How to calculate Area Under the Curve (AUC), or the c-statistic, by hand

I am interested in calculating area under the curve (AUC), or the c-statistic, by hand for a binary logistic regression model.

For example, in the validation dataset, I have the true value for the dependent variable, retention (1 = retained; 0 = not retained), as well as a predicted retention status for each observation generated by my regression analysis using a model that was built using the training set (this will range from 0 to 1).

My initial thoughts were to identify the "correct" number of model classifications and simply divide the number of "correct" observations by the number of total observations to calculate the c-statistic. By "correct", if the true retention status of an observation = 1 and the predicted retention status is > 0.5 then that is a "correct" classification. Additionally, if the true retention status of an observation = 0 and the predicted retention status is < 0.5 then that is also a "correct" classification. I assume a "tie" would occur when the predicted value = 0.5, but that phenomenon does not occur in my validation dataset. On the other hand, "incorrect" classifications would be if the true retention status of an observation = 1 and the predicted retention status is < 0.5 or if the true retention status for an outcome = 0 and the predicted retention status is > 0.5. I am aware of TP, FP, FN, TN, but not aware of how to calculate the c-statistic given this information.

regression logistic classification roc auc

edited Feb 23 at 23:50
amoeba
22.9k 5 82 140

asked Apr 9 '15 at 17:53
Matt Reichenbach
966 3 12 35

5 Answers

I would recommend Hanley's & McNeil's 1982 paper 'The meaning and use of the area under a receiver operating characteristic (ROC) curve'.

Example

They have the following table of disease status and test result (corresponding to, for example, the estimated risk from a logistic model). The first number on the right is the number of patients with *true* disease status 'normal' and the second number is the number of patients with *true* disease status 'abnormal':

(1) Definitely normal: 33/3
(2) Probably normal: 6/2
(3) Questionable: 6/2
(4) Probably abnormal: 11/11
(5) Definitely abnormal: 2/33

So there are in total 58 'normal' patients and '51' abnormal ones. We see that when the predictor is 1, 'Definitely normal', the patient is usually normal (true for 33 of the 36 patients), and when it is 5, 'Definitely abnormal' the patients is usually abnormal (true for 33 of the 35 patients), so the predictor makes sense. But how should we judge a patient with a score of 2, 3, or 4? What we set our cutoff for judging a patients as abnormal or normal to determines the sensitivity and specificity of the resulting test.

Sensitivity and specificity

We can calculate the *estimated* sensitivity and specificity for different cutoffs. (I'll just write 'sensitivity' and 'specificity' from now on, letting the estimated nature of the values be implicit.)

If we choose our cutoff so that we classify *all* the patients as abnormal, no matter what their test results says (i.e., we choose the cutoff 1+), we will get a sensitivity of 51/51 = 1. The specificity will be 0/58 = 0. Doesn't sound so good.

OK, so let's choose a less strict cutoff. We only classify patients as abnormal if they have a test result of 2 or higher. We then miss 3 abnormal patients, and have a sensitivity of 48/51 = 0.94. But we have a much increased specificity, of 33/58 = 0.57.

We can now continue this, choosing various cutoffs (3, 4, 5, >5). (In the last case, we won't classify *any* patients as abnormal, even if they have the highest possible test score of 5.)

The ROC curve

If we do this for all possible cutoffs, and the plot the sensitivity against 1 minus the specificity, we get the ROC curve. We can use the following R code:

```
# Data
norm     = rep(1:5, times=c(33,6,6,11,2))
abnorm   = rep(1:5, times=c(3,2,2,11,33))
testres  = c(abnorm,norm)
truestat = c(rep(1,length(abnorm)), rep(0,length(norm)))

# Summary table (Table I in the paper)
( tab=as.matrix(table(truestat, testres)) )
```

The output is:

