

Resource Summary Report

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GeneWalk

RRID:SCR_023787

Type: Tool

Proper Citation

GeneWalk (RRID:SCR_023787)

Resource Information

URL: <https://github.com/churchmanlab/genewalk>

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Description: Software for individual genes functions determination that are relevant in particular biological context and experimental condition. Quantifies similarity between vector representations of gene and annotated GO terms through representation learning with random walks on condition specific gene regulatory network. Similarity significance is determined through comparison with node similarities from randomized networks.

Resource Type: software resource, software application

Defining Citation: [PMID:33526072](#)

Keywords: genes functions determination, vector representations of gene, annotated GO terms, similarity significance, node similarities, randomized networks,

Funding: NHGRI R01 HG007173

Availability: Free, Available for download, Freely available

Resource Name: GeneWalk

Resource ID: SCR_023787

Old URLs: <https://churchman.med.harvard.edu/genewalk>

License: BSD 2-Clause

Record Creation Time: 20230714T050221+0000

Record Last Update: 20260801T191122+0000

Ratings and Alerts

No rating or validation information has been found for GeneWalk.

No alerts have been found for GeneWalk.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Montani C, et al. (2024) Sex-biasing influence of autism-associated Ube3a gene overdosage at connectomic, behavioral, and transcriptomic levels. Science advances, 10(28), eadg1421.

Newsham I, et al. (2024) Early detection and diagnosis of cancer with interpretable machine learning to uncover cancer-specific DNA methylation patterns. Biology methods & protocols, 9(1), bpae028.

Ietswaart R, et al. (2021) GeneWalk identifies relevant gene functions for a biological context using network representation learning. Genome biology, 22(1), 55.