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Classification – Part 2

- Classification – Part I
  - Logistic Regression
- Classification – Part 2
  - Linear Discriminant Analysis
  - Naïve Bayes
  - Decision Trees
  - Support Vector Machines

ISL Chapter 4

ISL Chapter 8

There are hundreds of classification algorithms available *(regression too)*. But most of the them fall into the broad categories outlined here *(and in ch 4 and 8 of ISL)*.

Which one should you use? What's the best car to buy?

It depends on what you need. Model selection is art and science. The science piece is understanding how the algorithm works, and how that fits your data and analysis, how to "tune" the algorithm parameters and compare results.

The tradeoffs: Bias and Variance, and Prediction Accuracy and Interpretability, apply here. As does intuition based on case study – as we look into these algorithms, note how they treat continuous vs discrete data *(or can the data be transformed?)* – that will be a clue that can guide you…

http://topepo.github.io/caret/available-models.html

Show 238 entries

Search:

Model	*method* Value	Type	Libraries	Tuning Parameters
AdaBoost Classification Trees	adaboost	Classification	fastAdaboost	nIter, method
AdaBoost.M1	AdaBoost.M1	Classification	adabag, plyr	mfinal, maxdepth, coeflearn
Adaptive Mixture Discriminant Analysis	amdai	Classification	adaptDA	model
Adjacent Categories Probability Model for Ordinal Data	vglmAdjCat	Classification	VGAM	parallel, link
Bagged AdaBoost	AdaBag	Classification	adabag, plyr	mfinal, maxdepth
Bagged FDA using gCV Pruning	bagFDAGCV	Classification	earth	degree
Bagged Flexible Discriminant Analysis	bagFDA	Classification	earth, mda	degree, nprune
Binary Discriminant	binda	Classification	binda	lambda.freqs

Homework Review

default		balGrp			student	n	
No	9667	96.7%	1	1261	13% No	1066	85%
					Yes	195	15%
			2	3145	33% No	2408	77%
					Yes	737	23%
			3	3569	37% No	2410	68%
					Yes	1159	32%
			4	1514	16% No	904	60%
					Yes	610	40%
			5	174	2% No	61	35%
					Yes	113	65%
			6	4	0% No	1	25%
					Yes	3	75%
Yes	333	3.3%	1	0	0% No	0	0%
					Yes	0	0%
			2	2	1% No	2	100%
					Yes	0	0%
			3	24	7% No	19	79%
					Yes	5	21%
			4	130	39% No	91	70%
					Yes	39	30%
			5	159	48% No	90	57%
					Yes	69	43%
			6	18	5% No	4	22%
					Yes	14	78%

$$\mathbb{P}(A \mid B) = \frac{\mathbb{P}(A)\mathbb{P}(B \mid A)}{\mathbb{P}(B)}$$

$$\mathbb{P}(\text{default} = \text{“Yes”} \mid \text{balGrp} = 3, \text{student} = \text{“Yes”}) = \frac{(.033 * .072) * .21}{(.37 * .96 * .32) + (.033 * .07 * .21)} = .004$$

So, there's a .4% chance of default, given the balance is between (750,1.25e+03) and a student

0.05%
F72*C68) = 0.43%

Notice how P $_{\text{level 1, level 2}}$ becomes the prior for level 3

Also notice that the prior probability is

$$P(A \cap B) = P(B) * P(A \mid B) =$$

$$.03 * .07 = .002$$

Hypothesis	Prior	Likelihood	Bayes Numerator	Posterior
Default = No	0.357	0.325	0.1159	0.996
Default = Yes	0.002	0.208	0.0005	0.004
			0.1164	**1.000**

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Homework Extension

Lets assume that dfDefault is month 1, and that month 2 is a little different. The change is an increase in student defaults in balGrp 3 – from 5 to 24 (maybe the recent grad job market stalls out).

So, if we go through the same process, then we'll get an increase in posterior probability from .4% to 2%.

But is that the best projection for month 3? Should we start getting tougher on student credit? Is month 2 a trend or a deviation *(randomness)*?

Hypothesis	Prior	Likelihood	Bayes Numerator	Posterior
Default = No	0.356	0.325	0.116	0.980
Default = Yes	0.004	0.558	0.002	**0.020**
			0.118	**1.000**

```
dfDefault1 = dfDefault %>%
  dplyr::select(default, student, balance, balGrp, income) %>%
  mutate (month = 1)

dfDefault2 = dfDefault1 %>%
  filter(default == "Yes", balGrp == 3, student == "Yes") %>%
  sample_n(20, replace = T) %>%
  mutate (balance = balance + rnorm(balance, 0, 30)) %>%
  filter(balance > 750, balance <1250) %>%
  bind_rows(dfDefault1) %>%
  mutate(month = 2)

dfDefaultNew = bind_rows(dfDefault1, dfDefault2)

dfDefaultNew %>%
  filter(student == "Yes", balGrp == 3, default == "Yes", month == 2) %>%
  summarise(Tot = n())
Tot
 24

Bayes2N = dfDefault2 %>% filter(student == "Yes", balGrp == 3, default == "Yes")
%>%
  summarise(Tot = n())
Bayes2D = dfDefault2 %>% filter(student == "Yes", balGrp == 3) %>%
  summarise(Tot = n())
Bayes2N/Bayes2D
       Tot
0.0202874
```

We could also analyze ALL *(month1 + month 2)* the data *(in which case, the posterior becomes 1.2%)*

A more conservative *(and Bayesian)* approach would be to set the priors based on Month 1 posteriors. This will adjust the posterior with more weight of prior probability – based on data. This is essentially a compromise between prior probability and current data. It's also more practical because we don't always have every period we need, and even if we do, we often don't have time to sample and analyze. Also, keep in mind that we're generally projecting imaginary data – regardless of whether we're forecasting, planning or validating.

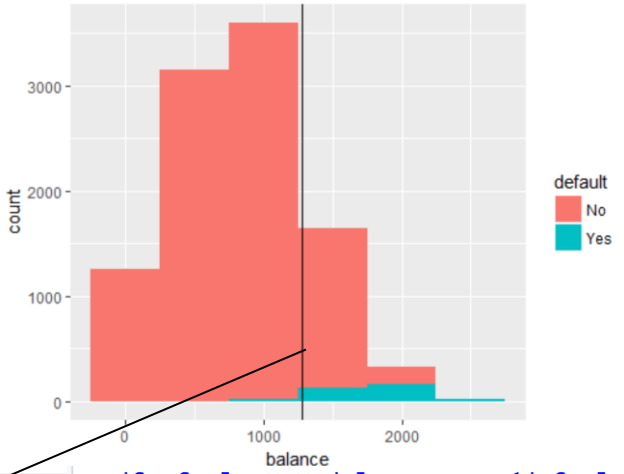
Hypothesis	Prior	Likelihood	Bayes Numerator	Posterior
Default = No	0.996	0.325	0.323	0.993
Default = Yes	0.004	0.558	0.002	**0.007**
			0.326	**1.000**

Note that .7% is a compromise between mo 1 (.4%), and mo2 (2%).

As we move into Bayesian analysis is the 2nd half, you'll see that we can adjust and weigh priors based on evidence and credibility, also based on expert knowledge and judgment.

