OME Core Ontology: An OWL-based Life Science Imaging Data Model

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Abstract. The Open Microscopy Environment (OME) is a consortium that produces open-source tools and format standards for microscopy data. The OME model is a specification for sharing biological imaging data in two parts: metadata as OME-XML and binary data as OME-TIFF. We built an OWL ontology translation of the OME-XML specification called OME core ontology so as to catch up with the rapid progress and diversification of imaging technology and to facilitate integrated analysis with various life science data. This poster presents the details and status of the ontology, associated tools, and future plans.

Keywords: Open Microscopy Environment, microscopy imaging, imaging ontology, semantic integration

1 Introduction

Imaging is one of the fundamental techniques and data types for understanding life phenomena intuitively through human vision. Because imaging data itself does not describe explicit knowledge, imaging metadata is fundamental to enable data sharing and integration of multi-modal imaging data with various other types of life science data.

Having multiple life science centers and laboratories, RIKEN employs various imaging apparatus covering a comprehensive range of scale, from organelle through organ to organism. For integrating the imaging data produced and the experimental conditions, a multi-modal ontology for electron microscopy, X-ray computed tomography and magnetic resonance imaging was developed as an OWL-based extension of the OME data model[1] which describes imaging metadata for OMERO[2], a *de facto*-standard imaging tool. Having confirmed the core ontology through this multi-modal extension in different practical research projects, the OME consortium has adopted the newly developed OWL-based OME model as an official companion to their XSD-based model.

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[1] `https://docs.openmicroscopy.org/ome-model/6.0.0/`

[2] `https://www.openmicroscopy.org`

2 Development of the OME core ontology and tools

The OME core ontology is a translation of the OME-XML format of the OME data model version 2016-06[3] that covers all its concepts and attributes. The ontology contains 130 classes and 210 properties. In addition, we implemented tools written in Java and a spreadsheet template for describing RDF data using the OME core ontology. The data converter is a tool for converting OME-XML format data into RDF using the OME core ontology. Another tool, the OME compatibility checker, determines if the given ontology includes OME core sub-classes and sub-properties. This checker is used for the 4DN-OME ontology for confirming if it is an extended ontology of the OME core ontology [1].

Finally, a spreadsheet template facilitates the users' description of RDF data for entry in the RIKEN MetaDatabase [2]. These tools and templates have been published at GitLab[4] with sample OME-XML and converted RDF data[5].

3 Discussion and future directions

Herein, we report our progress on the development of the OME core ontology and tools. With the publication of the ontology, members of the bioimaging community can develop an extended ontology converting the complete original imaging environment.Though the OME core ontology is designed for bioimaging, it can be connected to healthcare metadata such as DICOM data. Further, the distribution of imaging data in a FAIR representation accelerates advanced data analysis, critical for Open Science. Our goal is to enable integrated multi-omics knowledge analysis, artificial intelligence-supported image diagnosis, and scale-continuous image analysis as well as the realization of a standardized image analysis platform based on OMERO technology.

Acknowledgements

References

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`OME-2016-06/ome.html`

[4] `https://gitlab.com/openmicroscopy/incubator/ome-owl/`

[5] `https://downloads.openmicroscopy.org/images/OME-XML/2016-06/`