Resource Summary Report

Generated by NIF on Apr 28, 2025

<u>GSVA</u>

RRID:SCR_021058 Type: Tool

Proper Citation

GSVA (RRID:SCR_021058)

Resource Information

URL: https://www.bioconductor.org/packages/release/bioc/html/GSVA.html

Proper Citation: GSVA (RRID:SCR_021058)

Description: Open source software R package for assaying variation of gene set enrichment over sample population.Used for microarray and RNA-seq data analysis. Gene set enrichment method that estimates variation of pathway activity over sample population in unsupervised manner.

Abbreviations: GSVA

Synonyms: Gene Set Variation Analysis

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

Defining Citation: PMID:23323831

Keywords: Gene set enrichment, variation estimation, pathway activity, sample population, microarray, RNA-seq, data analysis

Funding: ISCIII COMBIOMED ; Spanish MINECO ; NCI U54 CA149237

Availability: Free, Available for download, Freely available

Resource Name: GSVA

Resource ID: SCR_021058

License: GPL

Record Creation Time: 20220129T080353+0000

Record Last Update: 20250428T054219+0000

Ratings and Alerts

No rating or validation information has been found for GSVA.

No alerts have been found for GSVA.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 191 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Klein L, et al. (2025) Spatial tumor immune heterogeneity facilitates subtype co-existence and therapy response in pancreatic cancer. Nature communications, 16(1), 335.

Liu Z, et al. (2024) Spatial transcriptomics reveals that metabolic characteristics define the tumor immunosuppression microenvironment via iCAF transformation in oral squamous cell carcinoma. International journal of oral science, 16(1), 9.

Shea A, et al. (2024) Modeling Drug Responses and Evolutionary Dynamics using Patient-Derived Xenografts Reveals Precision Medicine Strategies for Triple Negative Breast Cancer. Cancer research.

Versi A, et al. (2024) A severe asthma phenotype of excessive airway Haemophilus influenzae relative abundance associated with sputum neutrophilia. Clinical and translational medicine, 14(9), e70007.

Thatikonda V, et al. (2024) Co-targeting SOS1 enhances the antitumor effects of KRASG12C inhibitors by addressing intrinsic and acquired resistance. Nature cancer, 5(9), 1352.

Ou L, et al. (2024) Helicobacter pylori infection facilitates cell migration and potentially impact clinical outcomes in gastric cancer. Heliyon, 10(17), e37046.

Pan H, et al. (2024) FN1, a reliable prognostic biomarker for thyroid cancer, is associated with tumor immunity and an unfavorable prognosis. Oncology letters, 28(5), 510.

Lewis K, et al. (2024) p66ShcA promotes malignant breast cancer phenotypes by alleviating energetic and oxidative stress. Redox biology, 70, 103028.

Lu Y, et al. (2024) Development and experimental validation of an energy metabolismrelated gene signature for diagnosing of osteoporosis. Scientific reports, 14(1), 8153.

Wang D, et al. (2024) Identification of a 5-Gene Cuproptosis Signature Predicting the Prognosis for Colon Adenocarcinoma Based on WGCNA. Technology in cancer research & treatment, 23, 15330338241250285.

Zhao YC, et al. (2024) The role of SLC39A4 in the prognosis, immune microenvironment, and contribution to malignant behavior in vivo and in vitro of cervical cancer. Translational oncology, 40, 101839.

Ling T, et al. (2024) Single-cell analysis revealed a potential role of T-cell exhaustion in colorectal cancer with liver metastasis. Journal of cellular and molecular medicine, 28(8), e18341.

Zhu J, et al. (2024) Exploring the role of KIR3DL2 on NK cells in hepatocellular carcinoma and its potential prognostic implications. iScience, 27(9), 110637.

Lee S, et al. (2024) CRIF1 deficiency induces FOXP3LOW inflammatory non-suppressive regulatory T cells, thereby promoting antitumor immunity. Science advances, 10(13), eadj9600.

Liu J, et al. (2024) Construction and validation of m6A-related diagnostic model for psoriasis. PeerJ, 12, e17027.

Zhang J, et al. (2024) Immune microenvironment heterogeneity of concurrent adenocarcinoma and squamous cell carcinoma in multiple primary lung cancers. NPJ precision oncology, 8(1), 55.

Zhao Y, et al. (2024) Identification of potential biomarkers from amino acid transporter in the activation of hepatic stellate cells via bioinformatics. Frontiers in genetics, 15, 1499915.

Xue Y, et al. (2024) The IncRNA GAS5 upregulates ANXA2 to mediate the macrophage inflammatory response during atherosclerosis development. Heliyon, 10(2), e24103.

Goralski TM, et al. (2024) Spatial transcriptomics reveals molecular dysfunction associated with cortical Lewy pathology. Nature communications, 15(1), 2642.

Lu Y, et al. (2024) ALDH1A3-acetaldehyde metabolism potentiates transcriptional heterogeneity in melanoma. Cell reports, 43(7), 114406.