Logistic Regression

Supervised vs. Unsupervised Learning (Machine Learning Basics)

Supervised and unsupervised learning describe two ways in which machines algorithms can be set loose on a data set and expected to learn something useful from it.

The fundamental difference is that with supervised learning, the output of your algorithm is already known – just like when a student is learning from an instructor. All that needs to be done is work out the process necessary to get from your input, to your output. This is usually the case when an algorithm is being “taught” from a training data set. If the algorithms are coming up with results which are widely different from those which the training data says should be expected, the instructor can step in to guide them back to the right path.

In unsupervised learning, there is no training data set and outcomes are unknown. Essentially the model goes into the problem blind. Incredible as it seems, unsupervised machine learning is the ability to solve complex problems using just the input data. No reference data at all.

Classification vs. Clustering

In the terminology of machine learning, classification is considered an instance of supervised learning, i.e. learning where a training set of correctly identified observations is available. The corresponding unsupervised procedure is known as clustering, and involves grouping data into categories based on some measure of inherent similarity or distance.

Classification vs Clustering

Criteria	Classification	Clustering
Prior Knowledge of classes	Yes	No
Use case	Classify new sample into known classes	Suggest groups based on patterns in data
Algorithms	Decision Trees, Bayesian classifiers	K-means, Expectation Maximization
Data Needs	Labeled samples from a set of classes	Unlabeled samples

Figure 1:

In machine learning and statistics, classification is the problem of identifying to which of a set of categories (sub-populations) a new observation belongs, on the basis of a training set of data containing observations (or instances) whose category membership is known. An example would be assigning a given email into “spam” or “non-spam” classes or assigning a diagnosis to a given patient as described by observed characteristics of the patient (gender, blood pressure, presence or absence of certain symptoms, etc.).

An algorithm that implements classification, especially in a concrete implementation, is known as a classifier. The term “classifier” sometimes also refers to the mathematical function, implemented by a classification algorithm, that maps input data to a category.

Logistic Regression is one type of Classification Models

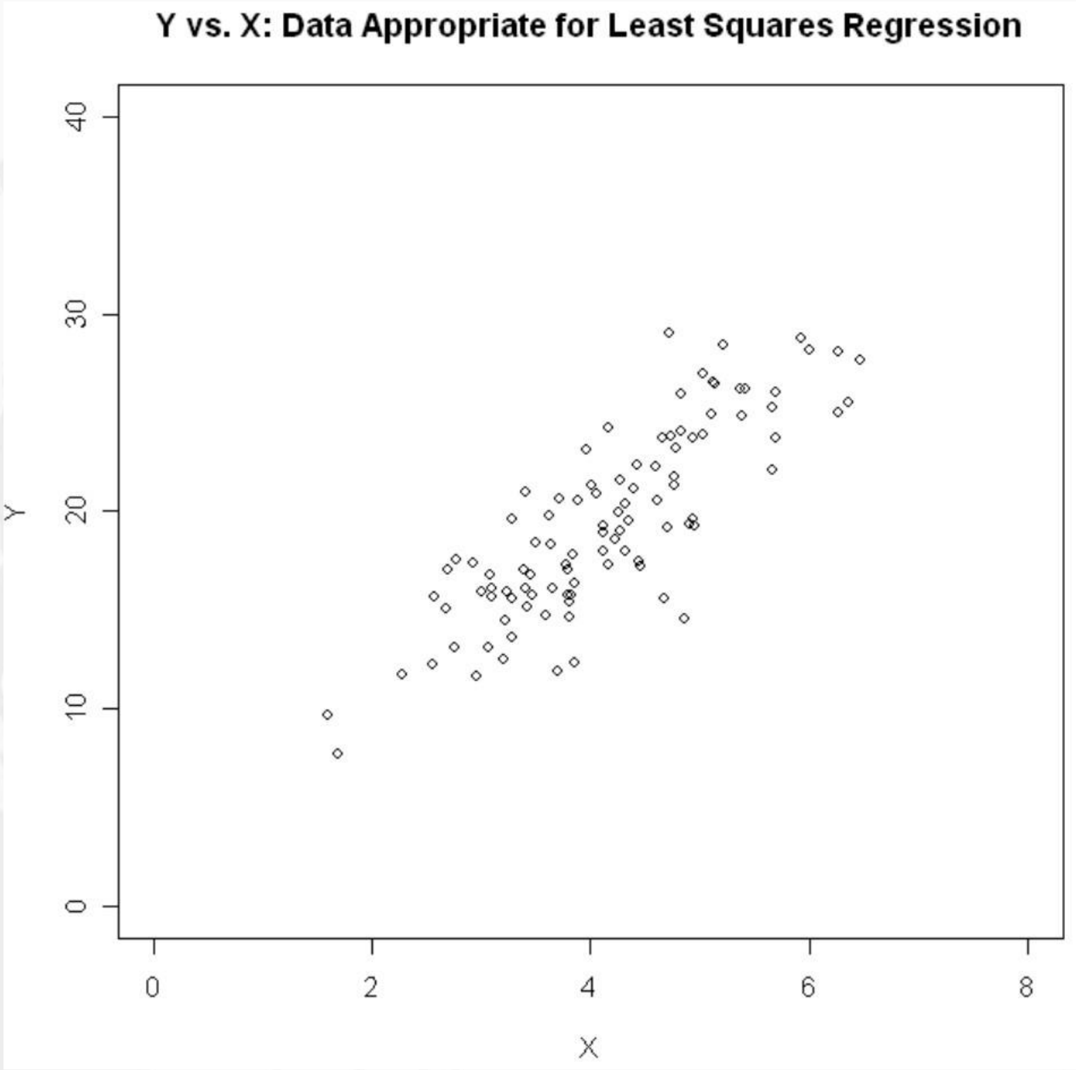
https://www.youtube.com/watch?v=zAULhNrnuL4

