

Introduction to Data Science-Topic 7

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- WWW: <http://www.stat.nctu.edu.tw/misg/hslu/course/DataScience.htm>
- Reference:
M. A. Pathak, Beginning Data Science with R, 2014, Springer-Verlag.
- Evaluation: Homework: 50%, Term Project: 50%
- Office hours: By appointment

Course Outline

- Introduction of Data Science
- Introduction of R
- More on R
- Process Real Data by R
- Data Visualization
- Exploratory Data Analysis
- Regression
- **Classification**
- Text Mining
- Clustering

Classification

References:

Ch. 7, M. A. Pathak, Beginning Data Science with R, 2014, Springer-Verlag.



7.1 Introduction

Regression - predicting a **numeric value**

Classification - classify data points into multiple **categories or classes**

Application: spam filtering, computational advertising, speech and handwriting recognition, and biometric authentication...and so on.

In this chapter, we'll introduce:

Parametric model: Naïve Bayes, Logistic Regression, SVM

Nonparametric: Nearest Neighbors, Decision Tree-based models

In this topic, we'll use the Titanic Dataset on Kaggle:

<https://www.kaggle.com/c/titanic/data>

```
> titanic <- read.csv("train.csv")
```

In this topic, we'll use the Titanic Dataset on Kaggle:

<https://www.kaggle.com/c/titanic/data>

```
> titanic <- read.csv("train.csv")
```

Preprocessing:

Select the columns we want to build a model.

```
> titanic <- titanic[, c(2,3,5,6,7,8,10,12)]
```

Remove NA.

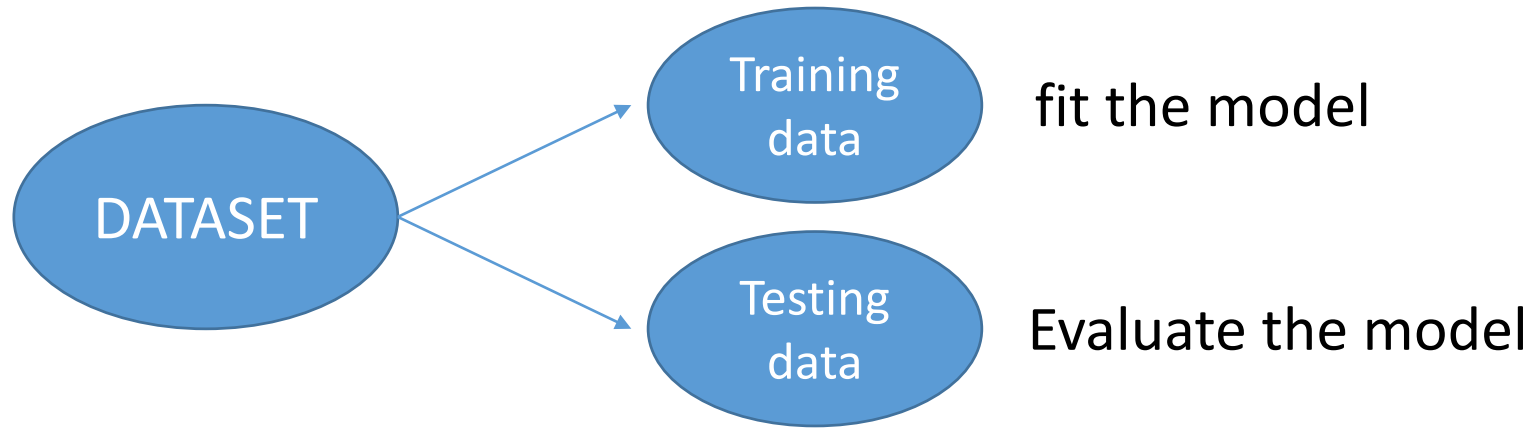
```
> titanic <- na.omit(titanic)
```

Turn factor variables into correct type.

```
> titanic$Survived <- as.factor(titanic$Survived)  
> titanic$Pclass <- as.factor(titanic$Pclass)
```

Variable name	Variable type	Description
PassengerId	Unique ID	Passenger's id
Survived	Categorical	Survival, 0 = No, 1 = Yes
Pclass	Categorical	Ticket class, 1 = 1st, 2 = 2nd, 3 = 3rd
Name	Character	Passenger's name
Sex	Categorical	Passenger's sex
Age	Numeric	Age in years
SibSp	Numeric	# of siblings / spouses aboard the Titanic
Parch	Numeric	# of parents / children aboard the Titanic
Ticket	ID	Ticket number
Fare	numeric	Passenger fare
Cabin	ID	Cabin number
Embarked	Categorical	Port of Embarkation, C = Cherbourg, Q = Queenstown, S = Southampton

