

Resource Summary Report

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ConsensusClusterPlus

RRID:SCR_016954

Type: Tool

Proper Citation

ConsensusClusterPlus (RRID:SCR_016954)

Resource Information

URL: <http://bioconductor.org/packages/release/bioc/html/ConsensusClusterPlus.html>

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Description: Software written in R for determining cluster count and membership by stability evidence in unsupervised analysis. Provides quantitative and visual stability evidence for estimating the number of unsupervised classes in a dataset with item tracking, item consensus and cluster consensus plots.

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

Defining Citation: [PMID:20427518](#)

Keywords: cluster, count, stability, evidence, unsupervised, analysis, , bio.tools

Funding: NCI F32CA142039;
Thomas G. Labrecque Foundation ;
NCI U24 CA126554

Availability: Free, Available for download, Freely available

Resource Name: ConsensusClusterPlus

Resource ID: SCR_016954

Alternate IDs: biotools:consensusclusterplus

Alternate URLs: <https://bio.tools/consensusclusterplus>

License: GPL 2

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260728T043523+0000

Ratings and Alerts

No rating or validation information has been found for ConsensusClusterPlus.

No alerts have been found for ConsensusClusterPlus.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 160 mentions in open access literature.

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

Zheng L, et al. (2025) A gene signature related to programmed cell death to predict immunotherapy response and prognosis in colon adenocarcinoma. PeerJ, 13, e18895.

Liu Y, et al. (2025) Identification of HES4 as a novel prognostic marker and therapeutic target in hepatocellular carcinoma. Discover oncology, 16(1), 156.

Ding C, et al. (2025) The signature based on interleukin family and receptors identified IL19 and IL20RA in promoting nephroblastoma progression through STAT3 pathway. Scientific reports, 15(1), 11639.

Shen Y, et al. (2025) Development of a novel risk signature revealing prognostic and tumor microenvironmental features in breast cancer. Medicine, 104(5), e41369.

Qian C, et al. (2025) Single-cell stemness analysis highlights Midkine-LRP1 pathway and identifies new bladder cancer subtypes. Cancer cell international, 25(1), 376.

Farrar JT, et al. (2025) Widespread pain phenotypes impact treatment efficacy results in randomized clinical trials for interstitial cystitis/bladder pain syndrome: a Multidisciplinary Approach to the Study of Chronic Pelvic Pain network study. Pain, 166(5), 1179.

Zhang J, et al. (2025) Characterization of PANoptosis-based markers for ischemic stroke and their appealing implications in improving prognosis and in glioma patients. Discover oncology, 16(1), 1987.

Mayer M, et al. (2025) Deciphering the cellular tumor microenvironment landscape in salivary gland carcinomas using multiplexed imaging mass cytometry. Journal of experimental & clinical cancer research : CR, 44(1), 288.

Helleux A, et al. (2025) TFE3 fusions drive oxidative metabolism and ferroptosis resistance in translocation renal cell carcinoma. EMBO molecular medicine, 17(5), 1041.

Chen J, et al. (2025) Identification and validation of biomarkers related to mitophagy in chronic obstructive pulmonary disease. Molecular medicine reports, 31(4).

Wang M, et al. (2025) A nicotinamide metabolism-related gene signature for predicting immunotherapy response and prognosis in lung adenocarcinoma patients. *PeerJ*, 13, e18991.

Chen Y, et al. (2025) Targeting the cuproptosis-associated gene COL22A1 in glioblastoma using EMD-1204831 and kaempferol. *International journal of oncology*, 66(5).

Cho Y, et al. (2025) Modeling cellular influence delineates functionally relevant cellular neighborhoods in primary and metastatic pancreatic ductal adenocarcinoma. *bioRxiv : the preprint server for biology*.

Jia X, et al. (2025) Comprehensive multi-omics analyses expose a precision therapy strategy that targets replication stress in hepatocellular carcinoma using WEE1 inhibition. *Journal of advanced research*, 78, 497.

Zhuo Z, et al. (2025) Machine learning-based integration reveals immunological heterogeneity and the clinical potential of T cell receptor (TCR) gene pattern in hepatocellular carcinoma. *Apoptosis : an international journal on programmed cell death*, 30(3-4), 955.

Liu X, et al. (2025) SpatialDeX Is a Reference-Free Method for Cell-Type Deconvolution of Spatial Transcriptomics Data in Solid Tumors. *Cancer research*, 85(1), 171.

Fox NS, et al. (2024) iSubGen generates integrative disease subtypes by pairwise similarity assessment. *Cell reports methods*, 4(11), 100884.

Yao J, et al. (2024) Integration of multi-omics data revealed the orphan CpG islands and enhancer-dominated cis-regulatory network in glioma. *iScience*, 27(10), 110946.

Shi HZ, et al. (2024) m6A- and m5C- modified lncRNAs orchestrate the prognosis in cutaneous melanoma and m6A- modified LINC00893 regulates cutaneous melanoma cell metastasis. *Skin research and technology : official journal of International Society for Bioengineering and the Skin (ISBS) [and] International Society for Digital Imaging of Skin (ISDIS) [and] International Society for Skin Imaging (ISSI)*, 30(7), e13842.

Liu H, et al. (2024) Identification of the novel exhausted T cell CD8 + markers in breast cancer. *Scientific reports*, 14(1), 19142.