Journal of Statistical Software

MMMMMM YYYY, Volume VV, Issue II.

doi: 10.18637/jss.v000.i00

ROC and AUC in R with a Single Binary Predictor

John Muschelli

Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health

Abstract

The abstract of the article.

Keywords: roc, auc, area under the curve, R.

1. Introduction

```
R> library(cranlogs)
R> library(ggplot2)
R> library(dplyr)
```

In many applications receiver operator characteristic (ROC) curves are used to show In this tutorial, we will show the calculation of the AUC

2. Simple Example

Here we will create a simple scenario where there is a binary predictor X and a binary outcome Y.

```
R> x = c(rep(0, 52), rep(1, 32),
R+ rep(0, 35), rep(1, 50))
R> y = c(rep(0, 84), rep(1, 85))
R> tab = table(x, y)
R> tab
```

2.1. Mathematical Proof of AUC for Single Binary Predictor

As there are only two outcomes for X, we can expand the probability using the law of total probability:

$$P(X_1 > X_0) = P(X_1 > X_0 | X_1 = 1) P(X_1 = 1)$$

$$+ P(X_1 > X_0 | X_1 = 0) P(X_1 = 0)$$

$$= P(X_1 > X_0 | X_1 = 1) P(X_1 = 1)$$
(2)

where the second term of equation (1) is equal to zero because $X_0 \in \{0, 1\}$. Here we see that the second term of equation (2) is the sensitivity:

$$P(X_1 = 1) = P(X = 1|Y = 1)$$

$$= \frac{TP}{TP + FN}$$

$$= \text{sensitivity}$$

Here we show the first term of equation (2) is the specificity:

$$\begin{split} P(X_1 > X_0 | X_1 = 1) &= P(X_1 > X_0 | X_1 = 1, X_0 = 1) P(X_0 = 1) \\ &+ P(X_1 > X_0 | X_1 = 1, X_0 = 0) P(X_0 = 0) \\ &= P(X_1 > X_0 | X_1 = 1, X_0 = 0) P(X_0 = 0) \\ &= P(X_0 = 0) \\ &= P(X = 0 | Y = 0) \\ &= \frac{TN}{TN + FP} \\ &= \text{specificity} \end{split}$$

Therefore, we combine these two to show that equation (2) reduces to:

$$P(X_1 > X_0) = \text{specificity} * \text{sensitivity}$$

Therefore, the true AUC should be equal to:

```
R> sens = tab[2,2] / sum(tab[,2])
R> spec = tab[1,1] / sum(tab[,1])
R> true_auc = sens * spec
R> print(true_auc)
```

[1] 0.3641457

```
Reverse Labeling
```

```
R> flip_auc = (1 - sens) * (1 - spec)
R> print(flip_auc)

[1] 0.1568627

R> fpr = 1-spec
R> area_of_tri = 1/2 * sens * fpr
R> area_of_quad = sens * spec + 1/2 * spec * (1-sens)
R> auc = area_of_tri + area_of_quad
```

We can also show that if we use a simple sampling method, we can estimate this true AUC. Here, the function est_auc samples $10^{\hat{}}{6}$ random samples from X_1 and X_0 , then calculates $\hat{P}(X_1 > X_0)$:

```
R> est_auc = function(x, y) {
R+     x1 = x[y == 1]
R+     x0 = x[y == 0]
R+     n = 1000000
R+     c1 = sample(x1, size = n, replace = TRUE)
R+     c0 = sample(x0, size = n, replace = TRUE)
R+     mean(c1 > c0)
R+ }
R> sample_est_auc = est_auc(x, y)
R> sample_est_auc
```

3. Current Implementations

3.1. R

caTools Package

[1] 0.364464

The **caTools** package is one of the most popular packages in R, and has analysis for doing area under the curve:

```
R> library(caTools)
R> colAUC(x, y)
```

ROCR Package

The **ROCR** package is one of the most popular packages for doing ROC analysis (Sing, Sander, Beerenwinkel, and Lengauer 2005). Using prediction and performance functions, we see that the estimated AUC is much higher than the true AUC:

```
R> library(ROCR)
```

Loading required package: gplots

Attaching package: 'gplots'

The following object is masked from 'package:stats':

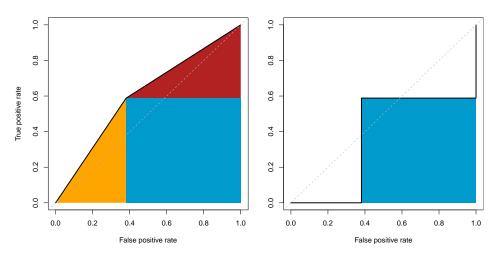
lowess

```
R> pred = prediction(x, y)
R> auc_est = performance(pred, "auc")
R> auc_est@y.values[[1]]
```

[1] 0.6036415

Looking at the plot for the ROC curve in ROCR, we can see why this may be:

```
R> par(mfrow = c(1, 2))
R> perf = performance(pred, "tpr", "fpr")
R> plot(perf)
R> abline(a = 0, b = 1)
R> plot(perf, type = "s")
R> abline(a = 0, b = 1)
```



