

The EDAM Ontology

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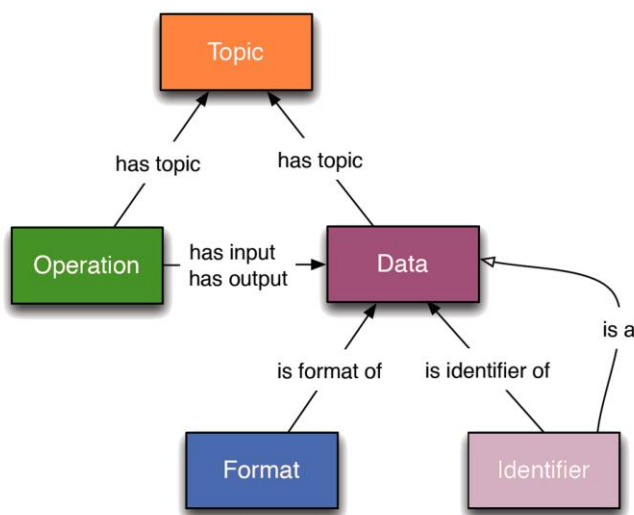
Project Website: <http://edamontology.org>

Source Code: <https://github.com/edamontology/edamontology>

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Bioinformaticians handle an increasingly large and diverse set of tools and data. Meanwhile, researchers demand ever more powerful and convenient means to organise, find, understand, compare, select, use and connect the available resources. These tasks often rely on consistent, machine-understandable descriptions of the underlying components, but these have been generally lacking in *ad hoc* resource descriptions. The urgent need - filled by EDAM - is for an ontology that unifies semantically the bioinformatics concepts in common use, provides the curator with a comprehensive nomenclature that is broadly applicable, and enables new and powerful search, browse and query functions.

EDAM is an ontology of well established, familiar concepts that are prevalent within bioinformatics, including types of data and data identifiers, data formats, operations and topics. EDAM is a simple ontology – essentially a set of concepts with terms, synonyms, definitions, and relations. EDAM is organised into an intuitive hierarchy for convenient use by curators, software developers, and end-users.



5 consecutive stable versions of EDAM have been released since July 2015, with version 1.14 being the current one at the time of submission. EDAM is developed in a participatory and transparent fashion, with a growing community of [contributors](#), connected *e.g.* to the **Bio.Tools** registry (<http://bio.tools>) of bioinformatics tools and data services, or to the development of various bioinformatics workbenches.