

Resource Summary Report

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scales

RRID:SCR_019295

Type: Tool

Proper Citation

scales (RRID:SCR_019295)

Resource Information

URL: <https://CRAN.R-project.org/package=scales>

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Description: Software R package as scale functions for visualization. Graphical scales map data to aesthetics, and provide methods for automatically determining breaks and labels for axes and legends.

Resource Type: data processing software, data visualization software, software application, software resource, software toolkit

Keywords: Scale functions, visualization, graphical scales, map data, axes, determining breaks, legend, determining labels

Availability: Free, Available for download, Freely available

Resource Name: scales

Resource ID: SCR_019295

Alternate URLs: <https://github.com/r-lib/scales>

License: MIT + file LICENSE

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260912T195912+0000

Ratings and Alerts

No rating or validation information has been found for scales.

No alerts have been found for scales.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Zambrano-Harvey AR, et al. (2026) Cancer incidence in the Pijao indigenous population of colombia using administrative health records, 1996-2022. Scientific reports, 16(1).

Al Souz J, et al. (2026) Organ injury in systemic autoimmunity is mediated by stem-like CD8+ T cells arising from tissue-draining lymph nodes. Immunity, 59(6), 1667.

Meghdadi B, et al. (2026) Digital twins for in vivo metabolic flux estimations in patients with brain cancer. Cell metabolism, 38(1), 228.

McLeod AA, et al. (2026) Classifying electric service disruptions under deep uncertainty: A comparative analysis of algorithms and their policy outcomes. iScience, 29(7), 116447.

Berger AH, et al. (2025) High-resolution transcriptional impact of AIRE: effects of pathogenic variants p.Arg257Ter, p.Cys311Tyr, and polygenic risk variant p.Arg471Cys. Frontiers in immunology, 16, 1572789.

Hamim I, et al. (2025) Insights into the viral landscape of the western honey bee and native bees in Bangladesh. Microbiology spectrum, 13(12), e0197125.

Sümer AP, et al. (2025) Earliest modern human genomes constrain timing of Neanderthal admixture. Nature, 638(8051), 711.

Tercan B, et al. (2025) Protocol for assessing distances in pathway space for classifier feature sets from machine learning methods. STAR protocols, 6(2), 103681.

Cao J, et al. (2025) A clinical feature-based nomogram for the personalized prediction of radioactive iodine therapy outcomes in patients with papillary thyroid carcinoma. Oncology letters, 30(6), 577.

Giovannetti M, et al. (2024) SIN-3 transcriptional coregulator maintains mitochondrial homeostasis and polyamine flux. iScience, 27(5), 109789.

Wang K, et al. (2024) Protocol for fast clonal family inference and analysis from large-scale B cell receptor repertoire sequencing data. STAR protocols, 5(2), 102969.

Zaychikova M, et al. (2024) Vic9 mycobacteriophage: the first subcluster B2 phage isolated in Russia. Frontiers in microbiology, 15, 1513081.

Kornienko M, et al. (2024) Multiomics analysis of Staphylococcus aureus ST239 strains resistant to virulent Herelleviridae phages. Scientific reports, 14(1), 29375.

Liu D, et al. (2024) Protocol for analyzing plasma cell-free DNA fragment end motifs from ultra-low-pass whole-genome sequencing. STAR protocols, 5(4), 103357.

Olkkonen E, et al. (2023) Analysis of population structure and genetic diversity in low-variance Saimaa ringed seals using low-coverage whole-genome sequence data. STAR protocols, 4(4), 102567.

Spari D, et al. (2023) Intestinal dysbiosis as an intraoperative predictor of septic complications: evidence from human surgical cohorts and preclinical models of peritoneal sepsis. Scientific reports, 13(1), 22921.

Han J, et al. (2023) AmpSeqR: an R package for amplicon deep sequencing data analysis. F1000Research, 12, 327.

Cardoso-Moreira M, et al. (2016) Evidence for the fixation of gene duplications by positive selection in *Drosophila*. Genome research, 26(6), 787.