Looking geometrically at the plot, we can see how

pROC Package

```
R> fpr = 1 - spec
R> area_of_left_tri = 1/2 * sens * fpr
R> area_of_top_tri = 1/2 * spec * (1 - sens)
R> false_auc = area_of_left_tri + true_auc + area_of_top_tri
R> false_auc
[1] 0.6036415
```

The **pROC** package is one of the most popular packages for doing ROC analysis (Robin, Turck, Hainard, Tiberti, Lisacek, Sanchez, and Müller 2011). Using prediction and performance functions, we see that the estimated AUC is much higher than the true AUC:

```
R> library(pROC)

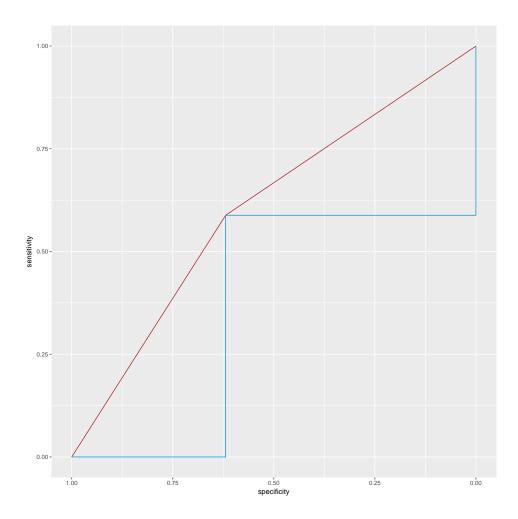
Type 'citation("pROC")' for a citation.

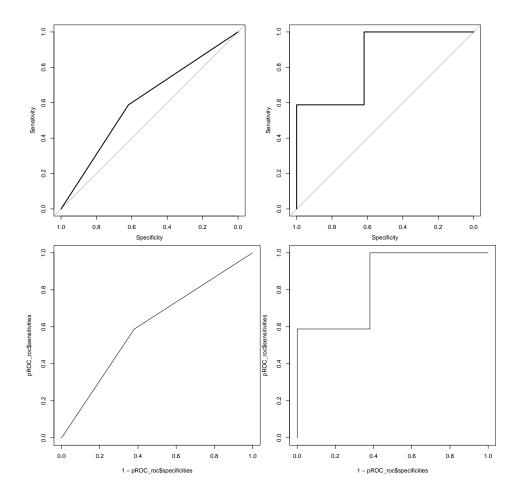
Attaching package: 'pROC'

The following objects are masked from 'package:stats':
    cov, smooth, var

R> pROC_roc = pROC::roc(predictor = x, response = y)
R> pROC_roc[["auc"]]
```

Area under the curve: 0.6036





fbroc Package

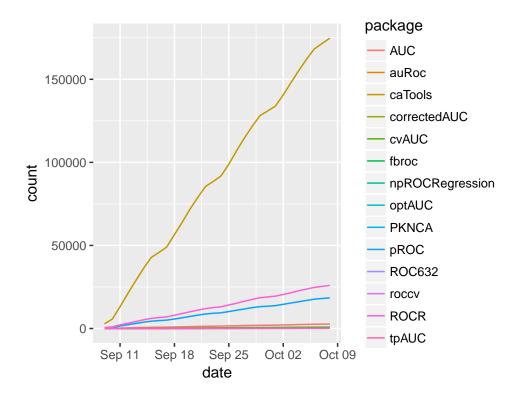
[1] 0.6036415

The **fbroc** package is one of the most popular packages for doing ROC analysis (Peter 2016). Using **prediction** and **performance** functions, we see that the estimated AUC is much higher than the true AUC:

```
R> library(fbroc)
R> fb_roc_default = boot.roc(x, as.logical(y), n.boot = 1000, tie.strategy = 2)
R> auc_def = perf(fb_roc_default, "auc")
R> auc_def[["Observed.Performance"]]

[1] 0.6036415

R> fb_roc_alternative = boot.roc(x, as.logical(y), n.boot = 1000, tie.strategy = 1)
R> auc_alt = perf(fb_roc_alternative, "auc")
R> auc_alt[["Observed.Performance"]]
```



3.2. Stata

R> roctab x y

. roctab x y

Obs	ROC Area	Std. Err.		c Normal Interval]
169	0.6037	0.0379	0.52952	0.67793

References

Peter E (2016). fbroc: Fast Algorithms to Bootstrap Receiver Operating Characteristics Curves. R package version 0.4.0, URL https://CRAN.R-project.org/package=fbroc.

Robin X, Turck N, Hainard A, Tiberti N, Lisacek F, Sanchez JC, Müller M (2011). "pROC: an open-source package for R and S+ to analyze and compare ROC curves." *BMC Bioinformatics*, **12**, 77.

Sing T, Sander O, Beerenwinkel N, Lengauer T (2005). "ROCR: visualizing classifier performance in R." *Bioinformatics*, **21**(20), 7881. URL http://rocr.bioinf.mpi-sb.mpg.de.

http://www.jstatsoft.org/

http://www.foastat.org/

Submitted: yyyy-mm-dd

Accepted: yyyy-mm-dd

Affiliation:

John Muschelli

 $\label{eq:continuous} \mbox{Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health}$

 $615~\mathrm{N}$ Wolfe St Baltimore, MD 21205

E-mail: jmuschel@jhsph.edu URL: http://johnmuschelli.