Why Regular Regression Does NOT Work

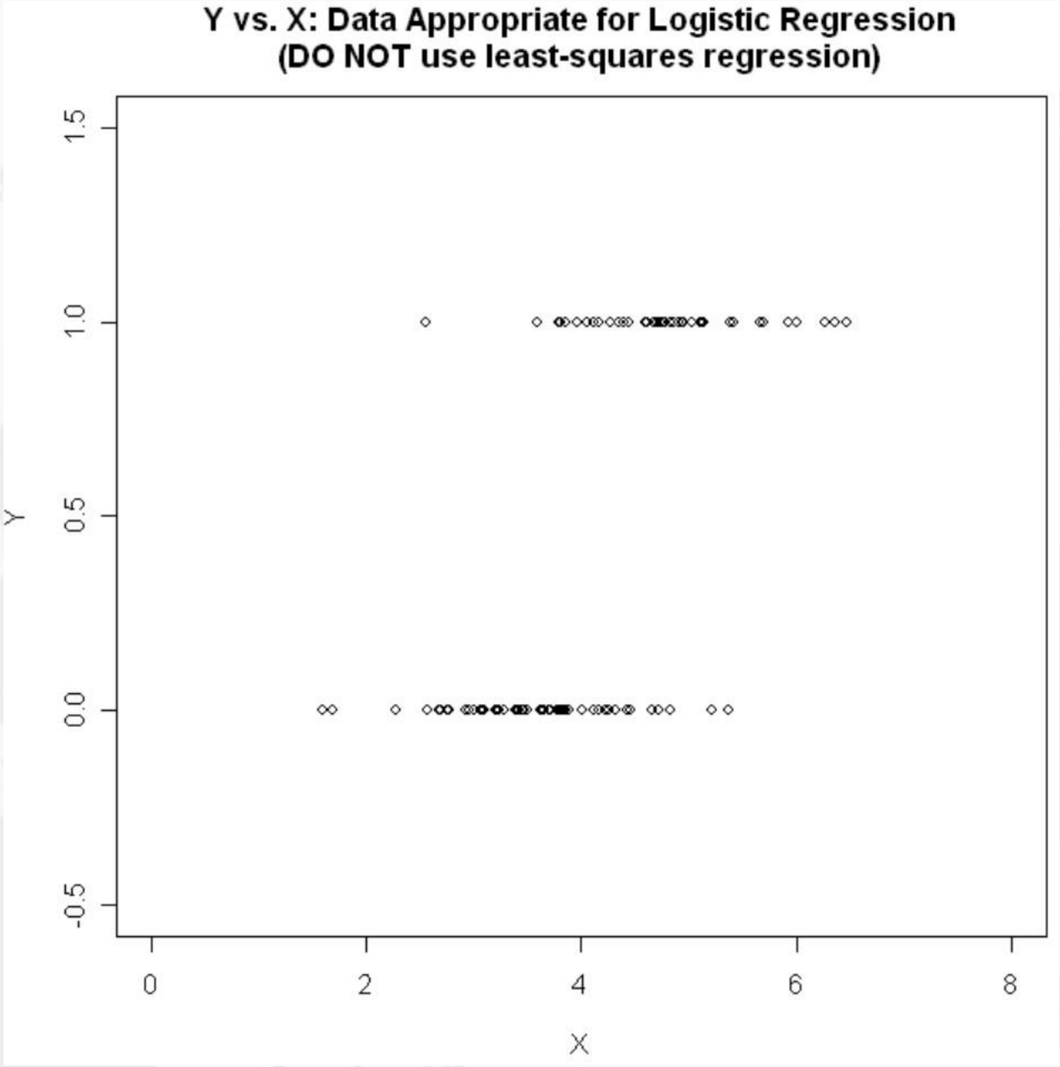
Recall that in least-squares regression, we model the Y-variable as a linear function of the X-variables plus a random error that is assumed to have a normal distribution. Then, if you use regular least-squares regression when you have a binary dependent variable (and should be using logistic regression) you are violating the least-squares requirement that the regression errors have a normal distribution.

When the assumptions that underlie the least-squares regression model are violated, you can no longer rely on the statistical inference (e.g., which regression coefficients are significant) or predictions that are made based on the least-squares model.

The first figure shows the kind of data that is appropriate for regular least-squares regression:



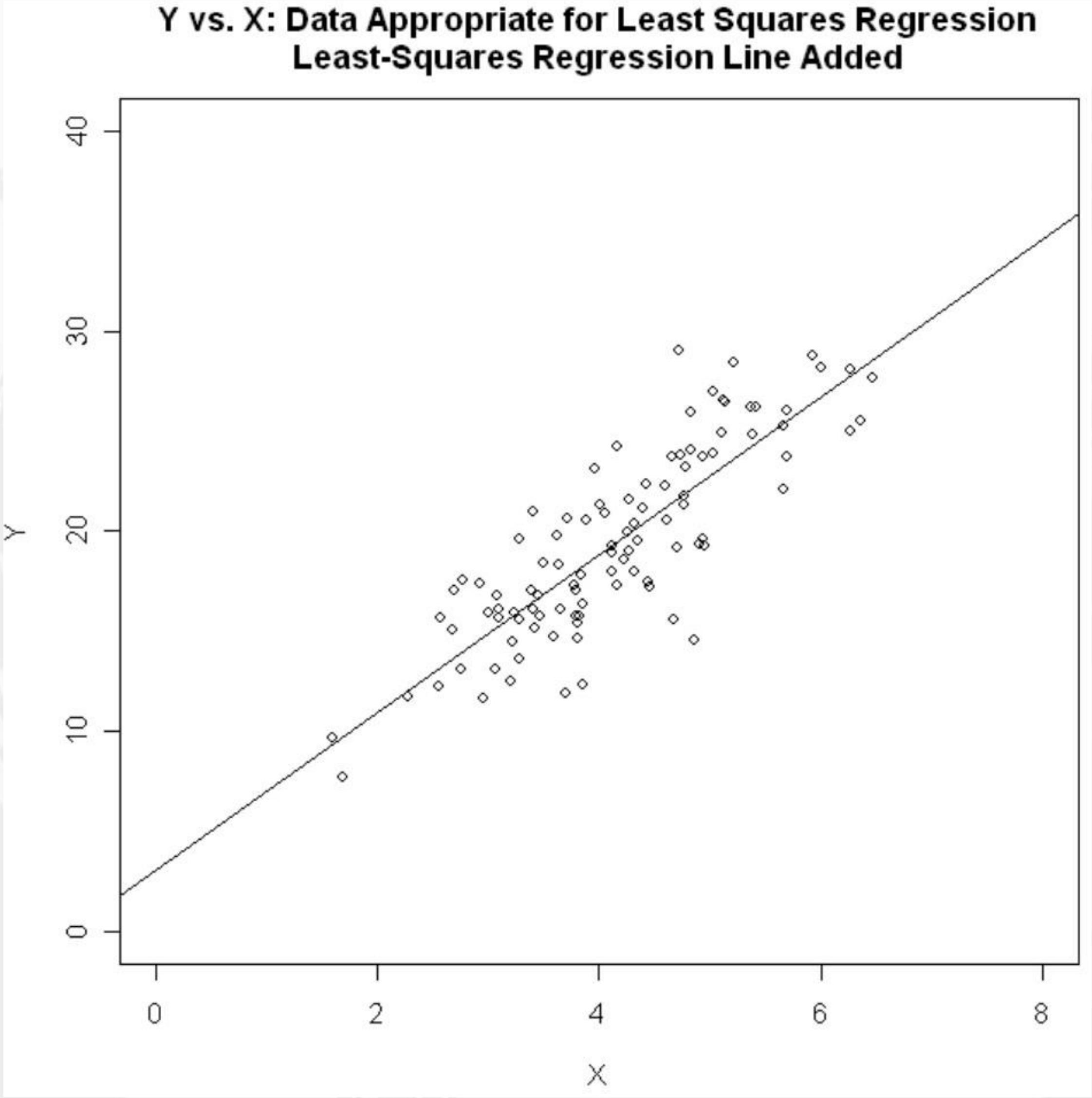
In this figure, you can see that the Y-variable takes on continuous values.The figure below shows data that is appropriate for logistic regression:



