

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

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Software

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Summary

The EDAM Browser is a client-side web-based visualization javascript widget for the navigation of the EDAM ontology (Ison et al. 2013). EDAM is a structured and controlled vocabulary describing bioinformatics and computational biology concepts. It is used to annotate resource descriptions (tools, web services) for discovery (Ison et al. 2015) and integration in platforms such as galaxy (Afgan et al. 2016). The EDAM Browser provides users a simple and performant interface to explore EDAM when annotating or searching for bioinformatics resources.

User interface and functionalities

The user interface (see Fig. 1) is divided in two main panels, a tree representation of the ontology on the left, and a properties card on the right. The tree on the left represents the different parts of the ontology (formats, data, operations and topics). By expanding or closing the nodes, users explore the hierarchy of the EDAM concepts. The selected concept is displayed in bold, and all the path(s) leading from the root to it are highlighted. The properties card panel on the right displays the main properties of the concept, such as its definition, comments, synonyms, and its non-hierarchical relations to other concepts (e.g. an operation has inputs, outputs, and belongs to a given topic). It also includes counts and links to entries in various databases that use this term, such as [bio.tools](#), [BioSphere](#) (Brancotte et al. 2017), [BioWeb](#) and [TeSS](#).

The user may directly suggest a modification on a concept by clicking on the “edit” icons at the top-right corner of this panel ; creating a new concept is also possible thanks to the “add a child” button. Both lead the user to a form that directly formats suggestions as github issues ready to be submitted by the user (see Fig. 2).

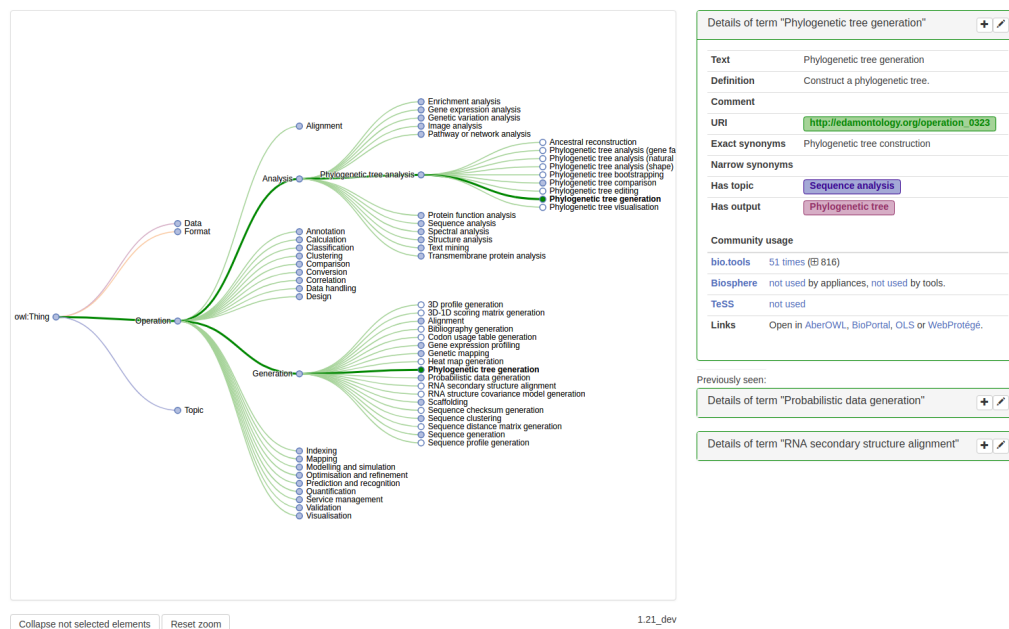
Additional components of the interface include a full-text search box to search for concepts on their names, synonyms or descriptions; a navigation toolbar to toggle the display of specific parts of the ontology only, or load locally modified versions of the ontology; and a history stack of the concepts that have been seen previously to the one currently selected, below the properties card panel.

