# Discovery and Exploration of Computational Models of Epithelial Transport

Dewan Sarwar, Tommy Yu, Peter Hunter, David Nickerson Auckland Bioengineering Institute (ABI), University of Auckland, New Zealand

#### Background

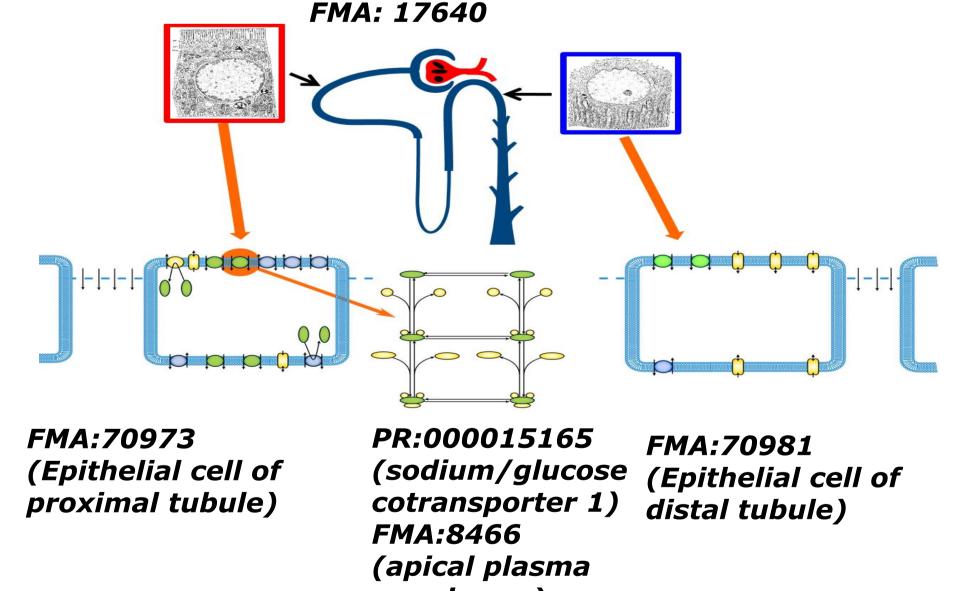
Comprehensive descriptions of mathematical models of biological systems captured in computable formats have the potential to significantly contribute to biomedical and clinical research. We achieve such computable descriptions with semantic annotation, using standard semantic web technologies to describe model entities using terms from common terminologies and ontologies. Such annotations capture the biological phenomena encapsulated by the model and aid in the discovery and comprehension of the model by independent scientists.

To annotate the typical range of biological phenomena seen in physiological models requires a diverse collection of reference ontologies and a repository to enable discovery and dissemination of such knowledge resources. To address this, computational tools and standards have evolved over the years such as CellML [1] to encode mathematical models of biological systems; SemGen [2] to annotate models; and the Physiome Model Repository (PMR) [3] to store these models and annotations to ensure the encoded knowledge is persistent, identifiable, discoverable, and sharable.

The discovery and reuse of data and models is a key component in achieving the goals of the IUPS Physiome Project [4] and the Virtual Physiological Human [5].

