

Resource Summary Report

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Harrell Miscellaneous

RRID:SCR_022497

Type: Tool

Proper Citation

Harrell Miscellaneous (RRID:SCR_022497)

Resource Information

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

Proper Citation: Harrell Miscellaneous (RRID:SCR_022497)

Description: Software R package for data analysis, graphics, utility operations, functions for computing sample size and power, simulation, importing and annotating datasets, imputing missing values, advanced table making, variable clustering, character string manipulation, conversion of R objects to LaTeX and html code, and recoding variables.

Abbreviations: Hmisc

Resource Type: software resource, software toolkit

Keywords: Graphics, utility operations, functions for computing sample size and power, simulation, importing and annotating datasets, imputing missing values, advanced table making, variable clustering, character string manipulation, conversion of R objects to LaTeX and html code, recoding variables

Availability: Free, Available for download, Freely available

Resource Name: Harrell Miscellaneous

Resource ID: SCR_022497

Alternate URLs: <https://github.com/harrelfe/Hmisc>

License: GPL v3

Record Creation Time: 20220616T050139+0000

Record Last Update: 20260904T000516+0000

Ratings and Alerts

No rating or validation information has been found for Harrell Miscellaneous.

No alerts have been found for Harrell Miscellaneous.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 56 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Guan R, et al. (2026) Influence of Age and Body Weight on Supramammary Lymph Node Morphology and Weight in Holstein Dairy Cows. *Veterinary sciences*, 13(6).

Gause EL, et al. (2026) Data needs for accelerating research at the intersection of climate stressors and health: an online survey. *Environmental research, health : ERH*, 4(1), 015007.

Liu XX, et al. (2026) SARS-CoV-2 infection during the first trimester leads to profound immune dysregulation at the maternal-fetal interface despite limited virus detection in placental tissues. *Nature communications*, 17(1).

Jaiswal A, et al. (2026) Spatial transcriptomics reveals altered communities and drivers of aberrant epithelia and pro-fibrotic fibroblasts in interstitial lung diseases. *Cell genomics*, 6(3), 101066.

Liu H, et al. (2026) Vaginal microbiota transfer ameliorates cesarean-associated neurodevelopmental deficits in mice via N-bc2S1P synthesis on neonatal skin. *Cell host & microbe*, 34(5), 942.

Wu G, et al. (2025) Wetland-to-Meadow Transition Alters Soil Microbial Networks and Stability in the Sanjiangyuan Region. *Microorganisms*, 13(6).

Sun H, et al. (2025) Multi-omics reveals the inhibition of asexual reproduction in the jellyfish *Aurelia coerulea* polyp by *Bacillus pacificus*. *Environmental microbiome*, 20(1), 78.

Jia F, et al. (2025) Responses of rhizosphere bacterial communities with different niche breadths to liquid fertilizer produced from Fuji apple wastes during planting process. *Microbiology spectrum*, 13(7), e0206824.

Tosi N, et al. (2025) Optimization of an In Vitro Colonic Fermentation: Insights into Flavan-3-ol Catabolism and Microbiota Modulation. *Journal of agricultural and food chemistry*, 73(26), 16429.

Savin C, et al. (2025) In-host evolution of *Yersinia enterocolitica* during a chronic human infection. *Nature communications*, 16(1), 5637.

Adnan D, et al. (2025) Oral microbiome brain axis and cognitive performance in older adults. *NPJ dementia*, 1.

Lugli GA, et al. (2025) Host interactions of *Lactococcus lactis* and *Streptococcus thermophilus* support their adaptation to the human gut microbiota. *Applied and environmental microbiology*, 91(12), e0154725.

Idkowiak J, et al. (2025) Best practices and tools in R and Python for statistical processing and visualization of lipidomics and metabolomics data. *Nature communications*, 16(1), 8714.

Gao X, et al. (2025) Identification of key genes in cuproptosis during acute kidney injury through weighted gene co-expression network analysis. *Medicine*, 104(43), e44592.

Guo W, et al. (2025) Phenotyping, genome-wide dissection, and prediction of maize root architecture for temperate adaptability. *iMeta*, 4(2), e70015.

Kasan M, et al. (2025) Genomic and phenotypic stability of fusion-driven pediatric sarcoma cell lines. *Nature communications*, 16(1), 380.

Peskett TR, et al. (2025) A network of P-body and Whi3 condensates adjusts cell fate decisions to cellular context. *Molecular cell*, 85(19), 3661.

Zheng Y, et al. (2024) Multi-omics data integration using ratio-based quantitative profiling with Quartet reference materials. *Nature biotechnology*, 42(7), 1133.

Ghaly TM, et al. (2024) Exploring virus-host-environment interactions in a chemotrophic-based underground estuary. *Environmental microbiome*, 19(1), 9.

Santos de Macedo BG, et al. (2024) Autophagy and inflammasome activation are associated with poor response to FLT3 inhibitors in patients with FLT3-ITD acute myeloid leukemia. *Scientific reports*, 14(1), 23882.