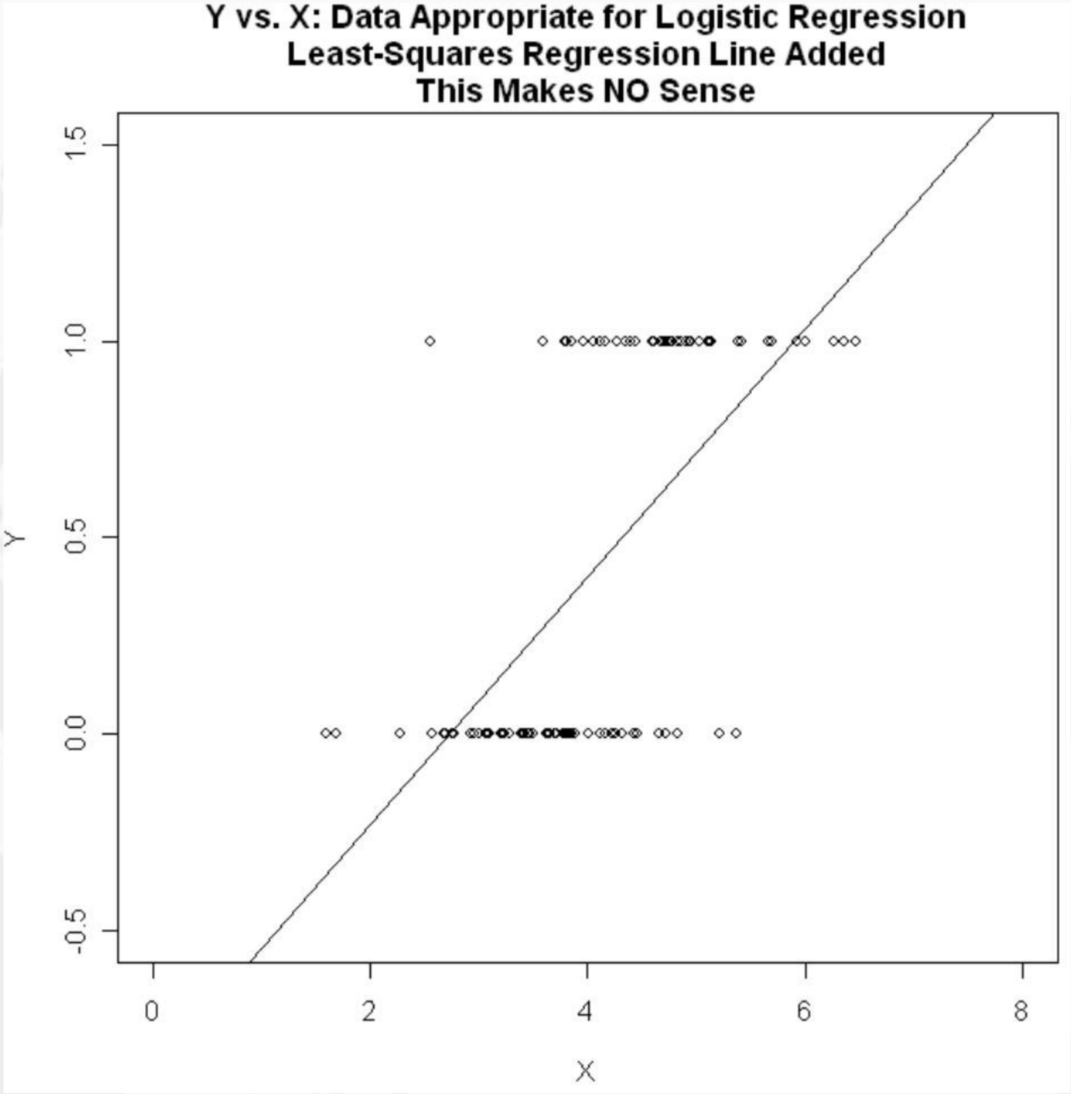
In this figure, you can see that the Y-variable only takes on two values, 0 and 1. This means that the data appear to be on two horizontal parallel lines, one at 0 and the other at 1. If you look carefully, you can see that the probability that Y is 1 increases as the value of X increases.

You can also see by looking at this picture that the equation above for the least-squares regression must give silly predictions for Y when Y takes on only binary values. The equation is linear. For any regression coefficient that is positive, increasing the corresponding X value will cause the prediction for Y to increase. You can make the predicted value of Y as large as you want just by moving the X value far enough. Thus, there will be X values for which the predicted Y value will far exceed 1. Similarly, there will be other X values for which the predicted Y value will negative and far below 0. Such predictions make no sense when the only values that the Y-variable can take on are 0and 1.

