

# Linking Computational Physiology Models with Clinical Data

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## Background

Linking Computational Physiology Models with Clinical Data can be instrumental for real-world model validation as well as enable personalised and predictive clinical decision support systems. Electronic health records (EHR) are sinks of biomedical knowledge and include manifestations of genomic and environmental aspects that impact on biological systems. However data quality and semantic interoperability remains a major challenge<sup>1</sup>.

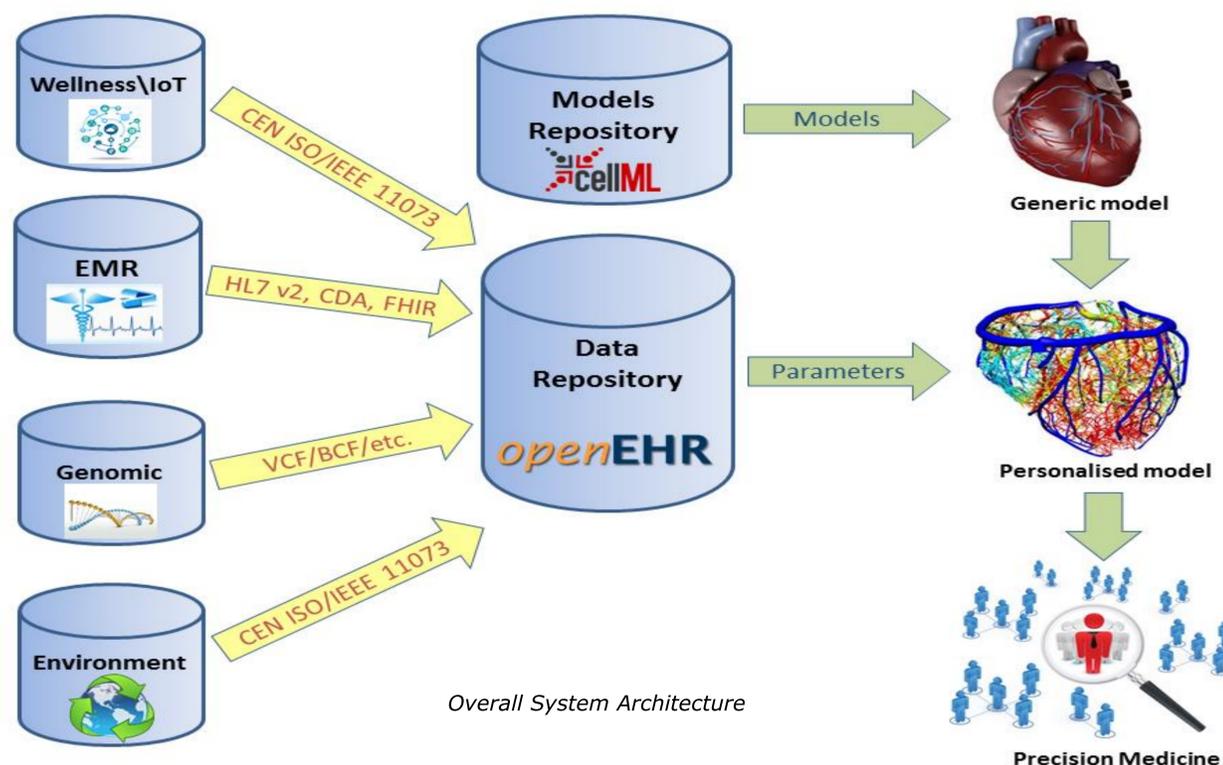
In the computational physiology domain recent attempts to enable semantic interoperability heavily rely on Semantic Web technologies and utilise ontology-based annotations but a wealth of useful information and knowledge sits in EHRs where Semantic Web technologies have very limited use.

## Step by Step Methodology

openEHR<sup>2</sup> provides open standards for structuring and exchange of healthcare data. We describe how to use openEHR to normalise, annotate and link clinical data with computational models.

At the heart of the openEHR formalism is the *Archetypes* which model clinical concepts like blood pressure, lab results or clinical diagnoses. openEHR provides the means to annotate whole or parts of the information model by a mechanism called *terminology binding*. This can then be used to semantically link to annotated CellML models through ontology mapping.

This linkage is bidirectional; e.g. from computational models to clinical data and vice versa. We're providing the necessary steps for the former.



Overall System Architecture

- 1) Select a CellML model with semantic annotations or biophysical ontology term(s) from which to find linked clinical data
- 2) Retrieve all semantic annotations from PMR for the selected model
- 3) Using mappings between ontology and clinical terminology concepts find matching clinical terms
- 4) Find Archetypes with matching terminology bindings leveraging all types of ontology relations (e.g. is-a, part-of) and display as a list/graph
- 5) Retrieve clinical data from clinical data repository with matching terminology bindings (both schema and instance level)
- 6) Display and export corresponding clinical data
- 7) Feed clinical data to model parameters (as per mappings), create SED-ML and simulate using openCOR / other

## 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)<sup>3</sup>.

## References

1. Nickerson DP, Atalag K, de Bono B, Hunter PJ. The Physiome Project, openEHR Archetypes, and the Digital Patient. In: Combs CD, Sokolowski JA, Banks CM, editors. The Digital Patient [Internet]. John Wiley & Sons, Inc; 2016. p. 101–25. Available from: <http://onlinelibrary.wiley.com/doi/10.1002/9781118952788.ch9/summary>
2. <http://www.openehr.org>
3. <http://www.openehr.org/ckm>

## Acknowledgements

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