

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 toolkit, software resource

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: 20260729T044540+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 38 mentions in open access literature.

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

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.

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.

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.

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

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.

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.

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.

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.

Chen M, et al. (2024) Community composition of phytopathogenic fungi significantly influences ectomycorrhizal fungal communities during subtropical forest succession. *Applied microbiology and biotechnology*, 108(1), 99.

Mancabelli L, et al. (2024) Taxonomic and metabolic development of the human gut microbiome across life stages: a worldwide metagenomic investigation. *mSystems*, 9(4), e0129423.

Zhang J, et al. (2024) From proteome to pathogenesis: investigating polycystic ovary syndrome with Mendelian randomization analysis. *Frontiers in endocrinology*, 15, 1442483.

Wiśniewski J, et al. (2024) Distinguishable topology of the task-evoked functional genome networks in HIV-1 reservoirs. *iScience*, 27(11), 111222.

Georgiev P, et al. (2024) Age-Associated Contraction of Tumor-Specific T Cells Impairs Antitumor Immunity. *Cancer immunology research*, 12(11), 1525.

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

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

DeFilipp Z, et al. (2024) Third-party fecal microbiota transplantation for high-risk treatment-naïve acute GVHD of the lower GI tract. *Blood advances*, 8(9), 2074.

Xu X, et al. (2024) Exploration of transcriptional regulation network between buffalo oocytes and granulosa cells and its impact on different diameter follicles. *BMC genomics*, 25(1), 1004.

Zhang J, et al. (2024) Scanning sample-specific miRNA regulation from bulk and single-cell RNA-sequencing data. *BMC biology*, 22(1), 218.