Resource Summary Report

Generated by NIF on May 25, 2025

clusterSim

RRID:SCR_023743
Type: Tool

Proper Citation

clusterSim (RRID:SCR_023743)

Resource Information

URL: https://CRAN.R-project.org/package=clusterSim

Proper Citation: clusterSim (RRID:SCR_023743)

Description: Software R package used for searching for optimal clustering procedure for data set.

Resource Type: software resource, software toolkit

Keywords: searching for optimal clustering procedure for data set, optimal clustering procedure, data set clustering procedure,

Funding:

Availability: Free, Freely available

Resource Name: clusterSim

Resource ID: SCR_023743

License: GPL v3

Record Creation Time: 20230701T050229+0000

Record Last Update: 20250525T032621+0000

Ratings and Alerts

No rating or validation information has been found for clusterSim.

No alerts have been found for clusterSim.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Komaki S, et al. (2024) Dimension reduction of microbiome data linked Bifidobacterium and Prevotella to allergic rhinitis. Scientific reports, 14(1), 7983.

Roussel C, et al. (2024) Human gut microbiota and their production of endocannabinoid-like mediators are directly affected by a dietary oil. Gut microbes, 16(1), 2335879.

Sun C, et al. (2024) Integrated analysis of facial microbiome and skin physio-optical properties unveils cutotype-dependent aging effects. Microbiome, 12(1), 163.

Wang J, et al. (2024) Protocol for identifying and comparing molecular prognosis subtypes of IgAN using R. STAR protocols, 5(3), 103138.

Carrara A, et al. (2024) Association of pathogenic determinants of Fusobacterium necrophorum with bacteremia, and Lemierre's syndrome. Scientific reports, 14(1), 19804.

Hoji A, et al. (2022) Cord blood sphingolipids are associated with atopic dermatitis and wheeze in the first year of life. The journal of allergy and clinical immunology. Global, 1(3), 162.

Li Z, et al. (2021) Characterization of the human skin resistome and identification of two microbiota cutotypes. Microbiome, 9(1), 47.

Szumowski P, et al. (2021) Pre-Processing Method for Contouring the Uptake Levels of [18F] FDG for Enhanced Specificity of PET Imaging of Solitary Hypermetabolic Pulmonary Nodules. Journal of clinical medicine, 10(7).

Li G, et al. (2021) Correlation Analysis between GDM and Gut Microbial Composition in Late Pregnancy. Journal of diabetes research, 2021, 8892849.

?obos K, et al. (2021) Management practices and their relation to success of Polish SMEs: The empirical verification. PloS one, 16(11), e0259892.

John CR, et al. (2020) Spectrum: fast density-aware spectral clustering for single and multi-omic data. Bioinformatics (Oxford, England), 36(4), 1159.

John CR, et al. (2020) M3C: Monte Carlo reference-based consensus clustering. Scientific reports, 10(1), 1816.

Hernandez I, et al. (2019) Epigenetic regulation of gene expression in Chinese Hamster Ovary cells in response to the changing environment of a batch culture. Biotechnology and bioengineering, 116(3), 677.

Khatri I, et al. (2019) Systems Biology Approach to Identify Novel Genomic Determinants for Pancreatic Cancer Pathogenesis. Scientific reports, 9(1), 123.

Chen QS, et al. (2017) Combining affinity propagation clustering and mutual information network to investigate key genes in fibroid. Experimental and therapeutic medicine, 14(1), 251.

Wang X, et al. (2013) Neural encoding of acupuncture needling sensations: evidence from a FMRI study. Evidence-based complementary and alternative medicine : eCAM, 2013, 483105.

Williams-DeVane CR, et al. (2013) Decision tree-based method for integrating gene expression, demographic, and clinical data to determine disease endotypes. BMC systems biology, 7, 119.

Hu Y, et al. (2013) Genetic background may contribute to PAM50 gene expression breast cancer subtype assignments. PloS one, 8(8), e72287.