

Bio-ontologies in OWL: Editing, sharing and curating



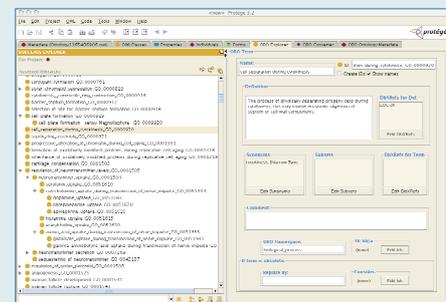
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The COBRa-CT project has developed tools for editing OBO ontologies, and for managing ontologies in the Web Ontology Language, OWL.

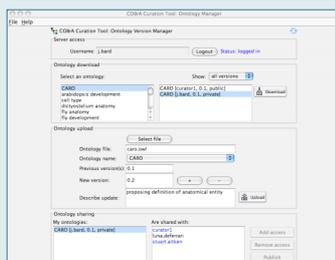
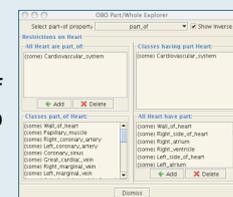
Bio-ontologies formalise our knowledge of molecular function, biological process, anatomy and cell type across the phyla. As with databases, bio-ontologies are created, published and updated over time. Ontology curation is typically a joint effort between subject matter experts, database curators and experimentalists. Hence tools for ontology curation should support sharing ontologies, managing versions, annotating changes to them, and visualising those changes over time.

The OBO Explorer Ontology Editor

OBO Explorer ontology editor is compatible with the proposed standard for transitioning Open Biomedical Ontologies (OBO) to OWL. The OBO-In-OWL format includes an agreed representation for synonyms, subsets and database cross-references as well as an interpretation of OBO relationships as Description Logic property restrictions. These standards have been incorporated into the OBO Explorer Protégé tab. We use the generic ontology editor Protégé for this work in order to have compatibility with, and reuse of, tools developed in the wider ontology research community, and the OBO Converter (Moreira and Musen, 2007) - also implemented as a Protégé tab. Because Protégé cannot easily handle OBO term annotations, tools such as the OBO Explorer are essential for end-users to be able to work with bio-ontologies that have been reformatted in OWL.



In on-going work we are developing alternative visualisations of the part-of hierarchies that bio-ontologists are familiar with. These get translated into Description Logic definitions that are complex to interpret.



Sharing and Curating

To allow users to publish, archive and exchange ontologies, and to record ontology versions, an ontology manager has been implemented. We have used Grid technology for the server: an eXist database is accessed via OGSA-DAI grid middleware to store or retrieve OWL ontologies on a central server. The server is accessed via web services.

The COBRa-CT Version Manager client allows a registered user to access ontologies (upload and download current and past versions) and share access to them. Ontologies can be either kept private, shared with named persons, or declared public and therefore shared with all users. The ontology server uses the OGSA-DAI API to access and query the eXist XML database, invoked by the client through OGSA-DAI activities.

Future work will explore visualisations of the differences between ontology versions and investigate more efficient ways to store OWL ontologies as XML documents – taking advantage of developments such as OWL 1.1.

References:

- Stuart Aitken, Yin Chen, Bonnie Webber, Wenfei Fan and Jonathan Bard (2007) Managing the transition from OBO to OWL: The COBRa-CT Bio-Ontology Tools, *Proc. AHM 2007*
- Dilvan Moreira and Mark Musen (2007) OBO to OWL: A Protégé OWL Tab to Read/Save OBO Ontologies *Bioinformatics* doi:10.1093/bioinformatics/btm258

Acknowledgements: Supported by BBSRC grant BB/D006473/1