

Logistic Regression Performance

Fundamental Techniques in Data Science



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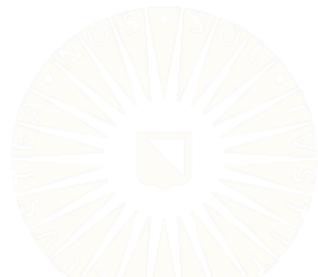
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Outline

Confusion Matrix

ROC Curve

Alternative Performance Measures



Example Model

First, we'll refit the logistic regression model that predicts the chances of Titanic passengers surviving based on their age, sex, and ticket price

```
## Read the data:  
titanic <- readRDS(here::here("data", "titanic.rds"))  
  
## Estimate the logistic regression model:  
glmFit <- glm(survived ~ age + sex + fare,  
                data = titanic,  
                family = "binomial")  
  
## Save the linear predictor estimates:  
titanic$etaHat <- predict(glmFit, type = "link")
```



Example Model

```
partSummary(glmFit, -1)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.837621  0.215121  3.894 9.87e-05
age         -0.007404  0.006040 -1.226    0.22
sexmale     -2.392422  0.171288 -13.967 < 2e-16
fare        0.011586  0.002338  4.955 7.23e-07

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1182.8 on 886 degrees of freedom
Residual deviance: 881.4 on 883 degrees of freedom
AIC: 889.4

Number of Fisher Scoring iterations: 5
```



Confusion Matrix

One of the most direct ways to evaluate classification performance is the *confusion matrix*.

```
library(magrittr)

## Add predictions to the dataset:
titanic %<%
  mutate(piHat = predict(glmFit, type = "response"),
         yHat = as.factor(ifelse(piHat <= 0.5, "no", "yes")))
  )
```

		True	
Predicted		no	yes
no	no	458	106
	yes	87	236

Confusion Matrix of Predicted Survival



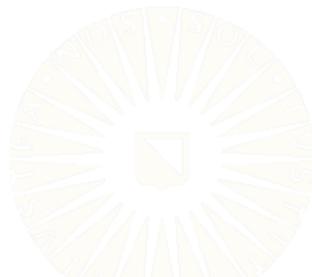
Confusion Matrix

Each cell in the confusion matrix represents a certain classification result.

		True	
Predicted	Died	Survived	
Died	True Negative	False Negative	
Survived	False Positive	True Positive	

Confusion Matrix of Predicted Survival

- **TP:** Correctly predict survival
- **TN:** Correctly predict death
- **FP:** Predict survival for dead people
- **FN:** Predict death for survivors



Confusion Matrix

```
library(caret)

cMat <- titanic %$% confusionMatrix(data = yHat, reference = survived)

cMat$table

      Reference
Prediction  no yes
          no 458 106
          yes 87 236

cMat$overall

      Accuracy      Kappa AccuracyLower AccuracyUpper
7.824126e-01 5.359709e-01 7.537802e-01 8.091549e-01
AccuracyNull AccuracyPValue McnemarPValue
6.144307e-01 7.471405e-27 1.950898e-01
```

Confusion Matrix

```
cMat$byClass
```

Sensitivity		Specificity	
Pos	Pred Value	Neg	Pred Value
	0.8403670		0.6900585
0.8120567		0.7306502	
Precision		Recall	
0.8120567		0.8403670	
F1		Prevalence	
0.8259693		0.6144307	
Detection Rate		Prevalence	
0.5163472		0.6358512	
Balanced Accuracy			
0.7652127			

Summaries of the Confusion Matrix

$$\text{Accuracy} = (TP + TN) / (P + N)$$

- In our example, Accuracy = 0.78
- 78% are correctly classified

$$\text{Error Rate} = (FP + FN) / (P + N) = 1 - \text{Accuracy}$$

- In our example, Error Rate = 0.22
- 22% are incorrectly classified

$$\text{Sensitivity} = TP / (TP + FN)$$

- In our example, Sensitivity = 0.84
- 84% of survivors are correctly classified

$$\text{Specificity} = TN / (TN + FP)$$

- In our example, Specificity = 0.69
- 69% of deaths are correctly classified



Summaries of the Confusion Matrix

False Positive Rate (FPR) = $FP / (TN + FP)$ = 1 - Specificity

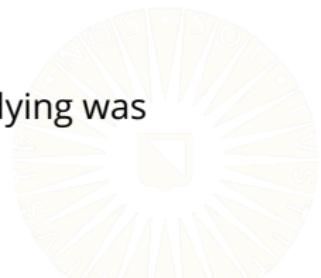
- In our example, FPR = 0.31
- 31% of deaths are incorrectly classified as survivors

Positive Predictive Value (PPV) = $TP / (TP + FP)$

- In our example, PPV = 0.81
- There is an 81% chance that a passenger classified as a survivor was classified correctly

Negative Predictive Value (NPV) = $TN / (TN + FN)$

- In our example, NPV = 0.73
- There is a 73% chance that a passenger classified as dying was classified correctly

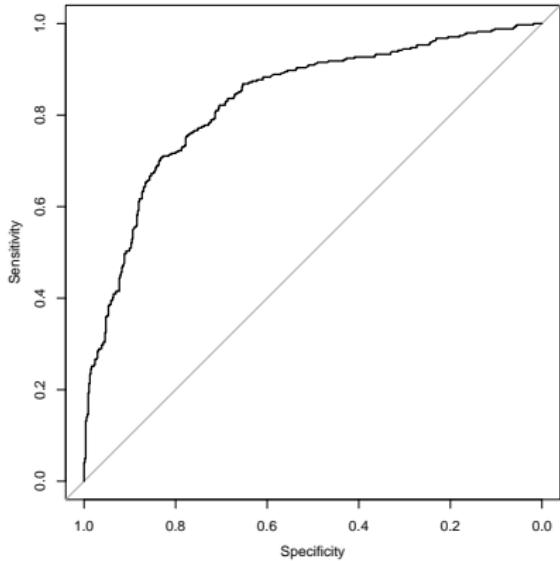


ROC Curve

```
rocData <- titanic %$%
  pROC::roc(survived, piHat)
plot(rocData)
```

A *receiver operating characteristic* (ROC) curve illustrates the diagnostic ability of a binary classifier for all possible values of the classification threshold.