To show this, I have added the least squares regression line to the two figures shown above. Here is the first one which was for data that is appropriate for least-squares regression.

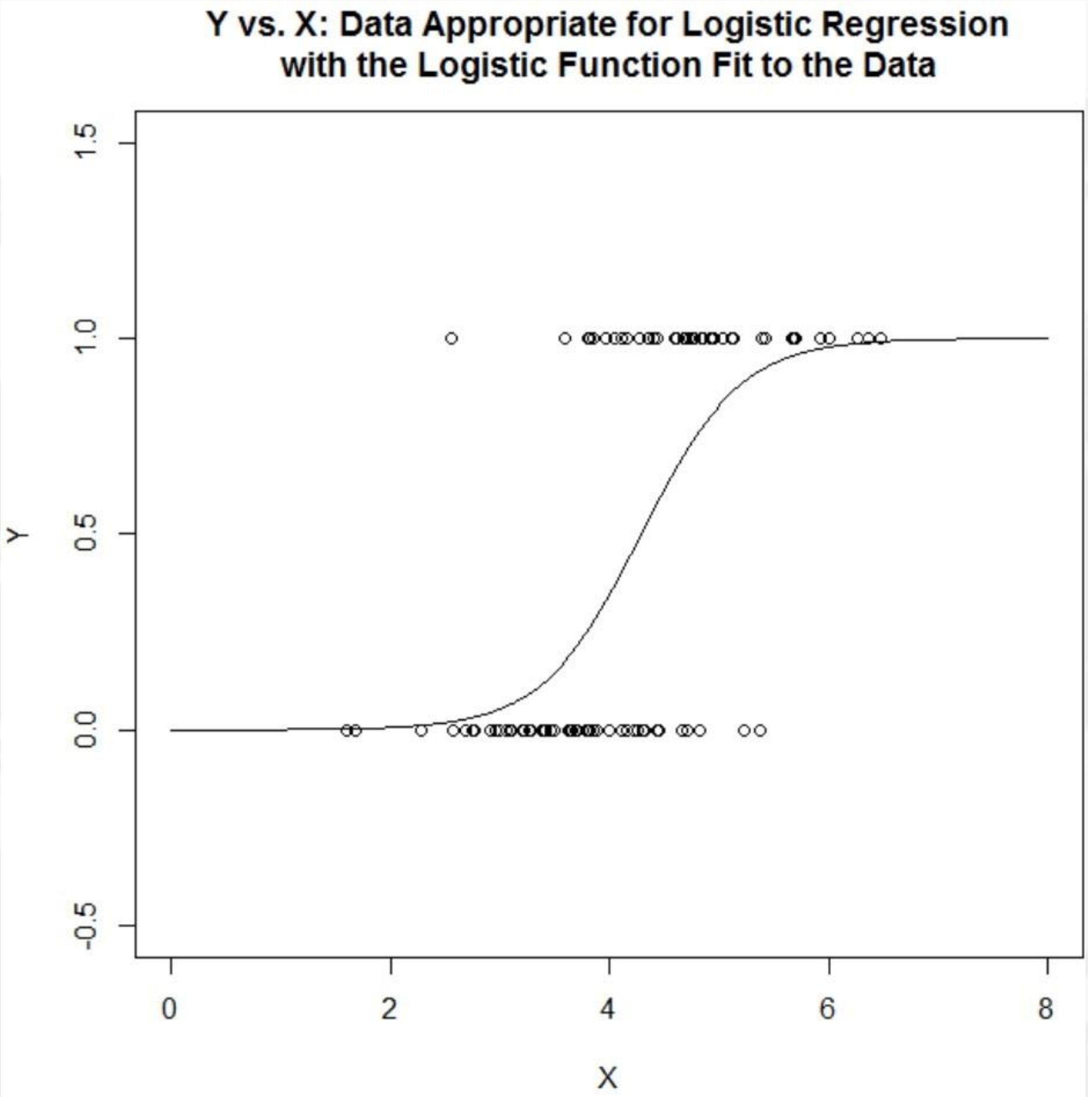


For this first figure, the regression line makes perfect sense and gives very reasonable predictions. Next, the figure for the data with the binary Y-variable is shown.

