

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

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## Software

- [Review](#) ↗
- [Repository](#) ↗
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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 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. It helps describing resources, and facilitates community contributions to EDAM.

## Availability and re-usability

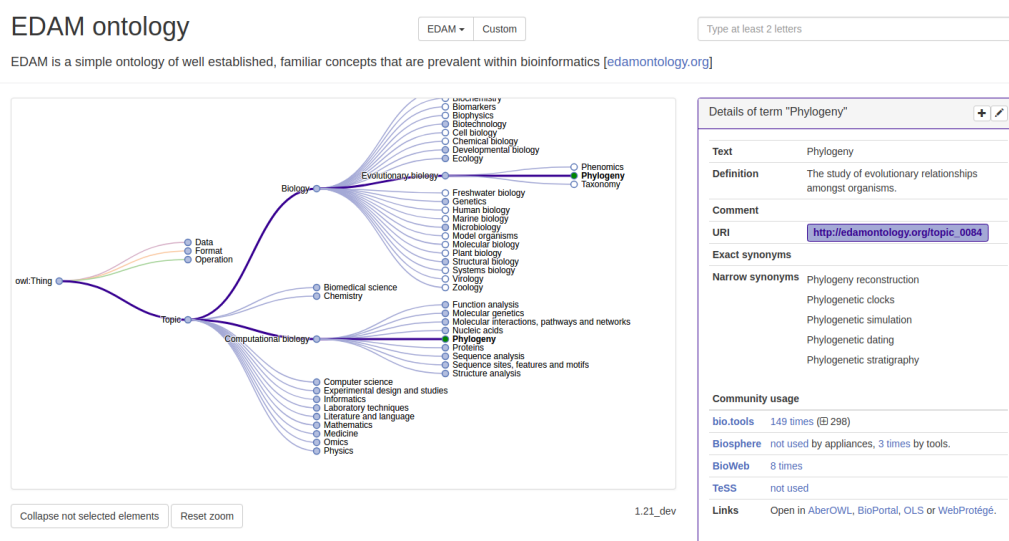
The EDAM browser is available publicly and anonymously at <https://ifb-elixirfr.github.io/edam-browser/>. Its lightweight architecture makes it easy to download and run, either as a local HTML file or on a web server. It is possible to integrate the EDAM Browser in external websites and applications, 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.

## Information display

The user interface aims at simplicity and relevance to the specific domain of EDAM. The interface displays all of the information necessary to users, and avoids ontology development jargon.

Users can navigate between different parts of the ontology, based on the 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*).

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



**Figure 1:** The term Phylogeny has two parents

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).

On the right part of Figure 1, details of the selected concept are displayed. One last salient feature is the presentation of the usage of the concept in annotated resource collections, such as [bio.tools](#), [BioSphere](#) (Brancotte et al. 2017), [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 [ashburner2000go, go2016go]. This reduced size makes it easy to load it entirely in the browser's memory, and enables a very fast navigation that does not rely on server calls (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).

## Facilitating community feedback.

EDAM users can contribute their own expertise to the ontology. In order to make these contributions easier, we have implemented a form that directly formats suggestions as github issues ready to be submitted by the user (cf Fig. 3).

## References

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Load custom ontology

The ontology can be loaded from an URL, or directly uploaded. Note that if one of the fields *URL* and *file* is provided, the other is disabled so empty one field before filling the other.

**Ontology URL**

media/regular.example.json

Either provide a URL or a file.

**Ontology File**

Choisissez un fichier Aucun fichier choisi

The ontology has to be in json following [this format](#), a validator is available [here](#). Note that slight modification of the schema are authorized

**How to access to the identifier of a term d**

☒ d.id  
☐ d.data.uri

**How to access to the text of a term d**

☒ d.text  
☐ d.name

Cancel Load ontology

**Figure 2:** Providing a custom ontology

Propose a change in "topic" of EDAM ontology

Label: PhylogenyYYY

Definition: The study of evolutionary relationships amongst organisms.

Parent: Computational biology, Evolutionary biology

Exact synonyms:

Narrow synonyms: Phylogenetic simulation|Phylogeny reconstruction|Phylogenetic stratigraphy|Phylogenetic clocks|Phylogenetic dating|phylogenetics

Issue comments: Adding phylogenetics as a narrow synonyms, and introducing a typo in the Label

Continue to GitHub

edamontology / edamontology

[Edam Browser User] Change proposition for [http://edamontology.org/topic\\_0084](http://edamontology.org/topic_0084)

Comments: Adding phylogenetics as a narrow synonyms, and introducing a typo in the Label

Hereafter are the initial version et proposed modification of attributes of the given term

key	value
Attr	label
Old	Phylogeny
New	PhylogenyYYY

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

Submit new issue

**Figure 3:** The edition form and the issue created

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