

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

[sandwich](#)

RRID:SCR_027691

Type: Tool

Proper Citation

sandwich (RRID:SCR_027691)

Resource Information

URL: <https://cran.r-project.org/web/packages/sandwich/index.html>

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Description: Object-oriented software for model-robust covariance matrix estimators. Starting out from the basic robust Eicker-Huber-White sandwich covariance methods include: heteroscedasticity-consistent (HC) covariances for cross-section data; heteroscedasticity- and autocorrelation-consistent (HAC) covariances for time series data (such as Andrews' kernel HAC, Newey-West, and WEAVE estimators); clustered covariances (one-way and multi-way); panel and panel-corrected covariances; outer-product-of-gradients covariances; and (clustered) bootstrap covariances. All methods are applicable to (generalized) linear model objects fitted by `lm()` and `glm()` but can also be adapted to other classes through S3 methods.

Synonyms: sandwich:Robust Covariance Matrix Estimators

Resource Type: software application, software resource

Keywords: covariance matrix estimators, Eicker-Huber-White sandwich covariance, sandwich covariance,

Availability: Free, Available for download, Freely available

Resource Name: sandwich

Resource ID: SCR_027691

License: GNU GPL v3

Record Creation Time: 20251122T055350+0000

Record Last Update: 20260810T040944+0000

Ratings and Alerts

No rating or validation information has been found for sandwich.

No alerts have been found for sandwich.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Ikegami M, et al. (2026) Germline Pathogenic Variant Prediction Model for Tumor-Only Sequencing Based on Japanese Clinicogenomic Database. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(4), 770.