

Resource Summary Report

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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 toolkit, software resource

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

Availability: Free, Freely available

Resource Name: clusterSim

Resource ID: SCR_023743

License: GPL v3

Record Creation Time: 20230701T050229+0000

Record Last Update: 20260729T044559+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 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Bollhagen A, et al. (2025) High-resolution imaging mass cytometry to map subcellular structures. *Nature methods*, 22(12), 2601.

Abdill RJ, et al. (2025) Integration of 168,000 samples reveals global patterns of the human gut microbiome. *Cell*, 188(4), 1100.

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.

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

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

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.

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

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).

Bobos 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.

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

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.