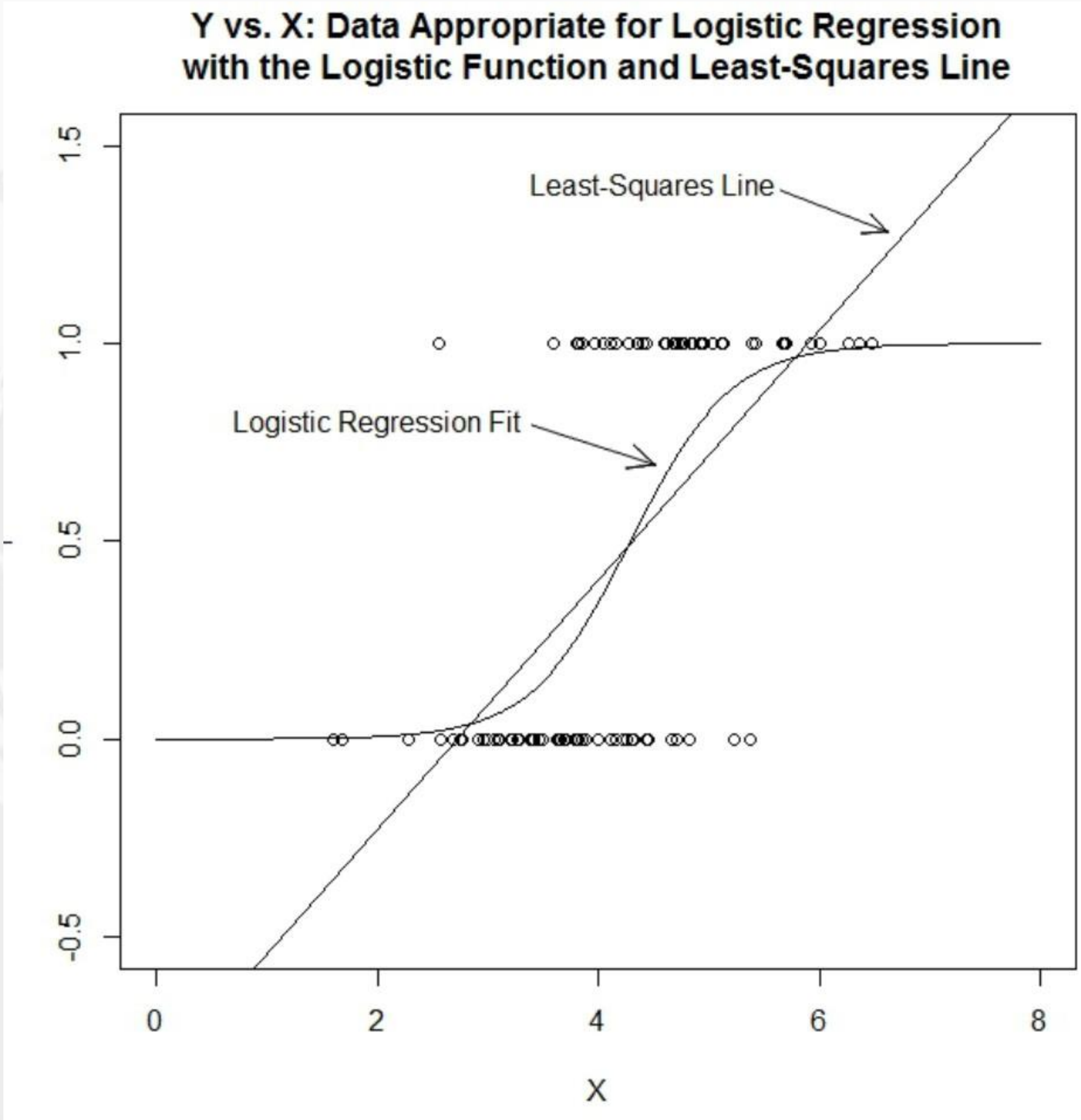


As you can see, the least-squares regression line gives predictions that make no sense. For example, for an X value of 8, the least-square regression line predicts that Y will be above 1.5. But Y can only take on values of 0 and 1.

So now I will show you in a graph what the logistic regression equation is doing.



In this figure, the smooth s-shaped trace shows the logistic function that is fit to the binary data. This function is an estimate of the probability that Y is one. As you can see, the probability that Y is 1 is very small on the left hand side of the figure. It increases through the middle of the figure and is nearly 1 on the right hand side of the figure. Just to contrast the logistic regression fit with the regular least-squares regression line, I will now add the least-squares line to the figure.



This figure clearly shows how silly the least-squares line is for this binary data and how well the logistic curve estimates the probability that the dependent Y variable is 1.

Odds Ratio

Odds are the number of times success occurred compared to the number of times failure occurred.

$Odds(Y = 1) = Pr(Y = 1)/Pr(Y = 0)$

$Pr(success) = successes/trials$

$Odds(success) = successes/failures = Pr(success)/Pr(failure)$

Log Odds

$log(Odds(Y = 1)) = log(Pr(Y = 1)/Pr(Y = 0))$

Logistic Regression Formula

$log(Pr(Y = 1)/Pr(Y = 0)) = a_0 + a_1x_1 + a_2x_2 + a_3x_3$

What is False Positive in Binary Classification Problem?

		Reality: True	Reality: False
Measured / Perceived	True	Correct ☺	Type I False Positive
	False	Type II False Negative	Correct ☺

Test	Disease: Present	Disease: Absent
Positive	TP	FP
Negative	FN	TN

TP = (Sensitivity)(Pretest probability)
FP = (1−Specificity)(1−Pretest probability)
FN = (1−Sensitivity)(Pretest probability)
TN = (Specificity)(1−Pretest probability)

$$\textit{Sensitivity} = \frac{\textit{Number of diseased patients with positive test}}{\textit{Number of diseased patients}} = \frac{TP}{TP + FN}$$

$$\textit{Specificity} = \frac{\textit{Number of nondiseased patients with negative test}}{\textit{Number of nondiseased patients}} = \frac{TN}{TN + FP}$$

$$\begin{aligned}\textit{Posttest probability after positive test} &= \textit{Probability of disease if test positive} = \frac{TP}{TP + FP} \\ &= \frac{\text{(Sensitivity)(Pretest probability)}}{\text{(Sensitivity)(Pretest probability)} + \text{(1−Specificity)(1−Pretest probability)}}\end{aligned}$$

Source: McPhee SJ, Papadakis MA: *Current Medical Diagnosis and Treatment 2011*, 50th Edition: http://www.accessmedicine.com

ROC Curve for Model Selection in Binary Classification

Receiver Operating Characteristic curve (or ROC curve). It is a plot of the true positive rate against the false positive rate for the different possible cutpoints of a binary classifier.

In a Receiver Operating Characteristic (ROC) curve the true positive rate (Sensitivity) is plotted in function of the false positive rate (100-Specificity) for different cut-off points. Each point on the ROC curve represents a sensitivity/specificity pair corresponding to a particular decision threshold. A test with perfect discrimination (no overlap in the two distributions) has a ROC curve that passes through the upper left corner (0% false positive and 100% true positive). Therefore the closer the ROC curve is to the upper left corner, the higher the overall accuracy of the test.