## **Kidney Model Annotation**

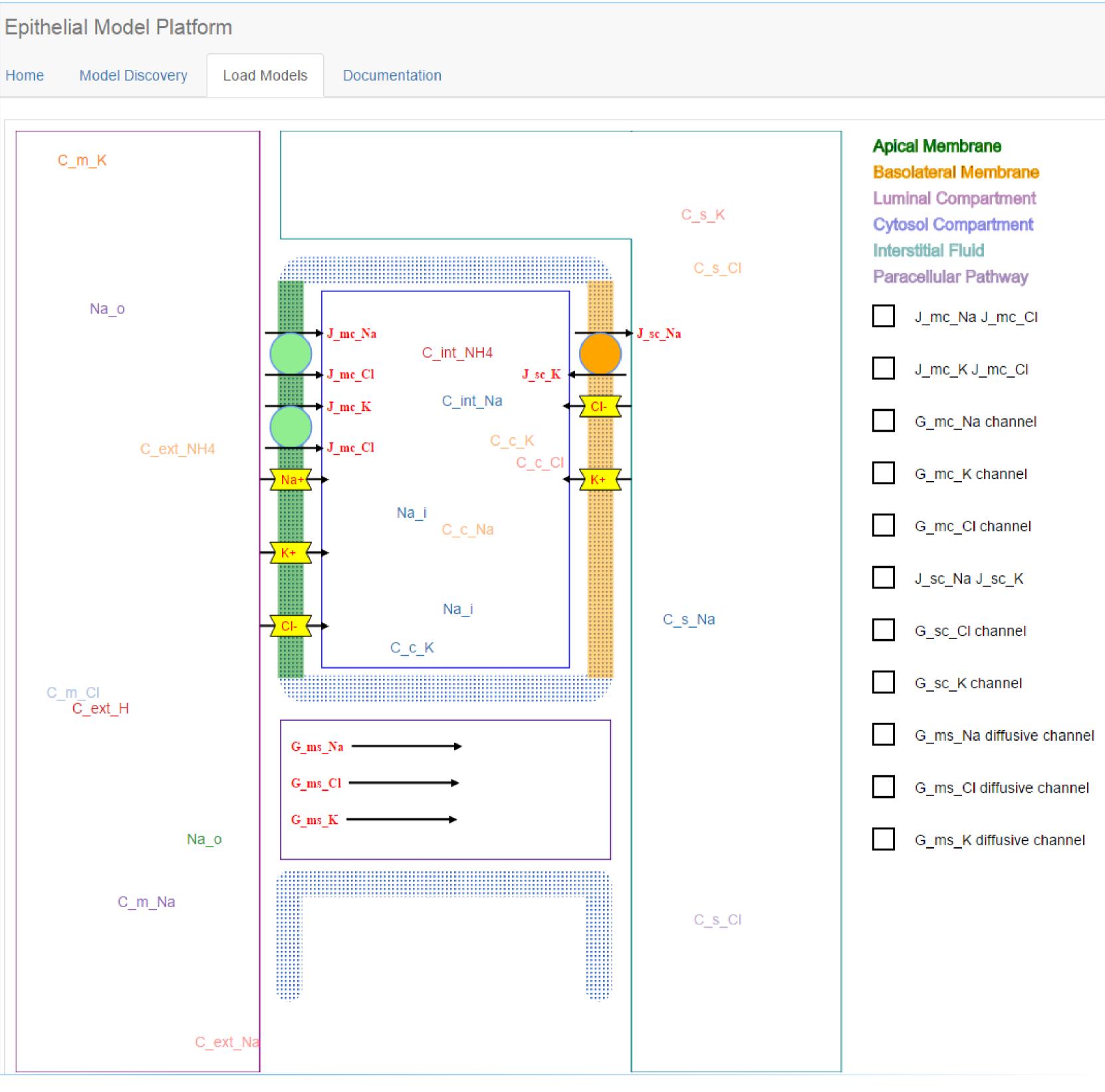
Presented below demonstrates some of the information with which we have extended existing descriptions of models relevant to the kidney.



#### membrane) HE3 exchanger/antiporter; NHE3 is a protein - UniProt ID: P26433; species - rattus norvegicus; Gene - Slc Weinstein\_1995\_NHE3.cellml#v035 component=NHE3 / variable=J\_NHE3\_Na Weinstein\_1995\_NHE3.cellml#v036 component=NHE3 / variable=J\_NHE3\_H Weinstein\_1995\_NHE3.cellml#v037 component=NHE3 / variable=J\_NHE3\_NH4 ??? not in the CellML model ??? component=NHE3 / variable=J\_NHE3\_Na\_Max component=NHE3 / variable=XTxP NHE3 Na Weinstein 1995 NHE3.cellml#v022 component=NHE3 / variable=XTxP\_NHE3\_H Weinstein\_1995\_NHE3.cellml#v023 component=NHE3 / variable=XTxP\_NHE3\_NH4 einstein\_1995\_NHE3.cellml#v024/ Weinstein\_1995\_NHE3.cellml#v028 component=NHE3 / variable=alpha\_ext\_Na Weinstein 1995 NHE3.cellml#v031 component=NHE3 / variable=alpha int Na Weinstein\_1995\_NHE3.cellml#v029 Weinstein\_1995\_NHE3.cellml#v032 component=NHE3 / variable=beta\_int\_H Weinstein 1995 NHE3.cellml#v030 component=NHE3 / variable=gamma\_ext\_NH4 Weinstein\_1995\_NHE3.cellml#v033 component=NHE3 / variable=gamma\_int\_NH4 Weinstein\_1995\_NHE3.cellml#v034 component=NHE3 / variable=sum NHE3 Weinstein\_1995\_NHE3.cellml#v001 component=concentrations / variable=C\_ext\_Na Concentration of Na+ in the extracellular (lumen) compartme Weinstein\_1995\_NHE3.cellml#v002 component=concentrations / variable=C ext H Concentration of H+ in the extracellular (lumen) compartment Weinstein\_1995\_NHE3.cellml#v003 Concentration of NH4+ in the extracellular (lumen) compartment component=concentrations / variable=C ext NH4 Weinstein\_1995\_NHE3.cellml#v004 Weinstein\_1995\_NHE3.cellml#v005 component=concentrations / variable=C int H Concentration of H+ in the intracellular (cytosol) compartment Weinstein 1995 NHE3.cellml#v006 component=concentrations / variable=C\_int\_NH4 Concentration of NH4+ in the intracellular (cytosol) compartment Weinstein\_1995\_NHE3.cellml#v007 Weinstein\_1995\_NHE3.cellml#v008 Weinstein\_1995\_NHE3.cellml#v009 Permeation velocity constant of H+ from intracellular (cytosol) to extracellular (lumen) compartment through the cell membrane Weinstein\_1995\_NHE3.cellml#v010 component=NHE3 Parameters / variable=XTxP0 NHE3 NH4 Permeation velocity constant of NH4+ from intracellular (cytosol) to extracellular (lumen) compartment through the cell membrane Weinstein 1995 NHE3.cellml#v01 Equilibrium binding contstant of H+ in the NHE3 protein model Weinstein\_1995\_NHE3.cellml#v012 component=NHE3 Parameters / variable=K NHE3 H Weinstein\_1995\_NHE3.cellml#v013 Equilibrium binding contstant of NH4+ in the NHE3 protein mode

