

Data and text mining

PRROC: computing and visualizing precision-recall and receiver operating characteristic curves in R

Jan Grau^{1,*}, Ivo Grosse^{1,2} and Jens Keilwagen^{3,†}

¹Institute of Computer Science and Universitätszentrum Informatik, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany, ²German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany and ³Institute for Biosafety in Plant Biotechnology, Julius Kühn-Institut (JKI) - Federal Research Centre for Cultivated Plants, Quedlinburg, Germany

*To whom correspondence should be addressed.

†The authors wish it to be known that, in their opinion, the first and last authors should be regarded as Joint First Authors.

Associate Editor: Jonathan Wren

Received on January 20, 2015; revised on February 27, 2015; accepted on March 11, 2015

Abstract

Summary: Precision-recall (PR) and receiver operating characteristic (ROC) curves are valuable measures of classifier performance. Here, we present the R-package PRROC, which allows for computing and visualizing both PR and ROC curves. In contrast to available R-packages, PRROC allows for computing PR and ROC curves and areas under these curves for soft-labeled data using a continuous interpolation between the points of PR curves. In addition, PRROC provides a generic plot function for generating publication-quality graphics of PR and ROC curves.

Availability and implementation: PRROC is available from CRAN and is licensed under GPL 3.

Contact: grau@informatik.uni-halle.de

1 Introduction

The assessment of classifier performance is a recurring task in machine learning and data mining, and in particular in bioinformatics applications. It assists researchers in identifying the most promising approach for the classification problem at hand. For binary classification tasks, the receiver operating characteristic (ROC) curve and the area under this curve (AUC-ROC) are widely accepted as a general measure of classifier performance. In many bioinformatics applications, however, positive examples are substantially less abundant than negative examples, resulting in a highly imbalanced class ratio. For instance, the number of target genes of a microRNA is substantially smaller than the number of non-target genes. In such cases, the precision-recall (PR) curve and AUC (AUC-PR) is better suited for comparing the performance of individual classifiers than the ROC curve and AUC-ROC (Davis *et al.*, 2005).

Often, the decision for the true class labels of a given data point is arguable and, for instance, based on an arbitrary threshold for

some continuous measurement or based on multiple, possibly contradictory, expert labelings. However, the choice of this threshold decisively influences classifier training and assessment. One solution to this problem is the transition from hard-labeling to soft-labeling, where each data point is assigned to both classes with a certain probability that reflects confidence in the labeling (Grau *et al.*, 2013; Mihaljevic *et al.*, 2014). Although soft-labeling has been used extensively for classifier training in the past, it has been neglected for classifier assessment (Keilwagen *et al.*, 2014).

Computing empirical AUC-PR and AUC-ROC values from a limited set of test data points requires interpolation between discrete supporting points corresponding to a series of classification threshold affecting the classification result. AUC-ROC can be computed by linear interpolation between the supporting points of the curve for hard-labeled and soft-labeled data. In contrast, Davis and Goadrich (2006) show that for AUC-PR an interpolation along the true positives is more accurate than linear interpolation for hard-

Table 1. R-packages for computing PR and ROC curves, and their AUCs; “both”: AUC and curve can be computed; “linear”: linear interpolation, “DG”: interpolation of Davis and Goadrich (2006), “con.”: interpolation of Boyd et al. (2013); Keilwagen et al. (2014)

Package	AUC	PerfMeas	pROC ^a	ROCR ^b	PRROC
Version	0.3.0	1.2.1	1.7.3	1.0–5	1.1
PR curve					
Hard-labeled	No	Both	No	Curve	Both
Interpolation	N/A	Linear	N/A	Linear	DG/con
Soft-labeled	No	No	No	No	Both
ROC curve					
Hard-labeled	Both	AUC	Both	Both	Both
Soft-labeled	No	No	No	No	Both
Plotting	Yes	Std. R	Yes	Yes	Yes

^aRobin et al. (2011); ^bSing et al. (2005).

labeled data, while Boyd et al. (2013) and Keilwagen et al. (2014) propose a more fine-grained, continuous interpolation between the supporting points of the PR curve. Only the latter can also be used for soft-labeled data (Keilwagen et al., 2014).

In Table 1, we list several common R-packages for computing PR or ROC curves or their AUCs, which in some cases provide further performance measures. For PR curves, however, none of the previous packages uses the more accurate interpolation of Davis and Goadrich (2006) or the continuous interpolation of Boyd et al. (2013) and Keilwagen et al. (2014). Hence, none of these packages is applicable to soft-labeled data.

In this article, we present the R-package PRROC, which closes both gaps by (i) using the continuous interpolation of Keilwagen et al. (2014) for computing and drawing PR curves and, by this means, (ii) enabling the computation of PR and ROC curves, and AUC-PR and AUC-ROC for soft-labeled and hard-labeled data. In addition, PRROC optionally computes curves and AUC values for the optimal, the worst and the random classifier as a reference. These references are particularly useful for (a) PR curves and (b) ROC and PR curves in case of soft-labeled data, where, for instance, the minimum and maximum AUC might differ from 0 and 1, respectively. Finally, PRROC provides a plotting function for generating publication-quality plots of PR and ROC curves.

