

A Study of Bio-ontologies

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Abstract:

Ontology has been adapted by the biologists that is widely used in biological and biomedical research which in itself is considered as a mode to constantly interpret characteristics from genotype to phenotype. Artifacts called ontologies in medicinal informatics that have been considerably applied for an extensive time duration to create and deliver governed terminologies for coding arrangements. It is an amalgamation of four chief characteristics that is existent in nearly all ontologies in which success lies: allocation of regular identifiers for courses and associations that characterize the portents present in a domain; allocation of a terminology for a domain; allocation of metadata that defines the proposed connotation of the courses and associations in ontologies; and the allocation of machine-readable adages and descriptions that permit computational entree to some facets of the connotation of courses and associations. In this paper, it is discussed regarding the chief characteristics of ontologies, kinds of gene ontologies and forthcoming fashion of ontologies.

Keywords: *Ontology, Phenotype, Genotype, Vocabulary*

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Introduction

Bioinformatics have relatively recent achievement which is Bio-ontologies that determination towards a competent institution and dispersal of living data. Bio-ontologies deliver a structure and organized vocabulary through which data particularly those collected through sequencing and genomics but results are increasing from other types of research. The usage of ontologies initiated in biological sciences about 1998 with the progress of gene ontology. Their attention and action are growing in the zone to value nationwide and worldwide synchronization exertions such as Open Biomedical Ontologies Foundry or National Center for Biomedical Ontologies in 2007. Ontology is referred to as mainly ‘ontologies’ as well as ‘vocabularies’ and ‘thesauri’ that offer numerous key characteristics and these characteristics are used in all their implementations, which is listed below:

- Courses and associations are stated to as identifier like as an Internationalized Resource Identifier

(IRI), a Uniform Resource Identifier (URI), or a database identifier string.

- A domain terminology may be a record of expressions linked with the ontology’s courses and associations.
- Documentary descriptions and explanations that deliver supplementary data about what type of belongings is a course or association.
- Official descriptions and adages that offer a computational complement to documentary explanations which is retrieved and oppressed spontaneously using dedicated software and adages regarding domain.

Here, discuss ontologies containing features and these characteristics offer a ‘functional’ perception on ontologies. These features are improve data analysis in biology and biomedicine, which is discuss in below table.

Table: Characteristics offered by ontologies in Biological and Biomedical Study

Ontology characteristic	Effectiveness in Research
Courses and associations	In ontologies, usage of customary identifiers for courses and associations, is what assists data incorporation across numerous databases because the identical identifiers can be used across numerous, detached databases, records or web sites.
Domain terminology	Through labels linked with courses and associations, ontologies offer a domain terminology that can be subjugated for uses extending from natural language handling, formation of user interfaces, etc.
Metadata and explanations	In ontologies, courses are linked with written descriptions, explanations, instances and additional metadata that are what permit domain specialists to comprehend the accurate connotation of course in the ontology. The meaning of courses in ontologies are consistent understood by definitions and related metadata.
Adages and official descriptions	Official descriptions and adages assist automatic and computational entree to (some parts of) the connotation of a course or relation.

Here, we also converse the categories of gene ontologies which is divided into three parts that is discuss into below:

- Molecular function
- Biological process
- Cellular component

Molecular function: It is described as biological occurrence that include definite bondage to ligands or arrangements which is a gene artefact of activity. It applies to the proficiency that a gene artefact holds as a potential. It is defines only that what has

occurred without postulating the where or when occurrence really took place. Instances of narrower practical rapports are ‘adenylate cyclase’ or ‘Toll receptor ligand’ and example of broad purposeful rapports are ‘enzyme’, ‘transporter’ or ‘ligand’.

Biological process: In which biological procedure mentions to a biological motive to which the gene or gene artefact donates. A method is fulfilled through one or more methodical associations of molecular utilities. This process comprise a physical or chemical conversion, in the logic that a certain thing goes into the procedure and something is dissimilar that come out of it. Example of broad (high level)

biological procedure terminology are “cell development and conservation” or “signal transduction” and more definite (lower level) procedure terms are ‘translation’, ‘pyrimidine metabolism’ or ‘Cyclic adenosine monophosphate (CAMP) bio-synthesis’.

Cellular component: It refers to the specific spot present within the cell where a gene artefact is dynamic. These terminologies showcase the apprehension of eukaryotic cell structure. It is correct for other ontologies but not for all terminologies which are can be applied to all the organisms; the series of terminologies is destined to be comprehensive. It comprises of terms such as ‘ribosome’ or ‘proteasome’, ‘nuclear membrane’ and ‘Golgi apparatus’, postulating where numerous gene products would be established.

Molecular function, biological process and cellular constituent are all characteristics of genes, gene artefacts or gene-artefact collections. All of these are allocated as an individualistically and simply recognizing that biological procedure, molecular occupation and cellular position characterize self-regulating characteristics is by itself expounding in several circumstances. The associations between a gene artefact (or gene-artefact group) to biological procedure, molecular occupation and cellular constituent are one-to-many, showcasing the biological authenticity that a specific protein may work out in numerous procedures, encompass domains that operate miscellaneous molecular purposes, and partake in numerous alternate interfaces with other proteins, organelles or sites present in the cell.

