

Resource Summary Report

Generated by [dkNET](#) on Aug 8, 2026

Sweave

RRID:SCR_013987

Type: Tool

Proper Citation

Sweave (RRID:SCR_013987)

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: standalone software, software resource, software application, data processing 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: 20260808T042802+0000

Ratings and Alerts

No rating or validation information has been found for Sweave.

No alerts have been found for Sweave.

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 [dkNET](#) .

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.