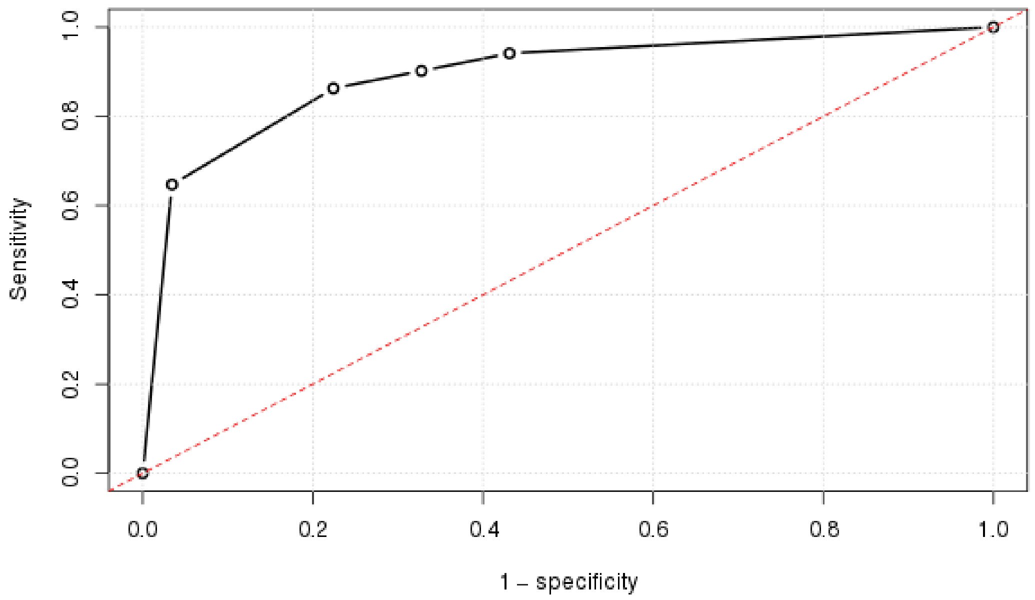
```
        testres
truestat  1  2  3  4  5
       0 33  6  6 11  2
       1  3  2  2 11 33
```

We can calculate various statistics:

```
( tot=colSums(tab) )                            # Number of patients w/ each test result
( truepos=unname(rev(cumsum(rev(tab[2,])))) )   # Number of true positives
( falsepos=unname(rev(cumsum(rev(tab[1,])))) )  # Number of false positives
( totpos=sum(tab[2,]) )                         # The total number of positives (one
number)
( totneg=sum(tab[1,]) )                         # The total number of negatives (one
number)
(sens=truepos/totpos)                           # Sensitivity (fraction true positives)
(omspec=falsepos/totneg)                        # 1 − specificity (false positives)
sens=c(sens,0); omspec=c(omspec,0)              # Numbers when we classify all as normal
```

And using this, we can plot the (estimated) ROC curve:

```
plot(omspec, sens, type="b", xlim=c(0,1), ylim=c(0,1), lwd=2,
     xlab="1 − specificity", ylab="Sensitivity") # perhaps with xaxs="i"
grid()
abline(0,1, col="red", lty=2)
```



Manually calculating the AUC

We can very easily calculate the area under the ROC curve, using the formula for the area of a trapezoid:

```
height = (sens[-1]+sens[-length(sens)])/2
width = -diff(omspec) # = diff(rev(omspec))
sum(height*width)
```

The result is 0.8931711.

A concordance measure

The AUC can also be seen as a concordance measure. If we take all possible *pairs* of patients where one is normal and the other is abnormal, we can calculate how frequently it's the abnormal one that has the highest (most 'abnormal-looking') test result (if they have the same value, we count that this as 'half a victory'):

