

# Resource Summary Report

Generated by [nidm-terms](#) on Aug 2, 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:** data analysis software, source code, software application, 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:** 20260801T190507+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 [nidm-terms](#) .

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.