Resource Summary Report

Generated by RRID on Apr 16, 2025

SEGS

RRID:SCR_003554
Type: Tool

Proper Citation

SEGS (RRID:SCR_003554)

Resource Information

URL: http://kt.ijs.si/software/SEGS/

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Description: A web tool for descriptive analysis of microarray data. The analysis is performed by looking for descriptions of gene sets that are statistically significantly over- or under-expressed between different scenarios within the context of a genome-scale experiments (DNA microarray). Descriptions are defined by using the terms from the Gene Ontology (GO), the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways and gene-gene interactions found in the ENTREZ database. Gene annotations by GO and KEGG terms can also be found in the ENTREZ database. The tool provides three procedures for testing the enrichment of the gene sets (over- or under-expressed): Fisher's exact test, GSEA and PAGE, and option for combining the results of the tests. Because of the multiple-hypothesis testing nature of the problem, all the p-values are computed using the permutation testing method.

Abbreviations: SEGS

Synonyms: Search for Enriched Gene Sets

Resource Type: analysis service resource, service resource, production service resource, data analysis service

Defining Citation: PMID:18234563

Keywords: microarray, pathway, gene-gene interaction, gene, interaction, annotation, gene expression, ortholog, molecular function, biological process, cellular component, enriched gene set, gene set

Funding:

Resource Name: SEGS

Resource ID: SCR_003554

Alternate IDs: nlx_157688

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250416T063330+0000

Ratings and Alerts

No rating or validation information has been found for SEGS.

No alerts have been found for SEGS.

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 RRID.

Cebrián-Tarancón C, et al. (2023) Chemical exchange in the vine shoots-wine system when used as an innovative enological procedure. Journal of the science of food and agriculture, 103(4), 1821.

Tine M, et al. (2021) Genome-wide analysis of European sea bass provides insights into the evolution and functions of single-exon genes. Ecology and evolution, 11(11), 6546.

Robinson J, et al. (2017) Distinguishing functional polymorphism from random variation in the sequences of >10,000 HLA-A, -B and -C alleles. PLoS genetics, 13(6), e1006862.