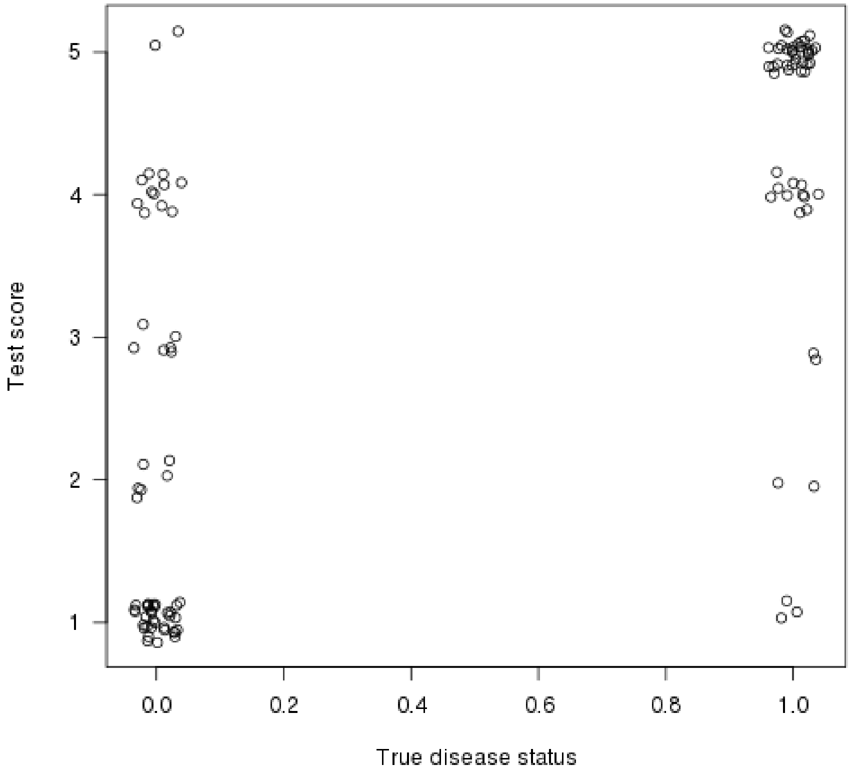
```
o = outer(abnorm, norm, "-")
mean((o>0) + .5*(o==0))
```

The answer is again 0.8931711, the area under the ROC curve. This will always be the case.

A graphical view of concordance

As pointed out by Harrell in his answer, this also has a graphical interpretation. Let’s plot test score (risk estimate) on the *y*-axis and true disease status on the *x*-axis (here with some jittering, to show overlapping points):

```
plot(jitter(truestat,.2), jitter(testres,.8), las=1,
     xlab="True disease status", ylab="Test score")
```