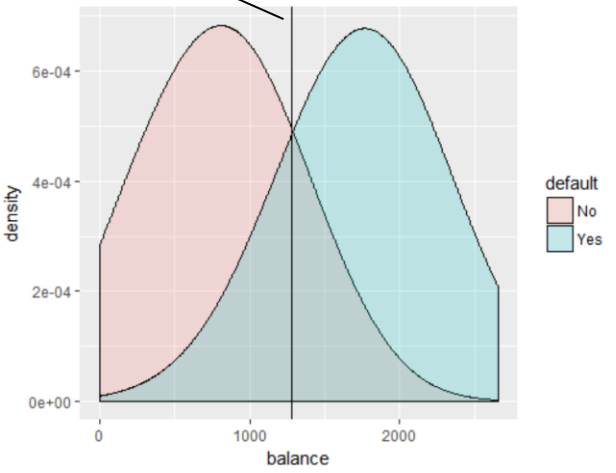
Linear Discriminant Analysis

```
library(tidyverse)
library(MASS)
library(ISLR)

dfDefault <- Default

p <- ggplot(dfDefault, aes(balance, fill = default)) +
  geom_histogram(binwidth = 500)
p

pl1 <- ggplot(dfDefault, aes(balance, fill = default))
pl1 <- pl1 + geom_density(alpha = 0.2, adjust = 5 )
pl1

lda.fit <- lda(default ~ balance, data = dfDefault)
lda.fit

lda.pred <- predict(lda.fit)

pl1 <- pl1 + geom_vline(xintercept = mean(lda.fit$means) )
pl1
p <- p + geom_vline(xintercept = mean(lda.fit$means) )
p
```



$$\frac{u_1 + u_2}{2}$$

```
> dfDefault %>% dplyr::count(default)
# A tibble: 2 x 2
  default     n
   <fctr> <int>
1      No  9667
2     Yes   333
```

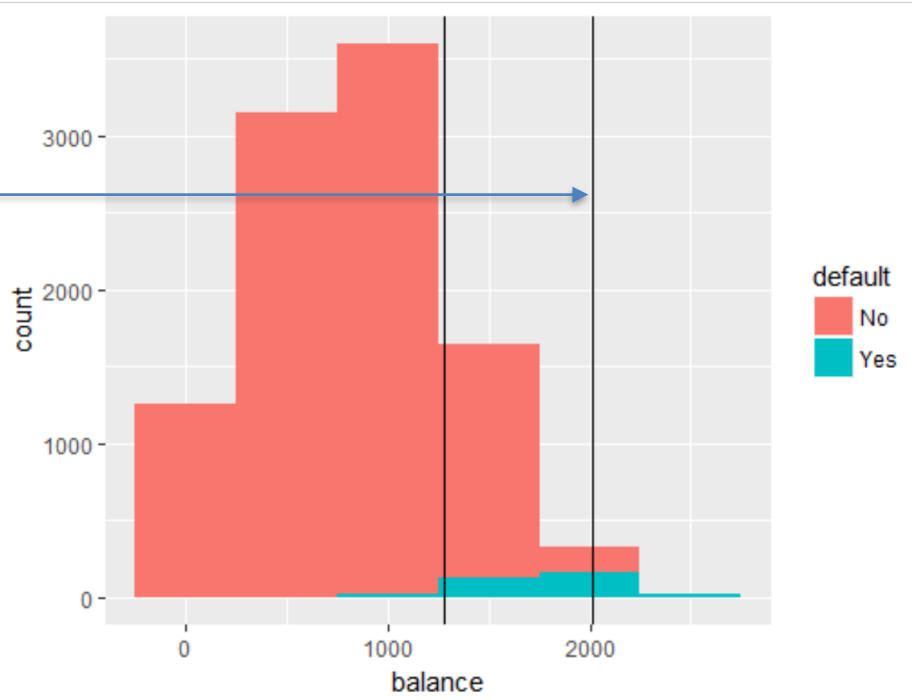


# get **decision rule**
A <- A <- mean(lda.fit$means)
B <- log(lda.fit$prior[2]) - log(lda.fit$prior[1])
s2.k <- t(tapply(dfDefault$balance, dfDefault$default, var)) %*%
lda.fit$prior
C <- s2.k/(lda.fit$means[1] - lda.fit$means[2])
dr <- A + B * C
dr

p <- p + geom_vline(xintercept = dr)
p

```
> dr <- A + B * C
> dr
          [,1]
[1,] 2008.554
```

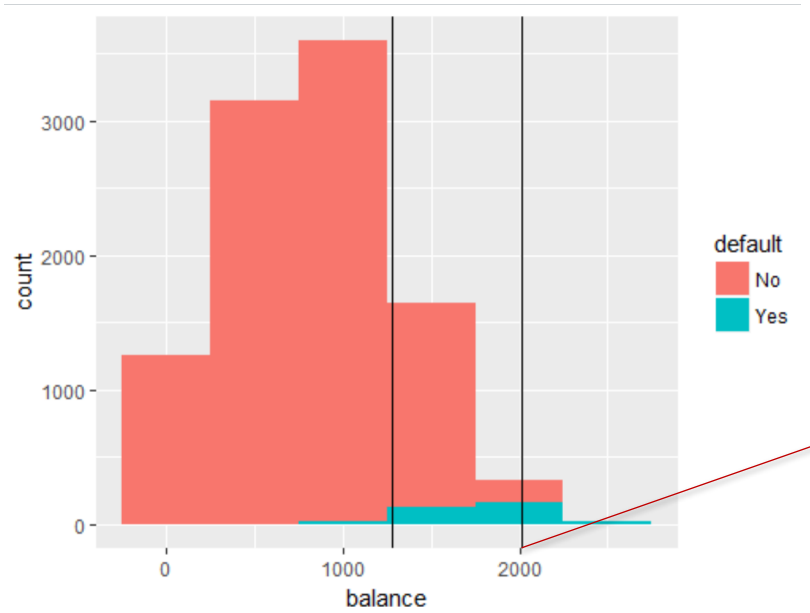
The classification boundary (decision rule) is not the average of the means.The decision rule is computed above (we're not going to cover the formula for the boundary)



The decision boundary where two log likelihood functions have the same value P(default = “Yes” | conditions) = P(default = “No” | conditions).
You can compare results by pulling the posterior for these classes:

```
firstAnalysis <- as_tibble(cbind(as.character(lda.pred$class),
                                 as.character(dfDefault$default),
                                 lda.pred$posterior))

firstAnalysis <- cbind(firstAnalysis,dplyr::select(dfDefault, student, balance, income))
```

Notice how the decision rule is implemented (2009 was the amt calculated by the dr function)



1	No	Yes	balance
92	47%	53%	2,033
93	48%	52%	2,027
94	48%	52%	2,025
95	48%	52%	2,025
96	48%	52%	2,024
97	48%	52%	2,024
98	48%	52%	2,023
99	49%	51%	2,018
100	49%	51%	2,014
101	50%	50%	2,010
102	50%	50%	2,008
103	50%	50%	2,008
104	50%	50%	2,007
105	50%	50%	2,006
106	50%	50%	2,005
107	50%	50%	2,004
108	51%	49%	1,997
109	52%	48%	1,994
110	52%	48%	1,994
111	52%	48%	1,992
112	52%	48%	1,991
113	52%	48%	1,989
114	53%	47%	1,985
115	53%	47%	1,983
116	53%	47%	1,981
117	54%	46%	1,976
118	54%	46%	1,974

```
Confusion Matrix and Statistics

          Reference
Prediction   No  Yes
       No  9643  257
       Yes   24   76

               Accuracy : 0.9719
                 95% CI : (0.9685, 0.9751)
    No Information Rate : 0.9667
    P-Value [Acc > NIR] : 0.001652

                  Kappa : 0.3409

 Mcnemar's Test P-Value : < 2.2e-16

            Sensitivity : 0.2282
            Specificity : 0.9975
         Pos Pred Value : 0.7600
         Neg Pred Value : 0.9740
             Prevalence : 0.0333
         Detection Rate : 0.0076
   Detection Prevalence : 0.0100
      Balanced Accuracy : 0.6129

       'Positive' Class : Yes
```

Review from last week:

Sensitivity (also called the **true positive rate**) measures the proportion of positives that are correctly identified. 76/(76+257) = **.22..**

Specificity (also called the **true negative rate**) measures the proportion of negatives that are correctly identified. 9643/(9643+24) = **.97…**

Prevalence = *(76+257)/(76+257+9643+257) = .03… Total Pos in Sample*

Positive Pred Value = *(sensitivity * prevalence)/((sensitivity*prevalence) + ((1-specificity)*(1-prevalence)))* **= .76** *(est % of predicted positives that were correctly predicted 76/(76+24) for rough)*

Neg Pred Value = *(specificity * (1-prevalence))/(((1-sensitivity)*prevalence) + ((specificity)*(1-prevalence)))… etc.*

lowering the threshold

```
pred[lda.pred$posterior[,2] >= 0.2] <- 'Yes'
dfPred <- data.frame(pred)
```

```
          Reference
Prediction   No  Yes
       No  9431  138
       Yes  236  195

               Accuracy : 0.9626
                 95% CI : (0.9587, 0.9662)
    No Information Rate : 0.9667
    P-Value [Acc > NIR] : 0.9886

                  Kappa : 0.4914

 Mcnemar's Test P-Value : 5.283e-07

            Sensitivity : 0.5856
            Specificity : 0.9756
         Pos Pred Value : 0.4524
         Neg Pred Value : 0.9856
             Prevalence : 0.0333
         Detection Rate : 0.0195
   Detection Prevalence : 0.0431
      Balanced Accuracy : 0.7806

       'Positive' Class : Yes
```

This doesn't change the probabilities, it just assigns a Yes to observations *(you can do this outside of the algorithm –classifiers usually give you access to the probabilities, and these values are usually updated to another analysis or process application).*

Now, you have increased Sensitivity *(proportion of positives that are correctly identified)*, but decreased Pos Pred Value (*% of predicted positives that were correctly identified).*

This should all makes sense to you – if not, go back and think it through.