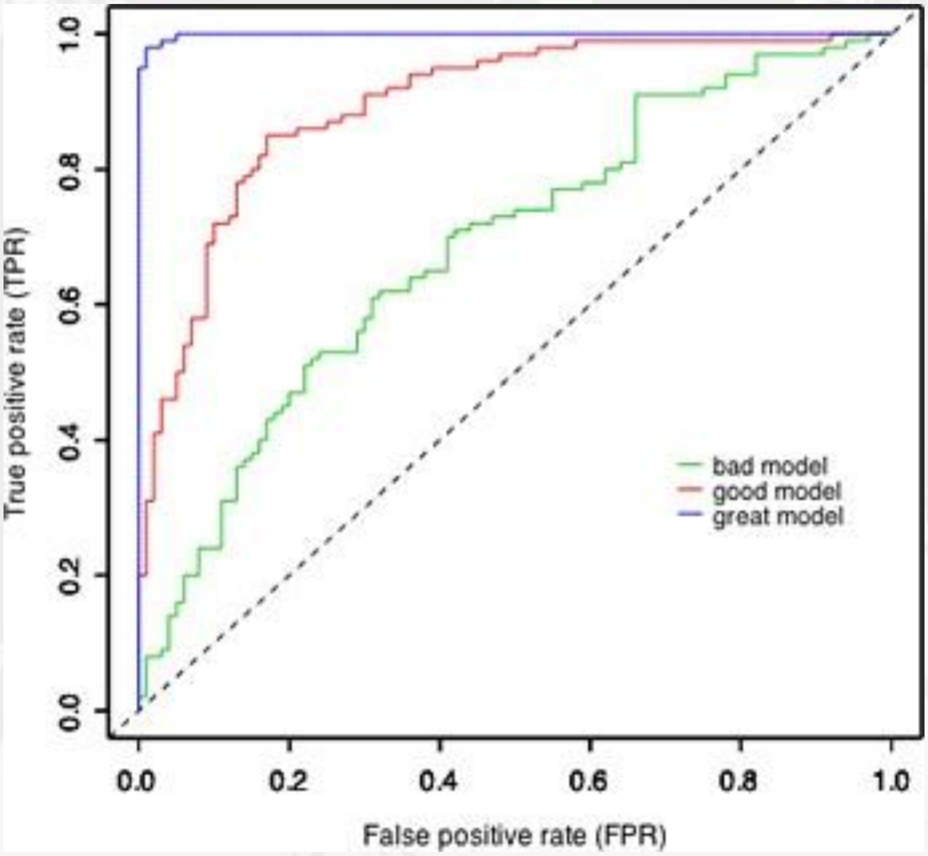
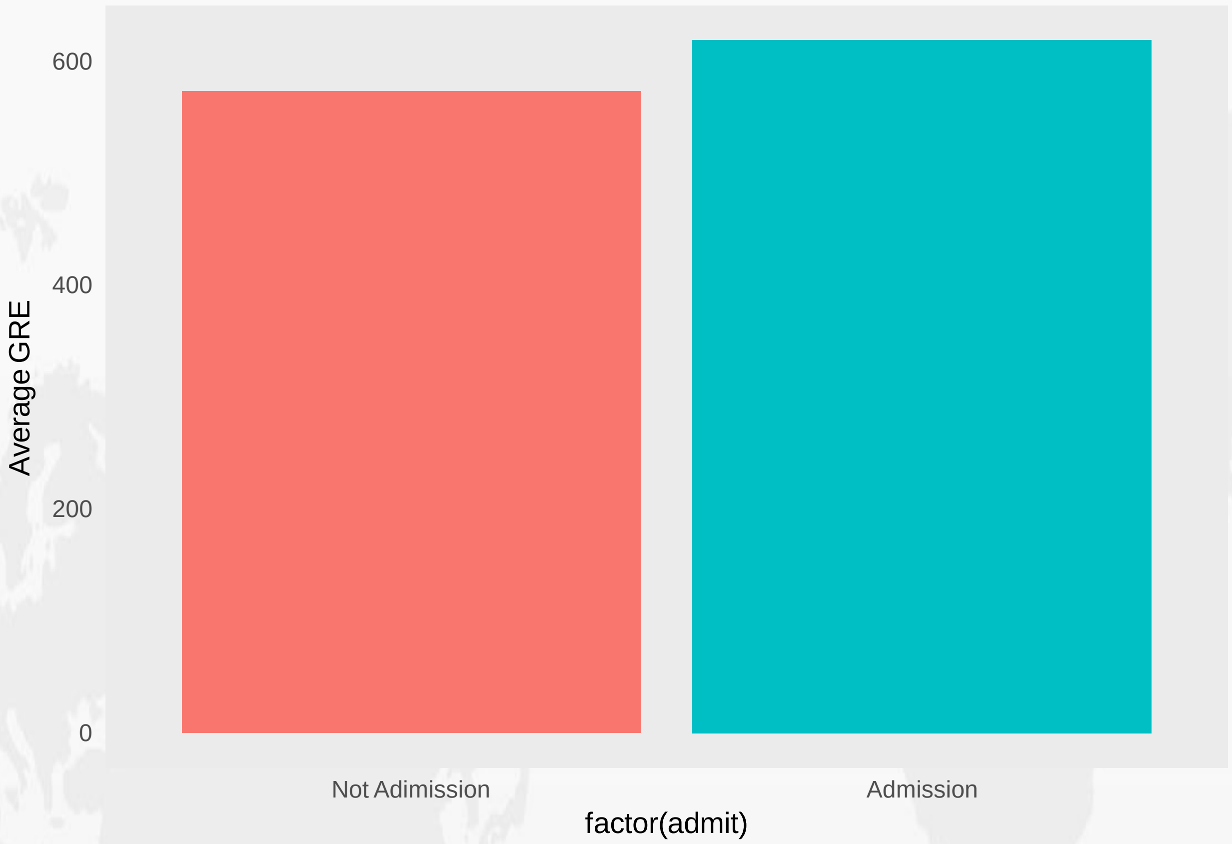


Figure 2:

