Resource Summary Report

Generated by dkNET on Apr 24, 2025

ConsensusClusterPlus

RRID:SCR 016954

Type: Tool

Proper Citation

ConsensusClusterPlus (RRID:SCR_016954)

Resource Information

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

Proper Citation: ConsensusClusterPlus (RRID:SCR_016954)

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

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: 20250423T060937+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 144 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Lei Y, et al. (2024) High temporal resolution prediction of mortality risk for single AML patient via deep learning. iScience, 27(8), 110458.

Shi HZ, et al. (2024) m6A- and m5C- modified IncRNAs 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.

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

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

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

Ulutekin C, et al. (2024) B cell depletion attenuates CD27 signaling of T helper cells in multiple sclerosis. Cell reports. Medicine, 5(1), 101351.

Gong H, et al. (2024) XRCC2 driven homologous recombination subtypes and therapeutic targeting in lung adenocarcinoma metastasis. NPJ precision oncology, 8(1), 169.

Watanabe K, et al. (2024) Inhibition of the galactosyltransferase C1GALT1 reduces osteosarcoma cell proliferation by interfering with ERK signaling and cell cycle progression. Cancer gene therapy, 31(7), 1049.

Xiong D, et al. (2024) Prediction significance of autophagy-related genes in survival probability and drug resistance in diffuse large B-cell lymphoma. Aging, 16(2), 1049.

Yang S, et al. (2024) Machine learning unveils immune-related signature in multicenter glioma studies. iScience, 27(4), 109317.

Patkar S, et al. (2024) Large-Scale Comparative Analysis of Canine and Human Osteosarcomas Uncovers Conserved Clinically Relevant Tumor Microenvironment Subtypes. Clinical cancer research: an official journal of the American Association for Cancer Research, 30(24), 5630.

Saulters EL, et al. (2024) Differential Regulation of the STING Pathway in Human Papillomavirus-Positive and -Negative Head and Neck Cancers. Cancer research communications, 4(1), 118.

Yang B, et al. (2024) Identification of ferroptosis-related gene signature for tuberculosis diagnosis and therapy efficacy. iScience, 27(7), 110182.

Huang Y, et al. (2024) Identification of a signature of histone modifiers in kidney renal clear cell carcinoma. Aging, 16(12), 10489.

Ma H, et al. (2024) Development of a Combined Oxidative Stress and Endoplasmic Reticulum Stress-Related Prognostic Signature for Hepatocellular Carcinoma. Combinatorial chemistry & high throughput screening, 27(19), 2850.

Fan Z, et al. (2024) A transcriptome based molecular classification scheme for cholangiocarcinoma and subtype-derived prognostic biomarker. Nature communications, 15(1), 484.

Rodriguez E, et al. (2024) The transcriptional landscape of glycosylation-related genes in cancer. iScience, 27(3), 109037.

Pan ZF, et al. (2024) Protocol for analysis of plasma proteomes from patients with hepatocellular carcinoma receiving combination therapy. STAR protocols, 5(4), 103308.

Yang Y, et al. (2024) Identification of costimulatory molecule signatures for evaluating prognostic risk in non-small cell lung cancer. Heliyon, 10(17), e36816.

Liu G, et al. (2024) Identification of mitochondria-related gene biomarkers associated with immune infiltration in acute myocardial infarction. iScience, 27(7), 110275.