All of this depends on the goals of your project.

Increasing dimensions and using a validation set:

```
dfDefault <- dfDefault %>% rownames_to_column("SampleID")
xTrain <- sample_n(dfDefault, round(nrow(dfDefault)*.6))
xTest <- dfDefault %>% anti_join(xTrain, by = "SampleID")
lda.fit <- lda(default ~ student + balance + income, xTrain)
lda.fit
```

```
          Reference
iction     No  Yes
     No  3838  118
     Yes   10   34

               Accuracy : 0.968
                 95% CI : (0.9621, 0.9732)
    No Information Rate : 0.962
    P-Value [Acc > NIR] : 0.02375

                  Kappa : 0.3356

 Mcnemar's Test P-Value : < 2e-16

            Sensitivity : 0.2237
            Specificity : 0.9974
         Pos Pred Value : 0.7727
         Neg Pred Value : 0.9702
             Prevalence : 0.0380
         Detection Rate : 0.0085
   Detection Prevalence : 0.0110
      Balanced Accuracy : 0.6105

       'Positive' Class : Yes
```

This is a more realistic approach. Remember, we never want to test an algorithm using data it's seen before – algorithms are cheaters.

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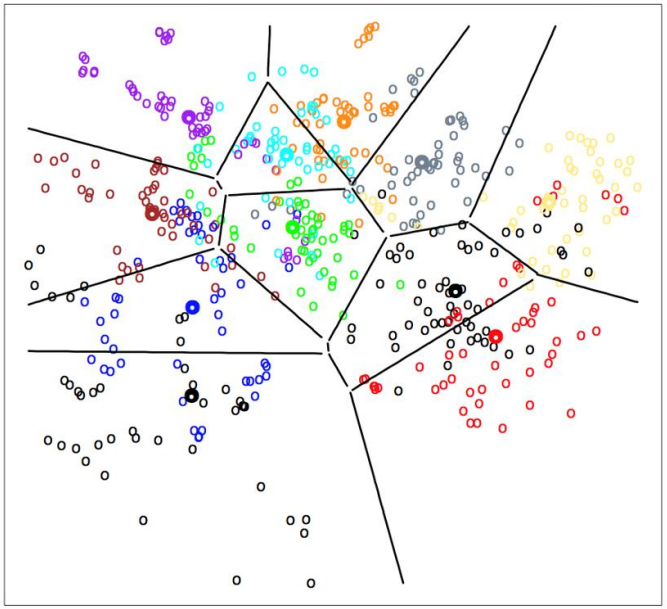
Multiclass LDA

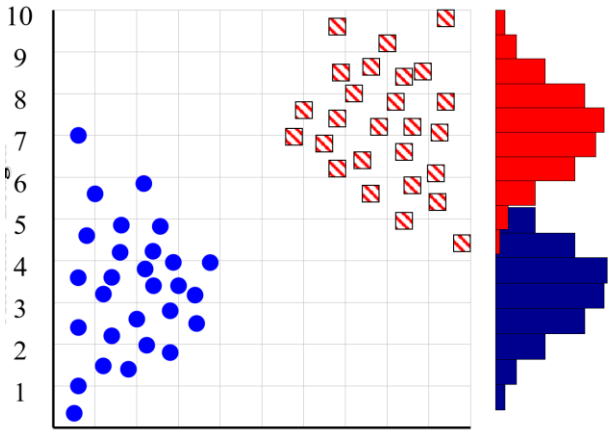


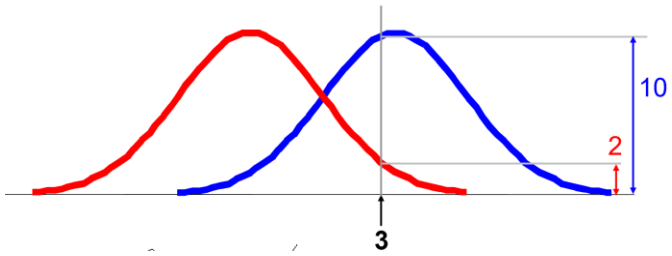
LDA is very common in complex multiclass analysis – you have more control and extensibility.

We touched on multiclass problems last week, and we may revisit.

But we're going to press on with other two-class algorithms for now.

Naïve Bayes

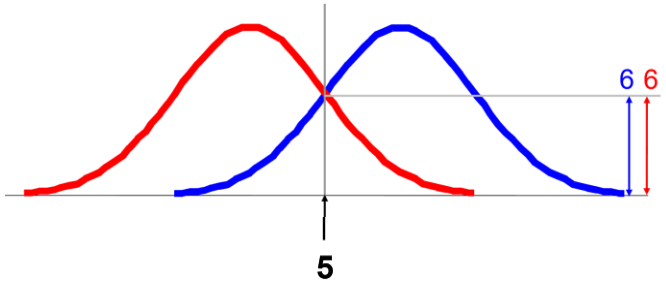




$$P(A \mid 3) = \frac{10}{(10+2)} = .833$$

$$P(B \mid 3) = \frac{2}{(10+2)} = .166$$

NB is a lot like LDA, in that both classifiers assume Gaussian within-class distributions. However, NB assumes *no correlations – i.e. NB assumes variables are independent (which is why it's naïve).*



$$P(A \mid 5) = \frac{6}{(6+6)} = .5$$

$$P(B \mid 5) = \frac{6}{(6+6)} = .5$$

Naïve Bayes

```
dfDefault <- dfDefault %>% rownames_to_column("SampleID")
xTrain <- sample_n(dfDefault, round(nrow(dfDefault)*.6))
xTest <- dfDefault %>% anti_join(xTrain, by = "SampleID")

model <- naiveBayes(default ~ student + balance +
xTest$pred <- predict(model, xTest[,-1], prob = TR

confusionMatrix((xTest$default), factor(xTest$pred
```

```
          Reference
Prediction   No  Yes
       No  3827  119
       Yes   21   33

               Accuracy : 0.965
                 95% CI : (0.9588, 0.9705)
    No Information Rate : 0.962
    P-Value [Acc > NIR] : 0.1711

                  Kappa : 0.3066

 Mcnemar's Test P-Value : 2.444e-16

            Sensitivity : 0.21711
            Specificity : 0.99454
         Pos Pred Value : 0.61111
         Neg Pred Value : 0.96984
             Prevalence : 0.03800
         Detection Rate : 0.00825
   Detection Prevalence : 0.01350
      Balanced Accuracy : 0.60582

       'Positive' Class : Yes
```

Improvement over LDA *(.19)*

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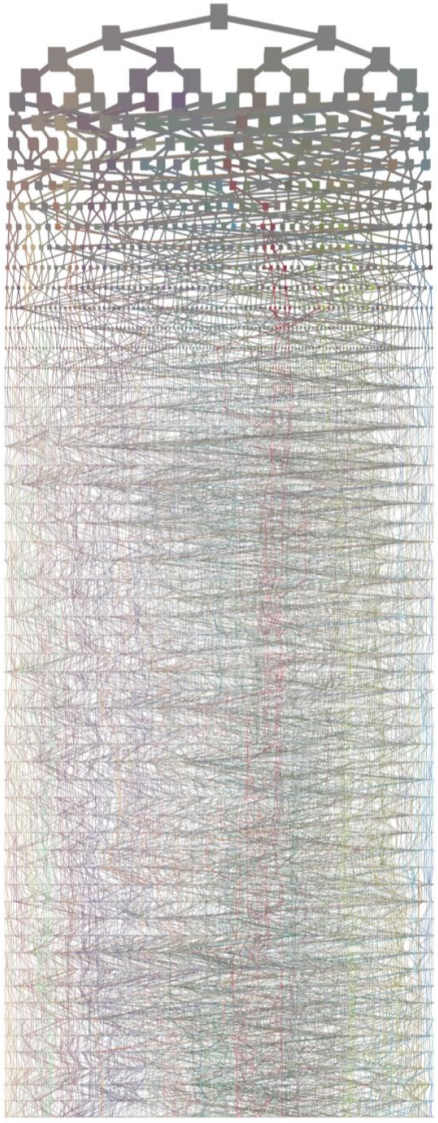
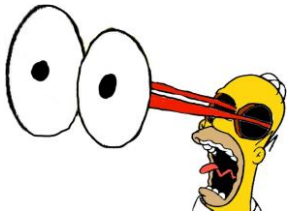
Decision Trees





We've looked at LDA and Naïve Bayes classifiers, which work by determining probability based on a likelihood of a distribution, and applying a decision rule to separate the classes.