7.1.1 Training and Test Datasets



```
> library(caret)
> set.seed(20180430)
> train.ind <- createDataPartition(titanic$Survived, p = 2/3, list = F)
> train <- titanic[train.ind, ]
> test <- titanic[-train.ind, ]
> dim(train) ; dim(test)
[1] 477    8
[1] 237    8
```

7.2 Parametric Classification Models

7.2.1 Naive Bayes

$P(\theta)$ = prior probability, $P(x|\theta)$ = likelihood of the data x

$$\text{posterior probability } P(\theta|x) = \frac{P(x|\theta)P(\theta)}{P(x)}$$

In a naive Bayes classifier, we compute the conditional probability of a data point having a class label $y = \{-1, 1\}$ and data point x ,

$$P(y = 1|x) = \frac{P(x|y = 1)P(y = 1)}{P(x)}$$

$$P(y = -1|x) = \frac{P(x|y = -1)P(y = -1)}{P(x)}$$

We can assign the label $y = 1$ or $y = -1$ to the data point x depending on which posterior probability is greater.

$P(y = 1)$ and $P(y = -1)$: *marginal probabilities or simply marginals*

$P(x|y = 1)$ is hard to compute while we have many features

To solve this problem, the NB model makes an assumption that the features of a data point are **conditional independence**:

$$P(x|y = 1) = P(x_1, x_2, \dots, x_p|y = 1) = P(x_1|y = 1)P(x_2|y = 1) \cdots P(x_p|y = 1)$$

7.2.1.1 Training an NB Classifier Using the e1071 Package

```
> library(e1071)
> model.nb <- naiveBayes(Survived ~ ., train)
```

```
> model.nb
```

Naive Bayes Classifier for Discrete Predictors

Call:

```
naiveBayes.default(x = X, y = Y, laplace = laplace)
```

A-priori probabilities:

Y

	0	1
0.5932914	0.4067086	

Conditional probabilities:

Pclass

Y	1	2	3
0	0.1554770	0.2190813	0.6254417
1	0.4175258	0.3041237	0.2783505

Sex

Y	female	male
0	0.1590106	0.8409894
1	0.6752577	0.3247423

...

Use `predict ()` to obtain predict result

```
> predict(model.nb, test)
 [1] 0 0 0 0 0 0 1 0 0 0 0 0 1 0 1 1 0 0 0 0 0 0 1 0 1 0 0 1 1 0 0 0
[33] 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 1 0 1 1 0 0 0 0 0 0 0 0 1 0
...
Levels: 0 1
> table(predict(model.nb,test) == test$Survived)/length(test$Survived)

      FALSE      TRUE
0.2025316 0.7974684
```

The accuracy of our naive Bayes classifier model is 79.7 %.

7.2.2 Logistic Regression

Sigmoid function: $\text{sig}(t) = \frac{1}{1+e^{-t}}$

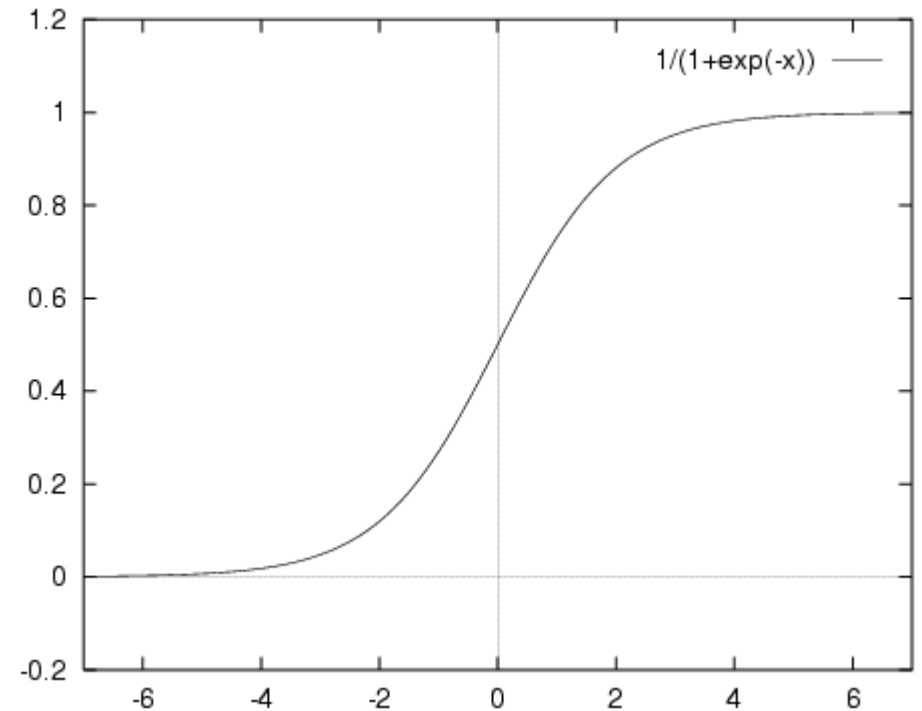
- Range: 0-1
- monotonically increasing

If the class label y takes two values 1 and -1, and has only one predictor variable, we have

