Resource Summary Report

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PATO

RRID:SCR_004782
Type: Tool

Proper Citation

PATO (RRID:SCR_004782)

Resource Information

URL: http://www.obofoundry.org/ontology/pato.html

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Description: Ontology of phenotypic qualities, intended for use in a number of applications, primarily defining composite phenotypes and phenotype annotation. The new PATO differs from the old in that the system of attributes and values has been abandoned in favor of a single hierarchy of qualities. PATO is designed to be used in conjunction with ontologies of quality-bearing entities. An example of such an entity is an insect eye (taken from the fly_anatomy ontology), which could be the bearer of the quality "red" (PATO:0000322). This combination is the red eye phenotype. We say that the phenotype term is "post-coordinated", as it is formed by coordinating two terms together. This is in contrast to ontologies of pre-coordinated phenotypes, such as the Mammalian Phenotype (MP) ontology. PATO is independent of any exchange format or database schema. One way of expressing phenotype annotation using PATO is pheno-syntax, or pheno-xml. They will also post recommendations for representing phenotypes using OWL. All representations share the same basic formal underpinnings, a combination of quality-bearing entity and a quality (the EQ model).

Abbreviations: PATO

Synonyms: PATO - Phenotypic Quality Ontology, Phenotype and Trait Ontology, Phenotypic Quality Ontology

Resource Type: ontology, controlled vocabulary, data or information resource

Keywords: plant trait, mammalian, phenotype, obo, quality, phenotypic quality

Funding:

Resource Name: PATO

Resource ID: SCR_004782

Alternate IDs: nlx_77534

Old URLs: http://obofoundry.org/wiki/index.php/PATO:Main_Page

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250416T063359+0000

Ratings and Alerts

No rating or validation information has been found for PATO.

No alerts have been found for PATO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Deans AR, et al. (2024) GallOnt: An ontology for plant gall phenotypes. Biodiversity data journal, 12, e128585.

Matentzoglu N, et al. (2024) The Unified Phenotype Ontology (uPheno): A framework for cross-species integrative phenomics. bioRxiv : the preprint server for biology.

Aracil-Gisbert S, et al. (2024) The ICU environment contributes to the endemicity of the "Serratia marcescens complex" in the hospital setting. mBio, 15(5), e0305423.

Flatgard BM, et al. (2024) Tracking antimicrobial resistance transmission in urban and rural communities in Bangladesh: a One Health study of genomic diversity of ESBL-producing and carbapenem-resistant Escherichia coli. Microbiology spectrum, 12(6), e0395623.

Pires J, et al. (2024) Development and implementation of a core genome multilocus sequence typing scheme for Yersinia enterocolitica: a tool for surveillance and outbreak detection. Journal of clinical microbiology, 62(8), e0004024.

Pérez-Viso B, et al. (2024) A long-term survey of Serratia spp. bloodstream infections revealed an increase of antimicrobial resistance involving adult population. Microbiology spectrum, 12(2), e0276223.

Molteni C, et al. (2024) Comparative genomics reveal a novel phylotaxonomic order in the genus Fusobacterium. Communications biology, 7(1), 1102.

Rodrigues C, et al. (2023) Phylogenomics of Globally Spread Clonal Groups 14 and 15 of Klebsiella pneumoniae. Microbiology spectrum, 11(3), e0339522.

Zhang X, et al. (2023) DEVO: an ontology to assist with dermoscopic feature standardization. BMC medical informatics and decision making, 23(Suppl 1), 162.

Langstroff A, et al. (2022) Opportunities and limits of controlled-environment plant phenotyping for climate response traits. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 135(1), 1.

Fisher ME, et al. (2022) The Xenopus phenotype ontology: bridging model organism phenotype data to human health and development. BMC bioinformatics, 23(1), 99.

Nowotarski SH, et al. (2021) Planarian Anatomy Ontology: a resource to connect data within and across experimental platforms. Development (Cambridge, England), 148(15).

Wineriter-Wright SA, et al. (2020) The Biology of Casmara subagronoma (Lepidoptera: Oecophoridae), a Stem-Boring Moth of Rhodomyrtus tomentosa (Myrtaceae): Descriptions of the Previously Unknown Adult Female and Immature Stages, and Its Potential as a Biological Control Candidate. Insects, 11(10).

Cui H, et al. (2020) Measurement Recorder: developing a useful tool for making species descriptions that produces computable phenotypes. Database : the journal of biological databases and curation, 2020.

Freitas AR, et al. (2020) Comparative genomics of global optrA-carrying Enterococcus faecalis uncovers a common chromosomal hotspot for optrA acquisition within a diversity of core and accessory genomes. Microbial genomics, 6(6).

Waller JT, et al. (2019) The odonate phenotypic database, a new open data resource for comparative studies of an old insect order. Scientific data, 6(1), 316.

Silva TSR, et al. (2019) Using controlled vocabularies in anatomical terminology: A case study with Strumigenys (Hymenoptera: Formicidae). Arthropod structure & development, 52, 100877.

Neveu P, et al. (2019) Dealing with multi-source and multi-scale information in plant

phenomics: the ontology-driven Phenotyping Hybrid Information System. The New phytologist, 221(1), 588.

Dahdul W, et al. (2018) Annotation of phenotypes using ontologies: a gold standard for the training and evaluation of natural language processing systems. Database : the journal of biological databases and curation, 2018.

Griffiths E, et al. (2017) Context Is Everything: Harmonization of Critical Food Microbiology Descriptors and Metadata for Improved Food Safety and Surveillance. Frontiers in microbiology, 8, 1068.