Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 12, 2025

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 dimentional data.

Resource Type: software toolkit, software resource

Defining Citation: DOI:10.18637/jss.v077.i01, DOI:10.48550/arXiv.1508.04409

Keywords: Random Forest, high dimentional data

Funding:

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: 20250412T060508+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.