Future and role of biomedical ontologies

Biomedical ontologies deliver the semantic arrangement that funds incorporation and assessment of huge, multifaceted data series in biology. To applied information of ontology improvement and usage has been on detention of domain information like as purpose and position. Ontologies sustain even data encrypting thus delivering semantic incorporation of data resultant from numerous means like as free-text periodicals or purposeful explanations of arrangements from manifold suppliers. Exchange and incorporation of data is the facilities of semantic incorporation that is in between the possessions and is crucial for forthcoming expansion of semantic web facilities. It is beneficial as expressions for explanation methods and that they

can be utilized in official ontological illustrations in biomedicine as these reserve progress. Bio-ontologies have substantial influence on data incorporation, admittance and examination through their practice in seizing and arranging biological data.

Review of Literature

Jupp et al., concluded that in life science ontologies, Simple Knowledge Organization System (SKOS) vocabulary has some adoption-in particularly the labeling and mapping properties. It permits prevailing apparatuses that use up the SKOS admittance to terminological data of bio-ontologies by taking standard approaches. It is required for an enhanced device support to permit life scientists to use SKOS more effortlessly. This paper reveals regarding the way to detach the protein with concern information and use demonstration into sheets and assuming ethics like as SKOS offer new prospects for new information.

Blake, Botstein and Butler 2000, by all eukaryotes, large fraction of genes are made by genomic sequencing that is specifying the core biological functions. Biological part knowledge of such mutual proteins in one organism can frequently be transported to other organism. The objective of gene ontology confederation is to generate an energetic, measured terminology that can be used on to all eukaryotes which have an information of gene and protein in cells which keeps amassing and altering.

Blake and Bult 2006, stated that generation of genome-scale data series are supported by new technologies and series of orders, order alternates, transcriptions and proteins; genetic rudiments reinforcing apprehension of biomedicine and ailment. These data is manage by information systems and by analysis of these data, biological knowledge have to come, assorted data series for fresh biologically appropriate arrangements, to producing theories for investigational authentication and eventually, to constructing replicas of the way biological system operate. Data integration and comparative genomics are two key approaches in role of bio-ontologies that is effectual explanation of genome-scale data series.

Huntley et.al 2014, in this paper, describing the some examples of gene ontology that is linked with annotation can change over time, using example how to manage the changes of UniPort. For analysis to understand that who make use of gene ontology and why such variations happen in order to conclude the suitable inferences for their elucidations.

Malone et.al 2016, dictated that metadata is describing by bio-ontologies that is important tool which is a progressively significant contemplation as scientifically logical group targets for exposed, reusable information. Ontology is choices by pick and not used as straightforward that is validated by number of times and writers are asked to applaud a specific ontology for a specified issue. First to select the bio-ontology is to apprehend the necessities before determining to engross with a specific

ontology or definitely before stamping one's own ontology.

Conclusion

Bio-ontologies play an important role is able to recognize the vital biology and medical research that is use within biomedicine is nowadays a conventional action. It is widely used to transport vocabularies for labelling information and upcoming aspect will see superior examination of information because of growing conventionalism of these ontologies. By using this conventionalism, will perceive the progress of mention ontologies in biology and biomedicine. Gene ontologies found accurately resembles modules that drives gene and protein boundary linkages, resulting to a data-driven method for authenticating ontology. By doing the scientific research, growing the methods for improving the use of ontologies for evaluating ontology quality.



References:

Blake, Judith A., and Carol J. Bult. "Beyond the Data Deluge: Data Integration and Bio-Ontologies." *Journal of Biomedical Informatics*, vol. 39, no. 3, 2006, pp. 314–320.

Blake, Judith A., et al. "Gene Ontology: Tool for the Unification of Biology." *2000 Nature America Inc.*, vol. 25, May 2000, pp. 25–29.

Bodenreider, Olivier, and Robert Stevens. "Bio-Ontologies: Current Trends and Future Directions." *Briefings in Bioinformatics*, vol. 7, no. 3, 2006, pp. 256–274.

Hoehndorf, R., et al. "The Role of Ontologies in Biological and Biomedical Research: a Functional Perspective." *Briefings in Bioinformatics*, vol. 16, no. 6, Oct. 2015, pp. 1069–1080.

Huntley, Rachael P, et al. "Understanding How and Why the Gene Ontology and Its Annotations Evolve: the GO within UniProt." *GigaScience*, vol. 3, no. 1, 2014.

Leonelli, Sabina. "Bio-Ontologies as Tools for Integration in Biology." *Biological Theory*, vol. 3, no. 1, 2008, pp. 7–11.

Malone, James, et al. "Ten Simple Rules for Selecting a Bio-Ontology." *PLOS Computational Biology*, vol. 12, no. 2, Nov. 2016.

Taking a view on bio-ontologies. Available at: <https://pdfs.semanticscholar.org/694b/5db6306f7a983f64df849ccc7637214bd8d5.pdf>