Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

OwlSim

RRID:SCR_006819
Type: Tool

Proper Citation

OwlSim (RRID:SCR_006819)

Resource Information

URL: http://owlsim.org

Proper Citation: OwlSim (RRID:SCR_006819)

Description: Software package that provides the ability to do a number of standard semantic similarity methods and includes novel methods for combining these with dynamic selection of anonymous grouping classes. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: OwlSim

Resource Type: data processing software, software application, software resource

Defining Citation: PMID:19956802

Keywords: functional similarity, semantic similarity, ontology, phenotype, annotation, windows, mac os x, linux, unix

Funding: Biomedical Information Science and Technology Initiative ;
National Center for Biomedical Ontology ;
NHGRI U54 HG004028;
NHGRI HG002659

Availability: Open unspecified license - Free for academic use

Resource Name: OwlSim

Resource ID: SCR_006819

Alternate IDs: nlx_149312

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260903T235940+0000

Ratings and Alerts

No rating or validation information has been found for OwlSim.

No alerts have been found for OwlSim.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Tanaka N, et al. (2020) An atlas of evidence-based phenotypic associations across the mouse phenome. Scientific reports, 10(1), 3957.

Wang RL, et al. (2019) Ontology-based semantic mapping of chemical toxicities. Toxicology, 412, 89.

Mungall CJ, et al. (2017) The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes across species. Nucleic acids research, 45(D1), D712.

Bone WP, et al. (2016) Computational evaluation of exome sequence data using human and model organism phenotypes improves diagnostic efficiency. Genetics in medicine : official journal of the American College of Medical Genetics, 18(6), 608.

Maynard SM, et al. (2013) A knowledge based approach to matching human neurodegenerative disease and animal models. Frontiers in neuroinformatics, 7, 7.