

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

caret

RRID:SCR_021138

Type: Tool

Proper Citation

caret (RRID:SCR_021138)

Resource Information

URL: <https://CRAN.R-project.org/package=caret>

Proper Citation: caret (RRID:SCR_021138)

Description: Software R package provides misc functions for training and plotting classification and regression models. Contains tools for data splitting, pre-processing, feature selection, model tuning using resampling, and variable importance estimation, as well as other functionality.

Synonyms: Classification And REgression Training

Resource Type: software resource, software toolkit

Keywords: Plotting classification, regression models, data splitting, pre processing, feature selection, model tuning using resampling, estimation

Availability: Free, Available for download, Freely available

Resource Name: caret

Resource ID: SCR_021138

Alternate URLs: <https://github.com/topepo/caret/>

License: GPL-3

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260905T133307+0000

Ratings and Alerts

No rating or validation information has been found for caret.

No alerts have been found for caret.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 96 mentions in open access literature.

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

Andersen L, et al. (2026) Cell-Free DNA-Derived Immune Cell Ratios Uncover Cancer-Associated Systemic Changes. *Cancer research communications*, 6(4), 811.

Xu R, et al. (2026) Identification of mitochondria metabolism-related biomarkers associated with the development of rheumatoid arthritis using bioinformatics: An observational study. *Medicine*, 105(2), e44435.

Lötsch J, et al. (2026) Dimensionality-modulated generative AI for safe biomedical dataset augmentation. *iScience*, 29(1), 114321.

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.

Lötsch J, et al. (2026) A model-agnostic framework for dataset-specific selection of missing value imputation methods in pain-related numerical data. *Canadian journal of pain = Revue canadienne de la douleur*, 10(1), 2595160.

Liao P, et al. (2026) Identification and validation of prognostic genes related to centrosome amplification in multiple myeloma. *PeerJ*, 14, e21283.

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.

Lazare S, et al. (2026) Postoperative Lymph Is a Proximal Source of ctDNA for Detection of Recurrence in HPV-Independent Head and Neck Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(1), 135.

Zhao J, et al. (2026) Identification and Validation of Mitophagy-Related Biomarkers in Colorectal Cancer: An Integrated Analysis of Single-Cell Transcriptome and Mendelian Randomization. *Genetics research*, 2026(1), e5579542.

Zhang X, et al. (2026) Identification and Analysis of Biomarkers Associated With Lipid Metabolism and Ferroptosis in Ulcerative Colitis. *Journal of immunology research*, 2026(1), e9283449.

Wei J, et al. (2026) Lovastatin Targets LIPA to Induce ER Stress-Mediated Apoptosis in Acute Myeloid Leukemia: A Multi-Omics Study. *International journal of general medicine*,

19, 591023.

Defrancesco M, et al. (2026) Plasma phospho-tau 217 outperforms plasma phospho-tau 181 analyzed with Lumipulse in detecting Alzheimer's dementia in a real-world memory clinic population. *Frontiers in aging neuroscience*, 18, 1714247.

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.

Canzoniero JV, et al. (2026) plasmaCHORD: A Machine Learning Approach to Distinguish Clonal Hematopoiesis-Derived Variants in Liquid Biopsies from Patients with Solid Tumors. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1729.

Ghoochani A, et al. (2026) Cell-type resolved protein atlas of brain lysosomes identifies SLC45A1-associated disease as a lysosomal disorder. *Cell*, 189(3), 765.

Liang Q, et al. (2025) Integration of multi-omics and machine learning strategies identifies immune related candidate biomarkers in inflammation-associated hypertrophic cardiomyopathy. *Frontiers in immunology*, 16, 1645382.

Gammon M, et al. (2025) An application of finite element analysis predicts unique temperatures and fates for flatback sea turtle embryos. *The Journal of experimental biology*, 228(23).

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.

Tognetti M, et al. (2025) Serum proteomics reveals survival-associated biomarkers in pancreatic cancer patients treated with chemoimmunotherapy. *iScience*, 28(4), 112230.

Xiao Z, et al. (2025) Inflammatory Biomarkers in Coronary Artery Disease: Insights From Mendelian Randomization and Transcriptomics. *Journal of inflammation research*, 18, 3177.