$$P(y = 1|x) = \text{sig}(w_0 + w_1x) = \frac{1}{1 + e^{-(w_0 + w_1x)}}$$

$$P(y = -1|x) = \frac{e^{-(w_0 + w_1x)}}{1 + e^{-(w_0 + w_1x)}} = \frac{1}{\frac{1}{e^{-(w_0 + w_1x)}} + 1} = \frac{1}{1 + e^{(w_0 + w_1x)}} = \text{sig}(-(w_0 + w_1x))$$

$$\Rightarrow P(y|x) = \text{sig}(y(w_0 + w_1x))$$



In logistic regression model, we select the coefficient vector w that maximizes the log-likelihood, given this log-likelihood function, we obtain w using optimization techniques such as gradient descent.

7.2.2.1 Using the glm() Function

Fit the logistic model with one variable Pclass

```
> model.lr.pclass <- glm(Survived ~ Pclass, data = train,  
+                         family = "binomial")  
> model.lr.pclass
```

```
Call:  glm(formula = Survived ~ Pclass, family = "binomial", data = train)
```

Coefficients:

(Intercept)	Pclass2	Pclass3
0.6103	-0.6599	-1.7974

Degrees of Freedom: 476 Total (i.e. Null); 474 Residual

Null Deviance: 644.6

Residual Deviance: 581.1 AIC: 587.1

```

> summary(model.lm.pclass)

Call:
glm(formula = Survived ~ Pclass, family = "binomial", data = train)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.4451  -0.7298  -0.7298   0.9315   1.7049

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.6103     0.1873   3.259  0.00112 **
Pclass2      -0.6599     0.2611  -2.528  0.01148 *
Pclass3      -1.7974     0.2434  -7.385 1.53e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 644.56  on 476  degrees of freedom
Residual deviance: 581.07  on 474  degrees of freedom
AIC: 587.07

Number of Fisher Scoring iterations: 4

```

`fit()` output the numeric score : $w_0 + w_1x$

```
> predict(model.lr.pclass, test)
      1      3      7      9     13
-1.18716569 -1.18716569  0.61025952 -1.18716569 -1.18716569
     14     16     19     24     31
-1.18716569 -0.04959694 -1.18716569  0.61025952  0.61025952
...
```

We can pass the above value to sigmoid function are simply use parameter `type="response"` to obtain the probabilities.

```
> predict(model.lr.pclass, test, type = "response")
      1      3      7      9     13     14     16
0.2337662 0.2337662 0.6480000 0.2337662 0.2337662 0.2337662 0.4876033
     19     24     31     39     41     44     50
0.2337662 0.6480000 0.6480000 0.2337662 0.2337662 0.4876033 0.2337662
...
```

We need to set a threshold to convert these probabilities into class labels. For example, we set 0.5 as threshold.

```
> p <- predict(model.lr.pclass, test, type = "response")
> labels <- ifelse(p > 0.5, "1", "0")
> labels
  1    3    7    9   13   14   16   19   24   31   39   41   44   50   54   57   61
"0" "0" "1" "0" "0" "0" "0" "0" "1" "1" "0" "0" "0" "0" "0" "0"
 69   72   75   81   82   85   86   89   92   95   98   99  101  106  109  116  117
"0" "0" "0" "0" "0" "0" "0" "1" "0" "0" "1" "0" "0" "0" "0" "0"
...
> table(labels == test$Survived)/length(test$Survived)

      FALSE      TRUE
0.3164557 0.6835443
```

The accuracy of our logistic regression model using `Pclass` alone is 68.4 %.