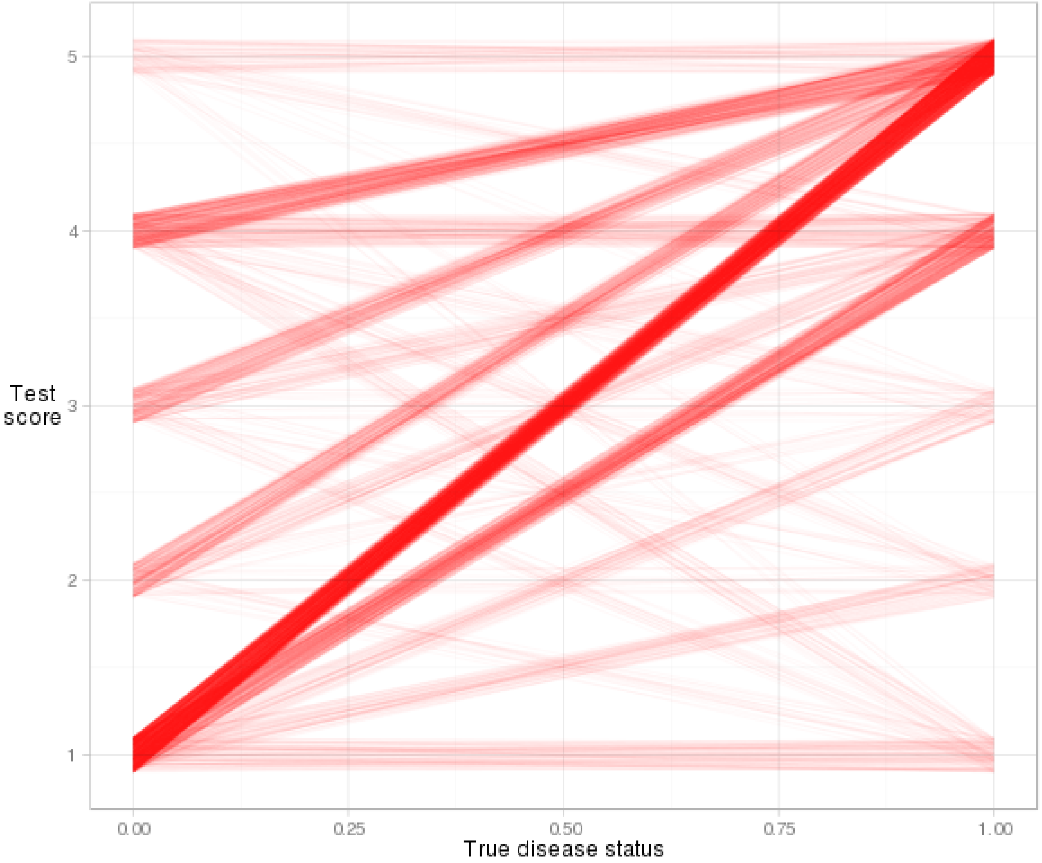


Let us now draw a line between each point on the left (a ‘normal’ patient) and each point on the right (an ‘abnormal’ patient). The proportion of lines with a positive slope (i.e., the proportion of *concordant* pairs) is the concordance index (flat lines count as ‘50% concordance’).

It’s a bit difficult to visualise the actual lines for this example, due to the number of ties (equal risk score), but with some jittering and transparency we can get a reasonable plot:

```
d = cbind(x_norm=0, x_abnorm=1, expand.grid(y_norm=norm, y_abnorm=abnorm))
```

```
library(ggplot2)
ggplot(d, aes(x=x_norm, xend=x_abnorm, y=y_norm, yend=y_abnorm)) +
  geom_segment(colour="#ff000006",
               position=position_jitter(width=0, height=.1)) +
  xlab("True disease status") + ylab("Test\nscore") +
  theme_light()  + theme(axis.title.y=element_text(angle=0))
```



We see that most of the lines slope upwards, so the concordance index will be high. We also see the contribution to the index from each type of observation pair. Most of it comes from normal patients with a risk score of 1 paired with abnormal patients with a risk score of 5 (1–5 pairs), but quite a lot also comes from 1–4 pairs and 4–5 pairs. And it's very easy to calculate the actual concordance index based on the slope definition:

```
d = transform(d, slope=(y_norm-y_abnorm)/(x_norm-x_abnorm))
mean((d$slope > 0) + .5*(d$slope==0))
```

The answer is again 0.8931711, i.e., the AUC.

The Wilcoxon–Mann–Whitney test

There is a close connection between the concordance measure and the Wilcoxon–Mann–Whitney test. Actually, the latter tests if the probability of concordance (i.e., that it's the abnormal patient in a *random* normal–abnormal pair that will have the most 'abnormal-looking' test result) is exactly 0.5. And its test statistic is just a simple transformation of the estimated concordance probability:

```
> ( wi = wilcox.test(abnorm,norm) )
    Wilcoxon rank sum test with continuity correction

data:  abnorm and norm
W = 2642, p-value = 1.944e-13
alternative hypothesis: true location shift is not equal to 0
```

The test statistic (`W = 2642`) counts the number of concordant pairs. If we divide it by the number of possible pairs, we get a familar number:

```
w = wi$statistic
w/(length(abnorm)*length(norm))
```

Yes, it's 0.8931711, the area under the ROC curve.