Architecture, installation and integration

One of the specificities of EDAM is its relatively small size in comparison with large ontologies like Gene Ontology (Ashburner et al. 2000)(“Expansion of the Gene Ontology Knowledgebase and Resources” 2016). This reduced size makes it easy to load it entirely in the browser’s memory, and enables a fast navigation that does not rely on server

EDAM ontology

EDAM is a simple ontology of well established, familiar concepts that are prevalent within bioinformatics [edamontology.org]

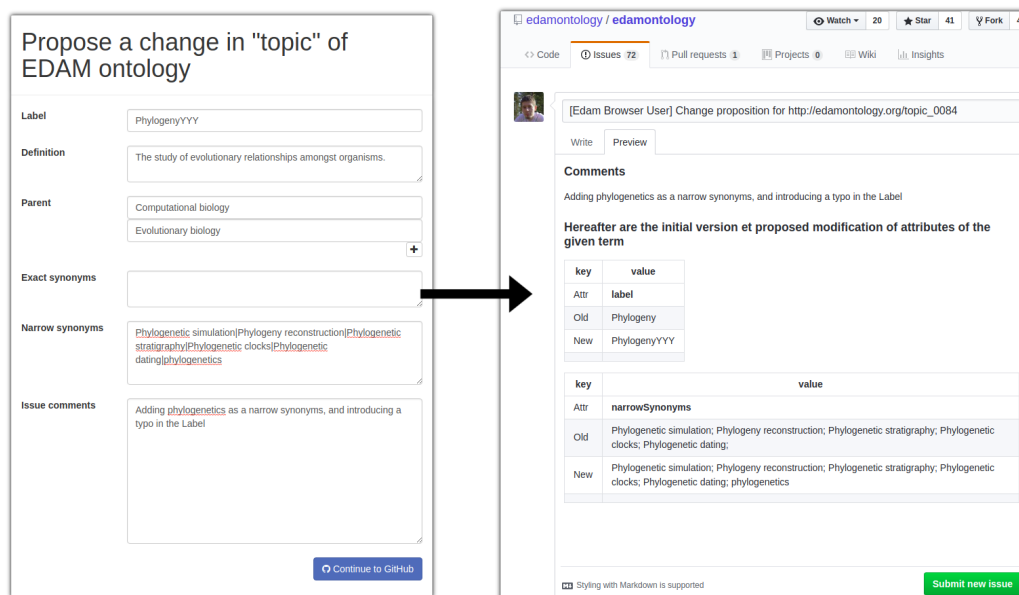


The interface shows a concept graph with 'Phylogenetic tree generation' as a central node. It has two parents: 'Phylogenetic tree analysis' and 'Phylogenetic tree generation'. The graph also shows other related concepts like 'Alignment', 'Annotation', 'Calculation', 'Classification', 'Clustering', 'Conversion', 'Correlation', 'Data handling', 'Design', 'Indexing', 'Mapping', 'Modelling and simulation', 'Optimization and refinement', 'Prediction and recognition', 'Quantification', 'Service management', 'Validation', and 'Visualisation'.

Details of term "Phylogenetic tree generation":

- Text:** Phylogenetic tree generation
- Definition:** Construct a phylogenetic tree.
- Comment:**
- URI:** http://edamontology.org/operation_0323
- Exact synonyms:** Phylogenetic tree construction
- Narrow synonyms:**
- Has topic:** Sequence analysis
- Has output:** Phylogenetic tree
- Community usage:** bio.tools 51 times (B 816)
- Biosphere:** not used by appliances, not used by tools.
- TeSS:** not used
- Links:** Open in AberOWL, BioPortal, OLS or WebProtégé.

Figure 1: EDAM Browser main interface with a concept that have two parents, and relations with others concepts



The left panel shows the "Propose a change in 'topic' of EDAM ontology" form. The label is "PhylogenyYYY", the definition is "The study of evolutionary relationships amongst organisms.", and the parent terms are "Computational biology" and "Evolutionary biology". The narrow synonyms are "Phylogenetic simulation|Phylogeny reconstruction|Phylogenetic stratigraphy|Phylogenetic clocks|Phylogenetic dating|phylogenetics". The issue comments are "Adding phylogenetics as a narrow synonyms, and introducing a typo in the Label".