2 Use cases

In this section, we present typical applications of the PRROC R-package. Complete listings of the corresponding R-code and further examples are available in the R vignette of PRROC.

First, we consider the scenario that we developed a novel approach for a classification problem with ‘hard class labels’ and now want to assess its performance on an independent test dataset. Further assume that the classification scores of the data points belonging to the positive class are stored in a vector `fg`, and those of the negative class in `bg`. Using PRROC, we can compute the ROC and PR curve, respectively, by

```
roc <- roc.curve(fg, bg, curve=T);
pr <- pr.curve(fg, bg, curve=T);
```

obtain the AUC values with `print(roc)`; `print(pr)`, and plot the curves with `plot(roc)`; `plot(pr)`. An ROC curve obtained by this procedure is shown in the left panel of Figure 1.

Alternatively, classification scores for both classes may be stored in one joint vector (`x`) and the corresponding class labels (1/0 for

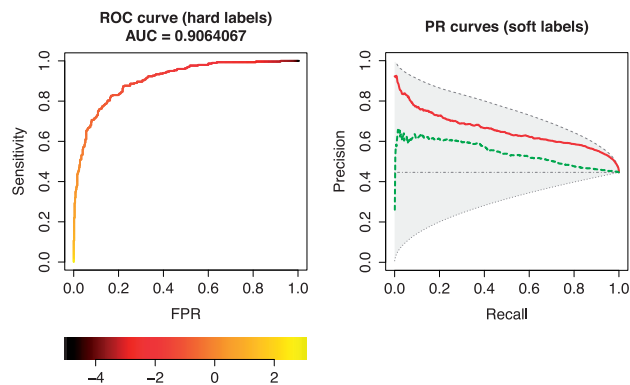


Fig. 1. Plots of ROC (left) and PR (right) curves generated by PRROC. For the ROC curve, we consider hard-labeled data and show the plotting variant with a color scale that indicates classification thresholds yielding the points on the curve. For the PR curve, we consider soft-labeled data and show a comparative plot for two classifiers as solid and dashed lines. We also include the maximal and minimal possible curves and the curve of a random classifier for the given soft-labels

positive/negative class) in another vector (`lab`). In this case, we can compute the ROC and PR curves by

```
roc <- roc.curve(x, weights.class0=lab, curve=T);
pr <- pr.curve(x, weights.class0=lab, curve=T);
```

Second, we consider a scenario for a classification problem with ‘soft class labels’, where each data point belongs to the positive class with probability P and to the negative class with probability $(1-P)$. We assume that the classification scores are again stored in one joint vector (`x`) and the soft-labels, i.e., the probability of belonging to the positive class for each data point, in another vector (`w`). Using PRROC, we can compute the PR curve as well as the minimum and maximum curve, and the curve for the random classifier by

```
pr.1 <- pr.curve(x, weights.class0=w, curve=T,
  max.compute=T, min.compute=T, rand.compute=T)
```

Analogously, we compute the PR curve `pr.2` for another classifier and plot both curves together with the maximum and minimum curve, and the curve of the random classifier by

```
plot(pr.1, col=2, max.plot=T, min.plot=T,
  rand.plot=T, fill.area=T, auc.main=F);
plot(pr.2, col=3, add=T)
```

A plot obtained by this procedure is shown in the right panel of Figure 1. We clearly see the difference in performance of the two classifiers and may conclude that the ranking implied by the classification scores behind the solid curve reconstructs the soft-labels with greater accuracy.

3 Discussion

We present PRROC, an R-package for computing PR and ROC curves as well as their AUCs for soft-labeled and hard-labeled data, which may be beneficial for typical bioinformatics applications. Additionally, PRROC provides a function for plotting PR and ROC curves within R. The PRROC package provides R documentation files and a vignette.

Conflict of Interest: none declared.

References

- Boyd, K. *et al.* (2013) Area under the precision-recall curve: point estimates and confidence intervals. In: Blockeel, H., Kersting, K., Nijssen, S., and Železný, F. (ed.) *Machine Learning and Knowledge Discovery in Databases*. Vol. 8190 of LNCS. Springer, Berlin, pp. 451–466.
- Davis, J. and Goadrich, M. (2006) The relationship between precision-recall and ROC curves. In: *Proceedings of the 23rd International Conference on Machine Learning*. ACM, New York, pp. 233–240.
- Davis, J. *et al.* (2005) View learning for statistical relational learning: with an application to mammography. In: *Proceeding of the 19th International Joint Conference on Artificial Intelligence*, pp. 677–683.
- Grau, J. *et al.* (2013) A general approach for discriminative de novo motif discovery from high-throughput data. *Nucleic Acids Res.*, **41**, e197.
- Keilwagen, J. *et al.* (2014) Area under precision-recall curves for weighted and unweighted data. *PLoS One*, **9**, e92209.
- Mihaljevic, B. *et al.* (2014) Multi-dimensional classification of GABAergic interneurons with Bayesian network-modeled label uncertainty. *Front. Comput. Neurosci.*, **8**, 150.
- Robin, X. *et al.* (2011) pROC: an open-source package for R and S+ to analyze and compare ROC curves. *BMC Bioinformatics*, **12**, 77.
- Sing, T. *et al.* (2005) ROCR: visualizing classifier performance in R. *Bioinformatics*, **21**, 3940–3941.