- The ROC curve plots sensitivity against specificity at different threshold values.



ROC Curve

The *area under the ROC curve* (AUC) is a one-number summary of the potential performance of the classifier.

- The AUC does not depend on the classification threshold.

```
pROC::auc(rocData)
```

```
Area under the curve: 0.8298
```

According to Mandrekar (2010):

- AUC value from 0.7 – 0.8: Acceptable
- AUC value from 0.8 – 0.9: Excellent
- AUC value over 0.9: Outstanding



Threshold Selection

We can use numerical methods to estimate an optimal threshold value.

```
library(OptimalCutpoints)

ocOut <- optimal.cutpoints(X = "piHat",
                            status = "survived",
                            tag.healthy = "no",
                            data = titanic,
                            method = "ROC01"
                           )
```

Threshold Selection

```
partSummary(ocOut, -1)
```

```
Area under the ROC curve (AUC): 0.83 (0.802, 0.858)
```

```
CRITERION: ROC01
```

```
Number of optimal cutoffs: 1
```

	Estimate
cutoff	0.2360978
Se	0.7543860
Sp	0.7761468
PPV	0.6789474
NPV	0.8343195
DLR.Positive	3.3700029
DLR.Negative	0.3164531
FP	122.0000000
FN	84.0000000
Optimal criterion	0.1104365

Optimized Confusion Matrix

```
library(caret)
optThresh <- ocOut$ROC01$Global$optimal.cutoff$cutoff

## Add optimized predictions to the dataset:
titanic %<%
  mutate(yHat2 = as.factor(ifelse(piHat <= optThresh, "no", "yes")))

## Compute the optimized confusion matrix:
cMat2 <- titanic %$% confusionMatrix(data = yHat2, reference = survived)

cMat2$table
```

		Reference
Prediction	no	yes
no	423	85
yes	122	257

```
cMat2$overall
```

Accuracy	Kappa	AccuracyLower	AccuracyUpper
7.666291e-01	5.171882e-01	7.373697e-01	7.941051e-01
AccuracyNull	AccuracyPValue	McnemarPValue	
6.144307e-01	3.688756e-22	1.234336e-02	

Alternative Performance Measures

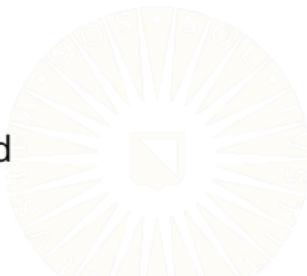
Measuring classification performance from a confusion matrix can be problematic.

- Sometimes too coarse.

We can also base our error measure on the residual deviance with the *Cross-Entropy Error*:

$$CEE = -N^{-1} \sum_{n=1}^N Y_n \ln(\hat{\pi}_n) + (1 - Y_n) \ln(1 - \hat{\pi}_n)$$

- The CEE is sensitive to classification confidence.
- Stronger predictions are more heavily weighted.
- The CEE doesn't depend on the classification threshold



Benefits of CEE

The misclassification rate is a naively appealing option.

- The proportion of cases assigned to the wrong group

Consider two perfect classifiers:

1. $P(\hat{Y}_n = 1|Y_n = 1) = 0.90, P(\hat{Y}_n = 1|Y_n = 0) = 0.10, n = 1, 2, \dots, N$
2. $P(\hat{Y}_n = 1|Y_n = 1) = 0.55, P(\hat{Y}_n = 1|Y_n = 0) = 0.45, n = 1, 2, \dots, N$

Both of these classifiers will have the same misclassification rate.

- Neither model ever makes an incorrect group assignment.

The first model will have a lower CEE.

- The classifications are made with higher confidence.
- $CEE_1 = 0.105, CEE_2 = 0.598$



CEE Example

```
glmFit2 <- update(glmFit, ". ~ . + class")
partSummary(glmFit2, 2:4)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.5933885	0.4261192	8.433	< 2e-16
age	-0.0340848	0.0072237	-4.718	2.38e-06
sexmale	-2.5851093	0.1878983	-13.758	< 2e-16
fare	0.0004142	0.0021066	0.197	0.844
class2nd	-1.1739314	0.2911585	-4.032	5.53e-05
class3rd	-2.4261391	0.2936692	-8.261	< 2e-16

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1182.77 on 886 degrees of freedom
Residual deviance: 801.56 on 881 degrees of freedom
AIC: 813.56

CEE Example

```
library(MLmetrics)

# Create a numeric version of our outcome variable:
survived <- ifelse(titanic$survived == "yes", 1, 0)

# Compute the CEE for the smaller model:
LogLoss(y_pred = predict(glmFit, type = "response"), y_true = survived)
[1] 0.496846

# Compute the CEE for the larger model:
LogLoss(y_pred = predict(glmFit2, type = "response"), y_true = survived)
[1] 0.451835
```

References

Mandrekar, J. N. (2010). Receiver operating characteristic curve in diagnostic test assessment. *Journal of Thoracic Oncology*, 5(9), 1315–1316.

