

Resource Summary Report

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RandomForest Package in R

RRID:SCR_015718

Type: Tool

Proper Citation

RandomForest Package in R (RRID:SCR_015718)

Resource Information

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

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Description: Software package for classification and regression based on a forest of trees using random inputs.

Synonyms: randomForest: Breiman and Cutler's Random Forests for Classification and Regression

Resource Type: software application, software resource

Defining Citation: [PMID:14632445](https://pubmed.ncbi.nlm.nih.gov/14632445/)

Keywords: classification, cluster, regression, random input, qsar model

Availability: Free, Available for download

Resource Name: RandomForest Package in R

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Alternate URLs: <https://CRAN.R-project.org/package=randomForest>,
<https://www.stat.berkeley.edu/~breiman/RandomForests/>

License: GPL 2, GPL 3

License URLs: <http://www.gnu.org/licenses/gpl.txt>

Record Creation Time: 20220129T080327+0000

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Ratings and Alerts

No rating or validation information has been found for RandomForest Package in R.

No alerts have been found for RandomForest Package in R.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 203 mentions in open access literature.

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

Sirc N, et al. (2026) Functionally Characterizing the Renal Cell Carcinoma Tumor-Immune Microenvironment via Patient-Derived Ex Vivo Models. Cancer research communications, 6(2), 402.

Xue M, et al. (2026) HIF3A-mediated aberrant activation of TXNIP promotes Alzheimer's disease progression. Scientific reports, 16(1).

Yuan Y, et al. (2026) Unveiling preeclampsia: diagnostic value and potential molecular mechanisms of abnormally methylated immune-related genes. Brazilian journal of medical and biological research = Revista brasileira de pesquisas medicas e biologicas, 59, e15317.

Matsuda K, et al. (2026) Tumor vessel phenotype in colorectal cancer microenvironment according to age at diagnosis. British journal of cancer, 134(10), 1375.

Wu B, et al. (2026) Proteomic profiling of single extracellular vesicles as a promising new approach for the diagnosis and treatment modality of advanced ovarian cancer. NPJ precision oncology, 10(1), 65.

Guo X, et al. (2026) Diagnostic Model for Obesity and Type 2 Diabetes Mellitus Based on Feature Selection from Fatty Acids, Amino Acids, and Clinical Characteristics. Diabetes, metabolic syndrome and obesity : targets and therapy, 19, 583656.

Sun Z, et al. (2026) Intrapartum caesarean delivery and childhood BMI trajectories in relation to the infant gut microbiome in the VDAART prospective birth cohort. EBioMedicine, 129, 106347.

Lötsch J, et al. (2026) Resolving Interpretation Challenges in Machine Learning Feature Selection With an Iterative Approach in Biomedical Pain Data. European journal of pain (London, England), 30(2), e70221.

Williams EA, et al. (2026) The Typability Index: A tool for measuring and controlling for typing difficulty in text stimuli. Behavior research methods, 58(2), 61.

Fernandez Garcia M, et al. (2026) Transcriptomic and phenotypic convergence of neurodevelopmental disorder risk genes in vitro and in vivo. Nature neuroscience, 29(5),

Thursby SJ, et al. (2026) Epigenetic Instability-Based Metrics in Cell-Free DNA for Early Cancer Detection. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(8), 1528.

Hofvander J, et al. (2026) Transcriptomic Subgroups in Soft Tissue Tumors Correlate with Morphologic Subtype, Genomic Features, and Outcome. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1825.

Su Q, et al. (2026) Integrated bulk RNA-seq and scRNA-seq identification of a novel "PET-SPI1-MYL9" transcriptional axis in lung adenocarcinoma driven by polyethylene terephthalate exposure. *Translational cancer research*, 15(3), 173.

Jiang K, et al. (2026) Soil microbial community assembly drives ecosystem multifunctionality under grazing disturbance by regulating diversity and network structure. *Scientific reports*, 16(1).

Xu Q, et al. (2026) Identification of diagnostic markers for diabetic kidney disease by weighted gene co-expression network analysis and machine learning. *International journal of molecular medicine*, 58(1).

Zeng Q, et al. (2026) Intratumoral Tertiary Lymphoid Structures Characterized by a B Cell-Related Signature Elicit Antitumor Effect through HAPLN3 in Hepatocellular Carcinoma. *Cancer immunology research*, 14(5), 771.

Matchett CL, et al. (2026) Validation of Methylated DNA Markers for Esophageal Squamous Cancer: An International Study. *Cancer prevention research (Philadelphia, Pa.)*, 19(4), 197.

Ma T, et al. (2026) Multiomic analysis of ART-interruption cohorts identifies cell-extrinsic and -intrinsic mechanisms driving lymphocyte-mediated control of HIV rebound. *Immunity*, 59(5), 1454.

Chen S, et al. (2026) Diversity-triggered 2-naphthoic acid exudation recruits keystone microbial taxa to promote soybean drought tolerance. *Cell host & microbe*, 34(5), 844.

Guillon M, et al. (2026) MECP2 mutations rewire human ESC fate and bias cortical lineage commitment. *Stem cell reports*, 21(5), 102895.