Trees work in a very different way

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Decision Tree Algorithms

CART (Classification and Regression Trees) Algorithm
C4.5 (Quinlan 1993) and others

CART works by ***Recursive Binary Splitting*** which is a top-down, greedy approach. It is top-down because it begins at the top of the tree *(at which point all observations belong to a single region)* and then successively splits the predictor space; each split is indicated via **two new branches** further down on the tree, until we can't divide it any longer – in which case we add a leaf *(the number of leaves can be limited)*.

It is greedy because at each step of the tree-building process, **the best split is made at that particular step, rather than looking ahead** and picking a split that will lead to a better tree in some future step. Then, we;

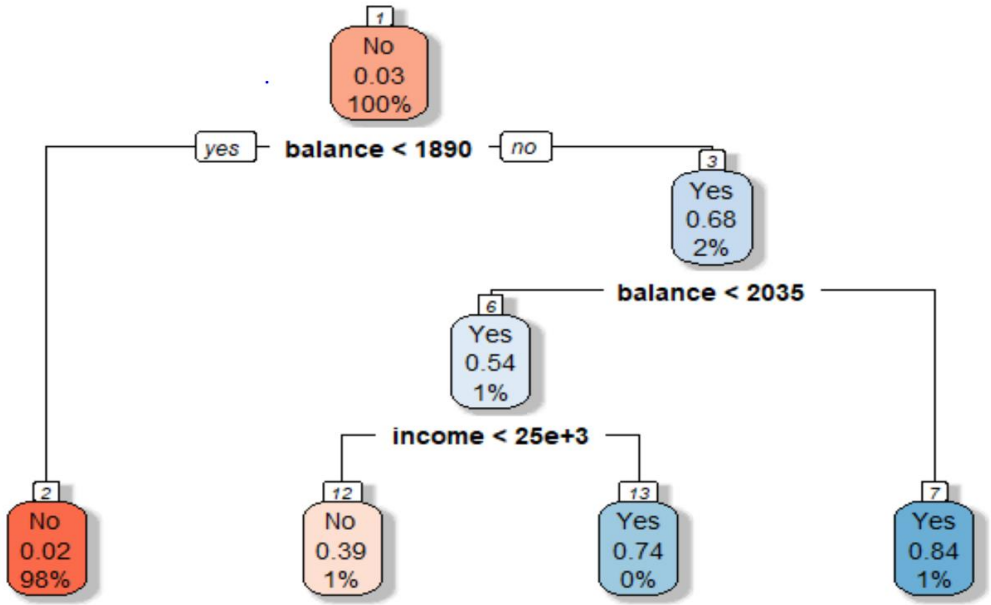
1. Apply cost complexity **pruning** to the large tree in order to obtain a sequence of best subtrees, as a function of α *(a cost function)*
2. Use K-fold ***cross-validation*** to choose α *(usually a parameter)*. That is, divide the training observations into K folds. For each k =1,...,K:.
3. Return the subtree from Step 2 that corresponds to the chosen value of α, which minimizes error.

	Result	QuoteDiff	ATPDiff
1	L	-6200	14
2	W	3500	14
3	L	-6200	75
4	L	-6200	14
5	W	3500	14
6	L	3500	-17
7	L	-6200	75
8	L	-10200	45
9	W	-500	49
10	L	3500	-17
11	L	-10200	45
12	W	3500	18

The algorithm iterates over the dimensions and selects a dimension / value combination based on a cost function, and creates a question. It then partitions the data into two groups based on that question (true or false). The best question is the one that that reduced uncertainty the most (the metric for this is called Gini impurity)

```
> fit <- rpart(Result ~ QuoteDiff + ATPDiff,
+              data=SampleData,
+              method="class")
>
> fancyRpartPlot(fit)
```

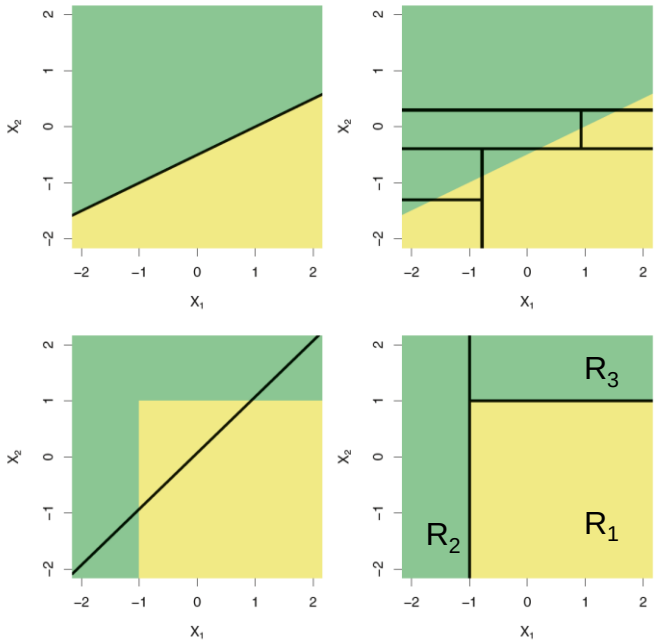
Improvement over NB *(sensitivity of .21)*




```
          Reference
Prediction   No  Yes
       No  3834  107
       Yes   14   45

               Accuracy : 0.9698
                 95% CI : (0.964, 0.9748)
    No Information Rate : 0.962
    P-Value [Acc > NIR] : 0.004692

                  Kappa : 0.4141

 Mcnemar's Test P-Value : < 2.2e-16

            Sensitivity : 0.29605
            Specificity : 0.99636
         Pos Pred Value : 0.76271
         Neg Pred Value : 0.97285
             Prevalence : 0.03800
         Detection Rate : 0.01125
   Detection Prevalence : 0.01475
      Balanced Accuracy : 0.64621

       'Positive' Class : Yes
```

Trees vs. Linear Models

Regions *(leaves)*



From the Book *(pg 315)*.

Top Row: A two-dimensional classification example in which the true decision boundary is linear, and is indicated by the shaded regions. A classical approach that assumes a linear boundary (left) will outperform a decision tree that performs splits parallel to the axes (right).

Bottom Row: Here the true decision boundary is non-linear. Here a linear model is unable to capture the true decision boundary (left), whereas a decision tree is successful (right).

