

Resource Summary Report

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ranger

RRID:SCR_022521

Type: Tool

Proper Citation

ranger (RRID:SCR_022521)

Resource Information

URL: <https://cran.r-project.org/web/packages/ranger/>

Proper Citation: ranger (RRID:SCR_022521)

Description: Software R package as fast implementation of Random Forests for high dimensional data.

Resource Type: software toolkit, software resource

Defining Citation: [DOI:10.18637/jss.v077.i01](https://doi.org/10.18637/jss.v077.i01), [DOI:10.48550/arXiv.1508.04409](https://doi.org/10.48550/arXiv.1508.04409)

Keywords: Random Forest, high dimensional data

Availability: Free, Available for download, Freely available

Resource Name: ranger

Resource ID: SCR_022521

Alternate URLs: <https://github.com/imbs-hl/ranger>

License: GPL v3

Record Creation Time: 20220628T050153+0000

Record Last Update: 20260803T040826+0000

Ratings and Alerts

No rating or validation information has been found for ranger.

No alerts have been found for ranger.

Data and Source Information

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Niu W, et al. (2025) Patterns of childhood trauma co-occurrence and its predictivity for suicidality: A machine learning approach. *iScience*, 28(2), 111877.

Elias R, et al. (2025) Clear-Cell Renal Cell Carcinoma Molecular Subtypes Differ by African and European Genetic Similarity. *Cancer research communications*, 5(5), 743.

Abdill RJ, et al. (2025) Integration of 168,000 samples reveals global patterns of the human gut microbiome. *Cell*, 188(4), 1100.

De Barros A, et al. (2024) Determining Prior Authorization Approval for Lumbar Stenosis Surgery With Machine Learning. *Global spine journal*, 14(6), 1753.

Golov AK, et al. (2024) A genome-wide nucleosome-resolution map of promoter-centered interactions in human cells corroborates the enhancer-promoter looping model. *eLife*, 12.

Leiendecker L, et al. (2023) Human Papillomavirus 42 Drives Digital Papillary Adenocarcinoma and Elicits a Germ Cell-like Program Conserved in HPV-Positive Cancers. *Cancer discovery*, 13(1), 70.

Saha A, et al. (2022) RandomForestsGLS: An R package for Random Forests for dependent data. *Journal of open source software*, 7(71).

Farooq M, et al. (2022) Genomic prediction in plants: opportunities for ensemble machine learning based approaches. *F1000Research*, 11, 802.

Verma SS, et al. (2018) Collective feature selection to identify crucial epistatic variants. *BioData mining*, 11, 5.