The right panel shows the resulting GitHub issue. The title is "[Edam Browser User] Change proposition for http://edamontology.org/topic_0084". The comments section contains the following text: "Adding phylogenetics as a narrow synonyms, and introducing a typo in the Label". Below this, there is a table with the following content:

key	value
Attr	label
Old	Phylogeny
New	PhylogenyYYY

Below the table, there is another table with the following content:

key	value
Attr	narrowSynonyms
Old	Phylogenetic simulation; Phylogeny reconstruction; Phylogenetic stratigraphy; Phylogenetic clocks; Phylogenetic dating;
New	Phylogenetic simulation; Phylogeny reconstruction; Phylogenetic stratigraphy; Phylogenetic clocks; Phylogenetic dating; phylogenetics

Figure 2: The edition form and the issue created

calls (except for displaying usage statistics from external annotated resources). The architecture of EDAM Browser is therefore very simple: it uses the D3.js library (Bostock, Ogievetsky, and Heer 2011) for visualisation, and loads EDAM from a JSON-based format, which is lighter and easier to parse than the native OWL/XML format. This makes the system easy to download and run, either as a local HTML file or on a web server. It is also possible to integrate it in external websites and applications: the autocomplete input field and the tree visualization are re-usable, and demonstration code is [available online](#), showing how the tree can be integrated, and how to programmatically interact with the tree in JavaScript.

Conclusion

The EDAM Browser is publicly available at <https://ifb-elixirfr.github.io/edam-browser/>. The interface displays all of the information necessary to users, and avoids ontology development jargon. The EDAM Browser is not a generic ontology navigation and/or edition platform, like 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 is tailored to the structure and properties of EDAM, and targets both contributors and users who might not be ontology experts. With this interface, users can both explore quickly and efficiently EDAM, and contribute their own expertise to the ontology.

References

- Afgan, Enis, Dannon Baker, Marius van den Beek, Daniel Blankenberg, Dave Bouvier, Martin Čech, John Chilton, et al. 2016. “The Galaxy Platform for Accessible, Reproducible and Collaborative Biomedical Analyses: 2016 Update.” *Nucleic Acids Research* 44 (W1):W3–W10. <https://doi.org/10.1093/nar/gkw343>.
- Ashburner, Michael, Catherine A. Ball, Judith A. Blake, David Botstein, Heather Butler, J. Michael Cherry, Allan P. Davis, et al. 2000. “Gene Ontology: Tool for the Unification of Biology.” *Nature Genetics* 25 (1). Springer Nature:25–29. <https://doi.org/10.1038/75556>.
- Bostock, Michael, Vadim Ogievetsky, and Jeffrey Heer. 2011. “D³ Data-Driven Documents.” *IEEE Transactions on Visualization and Computer Graphics* 17 (12). IEEE:2301–9. <https://doi.org/10.1109/TVCG.2011.185>.
- Brancotte, Bryan, Mohamed Bedri, Jonathan Lorenzo, Perrin Sandrine, Frédéric Séné, Awa Sepou Ngailo, Christophe Blanchet, and Jean-François Gibrat. 2017. “Biosphere Web : un portail haut niveau pour une utilisation bioinformatique des clouds.” JOBIM (Journées Ouvertes Biologie Informatique Mathématiques). <https://www.youtube.com/watch?v=gaopunffqnc>.
- “Expansion of the Gene Ontology Knowledgebase and Resources.” 2016. *Nucleic Acids Research* 45 (D1). Oxford University Press (OUP):D331–D338. <https://doi.org/10.1093/nar/gkw1108>.
- Hoehndorf, 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):26. <https://doi.org/10.1186/s12859-015-0456-9>.
- 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. <https://doi.org/10.1093/bioinformatics/btt113>.

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. <https://doi.org/10.1093/nar/gkv1116>.

Jupp, Simon, Tony Burdett, Catherine Leroy, and Helen E Parkinson. 2015. “A New Ontology Lookup Service at Embl-Ebi.” In *SWAT4LS*, 118–19. http://ceur-ws.org/Vol-1546/paper_29.pdf.

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. <https://doi.org/10.3233/SW-2012-0057>.

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 Ontologies in Software Applications.” *Nucleic Acids Research* 39 (suppl_2). Oxford University Press:W541–W545. <https://doi.org/10.1093/nar/gkr469>.

Xiang, Zuoshuang, Chris Mungall, Alan Ruttenberg, and Yongqun He. 2011. “Ontobee: A Linked Data Server and Browser for Ontology Terms.” In *ICBO*. <https://doi.org/10.1093/nar/gkw918>.