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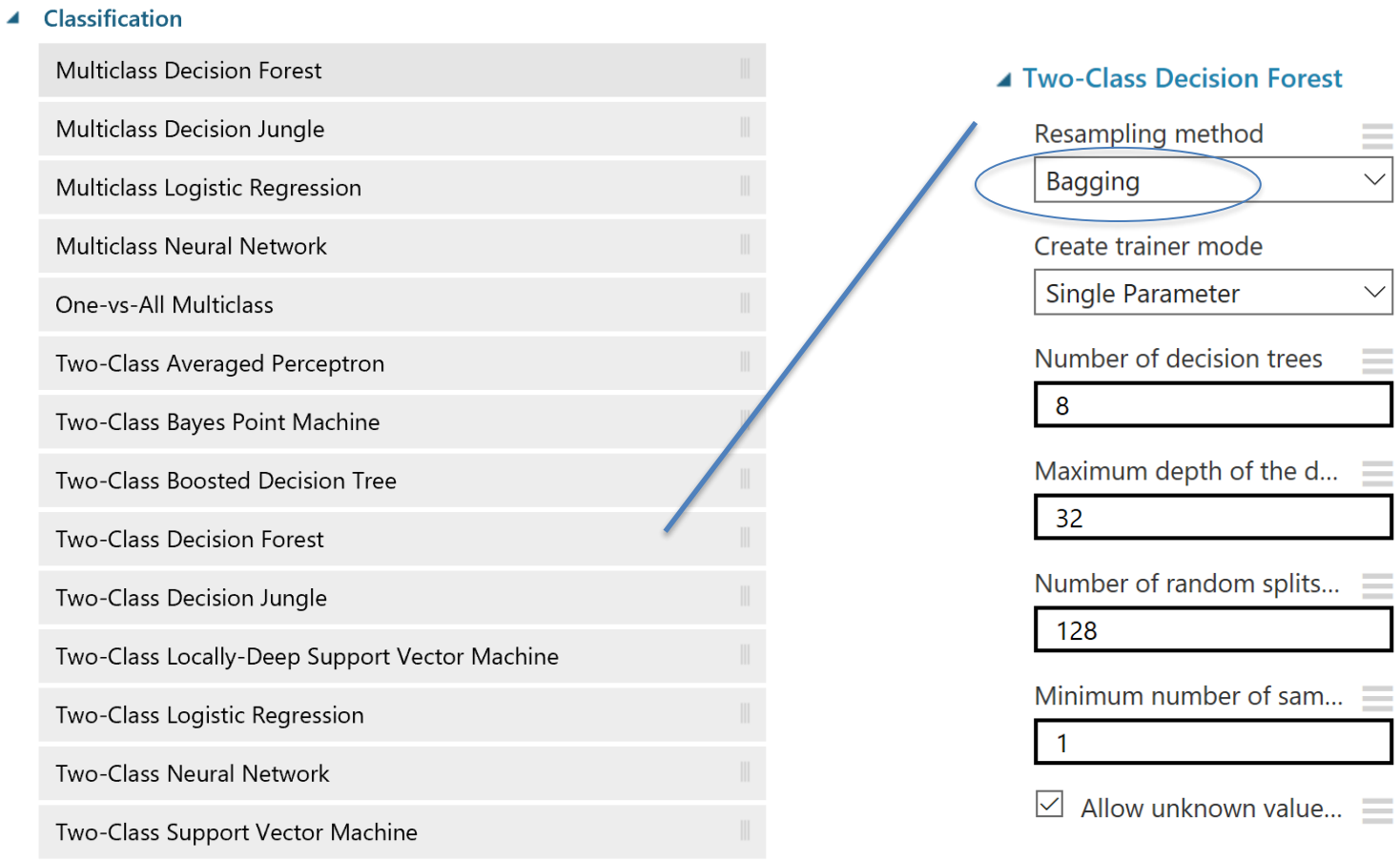
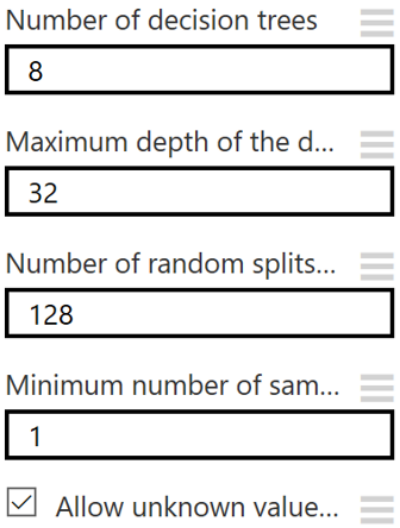
Decision Tree Models



Every tree algorithm behaves differently with different datasets. You will have to read the manual. Here's an description with an Azure tree parameters:



Many algorithms can create new trees as needed

Increasing the levels increases precision, but overfitting becomes a problem *(you have to watch variance with trees – error in actual data)*

type the number of splits to use when building each node of the tree.

minimum number of cases that are required to create any terminal node (leaf) in a tree - the threshold for creating new rules.

https://docs.microsoft.com/en-us/azure/machine-learning/studio-module-reference/

ranger *Ranger*

Description

Ranger is a fast implementation of random forests (Breiman 2001) or recursive partitioning, particularly suited for high dimensional data. Classification, regression, and survival forests are supported. Classification and regression forests are implemented as in the original Random Forest (Breiman 2001), survival forests as in Random Survival Forests (Ishwaran et al. 2008). Includes implementations of extremely randomized trees (Geurts et al. 2006) and quantile regression forests (Meinshausen 2006).

Usage

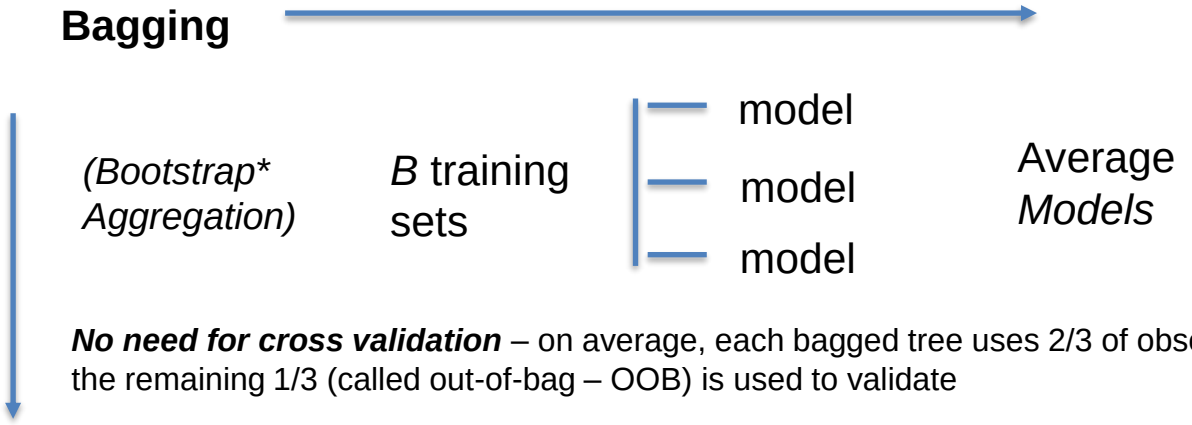
```
ranger(formula = NULL, data = NULL, num.trees = 500, mtry = NULL,
  importance = "none", write.forest = TRUE, probability = FALSE,
  min.node.size = NULL, replace = TRUE, sample.fraction = ifelse(replace,
  1, 0.632), case.weights = NULL, class.weights = NULL, splitrule = NULL,
  num.random.splits = 1, alpha = 0.5, minprop = 0.1,
  split.select.weights = NULL, always.split.variables = NULL,
  respect.unordered.factors = NULL, scale.permutation.importance = FALSE,
  keep.inbag = FALSE, holdout = FALSE, quantreg = FALSE,
  num.threads = NULL, save.memory = FALSE, verbose = TRUE, seed = NULL,
  dependent.variable.name = NULL, status.variable.name = NULL,
  classification = NULL)
```

R tree documentation is unique to each package. Here's ranger:
https://cran.r-project.org/web/packages/ranger/ranger.pdf

R trees are the same way.

There are some consistent concepts, and we will focus on those concepts in ISL for the exam.

Bagging



No need for cross validation – on average, each bagged tree uses 2/3 of observations. We then use the remaining 1/3 (called out-of-bag – OOB) is used to validate

Random Forests

Starts with bagging but restricts predictors (p) to a random sample of m predictors. This ***eliminates over-influence by strong predictors*** (i.e., the difference between random forests and bagging is the predictor subset size)

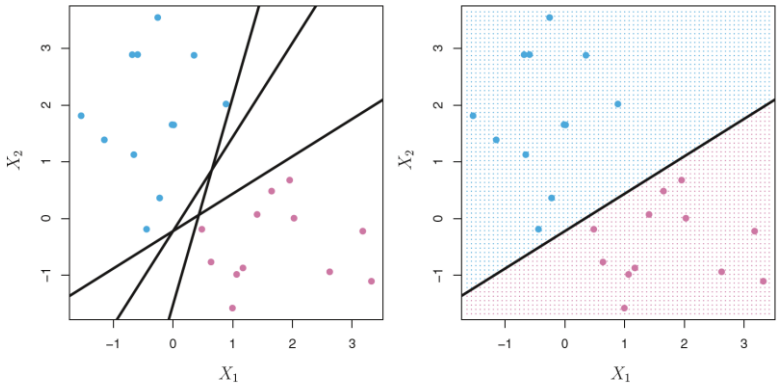
Boosting

Does not use bootstrapping, it uses a modified sampling that ***fits the residuals rather than the predicted value***. More complex, slower learning algorithm *(slower learners are often more accurate, but with higher processing costs)*

