A reusable tree-based web-visualization to browse EDAM ontology, and contribute to it.

Bryan Brancotte¹, Christophe Blanchet², and Hervé Ménager¹

¹ Bioinformatics and Biostatistics HUB, Centre de Bioinformatique, Biostatistique et Biologie Intégrative (C3BI, USR 3756 Institut Pasteur et CNRS), Paris, France
² French Institute of Bioinformatics, CNRS IFB-Core, Gif-sur-Yvette, France

Summary

Abstract

Labelling, indexing and describing a Bioinformatics resource, whether it is a software, a database, or a service is of a great help when it comes to promoting it to various user communities. As an example, the ELIXIR bio.tools (Ison et al. 2015) registry contains more than ten thousands software and service entries. In this context, the use of controlled vocabularies to describe the resources is of a paramount importance. In bio.tools, this need is addressed by the EDAM Ontology (Ison et al. 2013), which proposes a controlled vocabulary hierarchically organized around four axes which describe types of data, formats, operations and topics.

We here present the EDAM Browser, a client-side web-based visualization javascript widget that provides an interface to navigate EDAM. This browser is tailored to the needs of EDAM users who might not be ontology experts. It can, among other things, be used to help describing resources, and to facilitate and foster community contributions to EDAM. The EDAM Browser allows users to explore it with an interface tailored to its structure and properties. Its interface is not designed to be a generic ontology navigation and edition platform, a goal already achieved by many other systems such as AberOWL (Hoehndorf et al. 2015), BioPortal (Whetzel et al. 2011), OLS - Ontology Lookup Service (Jupp et al. 2015), Ontobee (Xiang et al. 2011) and WebProtégé (Tudorache et al. 2013).

Rather, it aims at providing features requested by most users and contributors, which we detail below.

Availability and re-usability

The EDAM browser is available publicly and anonymously at https://ifb-elixirfr.github.io/edam-browser/. In addition to this, its lightweight architecture makes it easy to download and run on any server or personal computer, either as a local HTML file or on a web server. It is possible to integrate the EDAM Browser and its tree representation in external websites and applications, providing a simple way for third party websites to promote EDAM-labeled resources. Both the autocomplete input field and the tree visualization are re-usable: a demonstration code is available here, showing how the tree can be integrated, how the user can interact with the tree, and how to programmatically interact with the tree in JavaScript.
As much as possible, the user interface aims at simplicity and relevance to the specific domain of EDAM. The creation of an interface that displays all of the information necessary to users, and avoids the use of ontology development jargon is a major goal of this project.

We also take into account the specificities of the structure of EDAM: while being represented as a tree, it is in fact a directed acyclic graph, meaning that a term can have more than one parent. In order to improve readability when a term is selected (1) all the term’s positions are shown; and (2) all paths from the root node are highlighted. A good example of this display is the Phylogeny topic (cf Fig. 1).

The interface also permits the navigation between different axes of the ontology, based on the EDAM properties that define their relationships (e.g. this format represents this type of data, this data is an output of this operation or is specific of this topic). One last salient feature of the interface is the representation of the usage of the selected concept in annotated resource collections, such as bio.tools, BioSphere, BioWeb and TeSS.

Performance and flexibility

One of the specificities of EDAM is its relatively small size in comparison with large ontologies like Gene Ontology. This reduced size makes it easy to load entirely the contents to be displayed in the browser’s memory, and enables a very fast navigation, with no need to rely on server calls during this navigation (except for displaying usage statistics from external annotated resources). Using the EDAM Browser to explore a local or in-development version is possible. The loaded file should be formatted as a JSON file following the schema accessible here. The edam2json utility can be used to generate the ontology in this format from any EDAM owl file.

An ontology is loaded into the EDAM Browser by clicking on the button labelled Custom at the top of its interface, and specifying either a public URL to the file or a local path to load it from (cf Fig. 2).
Figure 2: Providing a custom ontology

Ease of community contributions.

Letting users contribute to the ontology improves acceptance by the community as a user propose changes to the ontology to fit his/her needs. To facilitate these suggestions, the EDAM Browser lets users access a form letting them propose changes at any point of their exploration. These suggestions are automatically formatted as github issues ready to be submitted by the user (cf Fig. 3).

References

Höchndorf, Robert, Luke Slater, Paul N Schofield, and Georgios V Gkoutos. 2015. “Aber-Owl: A Framework for Ontology-Based Data Access in Biology.” *BMC Bioinformatics* 16 (1). BioMed Central:26.

Ison, Jon, Matúš Kalaš, Inge Jonassen, Dan Bolser, Mahmut Uludag, Hamish McWilliam, James Malone, Rodrigo Lopez, Steve Pettifer, and Peter Rice. 2013. “EDAM: An Ontology of Bioinformatics Operations, Types of Data and Identifiers, Topics and Formats.” *Bioinformatics* 29 (10). Oxford University Press:1325–32.

Ison, Jon, Kristoffer Rapacki, Hervé Ménager, Matúš Kalaš, Emil Rydza, Piotr Chmura, Christian Anthon, et al. 2015. “Tools and Data Services Registry: A Community Effort to Document Bioinformatics Resources.” *Nucleic Acids Research* 44 (D1). Oxford University Press:D38–D47.

Jupp, Simon, Tony Burdett, Catherine Leroy, and Helen E Parkinson. 2015. “A New Ontology Lookup Service at Embl-Ebi.” In *SWAT4LS*, 118–19.

Tudorache, Tania, Csongor Nyulas, Natalya F Noy, and Mark A Musen. 2013. “WebProtégé: A Collaborative Ontology Editor and Knowledge Acquisition Tool for the Web.” *Semantic Web* 4 (1). IOS Press:89–99.

Whetzel, Patricia L, Natalya F Noy, Nigam H Shah, Paul R Alexander, Csongor Nyulas, Tania Tudorache, and Mark A Musen. 2011. “BioPortal: Enhanced Functionality via New Web Services from the National Center for Biomedical Ontology to Access and Use Biological Resources.” *Journal of Open Source Software*, 3(24), 698. https://doi.org/10.21105/joss.00698
Propose a change in "topic" of EDAM ontology

Figure 3: The edition form and the issue created

Ontologies in Software Applications.” *Nucleic Acids Research* 39 (suppl_2). Oxford University Press:W541–W545.

Xiang, Zuoshuang, Chris Mungall, Alan Ruttenberg, and Yongjun He. 2011. “Ontobee: A Linked Data Server and Browser for Ontology Terms.” In *ICBO*. 

Brancotte et al., (2018). A reusable tree-based web-visualization to browse EDAM ontology, and contribute to it.. *Journal of Open Source Software*, 3(24), 698. https://doi.org/10.21105/joss.00698