타이타닉

1. 필요한 Library 호출

```
library('ggplot2')

library('caret')

library('dplyr')

library('randomForest')

library('rpart')

library('rpart.plot')

library('car')

library('e1071')
```

2. 데이터 입력

```
train.tit <- read.csv('train.csv', stringsAsFactors = F)
test.tit  <- read.csv('test.csv', stringsAsFactors = F)
test.tit$Survived <- NA

## train 와 test 데이터 결합
full_titanic <- rbind(train.tit, test.tit)

## 데이터 구조 확인
str(full_titanic)
```

```
## 'data.frame':    1309 obs. of  12 variables:
##  $ PassengerId: int  1 2 3 4 5 6 7 8 9 10 ...
##  $ Survived   : int  0 1 1 1 0 0 0 0 1 1 ...
##  $ Pclass     : int  3 1 3 1 3 3 1 3 3 2 ...
##  $ Name       : chr  "Braund, Mr. Owen Harris" "Cumings, Mrs. John Bradley
 (Florence Briggs Thayer)" "Heikkinen, Miss. Laina" "Futrelle, Mrs. Jacques H
eath (Lily May Peel)" ...
##  $ Sex        : chr  "male" "female" "female" "female" ...
##  $ Age        : num  22 38 26 35 35 NA 54 2 27 14 ...
##  $ SibSp      : int  1 1 0 1 0 0 0 3 0 1 ...
##  $ Parch      : int  0 0 0 0 0 0 0 1 2 0 ...
```

```
##  $ Ticket     : chr  "A/5 21171" "PC 17599" "STON/O2. 3101282" "113803" ...
##  $ Fare       : num  7.25 71.28 7.92 53.1 8.05 ...
##  $ Cabin      : chr  "" "C85" "" "C123" ...
##  $ Embarked   : chr  "S" "C" "S" "S" ...
```

2. 데이터 분석 및 결측치 확인

```
## 결측치 확인
colSums(is.na(full_titanic))
```

```
## PassengerId    Survived      Pclass        Name         Sex         Age
##           0         418           0           0           0         263
##       SibSp       Parch      Ticket        Fare       Cabin    Embarked
##           0           0           0           1           0           0
```

```
## 결측치 데이터
colSums(full_titanic=='')
```

```
## PassengerId    Survived      Pclass        Name         Sex         Age
##           0          NA           0           0           0          NA
##       SibSp       Parch      Ticket        Fare       Cabin    Embarked
##           0           0           0          NA        1014           2
```

Age 결측치: 263, Cabin 결측치: 1014, Embarked 결측치: 2

Embarked 의 결측치를 최빈값으로 입력한다.

```
table(full_titanic$Embarked)
```

```
##
##       C   Q   S
##   2 270 123 914
```

```
full_titanic$Embarked[full_titanic$Embarked==""]="S"
table(full_titanic$Embarked)
```

```
##
##   C   Q   S
## 270 123 916
```

Age 와 Cabin 은 결측치 많아, 분석과정 동안 결측값들을 확인 할 것이다.

