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Contents

Logistic Regression

> If linear regression serves to predict continuous Y variables, logistic regression is used for binary classification.

If we use linear regression to model a dichotomous variable (as *Y*), the resulting model might not restrict the predicted *Ys* within 0 and 1. Besides, other assumptions of linear regression (Assumptions-of-Linear-Regression.html) such as normality of errors may get violated. So instead, we model the log odds of the event $ln\left(\frac{P}{1-P}\right)$, where, *P* is the probability of event.

$$Z_i = ln\left(\frac{P_i}{1-P_i}\right) = \beta_0 + \beta_1 x_1 + .. + \beta_n x_n$$

The above equation can be modeled using the `glm()` by setting the `family` argument to `"binomial"`. But we are more interested in the probability of the event, than the log odds of the event. So, the predicted values from the above model, i.e. the log odds of the event, can be converted to probability of event as follows:

$$P_i = 1 - \left(\frac{1}{1 + e_i^z} \right)$$

This conversion is achieved using the `plogis()` function, as shown below when we build logit models and predict (Logistic-Regression-With-R.html#Build%20Logit%20Models%20and%20Predict).

Example Problem

Lets try and predict if an individual will earn more than $50K using logistic regression based on demographic variables available in the `adult` data (http://rstatistics.net/wp-content/uploads/2015/09/adult.csv). In this process, we will:

1. Import the data
2. Check for class bias
3. Create training and test samples
4. Compute information value to find out important variables
5. Build logit models and predict on test data
6. Do model diagnostics

Import data

```
inputData <- read.csv("http://rstatistics.net/wp-content/uploads/2015/09/adult.csv")
head(inputData)
#=>   AGE        WORKCLASS FNLWGT  EDUCATION EDUCATIONNUM       MARITALSTATUS
#=> 1  39        State-gov  77516  Bachelors           13       Never-married
#=> 2  50 Self-emp-not-inc  83311  Bachelors           13  Married-civ-spouse
#=> 3  38          Private 215646    HS-grad            9            Divorced
#=> 4  53          Private 234721       11th            7  Married-civ-spouse
#=> 5  28          Private 338409  Bachelors           13  Married-civ-spouse
#=> 6  37          Private 284582    Masters           14  Married-civ-spouse
#            OCCUPATION   RELATIONSHIP   RACE     SEX CAPITALGAIN CAPITALLOSS
#=> 1       Adm-clerical  Not-in-family  White    Male        2174           0
#=> 2    Exec-managerial        Husband  White    Male           0           0
#=> 3  Handlers-cleaners  Not-in-family  White    Male           0           0
#=> 4  Handlers-cleaners        Husband  Black    Male           0           0
#=> 5     Prof-specialty           Wife  Black  Female           0           0
#=> 6    Exec-managerial           Wife  White  Female           0           0
#     HOURSPERWEEK  NATIVECOUNTRY ABOVE50K
#=> 1           40  United-States        0
#=> 2           13  United-States        0
#=> 3           40  United-States        0
#=> 4           40  United-States        0
#=> 5           40           Cuba        0
#=> 6           40  United-States        0
```

Check Class bias

Ideally, the proportion of events and non-events in the Y variable should approximately be the same. So, lets first check the proportion of classes in the dependent variable `ABOVE50K`.

```
table(inputData$ABOVE50K)
#     0     1
# 24720  7841
```

Clearly, there is a class bias, a condition observed when the proportion of events is much smaller than proportion of non-events. So we must sample the observations in approximately equal proportions to get better models.

Create Training and Test Samples

One way to address the problem of class bias is to draw the 0’s and 1’s for the `trainingData` (development sample) in equal proportions. In doing so, we will put rest of the `inputData` not included for training into `testData` (validation sample). As a result, the size of development sample will be smaller that validation, which is okay, because, there are large number of observations (>10K).

```
# Create Training Data
input_ones <- inputData[which(inputData$ABOVE50K == 1), ]  # all 1's
input_zeros <- inputData[which(inputData$ABOVE50K == 0), ]  # all 0's
set.seed(100)  # for repeatability of samples
input_ones_training_rows <- sample(1:nrow(input_ones), 0.7*nrow(input_ones))  # 1's for
 training
input_zeros_training_rows <- sample(1:nrow(input_zeros), 0.7*nrow(input_ones))  # 0's fo
r training. Pick as many 0's as 1's
training_ones <- input_ones[input_ones_training_rows, ]
training_zeros <- input_zeros[input_zeros_training_rows, ]
trainingData <- rbind(training_ones, training_zeros)  # row bind the 1's and 0's

# Create Test Data
test_ones <- input_ones[-input_ones_training_rows, ]
test_zeros <- input_zeros[-input_zeros_training_rows, ]
testData <- rbind(test_ones, test_zeros)  # row bind the 1's and 0's
```

Next it is desirable to find the information value (Variable-Selection-and-Importance-With-R.html#7.%20Information%20value%20and%20Weight%20of%20evidence) of variables to get an idea of how valuable they are in explaining the dependent variable (ABOVE50K).