We train the logistic regression model to predict the Survived with all features.

```
> model.lr <- glm(Survived ~ ., data = train, family = "binomial")  
> model.lr
```

```
Call:  glm(formula = Survived ~ ., family = "binomial", data = train)
```

Coefficients:

(Intercept)	Pclass2	Pclass3	Sexmale	Age
16.07743	-1.17150	-2.62148	-2.64887	-0.04341
SibSp	Parch	Fare	EmbarkedC	EmbarkedQ
-0.53061	-0.02572	0.00173	-11.71033	-12.12269
EmbarkedS				
-11.93030				

Degrees of Freedom: 476 Total (i.e. Null); 466 Residual

Null Deviance: 644.6

Residual Deviance: 420.7 AIC: 442.7

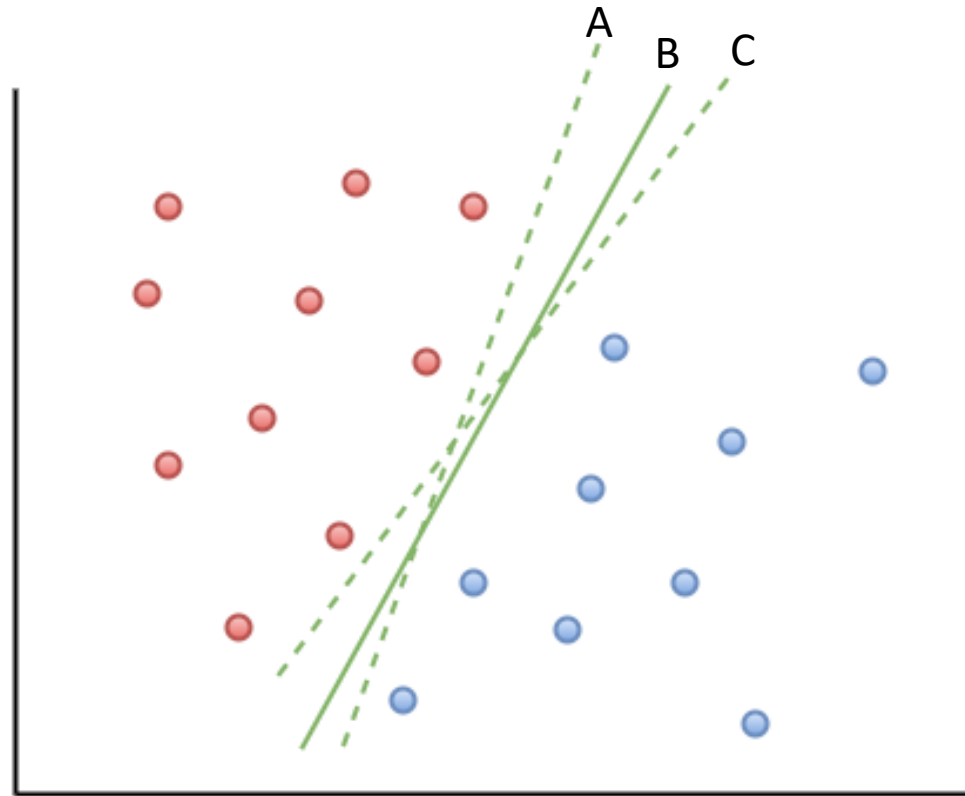
We need to set a threshold to convert these probabilities into class labels. For example, we set 0.5 as threshold.

```
> p <- predict(model.lr, test, type = "response")  
> labels <- ifelse(p > 0.5, "1", "0")  
> table(labels == test$Survived)/length(test$Survived)
```

