Resource Summary Report

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phenomeNET

RRID:SCR_006165
Type: Tool

Proper Citation

phenomeNET (RRID:SCR_006165)

Resource Information

URL: http://phenomebrowser.net/

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Description: PhenomeNet is a cross-species phenotype similarity network. It contains the experimentally observed phenotypes of multiple species as well as the phenotypes of human diseases. PhenomeNet provides a measure of phenotypic similarity between the phenotypes it contains. The latest release (from 22 June 2012) contains 124,730 complex phenotype nodes taken from the yeast, fish, worm, fly, rat, slime mold and mouse model organism databases as well as human disease phenotypes from OMIM and OrphaNet. The network is a complete graph in which edge weights represent the degree of phenotypic similarity. Phenotypic similarity can be used to identify and prioritize candidate disease genes, find genes participating in the same pathway and orthologous genes between species. To compute phenotypic similarity between two sets of phenotypes, we use a weighted Jaccard index. First, phenotype ontologies are used to infer all the implications of a phenotype observation using several phenotype ontologies. As a second step, the information content of each phenotype is computed and used as a weight in the Jaccard index. Phenotypic similarity is useful in several ways. Phenotypic similarity between a phenotype resulting from a genetic mutation and a disease can be used to suggest candidate genes for a disease. Phenotypic similarity can also identify genes in a same pathway or orthologous genes. PhenomeNet uses the axioms in multiple species-dependent phenotype ontologies to infer equivalent and related phenotypes across species. For this purpose, phenotype ontologies and phenotype annotations are integrated in a single ontology, and automated reasoning is used to infer equivalences. Specifically, for every phenotype, PhenomeNet infers the related mammalian phenotype and uses the Mammalian Phenotype Ontology for computing phenotypic similarity. Tools: * PhenomeBLAST - A tool for cross-species alignments of phenotypes * PhenomeDrug - method for drug-repurposing

Abbreviations: PhenomeNet

Synonyms: PhenomeNet - Cross Species Phenotype Network

Resource Type: source code, service resource, production service resource, data analysis service, database, analysis service resource, data or information resource, software resource

Defining Citation: PMID:21737429

Keywords: phenotype, disease, gene, genotype, allele, model organism, human disease, candidate disease gene, pathway, orthologous gene, ortholog, ontology, semantic similarity, mutant phenotype, disease pathway, alignment, pharmacogenomics, drug

Funding: European Union 7th FPRICORDO project 248502;
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BBSRC BBG0043581

Availability: The source code and all data are freely available on http://phenomeblast.googlecode.com

Resource Name: phenomeNET

Resource ID: SCR_006165

Alternate IDs: nlx_151667

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250517T055740+0000

Ratings and Alerts

No rating or validation information has been found for phenomeNET.

No alerts have been found for phenomeNET.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Alghamdi SM, et al. (2022) Contribution of model organism phenotypes to the computational identification of human disease genes. Disease models & mechanisms, 15(7).

Hinnerichs T, et al. (2021) DTI-Voodoo: machine learning over interaction networks and ontology-based background knowledge predicts drug-target interactions. Bioinformatics (Oxford, England), 37(24), 4835.

Kafkas ?, et al. (2021) Linking common human diseases to their phenotypes; development of a resource for human phenomics. Journal of biomedical semantics, 12(1), 17.

Smaili FZ, et al. (2020) Formal axioms in biomedical ontologies improve analysis and interpretation of associated data. Bioinformatics (Oxford, England), 36(7), 2229.

Boudellioua I, et al. (2017) Semantic prioritization of novel causative genomic variants. PLoS computational biology, 13(4), e1005500.

Hoehndorf R, et al. (2015) Analysis of the human diseasome using phenotype similarity between common, genetic, and infectious diseases. Scientific reports, 5, 10888.

Oellrich A, et al. (2015) An ontology approach to comparative phenomics in plants. Plant methods, 11, 10.

de Angelis MH, et al. (2015) Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. Nature genetics, 47(9), 969.

Hoehndorf R, et al. (2013) An integrative, translational approach to understanding rare and orphan genetically based diseases. Interface focus, 3(2), 20120055.

Pavlidis P, et al. (2013) Progress and challenges in the computational prediction of gene function using networks: 2012-2013 update. F1000Research, 2, 230.

Smedley D, et al. (2013) PhenoDigm: analyzing curated annotations to associate animal models with human diseases. Database : the journal of biological databases and curation, 2013, bat025.

Oellrich A, et al. (2012) Improving disease gene prioritization by comparing the semantic similarity of phenotypes in mice with those of human diseases. PloS one, 7(6), e38937.

Smith CL, et al. (2012) The Mammalian Phenotype Ontology as a unifying standard for experimental and high-throughput phenotyping data. Mammalian genome : official journal of the International Mammalian Genome Society, 23(9-10), 653.