R Example

```
binary <- read.csv("https://stats.idre.ucla.edu/stat/data/binary.csv")

head(binary)
##     admit gre  gpa  rank
## 1   0     380  3.61 3
## 2   1     660  3.67 3
## 3   1     800  4.00 1
## 4   1     640  3.19 4
## 5   0     520  2.93 4
## 6   1     760  3.00 2
```

```
str(binary)

##   'data.frame':         400 obs. of 4 variables:
##    $ admit :    int      0 1 1 1 0 1 1 0 1 0 ...
##    $ gre :       int      380 660 800 640 520 760 560 400 540 700 ...
##    $ gpa :       num   3.61 3.67 4 3.19 2.93 3 2.98 3.08 3.39 3.92 ...
##    $ rank :      int      3 3 1 4 4 2 1 2 3 2 ...

# summary(binary)
##   convert rank and admit to a factor
##   since they are not numeric values
binary$rank  <-  factor(binary$rank)
binary$admit  <-  factor(binary$admit)

str(binary)
##   'data.frame':      400 obs. of 4 variables:
##    $ admit :    Factor   w/ 2  levels   "0","1":    1 2 2 2 1 2 2 1 2 1 ...
##    $ gre :       int        380 660 800 640 520 760 560 400 540 700 ...
##    $ gpa :       num      3.61 3.67 4 3.19 2.93 3 2.98 3.08 3.39 3.92 ...
##    $ rank :      Factor    w/ 4  levels   "1","2","3","4": 3 3 1 4 4 2 1 2 3 2 ...

############################################
####### Explore and Visualize Data #######
############################################

require(dplyr)
##   Loading required package: dplyr
##
##   Attaching package: 'dplyr'
##   The following objects are masked from 'package:stats':
##
##   filter, lag
##   The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

require(ggplot2)
##   Loading required package: ggplot2

####   Admit vs. GRE
binary %>%
   group_by(admit) %>%
   summarise(gre = mean(gre))
## #    A tibble: 2 x 2
##       admit      gre
##       <fctr>     <dbl>
## 1     0           573.1868
## 2     1           618.8976

ggplot(binary, aes(x = factor(admit), y=gre)) +
   geom_bar(stat = "summary", fun.y = mean, aes(fill = factor(admit))) +
   ylab("Average GRE") +
   scale_x_discrete(label = c("0" = "Not Adimission", "1" = "Admission")) +
   theme(legend.position = "none")
```

