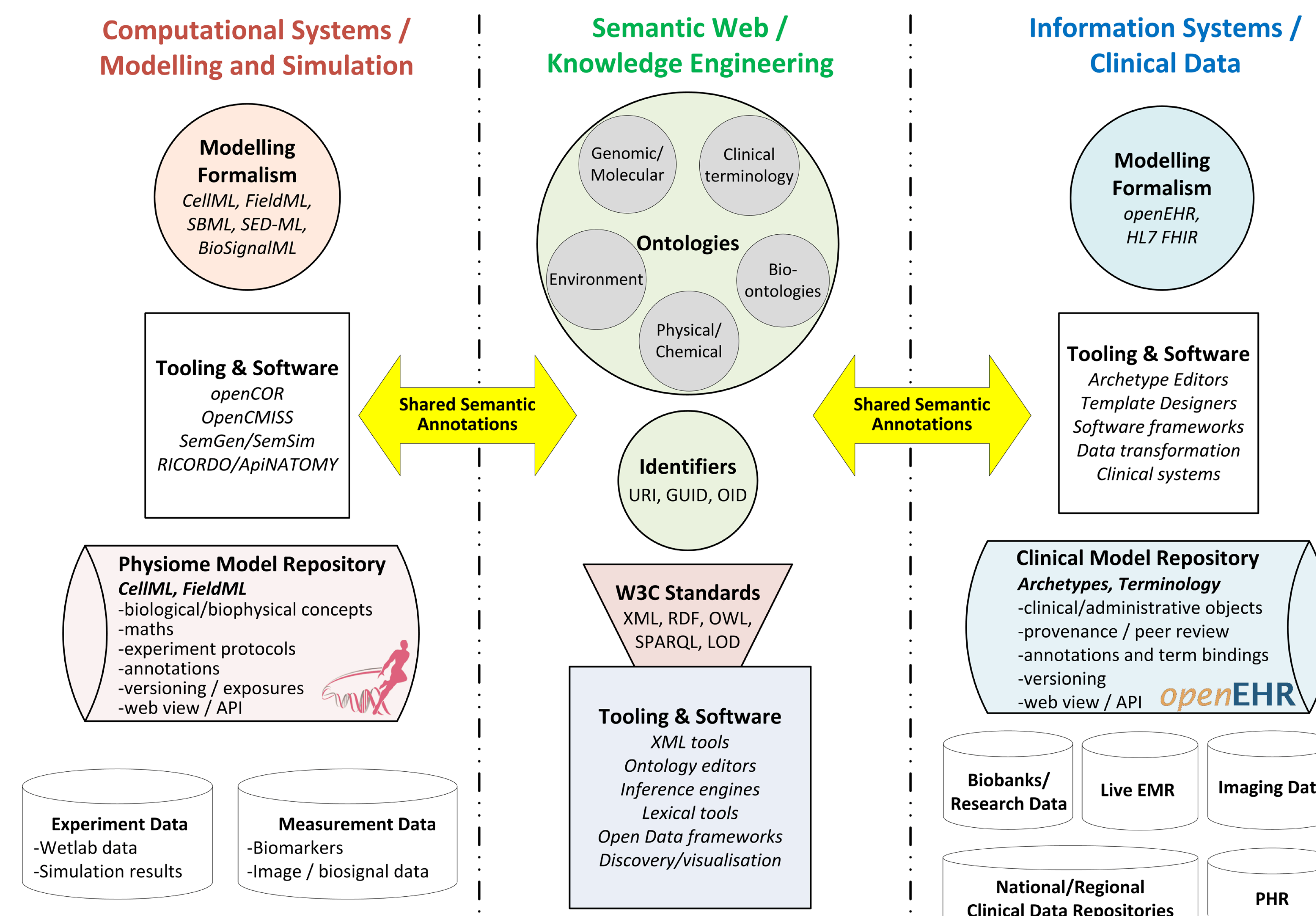
openEHR as the semantic glue between computational physiology and biomedical informatics

Summary

Computational models can be linked to corresponding clinical entities and healthcare processes using openEHR which can link the world of health ICT and Semantic Web based computational physiology and bioinformatics communities. More work is needed around shared ontologies, annotation methods and tooling.

openEHR models are freely available from the Clinical Knowledge Manager (CKM)[4].

References

1. Bono B de, Hoehndorf R, Wimalaratne S, Gkoutos G, Grenon P. The RICORDO approach to semantic interoperability for biomedical data and models: strategy, standards and solutions. BMC Research Notes. 2011 Aug 30; 4(1): 313.

2. http://www.openehr.org

3. ISO 13606 Health informatics-Electronic health record communication

4. http://openehr.org/ckm

Acknowledgements