Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 2, 2025

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

Funding:

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: 20250331T061827+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 28 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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

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.

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.

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

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.

Colman DR, et al. (2024) Covariation of hot spring geochemistry with microbial genomic diversity, function, and evolution. Nature communications, 15(1), 7506.

Argentini C, et al. (2024) Genomic and ecological approaches to identify the Bifidobacterium breve prototype of the healthy human gut microbiota. Frontiers in microbiology, 15, 1349391.

Hoekstra ME, et al. (2024) Distinct spatiotemporal dynamics of CD8+ T cell-derived cytokines in the tumor microenvironment. Cancer cell, 42(1), 157.

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.

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

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

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

Rachubinski AL, et al. (2024) JAK inhibition decreases the autoimmune burden in Down syndrome. eLife, 13.

Assaf ZJF, et al. (2023) A longitudinal circulating tumor DNA-based model associated with survival in metastatic non-small-cell lung cancer. Nature medicine, 29(4), 859.

Wang W, et al. (2023) Heritability and recursive influence of host genetics on the rumen microbiota drive body weight variance in male Hu sheep lambs. Microbiome, 11(1), 197.

Jang HJ, et al. (2023) A Phase II Trial of Guadecitabine plus Atezolizumab in Metastatic Urothelial Carcinoma Progressing after Initial Immune Checkpoint Inhibitor Therapy. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(11), 2052.

Xie F, et al. (2023) A universal AutoScore framework to develop interpretable scoring systems for predicting common types of clinical outcomes. STAR protocols, 4(2), 102302.