

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## Sweave

RRID:SCR\_013987

Type: Tool

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### Proper Citation

Sweave (RRID:SCR\_013987)

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### Resource Information

**URL:** <https://support.rstudio.com/hc/en-us/articles/200552056-Using-Sweave-and-knitr>

**Proper Citation:** Sweave (RRID:SCR\_013987)

**Description:** NO LONGER AVAILABLE. Documented on May 19, 2020. Software R tool for creating dynamic reports and reproducible research using LaTeX. Enables embedding of R code within LaTeX documents to generate PDF file that includes narrative and analysis, graphics, code, and results of computations. Software tool for complete data analyses in LaTeX documents.

**Resource Type:** software application, software resource, data processing software, standalone software

**Keywords:** software application, R code, LaTeX, standalone software

**Availability:** No longer available

**Resource Name:** Sweave

**Resource ID:** SCR\_013987

**Old URLs:** <http://www.statistik.lmu.de/~leisch/Sweave/>

**Record Creation Time:** 20220129T080318+0000

**Record Last Update:** 20260728T043431+0000

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### Ratings and Alerts

No rating or validation information has been found for Sweave.

No alerts have been found for Sweave.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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](#) .

Hautmann C, et al. (2021) Progress feedback in children and adolescents with internalizing and externalizing symptoms in routine care (OPTIE study): study protocol of a randomized parallel-group trial. BMC psychiatry, 21(1), 505.

Gupta N, et al. (2017) High Myc expression and transcription activity underlies intra-tumoral heterogeneity in triple-negative breast cancer. Oncotarget, 8(17), 28101.

Denaxas S, et al. (2017) Methods for enhancing the reproducibility of biomedical research findings using electronic health records. BioData mining, 10, 31.

Boerner V, et al. (2014) Accuracies of genomically estimated breeding values from pure-breed and across-breed predictions in Australian beef cattle. Genetics, selection, evolution : GSE, 46(1), 61.