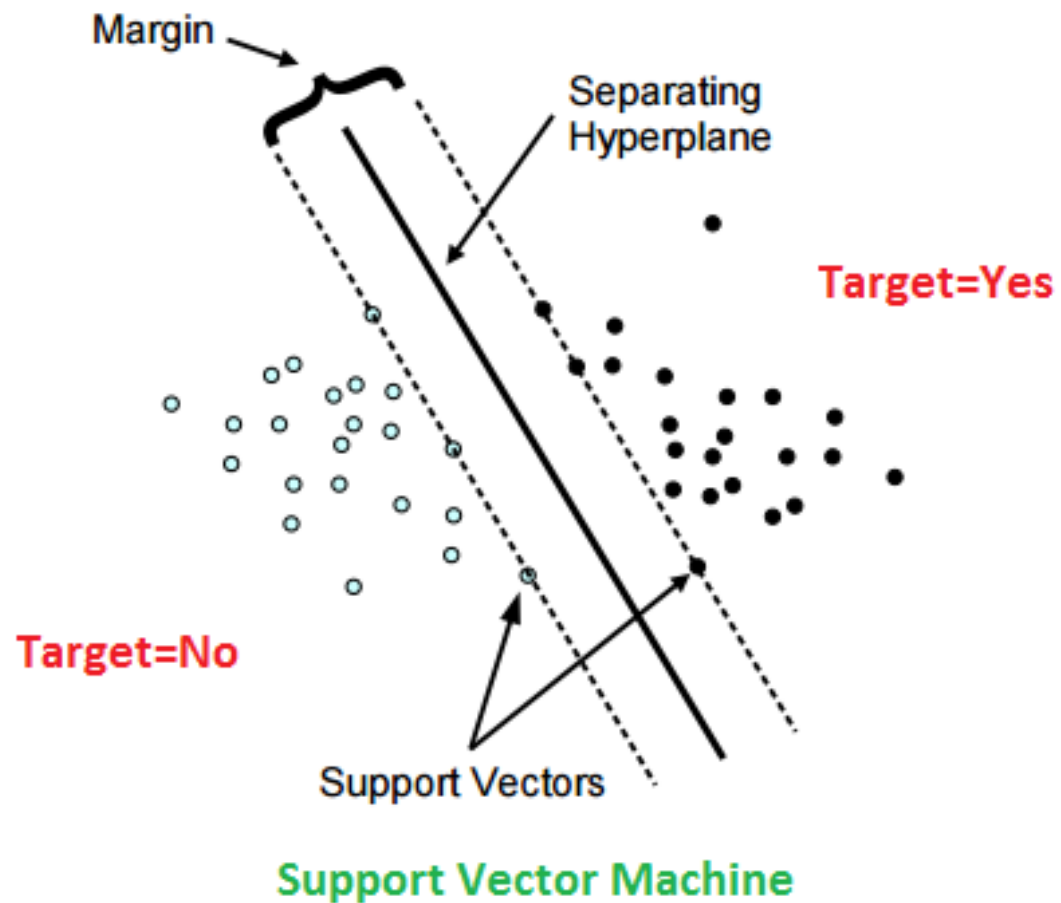
FALSE	TRUE
0.1687764	0.8312236

The accuracy of our logistic regression model is 83.1 %, is better than we use `Pclass` alone.

7.2.2 Support Vector Machines



All A, B and C can separate data points perfectly,
Which one is better?



The goal of SVM:
Maximized the margin

→ solving a quadratic optimization problem.

Use `svm()` in `e1071` package:
an interface to LIBSVM

<https://www.csie.ntu.edu.tw/~cjlin/libsvm/>

We can use `svm()` function to train a svm model

```
> model.svm <- svm(Survived ~ ., data = train, kernel = "linear")  
> model.svm
```

Call:

```
svm(formula = Survived ~ ., data = train, kernel = "linear")
```

Parameters:

```
  SVM-Type:  C-classification  
SVM-Kernel:  linear  
    cost:    1  
   gamma:    0.09090909
```

```
Number of Support Vectors:  236
```

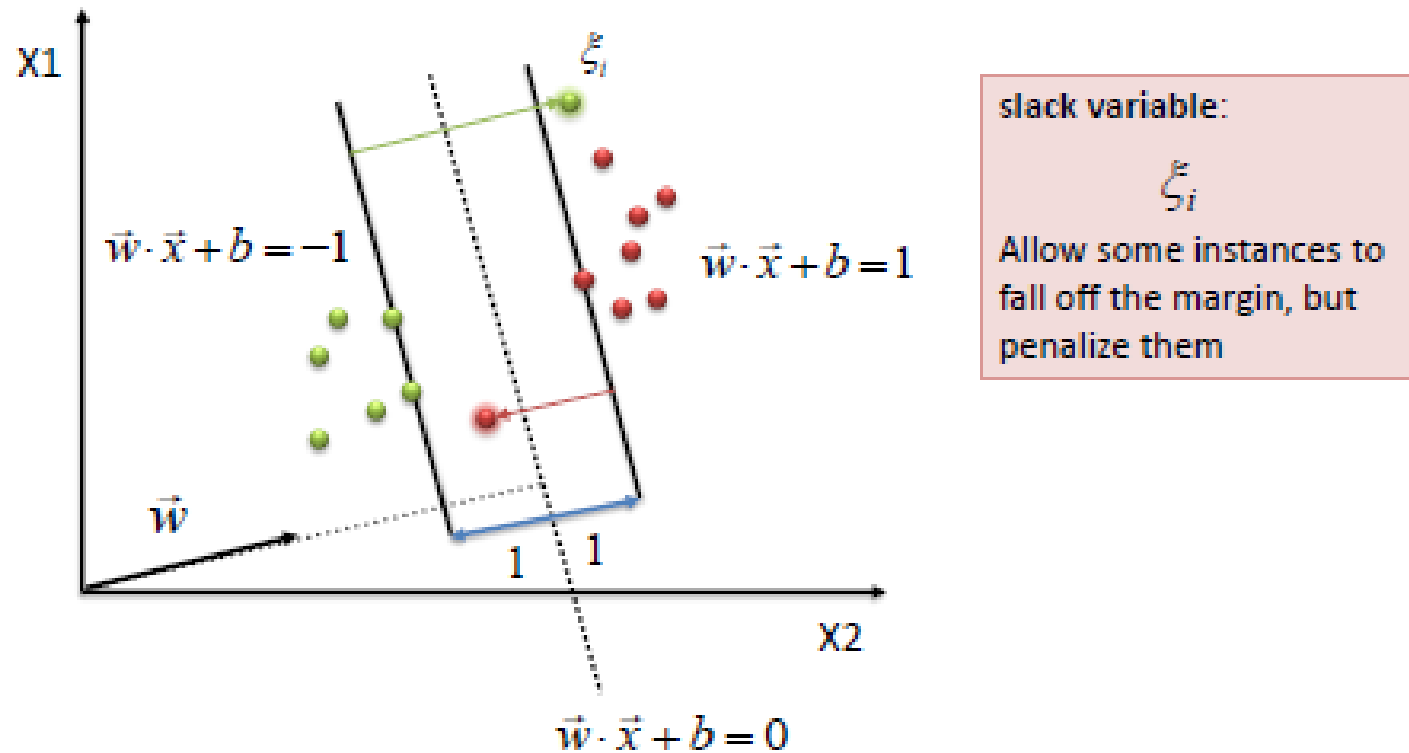
`predict ()` function to predict labels

```
> predict(model.svm, test)
 1    3    7    9   13   14   16   19   24   31   39   41   44   50   54   57   61
0    1    0    1    0    0    1    1    0    0    1    1    1    1    1    1    0
69   72   75   81   82   85   86   89   92   95   98   99  101  106  109  116  117
1    1    0    0    0    1    1    1    0    0    0    1    1    0    0    0    0
...
Levels: 0 1
> table(predict(model.svm, test) == test$Survived)/length(test$Survived)

      FALSE      TRUE
0.2067511 0.7932489
```

