

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 10, 2026

GeneWalk

RRID:SCR_023787

Type: Tool

Proper Citation

GeneWalk (RRID:SCR_023787)

Resource Information

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

Proper Citation: GeneWalk (RRID:SCR_023787)

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 application, software resource

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: 20260810T040841+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 4 mentions in open access literature.

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

Madhu LN, et al. (2026) Intranasal Human NSC-Derived EVs Therapy Can Restrain Inflammatory Microglial Transcriptome, and NLRP3 and cGAS-STING Signalling, in Aged Hippocampus. Journal of extracellular vesicles, 15(2), e70232.

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.

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.

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