**In simple terms: Bootstrapping refers to resampling with replacement*

Chapter 9: Support Vector Machines

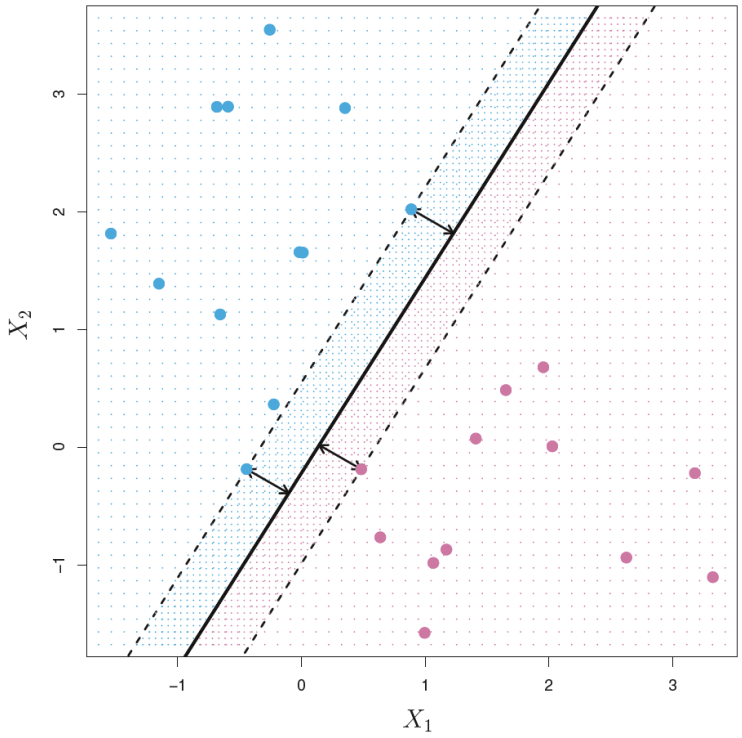
The Separating Hyperplane



The blue and purple grid indicates the decision rule *(recall the dr in LDA)* made by a classifier based on this separating hyperplane.

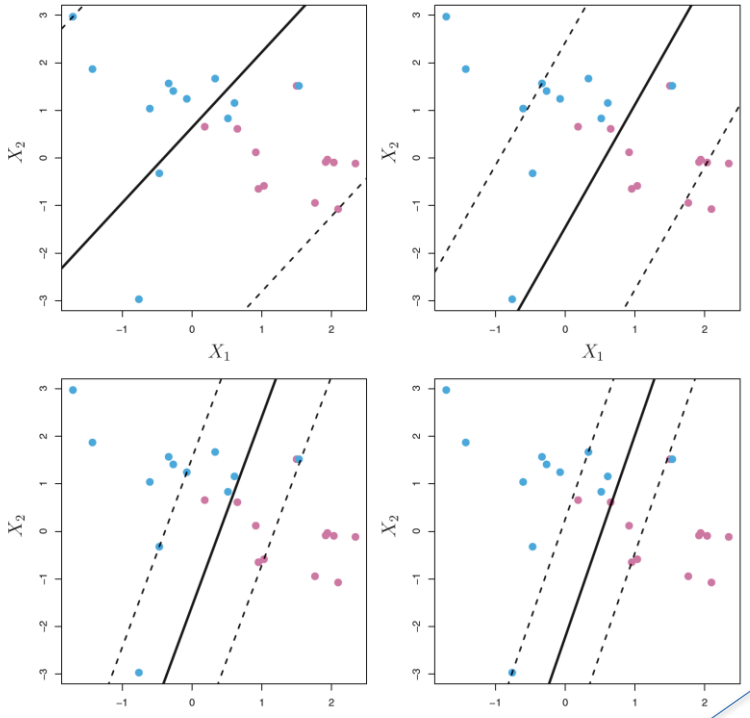
The right-hand panel shows an example of such a classifier. That is, we classify the test observation x based on the sign of $f(x) = \beta_0+\beta_1 x*1+\beta_2 x*2+...$ If $f(x)$ is positive, then we assign the test observation to class 1, and if $f(x)$ is negative, then we assign it to class −1.

We can also make use of the *magnitude* of $f(x)$. If $f(x)$ is far from zero, then this means that x lies far from the hyperplane, and so we can be confident about our class assignment for x. On the other hand, if $f(x)$ is close to zero, then x is located near the hyperplane, and so we are less certain about the class assignment for x. Not surprisingly, and as we see in Figure 9.2, a classifier that is based on a separating hyperplane leads to a linear decision boundary.



Maximal margin hyperplane (also known as the *optimal separating hyperplane*), is the separating hyperplane that is farthest from the training observations. That is, we can compute the perpendicular ***(orthogonal)*** distance from each training observation to a given separating hyperplane; the smallest such distance is the minimal distance from the observations to the hyperplane, and is known as the ***margin***.

(and the points on the margins are called support vectors)



$$\underset{\beta_0,\beta_1,\ldots,\beta_p,\epsilon_1,\ldots,\epsilon_n,M}{\text{maximize}} \; M \tag{9.12}$$

$$\text{subject to} \; \sum_{j=1}^{p} \beta_j^2 = 1, \tag{9.13}$$

$$y_i(\beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \ldots + \beta_p x_{ip}) \geq M(1 - \epsilon_i), \tag{9.14}$$

$$\epsilon_i \geq 0, \; \sum_{i=1}^{n} \epsilon_i \leq C, \tag{9.15}$$

Soft margin classifier. Rather than seeking the largest possible margin so that every observation is not only on the correct side of the hyperplane but also on the correct side of the margin, we instead allow some observations to be on the incorrect side of the margin, or even the incorrect side of the hyperplane *(The margin is soft because it can be violated by some of the training observations.)*

C is a nonnegative tuning parameter. *M* is the width of the margin; we seek to make M as large as possible.

We can create *slack variables* that allow individual observations to be on the wrong side of the margin or the hyperplane

These are the equations from the book – we're going to revise these a bit

SVM's use "kernels" *(functions)* to transform data to n dimensions. Then the additional data can be separated across multiple dimensions, creating non-linear separation. This is a good visualization:

[SVM with polynomial kernel visualization - YouTube]

We won't go deep into kernels here, but be aware that these open options for adapting analyses to data *(it also transforms coefficients and relationships into intractable values)*

	X	Y
1	1	7
2	-3	3
3	-6	1
4	2	6
5	3	8
6	4	5
7	7	3
8	-3	-2
9	-6	-5
10	-3	2
11	1	-6
12	5	3
13	1	-3
14	6	1

$$f(x) = w^\top \Phi(x)$$

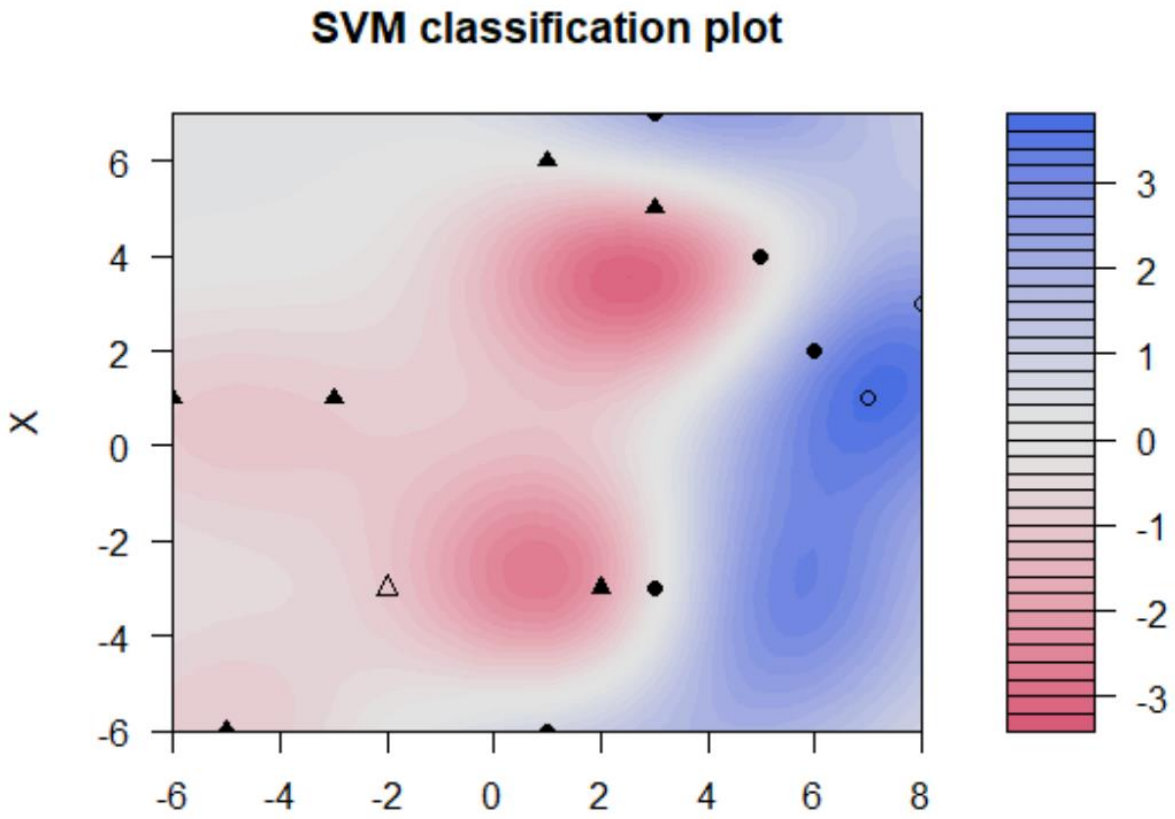
```
rbf <- function(x,y) exp(-0.1 *
sum((x-y)^2))
class(rbf) <- "kernel"
mTst <- as.matrix(tst[,1:2])
yTst <- as.matrix(tst[,3])

k2 <- kernelMatrix(rbf, mTst)

dim(k2)
dfK2 <- data.frame(k2)
```