Our SVM classifier has 79.3% accuracy.

If data points are not linear separable



We can control the slack using the cost parameter of `svm()`.

By default cost is set to 1,

```
> model.svm.cost <- svm(Survived ~ ., data = train, kernel = "linear",  
+                        cost = 0.1)
```

7.2.3.1 Kernel Trick

An alternative strategy of dealing with nonlinearly separable data is to use the **kernel trick**. The idea behind the kernel trick is to project the data points of the training data into a higher dimensional space, in which the dataset is linearly separable.

Some common kernels: polynomial, sigmoid and radial kernel.

We can specify the type of the kernel using the `kernel` argument

```
> model.svm.radial <- svm(Survived ~ ., data = train, kernel = "radial")
> model.svm.radial
```

Call:

```
svm(formula = Survived ~ ., data = train, kernel = "radial")
```

Parameters:

```
  SVM-Type:  C-classification
SVM-Kernel:  radial
    cost:    1
  gamma:    0.09090909
```

```
Number of Support Vectors: 267
```



```
> table(predict(model.svm.radial, test) == test$Survived)/length(test$Survived)
```

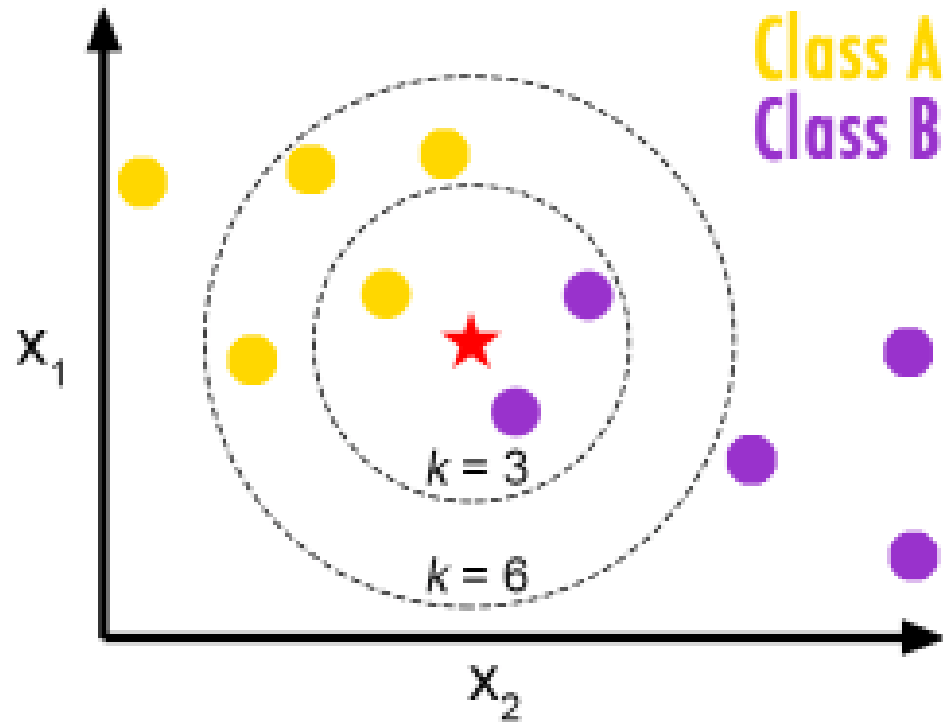
FALSE	TRUE
0.1940928	0.8059072

The accuracy is higher than we use linear kernel.