Factor 로 변환 가능한 변수 확인

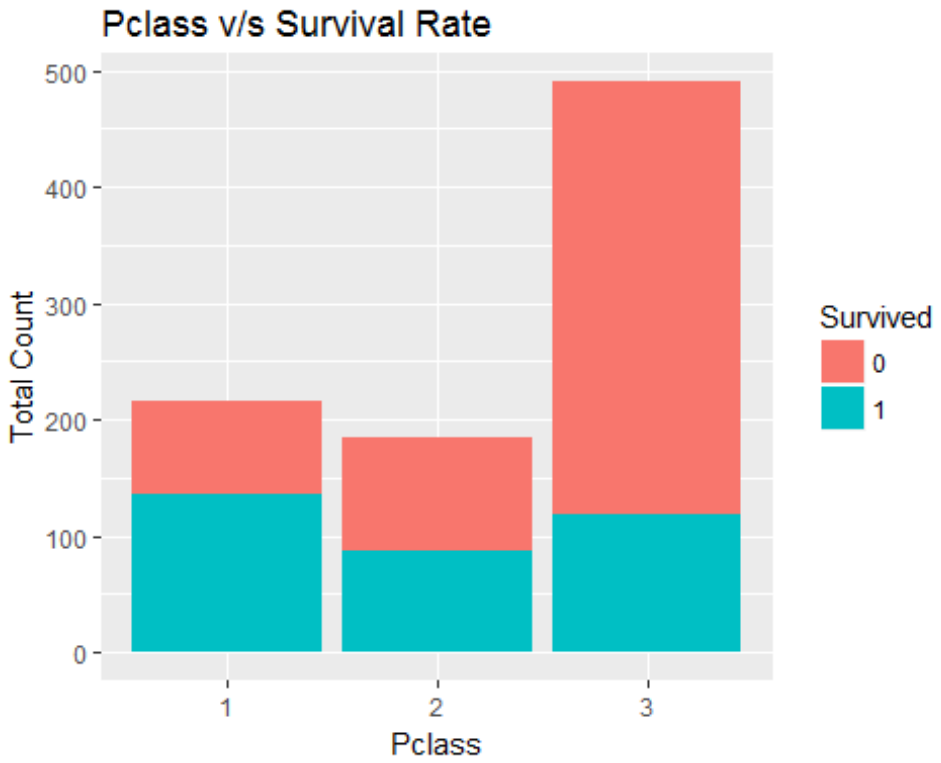
```
apply(full_titanic,2, function(x) length(unique(x)))
```

```
## PassengerId    Survived      Pclass        Name         Sex         Age
##        1309           3           3        1307           2          99
##       SibSp       Parch      Ticket        Fare       Cabin    Embarked
##           7           8         929         282         187           3
```

```
## 위 변수들 중 “Survived”, “Pclass”, “Sex”, “Embarked”를 Factor 로 변환한다.

cols=c("Survived","Pclass","Sex","Embarked")
for (i in cols){
  full_titanic[,i]=as.factor(full_titanic[,i])
}
```

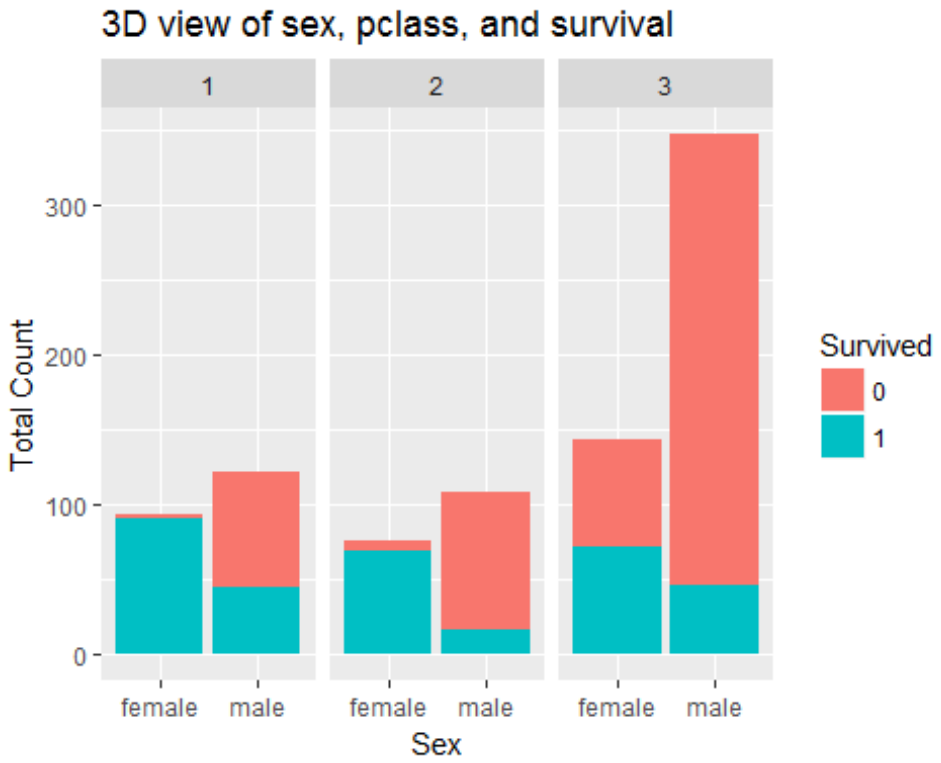
타이타닉호 에서 생존자 중 부유층이 가난한 사람들보다 더 많이 살아 남았다. 클라스별 생존자 비율을 그래프로 확인한다.

```
ggplot(full_titanic[1:891,],aes(x = Pclass,fill=factor(Survived))) +
geom_bar() +
ggtitle("Pclass v/s Survival Rate")+
xlab("Pclass") +
ylab("Total Count") +
labs(fill = "Survived")
```



