

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: software application, software resource, data processing software, data visualization software, 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: 20260729T044500+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 14 mentions in open access literature.

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

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

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.

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.

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

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.

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.

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.