Create WOE for categorical variables (optional)

Optionally, we can create `WOE` equivalents for all categorical variables. This is only an optional step, for simplicity, this step is NOT run for this analysis.

```
for(factor_var in factor_vars){
  inputData[[factor_var]] <- WOE(X=inputData[, factor_var], Y=inputData$ABOVE50K)
}
head(inputData)
#>   AGE  WORKCLASS FNLWGT  EDUCATION EDUCATIONNUM MARITALSTATUS OCCUPATION
#> 1  39  0.1608547  77516  0.7974104           13    -1.8846680  -0.713645
#> 2  50  0.2254209  83311  0.7974104           13     0.9348331   1.084280
#> 3  38 -0.1278453 215646 -0.5201257            9    -1.0030638  -1.555142
#> 4  53 -0.1278453 234721 -1.7805021            7     0.9348331  -1.555142
#> 5  28 -0.1278453 338409  0.7974104           13     0.9348331   0.943671
#> 6  37 -0.1278453 284582  1.3690863           14     0.9348331   1.084280

#>   RELATIONSHIP        RACE        SEX CAPITALGAIN CAPITALLOSS HOURSPERWEEK
#> 1    -1.015318  0.08064715  0.3281187        2174           0           40
#> 2     0.941801  0.08064715  0.3281187           0           0           13
#> 3    -1.015318  0.08064715  0.3281187           0           0           40
#> 4     0.941801 -0.80794676  0.3281187           0           0           40
#> 5     1.048674 -0.80794676 -0.9480165           0           0           40
#> 6     1.048674  0.08064715 -0.9480165           0           0           40

#>   NATIVECOUNTRY ABOVE50K
#> 1    0.02538318        0
#> 2    0.02538318        0
#> 3    0.02538318        0
#> 4    0.02538318        0
#> 5    0.11671564        0
#> 6    0.02538318        0
```

Compute Information Values

The `smbinning::smbinning` function converts a continuous variable into a categorical variable using recursive partitioning. We will first convert them to categorical variables and then, capture the information values for all variables in `iv_df`

```
library(smbinning)
# segregate continuous and factor variables
factor_vars <- c ("WORKCLASS", "EDUCATION", "MARITALSTATUS", "OCCUPATION", "RELATIONSHI
P", "RACE", "SEX", "NATIVECOUNTRY")
continuous_vars <- c("AGE", "FNLWGT","EDUCATIONNUM", "HOURSPERWEEK", "CAPITALGAIN", "CAP
ITALLOSS")

iv_df <- data.frame(VARS=c(factor_vars, continuous_vars), IV=numeric(14))  # init for IV
results

# compute IV for categoricals
for(factor_var in factor_vars){
  smb <- smbinning.factor(trainingData, y="ABOVE50K", x=factor_var)  # WOE table
  if(class(smb) != "character"){ # heck if some error occured
    iv_df[iv_df$VARS == factor_var, "IV"] <- smb$iv
  }
}

# compute IV for continuous vars
for(continuous_var in continuous_vars){
  smb <- smbinning(trainingData, y="ABOVE50K", x=continuous_var)  # WOE table
  if(class(smb) != "character"){  # any error while calculating scores.
    iv_df[iv_df$VARS == continuous_var, "IV"] <- smb$iv
  }
}

iv_df <- iv_df[order(-iv_df$IV), ]  # sort
iv_df
#>           VARS     IV
#>   RELATIONSHIP 1.5739
#>  MARITALSTATUS 1.3356
#>            AGE 1.1748
#>    CAPITALGAIN 0.8389
#>     OCCUPATION 0.8259
#>   EDUCATIONNUM 0.7776
#>      EDUCATION 0.7774
#>   HOURSPERWEEK 0.4682
#>            SEX 0.3087
#>      WORKCLASS 0.1633
#>    CAPITALLOSS 0.1507
#>  NATIVECOUNTRY 0.0815
#>           RACE 0.0607
#>         FNLWGT 0.0000
```

Build Logit Models and Predict

```
logitMod <- glm(ABOVE50K ~ RELATIONSHIP + AGE + CAPITALGAIN + OCCUPATION + EDUCATIONNUM,
data=trainingData, family=binomial(link="logit"))

predicted <- plogis(predict(logitMod, testData))  # predicted scores
# or
predicted <- predict(logitMod, testData, type="response")  # predicted scores
```

A quick note about the `plogis` function: The `glm()` procedure with `family="binomial"` will build the logistic regression model on the given formula. When we use the `predict` function on this model, it will predict the log(odds) of the Y variable. This is not what we ultimately want because, the predicted values may not lie within the 0 and 1 range as expected. So, to convert it into prediction probability scores that is bound between 0 and 1, we use the `plogis()`.