그래프를 보면 1 번째 클라스에 있는 사람들이 3 번째 클라스에 있는 사람들 보다 생존율이 더 높다

```
## Sex, Pclass, Survived 에 대한 관계를 그래프로 확인한다

ggplot(full_titanic[1:891,], aes(x = Sex, fill = Survived)) +
geom_bar() +
facet_wrap(~Pclass) +
ggtitle("3D view of sex, pclass, and survival") +
xlab("Sex") +
ylab("Total Count") +
labs(fill = "Survived")
```




```
## Name 컬럼에서 생존율과의 관계를 확인한다.

head(full_titanic$Name)

## [1] "Braund, Mr. Owen Harris"
## [2] "Cumings, Mrs. John Bradley (Florence Briggs Thayer)"
## [3] "Heikkinen, Miss. Laina"
## [4] "Futrelle, Mrs. Jacques Heath (Lily May Peel)"
## [5] "Allen, Mr. William Henry"
## [6] "Moran, Mr. James"

## 정규식을 이용해 Name 에서 title 을 축출한다.
names <- full_titanic$Name
title <-  gsub("^.*, (.*?)\\..*$", "\\1", names)

full_titanic$title <- title

table(title)

## title
##         Capt          Col          Don         Dona           Dr
##            1            4            1            1            8
##     Jonkheer         Lady        Major       Master         Miss
##            1            1            2           61          260
##         Mlle          Mme           Mr          Mrs           Ms
```

```
##            2            1          757          197            2
##          Rev          Sir the Countess
##            8            1            1
```

MISS, Mrs, Master, Mr 의 숫자가 많다. 생존율의 오버피팅을 막기 위해 여러 개의 다른 타이틀을 큰 그룹으로 합친다.

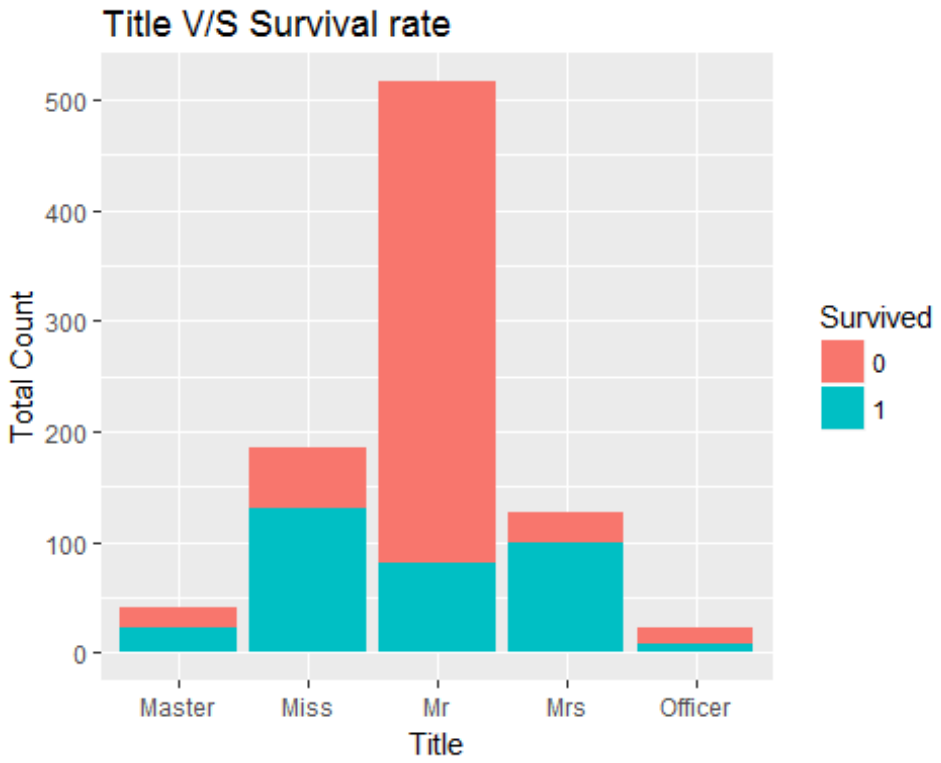
```
full_titanic$title[full_titanic$title == 'Mlle']        <- 'Miss'
full_titanic$title[full_titanic$title == 'Ms']          <- 'Miss'
full_titanic$title[full_titanic$title == 'Mme']         <- 'Mrs'
full_titanic$title[full_titanic$title == 'Lady']          <- 'Miss'
full_titanic$title[full_titanic$title == 'Dona']          <- 'Miss'
```