	X1	X2	X3	X4	X5	X6	X7
1	1.000000e+00	4.076220e-02	2.034684e-04	8.187308e-01	6.065307e-01	2.725318e-01	5.516
2	4.076220e-02	1.000000e+00	2.725318e-01	3.337327e-02	2.242868e-03	4.991594e-03	4.539
3	2.034684e-04	2.725318e-01	1.000000e+00	1.363889e-04	2.260329e-06	9.166088e-06	3.066
4	8.187308e-01	3.337327e-02	1.363889e-04	1.000000e+00	6.065307e-01	6.065307e-01	3.337
5	6.065307e-01	2.242868e-03	2.260329e-06	6.065307e-01	1.000000e+00	3.678794e-01	1.657
6	2.725318e-01	4.991594e-03	9.166088e-06	6.065307e-01	3.678794e-01	1.000000e+00	2.725
7	5.516564e-03	4.539993e-05	3.066941e-08	3.337327e-02	1.657268e-02	2.725318e-01	1.000(
8	6.128350e-05	8.208500e-02	1.652989e-01	1.363889e-04	1.240495e-06	5.545160e-05	3.726
9	4.150654e-09	6.755388e-04	2.732372e-02	9.237450e-09	1.388794e-11	2.061154e-09	7.602
10	1.657268e-02	9.048374e-01	3.678794e-01	1.657268e-02	7.465858e-04	3.027555e-03	4.107
11	4.575339e-08	6.128350e-05	5.545160e-05	5.043477e-07	2.061154e-09	2.260329e-06	8.293
12	4.076220e-02	1.661557e-03	3.726653e-06	1.652989e-01	5.502322e-02	6.065307e-01	6.703
13	4.539993e-05	5.516564e-03	1.503439e-03	2.746536e-04	3.726653e-06	6.755388e-04	7.465
14	2.242868e-03	2.034684e-04	5.573904e-07	1.657268e-02	3.027555e-03	1.353353e-01	6.065

```
dfDefault <- dfDefault %>% rownames_to_column("SampleID")
xTrain <- sample_n(dfDefault, round(nrow(dfDefault)*.6,0))
xTest <- dfDefault %>% anti_join(xTrain, by = "SampleID")

# showing equation with one categorical varible

svmMod <- svm(default ~ student + balance + inc
summary(svmMod)
```

SVMs generally do not perform well on imbalanced datasets. It finds a hyperplane decision boundary that best splits the examples into two classes. The split is made soft through the use of a margin that allows some points to be misclassified. This margin favors the majority class on imbalanced datasets, although it can be tuned *(we'll get into tuning later)*.

```
          Reference
Prediction   No  Yes
       No  3844  133
       Yes    4   19

               Accuracy : 0.9658
                 95% CI : (0.9596, 0.9712)
    No Information Rate : 0.962
    P-Value [Acc > NIR] : 0.1141

                  Kappa : 0.2092

 Mcnemar's Test P-Value : <2e-16

            Sensitivity : 0.12500
            Specificity : 0.99896
         Pos Pred Value : 0.82609
         Neg Pred Value : 0.96656
             Prevalence : 0.03800
         Detection Rate : 0.00475
   Detection Prevalence : 0.00575
      Balanced Accuracy : 0.56198

       'Positive' Class : Yes
```

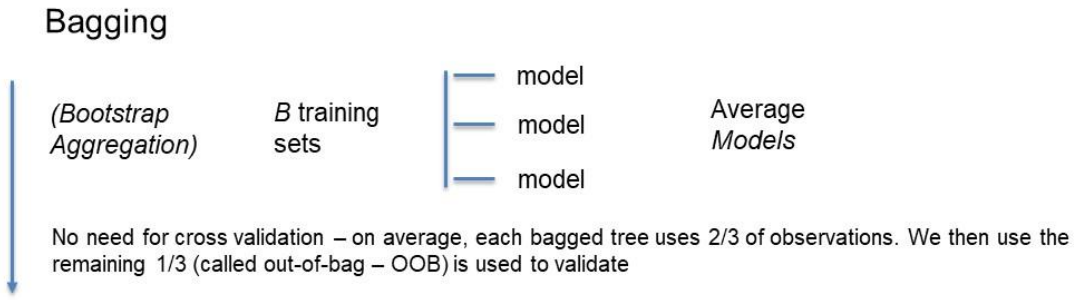


After the kernel transformation, the margins are still linear, but become non-linear with regard to the data. This is a pretty cool visualization.

https://www.youtube.com/watch?time_continue=3&v=3liCbRZPrZA&feature=emb_logo

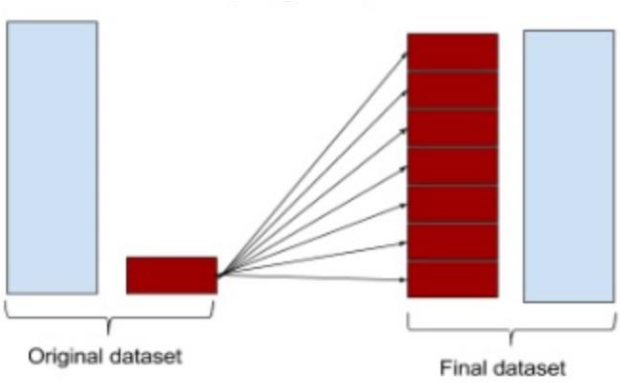
*If you don't have enough data to train your model, you may have to rely on **bootstrapping** where you (repeatedly sample the data with replacement).*

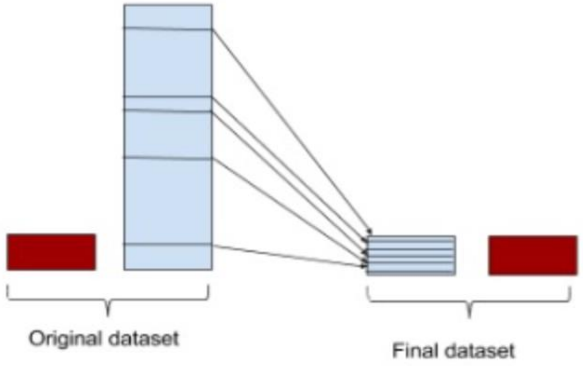
Bootstrapping is used to estimate errors in many models and is integral to ensemble methods. Recall from classification lecture:



Its also useful for finding starting values and estimating priors in Bayesian modelding