Decide on optimal prediction probability cutoff for the model

The default cutoff prediction probability score is 0.5 or the ratio of 1’s and 0’s in the training data. But sometimes, tuning the probability cutoff can improve the accuracy in both the development and validation samples. The `InformationValue::optimalCutoff` function provides ways to find the optimal cutoff to improve the prediction of 1’s, 0’s, both 1’s and 0’s and o reduce the misclassification error. Lets compute the optimal score that minimizes the misclassification error for the above model.

```
library(InformationValue)
optCutOff <- optimalCutoff(testData$ABOVE50K, predicted)[1]
#=> 0.71
```

Model Diagnostics

The `summary(logitMod)` gives the beta coefficients, Standard error, z Value and p Value. If your model had categorical variables with multiple levels, you will find a row-entry for each category of that variable. That is because, each individual category is considered as an independent binary variable by the `glm()`. In this case it is ok if few of the categories in a multi-category variable don’t turn out to be significant in the model (i.e. p Value turns out greater than significance level of 0.5).

```
summary(logitMod)
#> Call:
#>   glm(formula = ABOVE50K ~ RELATIONSHIP + AGE + CAPITALGAIN + OCCUPATION +
#>         EDUCATIONNUM, family = "binomial", data = trainingData)
#>
#>   Deviance Residuals:
#>       Min       1Q   Median       3Q      Max
#>   -3.8380  -0.5319  -0.0073   0.6267   3.2847
#>
#>   Coefficients:
#>                                  Estimate  Std. Error z value             Pr(>|z|)
#>   (Intercept)                 -4.57657130  0.24641856 -18.572 < 0.0000000000000002 *
**
#>   RELATIONSHIP Not-in-family   -2.27712854  0.07205131 -31.604 < 0.0000000000000002 *
**
#>   RELATIONSHIP Other-relative  -2.72926866  0.27075521 -10.080 < 0.0000000000000002 *
**
#>   RELATIONSHIP Own-child       -3.56051255  0.17892546 -19.899 < 0.0000000000000002 *
**
#>   ...
#>   ...
#>   Null deviance: 15216.0  on 10975  degrees of freedom
#>   Residual deviance:  8740.9  on 10953  degrees of freedom
#>   AIC: 8786.9
#>
#>   Number of Fisher Scoring iterations: 8
```

VIF

Like in case of linear regression, we should check for multicollinearity in the model. As seen below, all X variables in the model have VIF well below 4.

```
vif(logitMod)
#>                  GVIF Df GVIF^(1/(2*Df))
#> RELATIONSHIP 1.340895  5        1.029768
#> AGE          1.119782  1        1.058198
#> CAPITALGAIN  1.023506  1        1.011685
#> OCCUPATION   1.733194 14        1.019836
#> EDUCATIONNUM 1.454267  1        1.205930
```