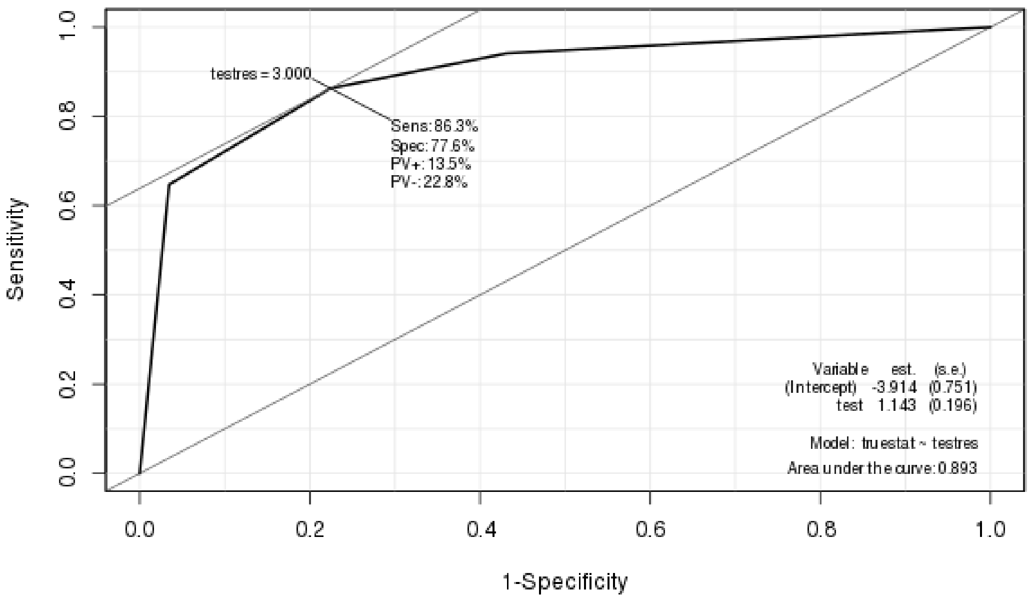
Easier ways to calculate the AUC (in R)

But let's make life easier for ourselves. There are various packages that calculate the AUC for us automatically.

The Epi package

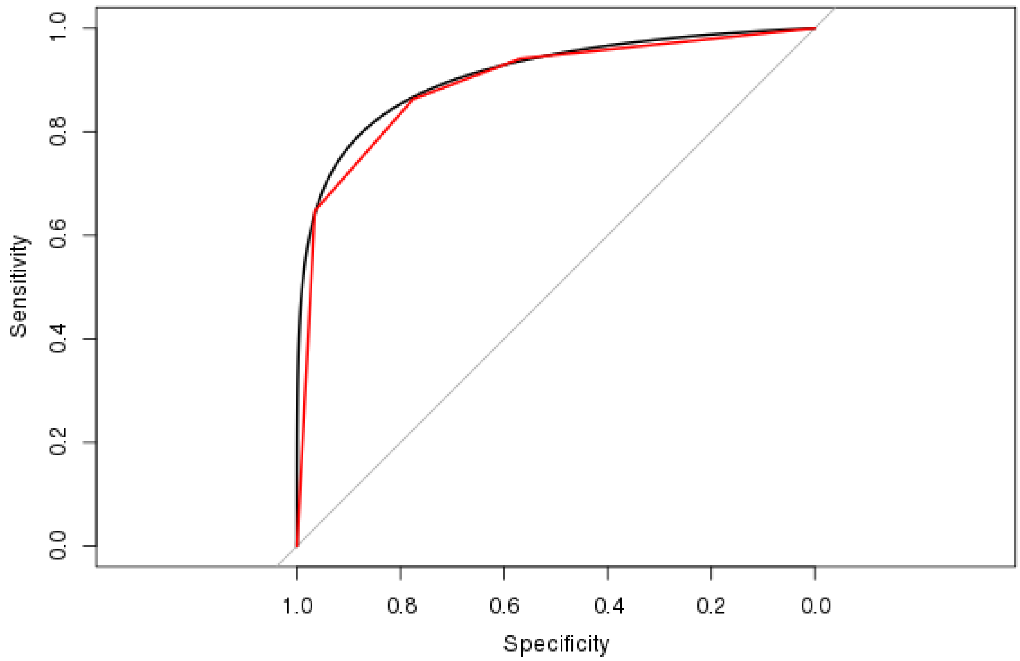
The `Epi` package creates a nice ROC curve with various statistics (including the AUC) embedded:

```
library(Epi)
ROC(testres, truestat) # also try adding plot="sp"
```



The pROC package

I also like the `pROC` package, since it can smooth the ROC estimate (and calculate an AUC estimate based on the smoothed ROC):



(The red line is the original ROC, and the black line is the smoothed ROC. Also note the default 1:1 aspect ratio. It makes sense to use this, since both the sensitivity and specificity has a 0–1 range.)

