

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

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>

Proper Citation: Hierarchical Clustering (RRID:SCR_014673)

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, data analysis software, source code, software resource, data processing software

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

Availability: Acknowledgement requested

Resource Name: Hierarchical Clustering

Resource ID: SCR_014673

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260729T044354+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 4 mentions in open access literature.

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

Buri MC, et al. (2025) Natural Killer Cell-Mediated Cytotoxicity Shapes the Clonal Evolution of B-cell Leukemia. Cancer immunology research, 13(3), 430.

Wu Y, et al. (2025) BEEEx Is an Open-Source Tool That Evaluates Batch Effects in Medical Images to Enable Multicenter Studies. Cancer research, 85(2), 218.

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.