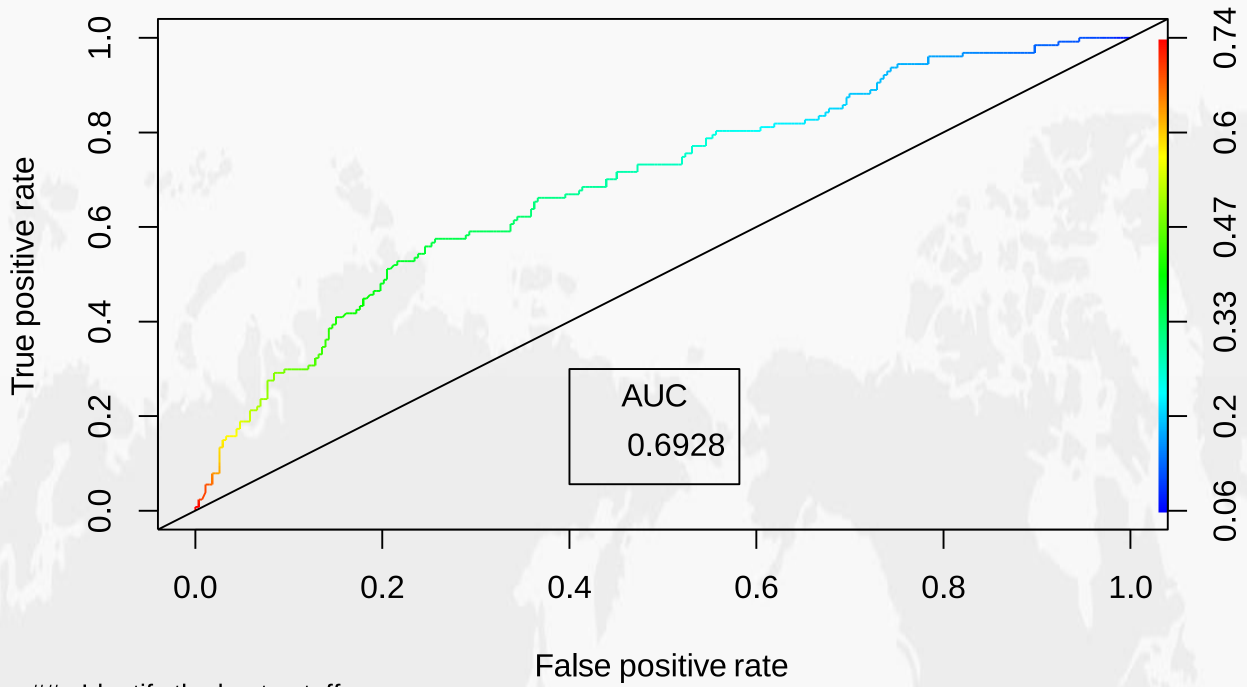


 # Average GRE is higher for students who have an offer.

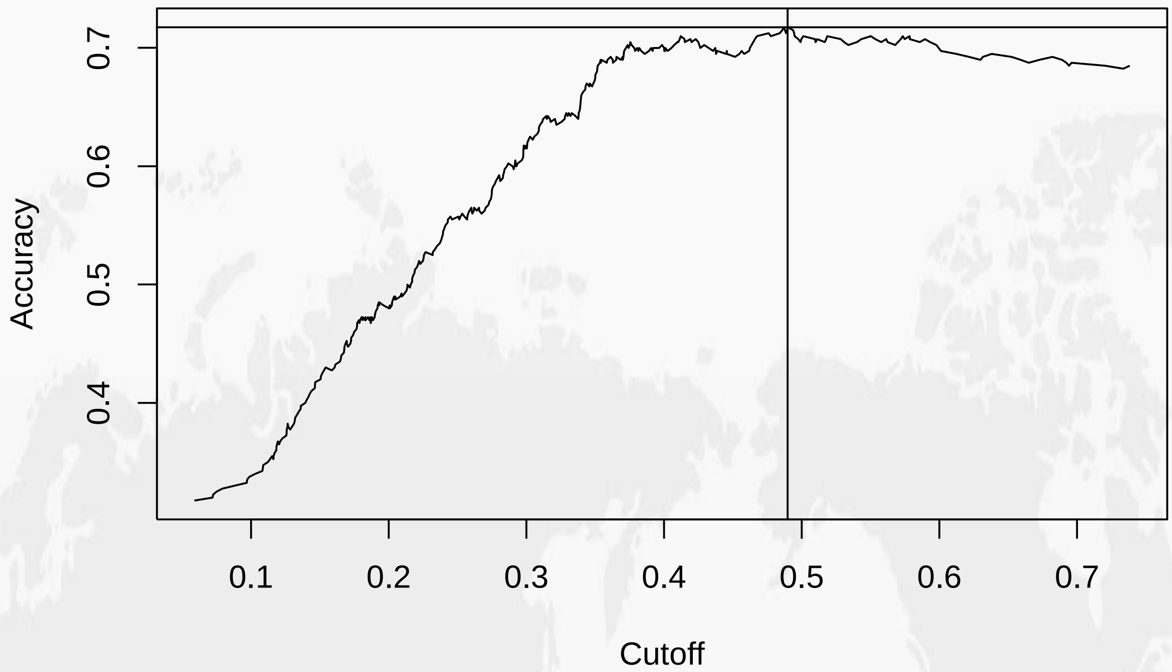
```
## Logistic Regression
model <- glm(admit ~., data = binary, family = "binomial")
summary(model)
##
## Call:
## glm(formula = admit ~ ., family = "binomial", data = binary)
##
## Deviance Residuals:
## Min      1Q       Median   3Q      Max
## -1.6268  -0.8662  -0.6388  1.1490  2.0790
##
## Coefficients:
##              Estimate   Std. Error  z value  Pr(>|z|)
## (Intercept)  -3.989979  1.139951    -3.500   0.000465 ***
## gre           0.002264  0.001094     2.070   0.038465 *
## gpa           0.804038  0.331819     2.423   0.015388 *
## rank2        -0.675443  0.316490    -2.134   0.032829 *
## rank3        -1.340204  0.345306    -3.881   0.000104 ***
## rank4        -1.551464  0.417832    -3.713   0.000205 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 499.98 on 399 degrees of freedom
## Residual deviance: 458.52 on 394 degrees of freedom
## AIC: 470.52
##
## Number of Fisher Scoring iterations: 4
## Deviance residuals: a measure of model fit.
## Coefficients interpretation:
## The log odds of admission increases by 0.002 when gre increase in 1 unit;
## The log odds of admission increases by 0.804 when gpa increase in 1 unit;
## Having attended an institution with rank of 2 versus an instituion with rank of 1,
## changes the log odds of admission by -0.675;
## Having attended an institution with rank of 3 versus an institution with rank of 1,
## changes the log odds of admission by -1.34;
## Having attended an institution with rank of 4 versus an institution with rank of 1,
## changes the log odds of admission by -1.551;

## odds ratio
OR <- exp(coef(model))
OR
## (Intercept)  gre        gpa        rank2      rank3      rank4
## 0.0185001    1.0022670  2.2345448  0.5089310  0.2617923  0.2119375
## OR interpretation:
## one unit increase in gre, the odds of being admitted (versus not being admitted) increase by a factor of 1.0022670
## one unit increase in gpa, the odds of being admitted increase by a factor of 2.234
## rank 2 school versus rank 1 school,
## the odds of being admitted increase by a factor of 0.5089
## rank 3 school versus rank 1 school,
## the odds of being admitted increase by a factor of 0.2618
## rank 4 school versus rank 1 school,
## the odds of being admitted increase by a factor of 0.2119

## Misclassification Rate
pred <- predict(model, newdata = binary, type = "response")
## If 0.5 as cutoff(we will change the cutoff later)
pred2 <- ifelse(pred > 0.5, 1, 0)
## if pred number is > 0.5, then assign class 1, otherwise assign the class 0
accuracy <- table(pred2, binary$admit)
## 2X2 table of the accuracy like the true positive vs. false positive 2X2 table
accuracy
##
## pred2  0    1
## 0      254  97
## 1      19   30
```

```
##   calculate the error rate (false positive + false negative)
1 - sum(diag(accuracy))/sum(accuracy)
##   [1] 0.29
##   Model Performance Evaluation
##   ROC Curve
##   We are concerned about the area under the ROC curve (AUROC)
##   The metric ranges from 0.5 to 1

require("ROCR")
##   Loading required package: ROCR
##   Loading required package: gplots
##
##   Attaching package: 'gplots'
##   The following object is masked from 'package:stats':
##
##   lowess

pred3 <- prediction(pred, binary$admit)
## Plot ROC using TPR and FPR
roc <- performance(pred3, "tpr", "fpr")
plot(roc,colorize = T)
abline(0, 1)

## AUC (area under ROC) for comparing models
## calculate the AUC
auc <- performance(pred3, 'auc')
auc <- slot(auc, 'y.values')[[1]]
## add the AUC to the plot
legend(0.4, 0.3, round(auc, 4), title = "AUC", cex = 1)
```




```
##   Identify the best cutoff
##   ACC(Accuracy): True Positive + True Negative
eval <- performance(pred3, "acc")
plot(eval)
max <- which.max(slot(eval, "y.values")[[1]])
acc <- max(slot(eval, "y.values")[[1]])

##   calculate the maximum in the ACC and choose out best cutoff
cutoff <- slot(eval, "x.values")[[1]][max]
cutoff
##   271 Identify the best cutoff
##   0.4899411

##   add the cutoff line to the ACC plot
abline(h = acc, v = cutoff)
```




```
## use the best cutoff instead of 0.5 to re-classify the outcome
cutoff
## 271
## 0.4899411

pred_best <- ifelse(pred > cutoff, 1, 0)
## 2X2 accuracy table
accuracy <- table(pred_best, binary$admit)
accuracy
##
## pred_best   0    1
## 0         252   93
## 1          21   34

## error rate (false positive + false negative)
1 - sum(diag(accuracy))/sum(accuracy)
## [1] 0.285
```

R Coding Style

Coding style is very important in the real world to make sure your code is readable and reproducible.. You can easily distinguish a coder is a profession or not simply based on their naming and spacing. Each company may have its own style guide, here I will use Google one as an example.

https://google.github.io/styleguide/Rguide.xml

Remember here, there is no right or wrong answer, as long as it is consistent and readable.

1. "<-" vs. "=".
2. File name, variable name and function name should be different naming style.

- file name: predict_ad_revenue.R
- variable name: avgClicks
- function name: CalculateAvgClicks

3. Spacing Good example:

```
###   Good Example
total <- sum(x[, 1])

###   Bad Example (space after comma)
total <- sum(x[,1])
total <- sum(x[ ,1])

###   Good Example
if (condition = TRUE) {
x = A
}

###   Bad Example
if (condition = TRUE){
x = A
}
if (condition = TRUE)
{
x = A

}
```