Dealing with Unbalanced Data: Up-Sampling, Down-Sampling and SMOTE





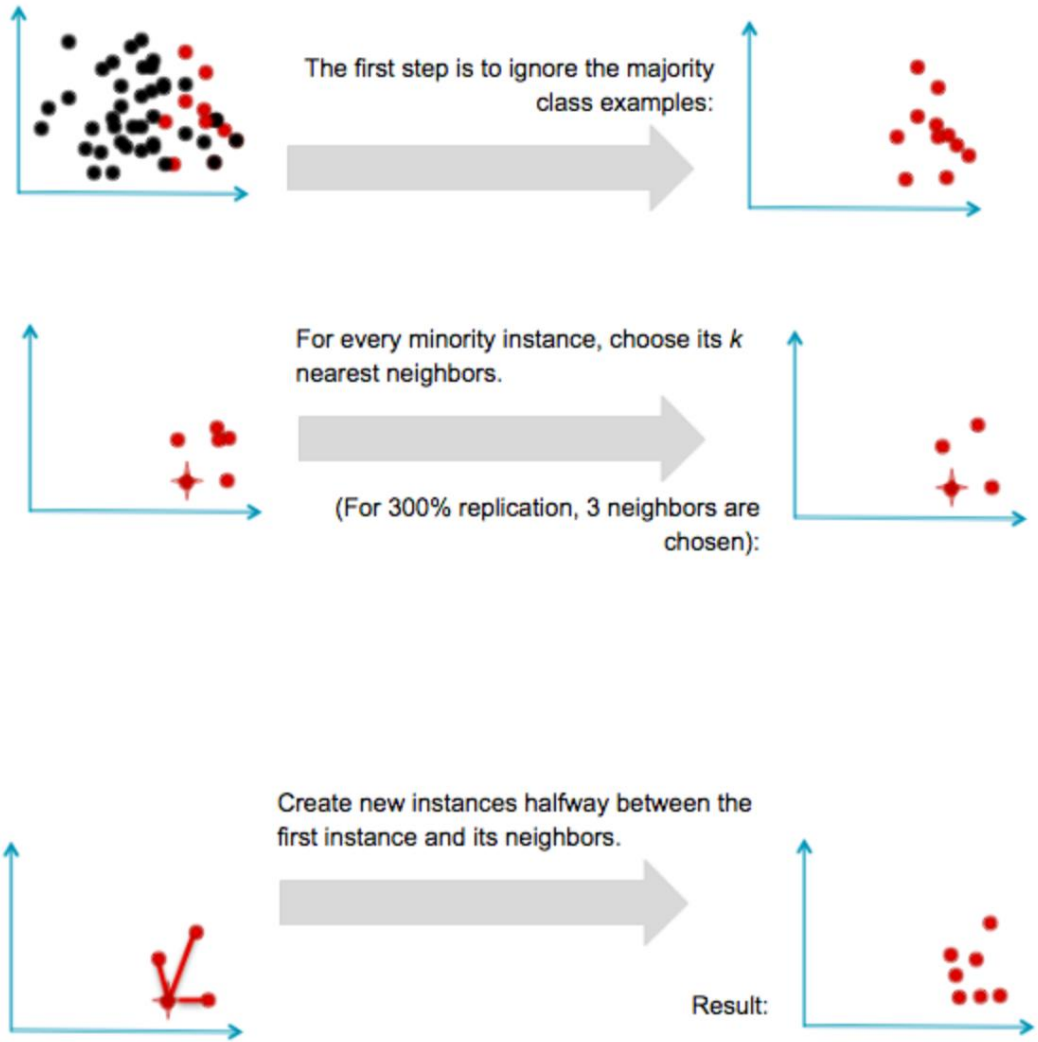
Up-Sampling randomly replicates minority instances to increase their population.

Down-Sampling randomly downsamples the majority class.

Up-Sampling is NOT necessarily superior because it results in more data, and replicating data is not without consequence—since it results in duplicate data, it makes variables appear to have lower variance than they do.

The positive consequence is that it duplicates the number of errors: if a classifier makes a false negative error on the original minority data set, and that data set is replicated five times, the classifier will make six errors on the new set. Conversely, down-sampling can make the independent variables look like they have a higher variance than they do.

Because expect mixed results and consider hybrid approaches.



SMOTE (Synthetic Minority Oversampling TEchnique) system creates new minority examples by interpolating between existing ones. The process is basically as follows:

Assume we have a set of majority and minority examples. SMOTE is generally successful and has led to many variants, extensions, and adaptations to different concept learning algorithms.

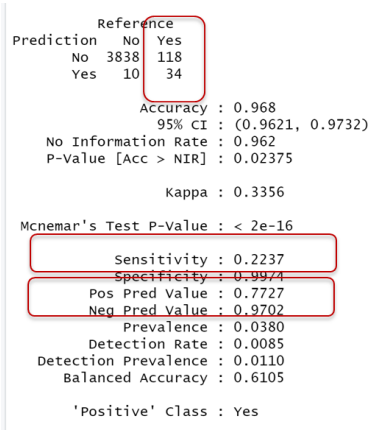
It is important to note a substantial limitation of SMOTE. Because it operates by interpolating between rare examples, it can only generate examples within the body of available examples—never outside.

```
> smoteData <- SMOTE(default ~ student + balance + income, data = Default,
+                    perc.over = 350, perc.under=130)
> # SMOTE only works with factors, so be careful
> prop.table(table(smoteData$default))

       No        Yes
0.4935361 0.5064639
>
```

So this has the same effect as lowering the threshold: increasing Sensitivity *(proportion of positives that are correctly identified)*, but decreasing Pos Pred Value (*% of predicted positives that were correctly identified).*

```
          Reference
Prediction   No  Yes
       No  3838  118
       Yes   10   34

               Accuracy : 0.968
                 95% CI : (0.9621, 0.9732)
    No Information Rate : 0.962
    P-Value [Acc > NIR] : 0.02375

                  Kappa : 0.3356

 Mcnemar's Test P-Value : < 2e-16

            Sensitivity : 0.2237
            Specificity : 0.9974
         Pos Pred Value : 0.7727
         Neg Pred Value : 0.9702
             Prevalence : 0.0380
         Detection Rate : 0.0085
   Detection Prevalence : 0.0110
      Balanced Accuracy : 0.6105

       'Positive' Class : Yes
```

```
          Reference
Prediction   No  Yes
       No  3237   19
       Yes  611  133

               Accuracy : 0.8425
                 95% CI : (0.8308, 0.8537)
    No Information Rate : 0.962
    P-Value [Acc > NIR] : 1

                  Kappa : 0.2495

 Mcnemar's Test P-Value : <2e-16

            Sensitivity : 0.87500
            Specificity : 0.84122
         Pos Pred Value : 0.17876
         Neg Pred Value : 0.99416
             Prevalence : 0.03800
         Detection Rate : 0.03325
   Detection Prevalence : 0.18600
      Balanced Accuracy : 0.85811

       'Positive' Class : Yes
```



```
          Reference
Prediction   No  Yes
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```

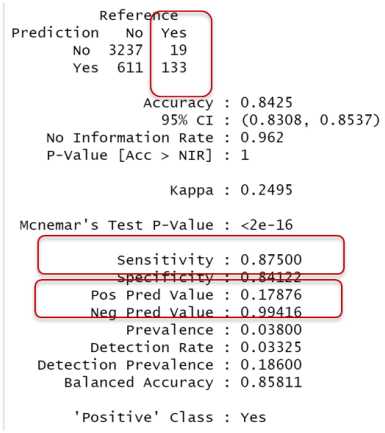

```
          Reference
Prediction   No  Yes
       No  3237   19
       Yes  611  133

               Accuracy : 0.8425
                 95% CI : (0.8308, 0.8537)
    No Information Rate : 0.962
    P-Value [Acc > NIR] : 1

                  Kappa : 0.2495

 Mcnemar's Test P-Value : <2e-16

            Sensitivity : 0.87500
            Specificity : 0.84122
         Pos Pred Value : 0.17876
         Neg Pred Value : 0.99416
             Prevalence : 0.03800
         Detection Rate : 0.03325
   Detection Prevalence : 0.18600
      Balanced Accuracy : 0.85811

       'Positive' Class : Yes
```

Sometimes, SMOTE can improve both sensitivity and Pos Pred Val. It depends on the data. Keep in mind that SMOTE is creating data much like you generate data in the regression exercises – random values within a range. But if that range overlaps with the other classes, it can make prediction more difficult. You have to decide based on the goals of your project.

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Classification Wrap-up

We've looked a an array for classifiers that can be used to build solutions. The data we've been using is challenging because separation is not discretely defined, and dimensions are limited.

As we get into sampling, you'll see how we can use resampling to improve model performance.

Model selection is an imprecise art based on experience and intuition. And there are many algorithms that could potentially solve a problem. For this reason, most ML platforms allow you to run multiple algorithms in parallel and will summarize results for you. Your homework is a manual walkthrough of this process.