Resource Summary Report

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BITOLA: Biomedical Discovery Support System

RRID:SCR_008175
Type: Tool

Proper Citation

BITOLA: Biomedical Discovery Support System (RRID:SCR_008175)

Resource Information

URL: http://www.mf.uni-lj.si/bitola/

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Description: An interactive literature-based biomedical discovery support system. The goal of this system is to discover new, potentially meaningful relations between a given starting concept of interest and other concepts, by mining the bibliographic database MEDLINE. To make the system more suitable for disease candidate-gene discovery and to decrease the number of candidate relations, we integrated background knowledge about the chromosomal location of the starting disease as well as the chromosomal location of the candidate genes from resources such as Entrez Gene, HUGO and OMIM. The BITOLA system can also be used as an alternative way of searching the Medline database. The system is available in two versions: closed discovery and open discovery. Closed discovery allows the input of two concepts (Example 1: a disorder and a gene. Example 2: a drug and a side effect) and generates potential explanations of the relationship between two entities. It does this by searching published literature to finds intermediate links. Open discovery allows the input of a single concept, then categories for first-order relatives of that concept, then categories for relatives of those first order concepts. Thus it can link from a disease to related drugs, then to genes related to those drugs and then test if those genes have been mentioned/tested in association with the disease. If the answer is no, then the gene is potentially related yet untested in the literature. Thus the open discovery tool is a nominator of new genes, drugs or neuroscience correlates to be investigated with diseases, disorders, physiological responses or any other phenotype.

Synonyms: BITOLA

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

Keywords: drug, gene, biomedical, chromosomal, concept, discovery, disease, disorder, literature, location, medline interfaces, neuroscience, phenotype, physiological, response

Resource Name: BITOLA: Biomedical Discovery Support System

Resource ID: SCR_008175

Alternate IDs: nif-0000-21062

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260815T182343+0000

Ratings and Alerts

No rating or validation information has been found for BITOLA: Biomedical Discovery Support System.

No alerts have been found for BITOLA: Biomedical Discovery Support System.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Toh H, et al. (2022) A haplotype-resolved genome assembly of the Nile rat facilitates exploration of the genetic basis of diabetes. BMC biology, 20(1), 245.

Zhang Y, et al. (2020) Identification of biological pathways and genes associated with neurogenic heterotopic ossification by text mining. PeerJ, 8, e8276.

Cifuentes RA, et al. (2012) The autoimmune tautology: an in silico approach. Autoimmune diseases, 2012, 792106.

Krallinger M, et al. (2005) Text-mining and information-retrieval services for molecular biology. Genome biology, 6(7), 224.