The estimated AUC from the *smoothed* ROC is 0.9107, similar to, but slightly larger than, the AUC from the unsmoothed ROC (if you look at the figure, you can easily see why it's larger). (Though we really have too few possible distinct test result values to calculate a smooth AUC).

The rms package

Harrell's `rms` package can calculate various related concordance statistics using the `rcorr.cens()` function. The `C Index` in its output is the AUC:

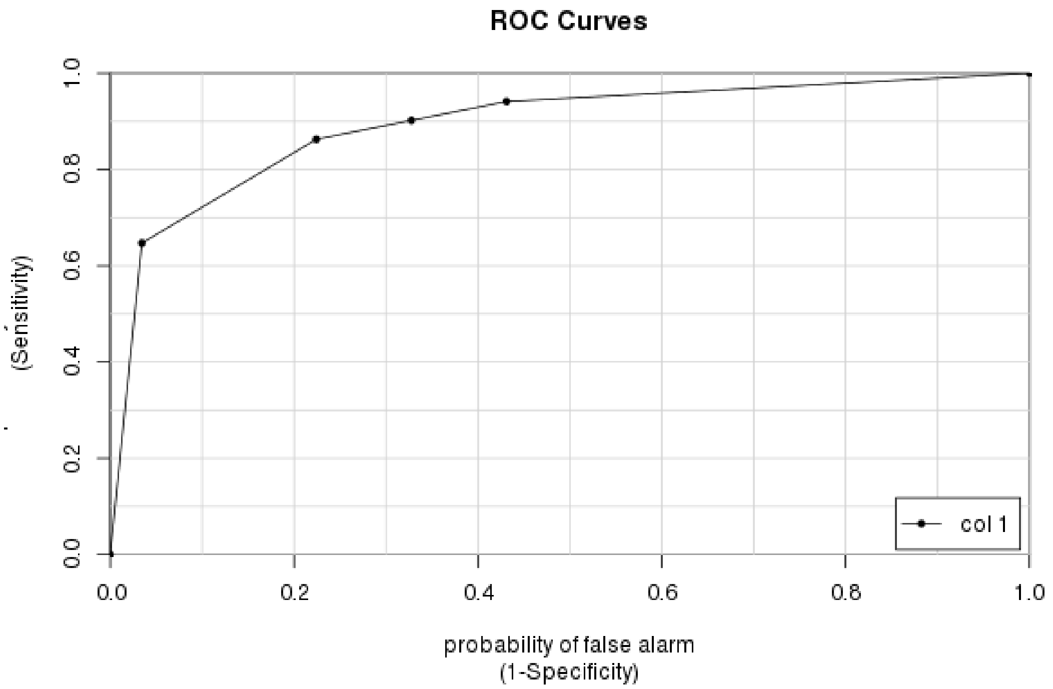
```
> library(rms)
> rcorr.cens(testres,truestat)[1]
  C Index
0.8931711
```

The caTools package

Finally, we have the `caTools` package and its `colAUC()` function. It has a few advantages over other packages (mainly speed and the ability to work with multi-dimensional data – see `?`

colAUC) that can *sometimes* be helpful. But of course it gives the same answer as we have calculated over and over:

```
library(caTools)
colAUC(testres, truestat, plotROC=TRUE)
             [,1]
0 vs. 1 0.8931711
```



Final words

Many people seem to think that the AUC tells us how ‘good’ a test is. And some people think that the AUC is the probability that the test will correctly classify a patient. It is **not**. As you can see from the above example and calculations, the AUC tells us something about a *family* of tests, one test for each possible cutoff.

And the AUC is calculated based on cutoffs one would never use in practice. Why should we care about the sensitivity and specificity of ‘nonsensical’ cutoff values? Still, that’s what the AUC is (partially) based on. (Of course, if the AUC is *very* close to 1, almost every possible test will have great discriminatory power, and we would all be very happy.)

The ‘random normal–abnormal’ pair interpretation of the AUC is nice (and can be extended, for instance to survival models, where we see if its the person with the highest (relative) hazard that dies the earliest). But one would never use it in practice. It’s a rare case where one *knows* one has *one* healthy and *one* ill person, doesn’t know which person is the ill one, and must decide which of them to treat. (In any case, the decision is easy; treat the one with the highest estimated risk.)