We can also tune these parameter using grid search to reach higher accuracy.

7.3 Nonparametric Classification Models

7.3.1 Nearest Neighbors



- without assuming any specific
- work well for nonlinear datasets

k: The only parameter we need to decide
We choose k based on the value that
gives the highest accuracy on test dataset
or using cross validation.

Distance metrics:

The most popular one is the **Euclidean distance**, which is given by the linear distance between two data points:

$$Euclidean(x_1, x_2) = \sqrt{\sum_i (x_{1i} - x_{2i})^2}$$

City-block or Manhattan distance:

$$Manhattan(x_1, x_2) = \sum_i |x_{1i} - x_{2i}|$$

Minkowski distance:

$$Minkowski(x_1, x_2) = \sqrt[p]{\sum_i (x_{1i} - x_{2i})^p}$$

p = 2 gives us Euclidean distance, while setting p = 1 gives us Manhattan distance

We can use a kernel function to assign weight based on the distance metric. We first use unweighted NN algorithm; this is equivalent to setting the `kernel` parameter to "rectangular". The default setting if `kknn()` function are use Minkowski distance with $p=2$ (equivalent to Euclidean distance), and $k = 7$.

```
> library(kknn)
> model <- kknn(Survived ~ ., train, test, kernel = "rectangular")
> model$fitted.values
  [1] 0 0 0 0 0 0 1 0 1 0 0 0 1 0 1 1 0 0 0 0 0 0 1 0 1 0 0 0 1 1 0 0
 [33] 0 0 0 0 0 1 0 0 0 0 0 0 0 0 1 0 0 0 1 0 1 1 0 0 0 0 0 1 0 0 1 0
      ...
> table(model$fitted.values == test$Survived)/length(test$Survived)

      FALSE      TRUE
0.185654 0.814346
```

The fitted value are return in `fitted.value`.
The accuracy of unweighted NN with $k=7$ is 81.4 %.

We can try different k:

```
> model.5 <- kknn(Survived ~ ., train, test, kernel = "rectangular",  
+                 k = 5)  
> table(model.5$fitted.values == test$Survived)/length(test$Survived)
```

FALSE	TRUE
0.1729958	0.8270042

The accuracy of unweighted NN with k=5 is 82.7 %, which is higher than the default k = 7. Similarly, we can also experiment with other kernels:

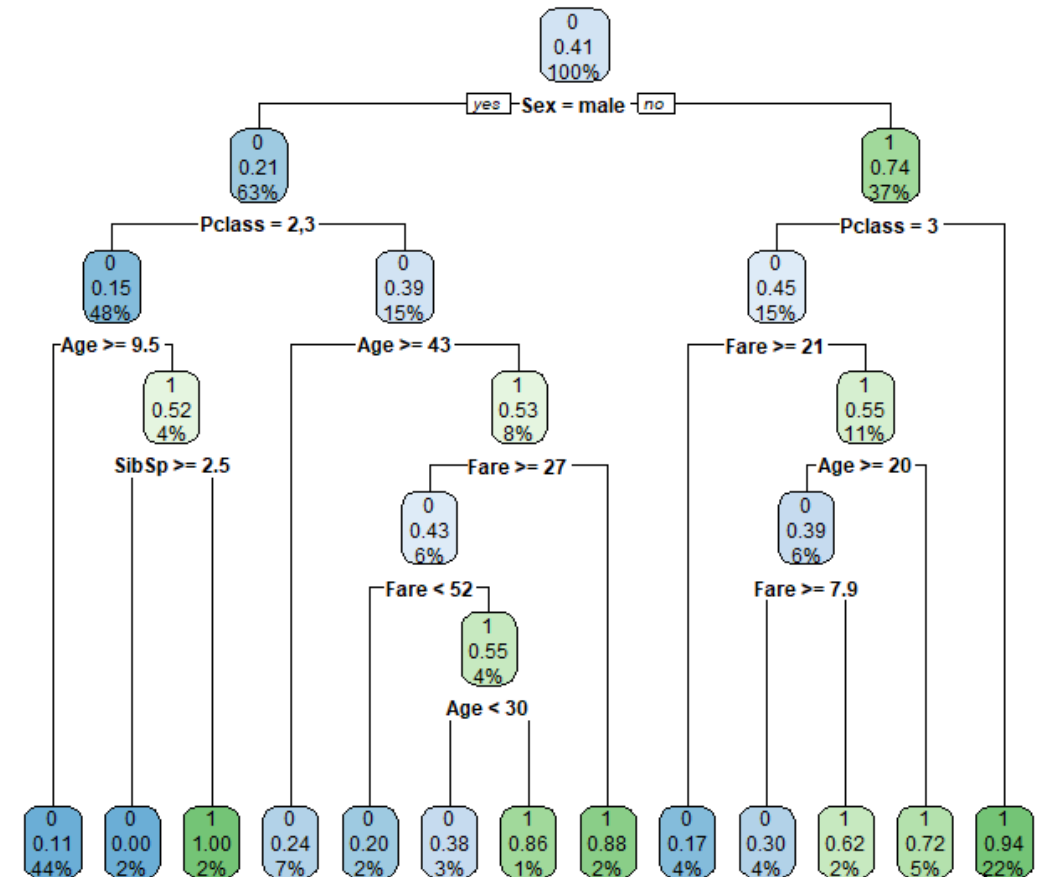
```
> model.gaussian <- kknn(Survived ~ ., train, test, kernel = "gaussian")  
> table(model.gaussian$fitted.values == test$Survived)/length(test$Survived)
```

