Resource Summary Report

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Hierarchical Clustering

RRID:SCR_014673
Type: Tool

Proper Citation

Hierarchical Clustering (RRID:SCR_014673)

Resource Information

URL: http://stat.ethz.ch/R-manual/R-patched/library/stats/html/hclust.html

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Description: R documentation for hierarchical cluster analysis on a set of dissimilarities for n objects. Each object is assigned to its own cluster, which an algorithm proceeds through iteratively. Two of the most similar clusters are joined at each stage until there is a single cluster. Distances between clusters are recomputed at each stage by the Lance–Williams dissimilarity update formula according to the particular clustering method being used. Clustering methods include: Ward's minimum variance method, complete linkage method, and single linkage method.

Synonyms: R: Hierarchical Clustering, R - Hierarchical Clustering

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

Keywords: statistical analysis, statistical analysis package, r, r package, data analysis, software, cluster, hierarchical, dissimilarity, clustering method, metabolomics

Funding:

Availability: Acknowledgement requested

Resource Name: Hierarchical Clustering

Resource ID: SCR_014673

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250514T061654+0000

Ratings and Alerts

No rating or validation information has been found for Hierarchical Clustering.

No alerts have been found for Hierarchical Clustering.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Umeda M, et al. (2024) A new genomic framework to categorize pediatric acute myeloid leukemia. Nature genetics, 56(2), 281.

Umeda M, et al. (2023) Proposal of a new genomic framework for categorization of pediatric acute myeloid leukemia associated with prognosis. Research square.