So I think studying the actual *ROC curve* will be more useful than just looking at the AUC summary measure. And if you use the ROC together with (estimates of the) *costs* of false positives and false negatives, along with base rates of what you’re studying, you can get somewhere.

Also note that the AUC only measures *discrimination*, not calibration. That is, it measures whether you can discriminate between two persons (one ill and one healthy), based on the risk score. For this, it only looks at *relative* risk values (or ranks, if you will, cf. the Wilcoxon–Mann–Whitney test interpretation), not the absolute ones, which you *should* be interested in. For example, if you divide each risk estimate from your logistic model by 2, you will get exactly the same AUC (and ROC).

When evaluating a risk model, *calibration* is also very important. To examine this, you will look at all patients with a risk score of around, e.g., 0.7, and see if approximately 70% of these actually were ill. Do this for each possible risk score (possibly using some sort of smoothing / local regression). Plot the results, and you’ll get a graphical measure of *calibration*.

If have a model with *both* good calibration and good discrimination, then you start to have good model. :)

edited Mar 14 at 23:51
gung
67.8k 19 148 280

answered Apr 13 '15 at 18:40
Karl Ove Hufthammer
2,580 1 11 25

4 Thank you, @Karl Ove Hufthammer, this is the most thorough answer that I have ever received. I especially appreciate your "Final Words" section. Excellent work! Thanks again! – Matt Reichenbach Apr 20 '15 at 12:16

Have a look at this question: Understanding ROC curve

Here's how to build a ROC curve (from that question):

Drawing ROC curve

given a data set processed by your ranking classifier

- rank test examples on decreasing score
- start in $(0, 0)$

- for each example x (in the decreasing order)
  - if x is positive, move $1/\text{pos}$ up
  - if x is negative, move $1/\text{neg}$ right

where pos and neg are the fractions of positive and negative examples respectively.

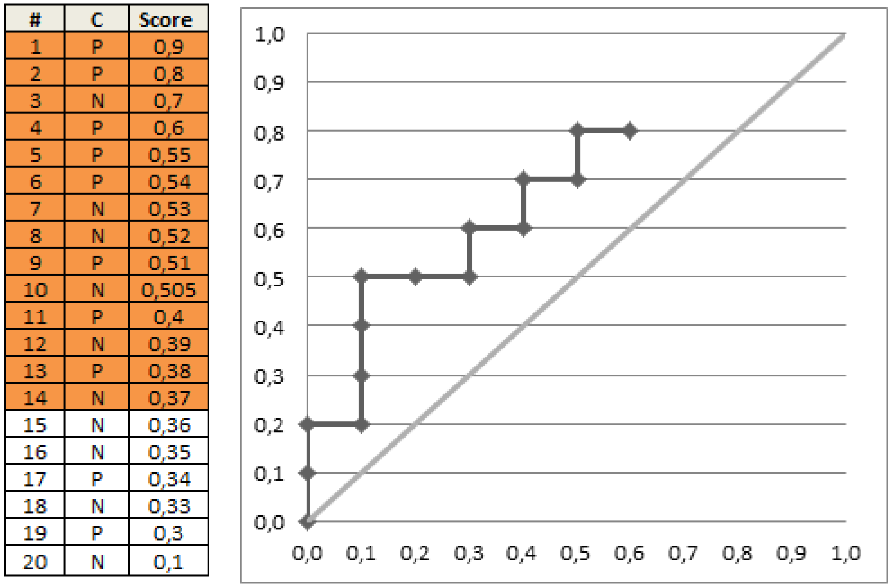
You can use this idea for manually calculating AUC ROC using the following algorithm:

```
auc = 0.0
height = 0.0

for each training example x_i, y_i
  if y_i = 1.0:
    height = height + tpr
  else
    auc = auc + height * fpr

return auc
```