FALSE	TRUE
0.1940928	0.8059072

7.3.2 Decision Trees

We also use the `rpart` package to fit decision trees.

```
> library(rpart)
> model.dt <- rpart(Survived ~ ., train)
> library(rpart.plot)
> rpart.plot(model.dt)
```



By default, the `predict()` function returns the class probabilities. We obtain the class labels by calling `predict()` with the argument `type="class"`.

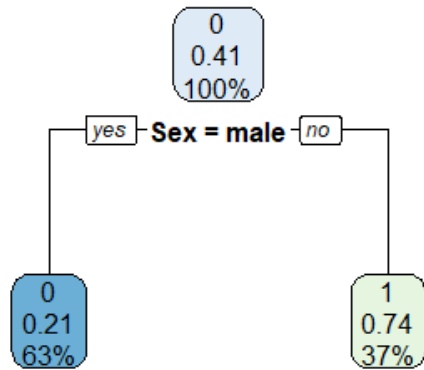
```
> predict(model.dt, test, type = "class")
 1   3   7   9  13  14  16  19  24  31  39  41  44  50  54
0   0   0   0   0   0   1   0   0   0   1   0   1   1   1
57  61  69  72  75  81  82  85  86  89  92  95  98  99 101
1   0   1   0   0   0   0   1   0   1   0   0   0   1   0
...
Levels: 0 1
> table(predict(model.dt, test, type = "class") ==
test$Survived)/length(test$Survived)

      FALSE      TRUE
0.1940928 0.8059072
```

The accuracy of our decision tree classifier is 80.6 %.

we set the `cp` parameter to prune some of the branches off by setting it to 0.04.
(default = 0.01)

```
> rpart.plot(model.dt)
> rpart.plot(model.dt.prune)
```



We can see the tree is smaller than the previous one.

```
> table(predict(model.dt.prune, test, type = "class") == test$Survived) /
+   length(test$Survived)
```

FALSE	TRUE
0.2067511	0.7932489

The accuracy is lower than the tree without pruning, maybe we can consider the larger value of `cp`, means more bigger(complex) tree.

Homework

- Basic
 - Find a dataset you want to analysis.
 - Do proper data preprocessing before building classification model.
 - Practice the models introduce in this chapter.
- Advanced
 - Explained the what preprocessing you done and why to do that.
 - Compare the different model by different evaluation metric (accuracy, recall, precision, ...), and choose one evaluation metric as the criteria of model selection, explain why you choose this evaluation metric.
more information about evaluation metric:
(https://en.wikipedia.org/wiki/Precision_and_recall)

Homework 7 (submitted to e3new.nctu.edu.tw before Nov 5, 2019)

- Use R and/or the other software practice classification model
- Explain the results you obtain
- Discuss possible problems you plan to investigate for future studies
- Possible source of open data:

UCI Machine Learning Repository

(<http://archive.ics.uci.edu/ml/datasets.php>)

References

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5. Chang, C.-C., & Lin, C.-J. (2011). LIBSVM: A library for support vector machines. ACM Transactions on Intelligent Systems and Technology, 2:27, 1–27:27. <http://www.csie.ntu.edu.tw/~cjlin/libsvm>. Accessed 1 Aug 2014.
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7. Geisser, S. (1993). Predictive inference. UK: Chapman and Hall.
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9. Karatzoglou, A., & Meyer, D. (2006). Support vector machines in R. Journal of Statistical Software, 15, 1–28.