

Resource Summary Report

Generated by [dkNET](#) on Aug 27, 2026

FastSemSim

RRID:SCR_006919

Type: Tool

Proper Citation

FastSemSim (RRID:SCR_006919)

Resource Information

URL: <http://sourceforge.net/p/fastsemsim/home/Home/>

Proper Citation: FastSemSim (RRID:SCR_006919)

Description: A package that implements several semantic similarity measures. It is both a library and an end-user application, featuring an intuitive graphical user interface (GUI). It has been implemented with the aim of being fast, expandable, and easy to use. It allows the user to work with the most updated version of GO database and customizable annotation corpora. It provides a set of logically-organized classes that can be easily exploited to both integrate semantic similarity into different analysis pipelines and extend the library with new measures. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: FastSemSim

Resource Type: software library, software resource, software toolkit

Keywords: software library, functional similarity, semantic similarity, graphical user interface, gene ontology, annotation, parse, gene, protein

Availability: Open unspecified license - Free for academic use. GNU GPL license. However, This software is currently unpublished work. You must contact us before using it or its results or any work/app. based on top of it in any published work.

Resource Name: FastSemSim

Resource ID: SCR_006919

Alternate IDs: nlx_149309

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260821T193816+0000

Ratings and Alerts

No rating or validation information has been found for FastSemSim.

No alerts have been found for FastSemSim.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Dosch J, et al. (2023) FAS: assessing the similarity between proteins using multi-layered feature architectures. Bioinformatics (Oxford, England), 39(5).

Gnanavel M, et al. (2021) Identifying the miRNA Signature Association with Aging-Related Senescence in Glioblastoma. International journal of molecular sciences, 22(2).

Wang Z, et al. (2018) PANDA: Protein function prediction using domain architecture and affinity propagation. Scientific reports, 8(1), 3484.

Saghaeian Jazi M, et al. (2018) SOX2OT knockdown derived changes in mitotic regulatory gene network of cancer cells. Cancer cell international, 18, 129.

Meng X, et al. (2015) CancerNet: a database for decoding multilevel molecular interactions across diverse cancer types. Oncogenesis, 4(12), e177.

Cao R, et al. (2015) Deciphering the association between gene function and spatial gene-gene interactions in 3D human genome conformation. BMC genomics, 16, 880.