This nice gif-animated picture should illustrate this process clearer



#	C	Score
1	P	0,9
2	P	0,8
3	N	0,7
4	P	0,6
5	P	0,55
6	P	0,54
7	N	0,53
8	N	0,52
9	P	0,51
10	N	0,505
11	P	0,4
12	N	0,39
13	P	0,38
14	N	0,37
15	N	0,36
16	N	0,35
17	P	0,34
18	N	0,33
19	P	0,3
20	N	0,1

edited Apr 15 '15 at 7:35

answered Apr 14 '15 at 8:23

Alexey Grigorev
2,223 1 9 27

Thanks @Alexey Grigorev, this is a great visual and it will likely prove useful in the future! +1 – Matt Reichenbach Apr 20 '15 at 12:13

Karl's post has a lot of excellent information. But I have not yet seen in the past 20 years an example of an ROC curve that changed anyone's thinking in a good direction. The only value of an ROC curve in my humble opinion is that its area happens to equal a very useful concordance probability. The ROC curve itself tempts the reader to use cutoffs, which is bad statistical practice.

As far as manually calculating the c-index, make a plot with $Y = 0, 1$ on the x-axis and the continuous predictor or predicted probability that $Y = 1$ on the y-axis. If you connect every point with $Y = 0$ with every point with $Y = 1$, the proportion of the lines that have a positive slope is the concordance probability.

Any measures that have a denominator of n in this setting are improper accuracy scoring rules and should be avoided. This includes proportion classified correctly, sensitivity, and specificity.

For the R `Hmisc` package `rcorr.cens` function, print the entire result to see more information, especially a standard error.

answered Apr 14 '15 at 12:41

Frank Harrell
36.3k 1 63 143

Thank you, @Frank Harell, I appreciate your perspective. I simply use the c-statistic as a concordance probability, as I don't like cutoffs. Thanks again! – Matt Reichenbach Apr 20 '15 at 12:12

Here is an alternative to the natural way of calculating AUC by simply using the trapezoidal rule to get the area under the ROC curve.

The AUC is equal to the probability that a randomly sampled positive observation has a predicted probability (of being positive) greater than a randomly sampled negative observation. You can use this to calculate the AUC quite easily in any programming language by going through all the pairwise combinations of positive and negative observations. You could also randomly sample observations if the sample size was too large. If you want to calculate AUC using pen and paper, this might not be the best approach unless you have a very small sample/a lot of time. For example in R:

```
n <- 100L
```

```
x1 <- rnorm(n, 2.0, 0.5)
x2 <- rnorm(n, -1.0, 2)
y <- rbinom(n, 1L, plogis(-0.4 + 0.5 * x1 + 0.1 * x2))

mod <- glm(y ~ x1 + x2, "binomial")

probs <- predict(mod, type = "response")

combinations <- expand.grid(positiveProbs = probs[y == 1L],
        negativeProbs = probs[y == 0L])

mean(combinations$positiveProbs > combinations$negativeProbs)
[1] 0.628723
```

We can verify using the `pROC` package:

```
library(pROC)
auc(y, probs)
Area under the curve: 0.6287
```

Using random sampling:

```
mean(sample(probs[y == 1L], 100000L, TRUE) > sample(probs[y == 0L], 100000L, TRUE))
[1] 0.62896
```

edited Apr 13 '15 at 22:06

answered Apr 13 '15 at 14:59

Jeff
294 1 15

Thank you, @Jeff, for your helpful response! +1 – Matt Reichenbach Apr 20 '15 at 12:10

1. You have true value for observations.
2. Calculate posterior probability and then rank observations by this probability.
3. Assuming cut-off probability of P and number of observations N:

$$\frac{\text{Sum of true ranks} - 0.5PN(PN+1)}{PN(N-PN)}$$

edited Apr 13 '15 at 17:48

gung
67.8k 19 148 280

answered Apr 13 '15 at 17:26

user73455
1

@user73455...1) Yes, I have the true value for observations. 2) Is posterior probability synonymous with predicted probabilities for each of the observations? 3) Understood; however, what is "Sum of true ranks" and how does one calculate this value? Perhaps an example would help you explain this answer more thoroughly? Thank you! – Matt Reichenbach Apr 13 '15 at 18:36