### **Epithelial Modelling Platform**

Presented below is the web-based epithelial modelling platform to discover, explore and assemble models where users would be able to create and validate new epithelial models. This platform allows users to drag and drop models between apical and basolateral membranes. Solutes, e.g. sodium, potassium, encoded in CellML will be floating in specific compartments. Novice modellers could use this platform as a learning tool.



#### References

- 1. A. Cuellar et al. An overview of CellML 1.1, a biological model description language SIMULATION, vol. 79, pp. 740-747, December 2003.
- 2. M. L. Neal, Modular, semantics-based composition of biosimulation models. Ph.D. Dissertation. University of Washington, 2010.
- 3. T. Yu et al. The Physiome Model Repository 2, Bioinformatics Oxford Journals, vol. 27, pp. 743-744,
- 4. P. Hunter, The IUPS Physiome Project: a framework for computational physiology, Progress in Biophysics and Molecular Biology, vol. 85, pp. 551–569, June-July 2004.
- 5. P. Hunter et al. A vision and strategy for the virtual physiological human in 2010 and beyond, Philos Transact A Math Phys Eng Sci, vol. 368, pp. 2595-614, June 2010.



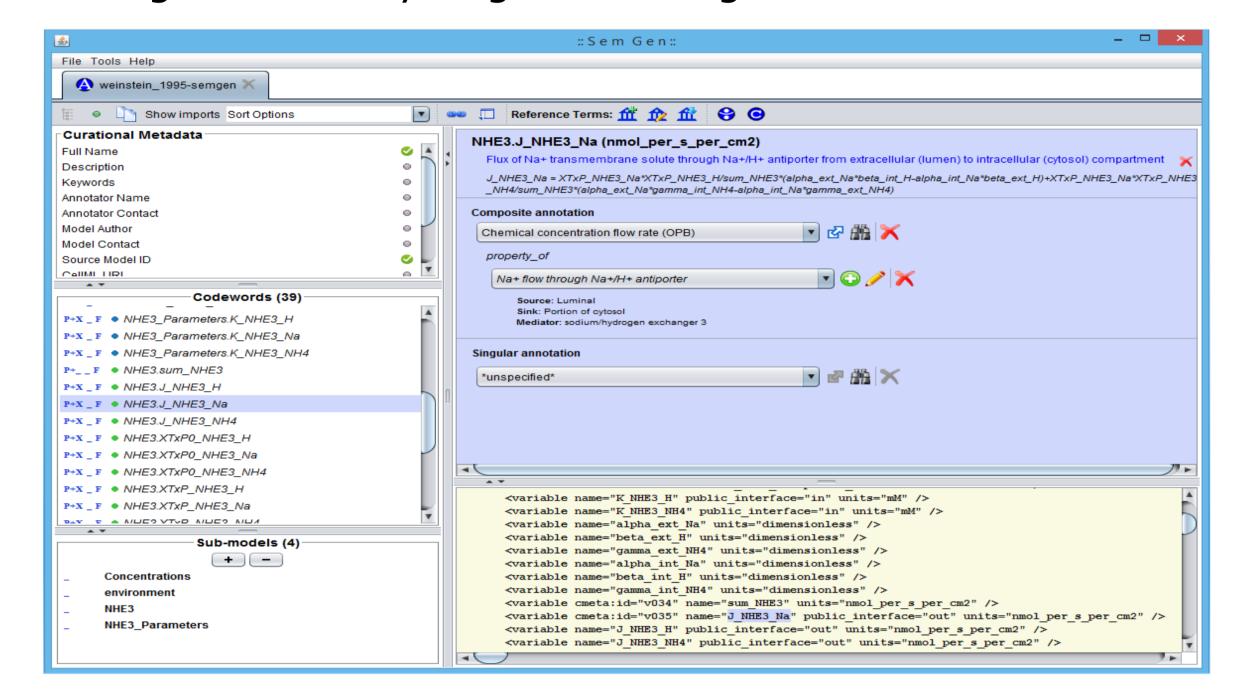




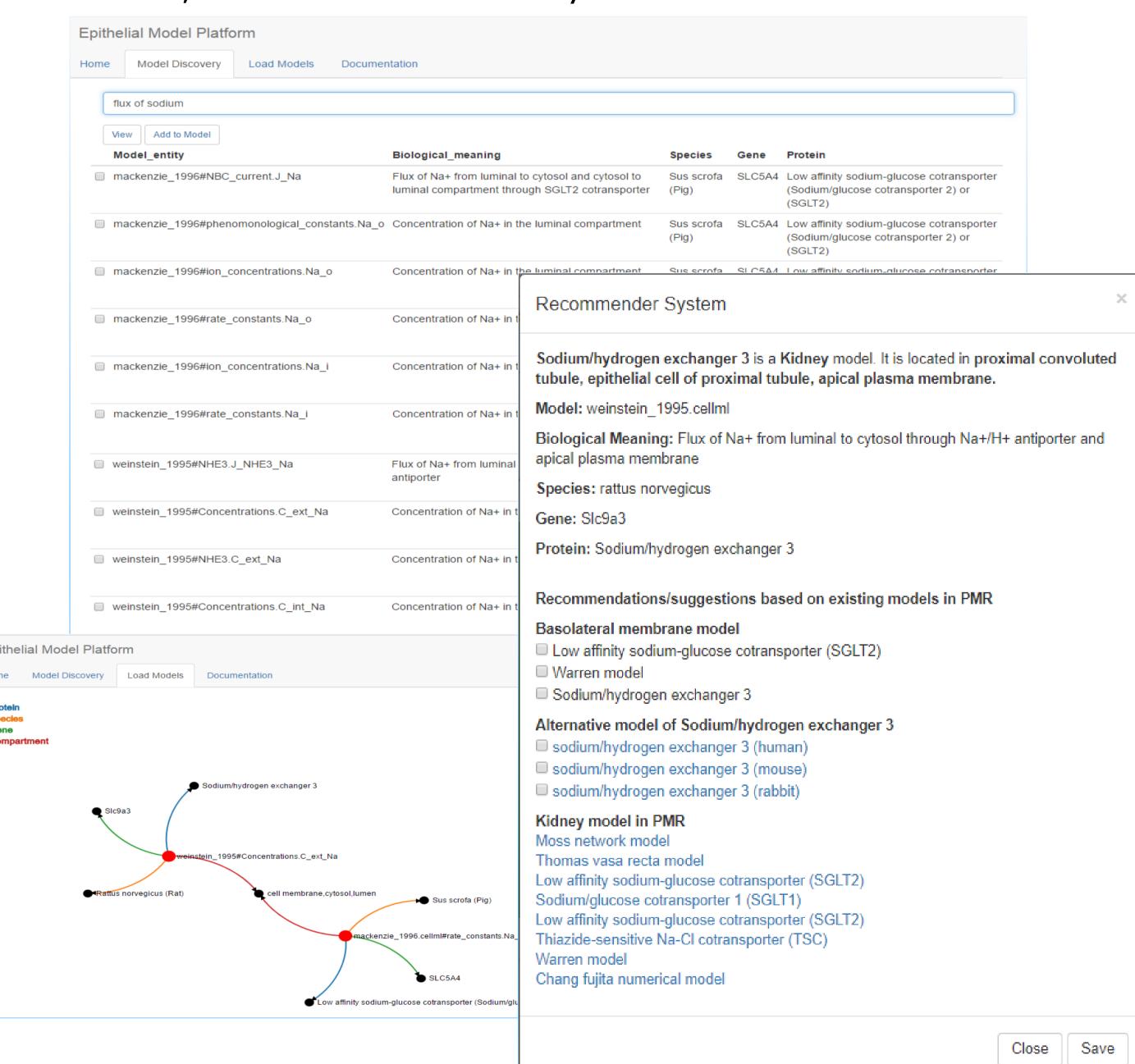
### **AUCKLAND** BIOENGINEERING **INSTITUTE**

#### **Semantic Annotation and Discovery**

Screenshot of the SemGen annotator interface of the Weinstein model for flux of sodium from lumen to cytosol through sodium hydrogen exchanger 3 is shown below.



Our prototype web interface presents the search results obtained from querying the PMR services, overlapping models, and a recommender system.



### Acknowledgements

PhD project supported by MedTech Center of Research Excellence (MedTech CoRE)







