

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Classifier Visualization in R

RRID:SCR_008551

Type: Tool

Proper Citation

Classifier Visualization in R (RRID:SCR_008551)

Resource Information

URL: <http://rocr.bioinf.mpi-sb.mpg.de/>

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Description: ROCR is a package for evaluating and visualizing the performance of scoring classifiers in the statistical language R. It features over 25 performance measures that can be freely combined to create two-dimensional performance curves. Standard methods for investigating trade-offs between specific performance measures are available within a uniform framework, including receiver operating characteristic (ROC) graphs, precision/recall plots, lift charts and cost curves. ROCR integrates tightly with R's powerful graphics capabilities, thus allowing for highly adjustable plots. Being equipped with only three commands and reasonable default values for optional parameters, ROCR combines flexibility with ease of usage. Performance measures that ROCR knows: Accuracy, error rate, true positive rate, false positive rate, true negative rate, false negative rate, sensitivity, specificity, recall, positive predictive value, negative predictive value, precision, fallout, miss, phi correlation coefficient, Matthews correlation coefficient, mutual information, chi square statistic, odds ratio, lift value, precision/recall F measure, ROC convex hull, area under the ROC curve, precision/recall break-even point, calibration error, mean cross-entropy, root mean squared error, SAR measure, expected cost, explicit cost. ROCR features: ROC curves, precision/recall plots, lift charts, cost curves, custom curves by freely selecting one performance measure for the x axis and one for the y axis, handling of data from cross-validation or bootstrapping, curve averaging (vertically, horizontally, or by threshold), standard error bars, box plots, curves that are color-coded by cutoff, printing threshold values on the curve, tight integration with Rs plotting facilities (making it easy to adjust plots or to combine multiple plots), fully customizable, easy to use (only 3 commands). ROCR can be used under the terms of the GNU General Public License. Running within R, it is platform-independent.

Synonyms: ROCR: Classifier Visualization in R, ROCR

Resource Type: software resource

Defining Citation: [PMID:16096348](#)

Resource Name: Classifier Visualization in R

Resource ID: SCR_008551

Alternate IDs: nif-0000-31415

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260905T132624+0000

Ratings and Alerts

No rating or validation information has been found for Classifier Visualization in R.

No alerts have been found for Classifier Visualization in R.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Jelcic I, et al. (2025) T-bet+ CXCR3+ B cells drive hyperreactive B-T cell interactions in multiple sclerosis. Cell reports. Medicine, 6(3), 102027.

Wang Y, et al. (2024) Expression profile of circular RNAs in blood samples of Northern Chinese males with intracerebral hemorrhage shows downregulation of hsa-circ-0090829. Heliyon, 10(16), e35864.

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

Workman MJ, et al. (2023) Large-scale differentiation of iPSC-derived motor neurons from ALS and control subjects. Neuron, 111(8), 1191.

Oliva G, et al. (2021) Three-Dimensional Dental Analysis for Sex Estimation in the Italian Population: A Pilot Study Based on a Geometric Morphometric and Artificial Neural Network Approach. Healthcare (Basel, Switzerland), 10(1).

Ho R, et al. (2021) Cross-Comparison of Human iPSC Motor Neuron Models of Familial and Sporadic ALS Reveals Early and Convergent Transcriptomic Disease Signatures. Cell systems, 12(2), 159.

Ruiz EML, et al. (2020) A novel gene panel for prediction of lymph-node metastasis and recurrence in patients with thyroid cancer. Surgery, 167(1), 73.

Kim J, et al. (2020) Tumor Mutational Burden Determined by Panel Sequencing Predicts Survival After Immunotherapy in Patients With Advanced Gastric Cancer. *Frontiers in oncology*, 10, 314.

Terrasi A, et al. (2019) Specific V-ATPase expression sub-classifies IDHwt lower-grade gliomas and impacts glioma growth in vivo. *EBioMedicine*, 41, 214.

Kunitoki K, et al. (2019) Clinical Utility of a Semiquantitative Method Using Lumbar Radiography as a Screening Tool for Osteoporosis in Elderly Subjects. *Medical science monitor : international medical journal of experimental and clinical research*, 25, 6928.

Clooney AG, et al. (2019) Whole-Virome Analysis Sheds Light on Viral Dark Matter in Inflammatory Bowel Disease. *Cell host & microbe*, 26(6), 764.

Wei DD, et al. (2018) Metabolomic Assessment of Acute Cholestatic Injuries Induced by Thioacetamide and by Bile Duct Ligation, and the Protective Effects of Huang-Lian-Jie-Du-Decoction. *Frontiers in pharmacology*, 9, 458.

Roy MF, et al. (2017) Prognostic Value and Development of a Scoring System in Horses With Systemic Inflammatory Response Syndrome. *Journal of veterinary internal medicine*, 31(2), 582.

Takahashi P, et al. (2014) MicroRNA expression profiling and functional annotation analysis of their targets in patients with type 1 diabetes mellitus. *Gene*, 539(2), 213.

Smedley D, et al. (2013) PhenoDigm: analyzing curated annotations to associate animal models with human diseases. *Database : the journal of biological databases and curation*, 2013, bat025.

Xu M, et al. (2011) Genome Wide Association Study to predict severe asthma exacerbations in children using random forests classifiers. *BMC medical genetics*, 12, 90.

Kim WK, et al. (2008) Inferring mouse gene functions from genomic-scale data using a combined functional network/classification strategy. *Genome biology*, 9 Suppl 1(Suppl 1), S5.