Misclassification Error

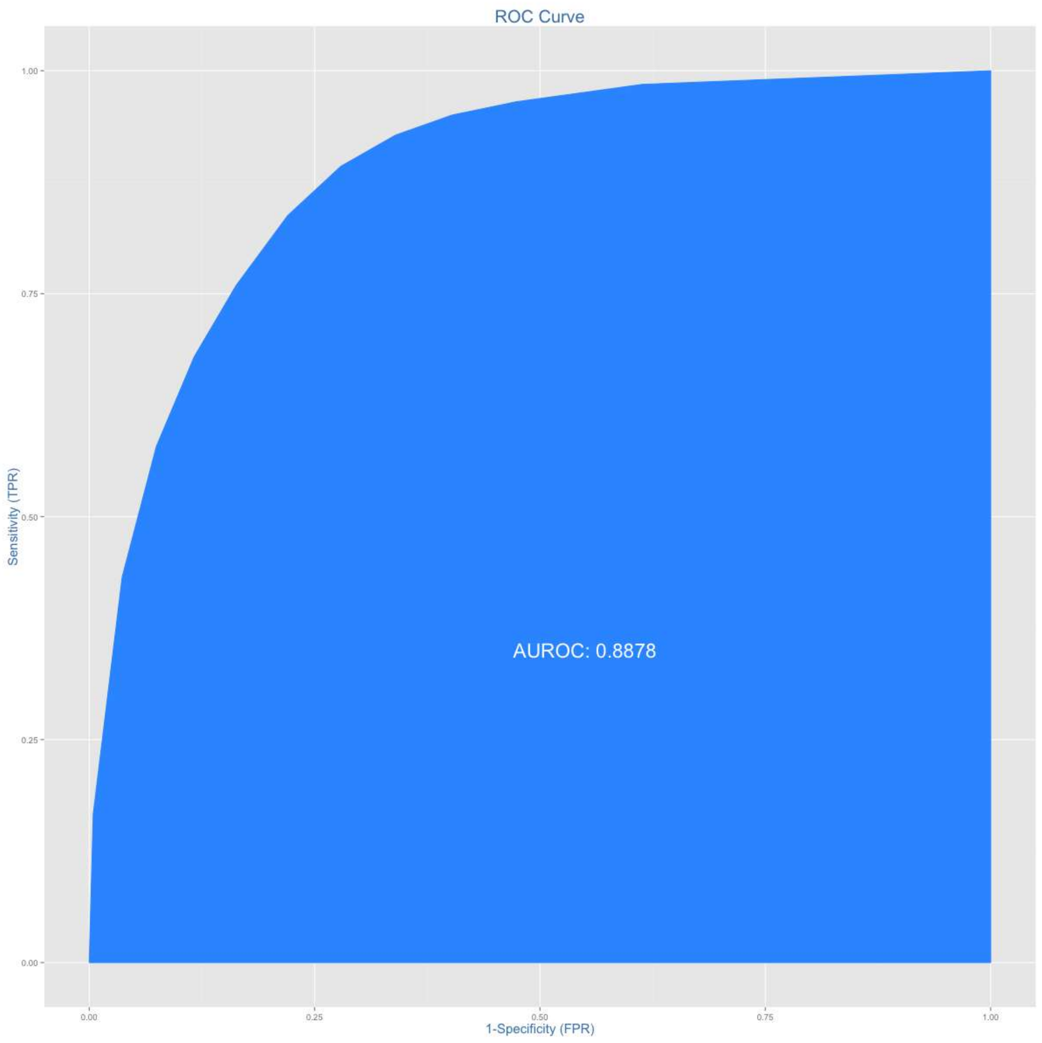
Misclassification error is the percentage mismatch of predcited vs actuals, irrespective of 1’s or 0’s. The lower the misclassification error, the better is your model.

```
misClassError(testData$ABOVE50K, predicted, threshold = optCutOff)
#=> 0.0899
```

ROC

Receiver Operating Characteristics Curve traces the percentage of true positives accurately predicted by a given logit model as the prediction probability cutoff is lowered from 1 to 0. For a good model, as the cutoff is lowered, it should mark more of actual 1’s as positives and lesser of actual 0’s as 1’s. So for a good model, the curve should rise steeply, indicating that the TPR (Y-Axis) increases faster than the FPR (X-Axis) as the cutoff score decreases. Greater the area under the ROC curve, better the predictive ability of the model.

```
plotROC(testData$ABOVE50K, predicted)
```



The above model has area under ROC curve 88.78%, which is pretty good.

Concordance

Ideally, the model-calculated-probability-scores of all actual Positive's, (aka Ones) should be greater than the model-calculated-probability-scores of ALL the Negatives (aka Zeroes). Such a model is said to be perfectly concordant and a highly reliable one. This phenomenon can be measured by Concordance and Discordance.

In simpler words, of all combinations of 1-0 pairs (actuals), *Concordance* is the percentage of pairs, whose scores of actual positive's are greater than the scores of actual negative's. For a perfect model, this will be 100%. So, the higher the concordance, the better is the quality of model.

```
Concordance(testData$ABOVE50K, predicted)
#> 0.8915
```

The above model with a concordance of 89.2% is indeed a good quality model.

Specificity and Sensitivity

Sensitivity (or True Positive Rate) is the percentage of 1’s (actuals) correctly predicted by the model, while, specificity is the percentage of 0’s (actuals) correctly predicted. Specificity can also be calculated as 1 − *False Positive Rate*.

$$Sensitivity = \frac{\#\ Actual\ 1's\ and\ Predicted\ as\ 1's}{\#\ of\ Actual\ 1's}$$

$$Specificity = \frac{\#\ Actual\ 0's\ and\ Predicted\ as\ 0's}{\#\ of\ Actual\ 0's}$$

```
sensitivity(testData$ABOVE50K, predicted, threshold = optCutOff)
#> 0.3089
specificity(testData$ABOVE50K, predicted, threshold = optCutOff)
#> 0.9836
```

The above numbers are calculated on the validation sample that was not used for training the model. So, a truth detection rate of 31% on test data is good.

Confusion Matrix

```
confusionMatrix(testData$ABOVE50K, predicted, threshold = optCutOff)
# The columns are actuals, while rows are predicteds.
#>       0    1
#> 0 18918 1626
#> 1   314  727
```

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