작은 데이터를 새로운 변수로 생성하는 것에 대한 우려가 있어, 기존의 변수에 합치는 것으로 결정한다. 군인, 의사, 일반인 등을 아래 분류로 합친다.

```
full_titanic$title[full_titanic$title == 'Capt']        <- 'Officer'
full_titanic$title[full_titanic$title == 'Col']        <- 'Officer'
full_titanic$title[full_titanic$title == 'Major']   <- 'Officer'
full_titanic$title[full_titanic$title == 'Dr']   <- 'Officer'
full_titanic$title[full_titanic$title == 'Rev']   <- 'Officer'
full_titanic$title[full_titanic$title == 'Don']   <- 'Officer'
full_titanic$title[full_titanic$title == 'Sir']   <- 'Officer'
full_titanic$title[full_titanic$title == 'the Countess']   <- 'Officer'
full_titanic$title[full_titanic$title == 'Jonkheer']   <- 'Officer'
```

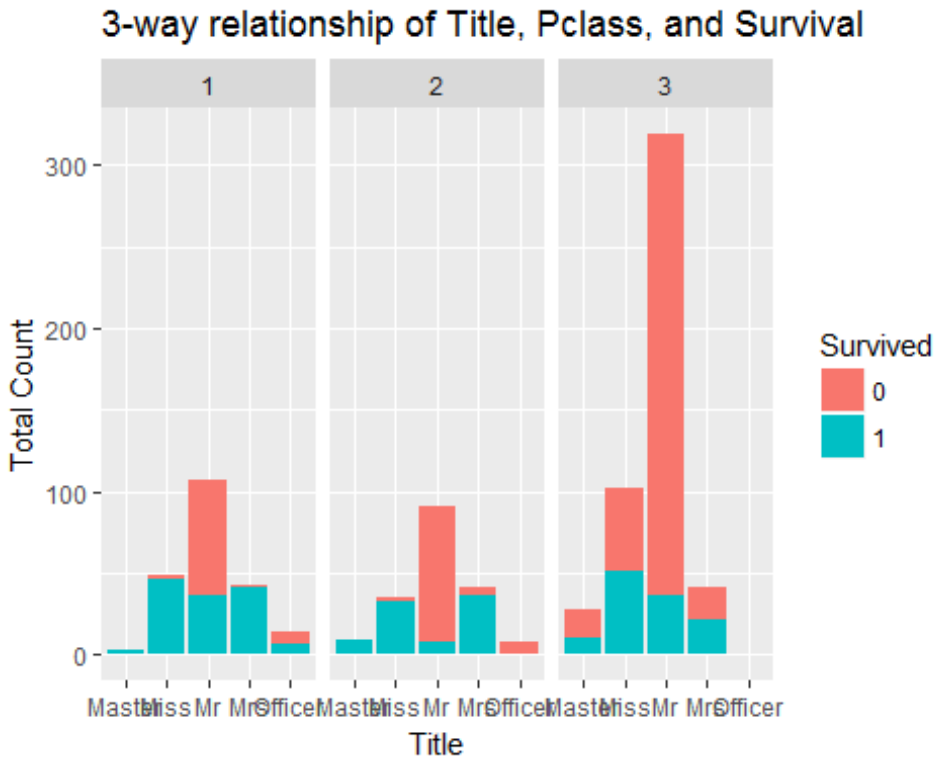
높은 생존율을 갖는 title 에대한 점검

```
ggplot(full_titanic[1:891,],aes(x = title,fill=factor(Survived))) +
  geom_bar() +
  ggtitle("Title V/S Survival rate")+
  xlab("Title") +
  ylab("Total Count") +
  labs(fill = "Survived")
```

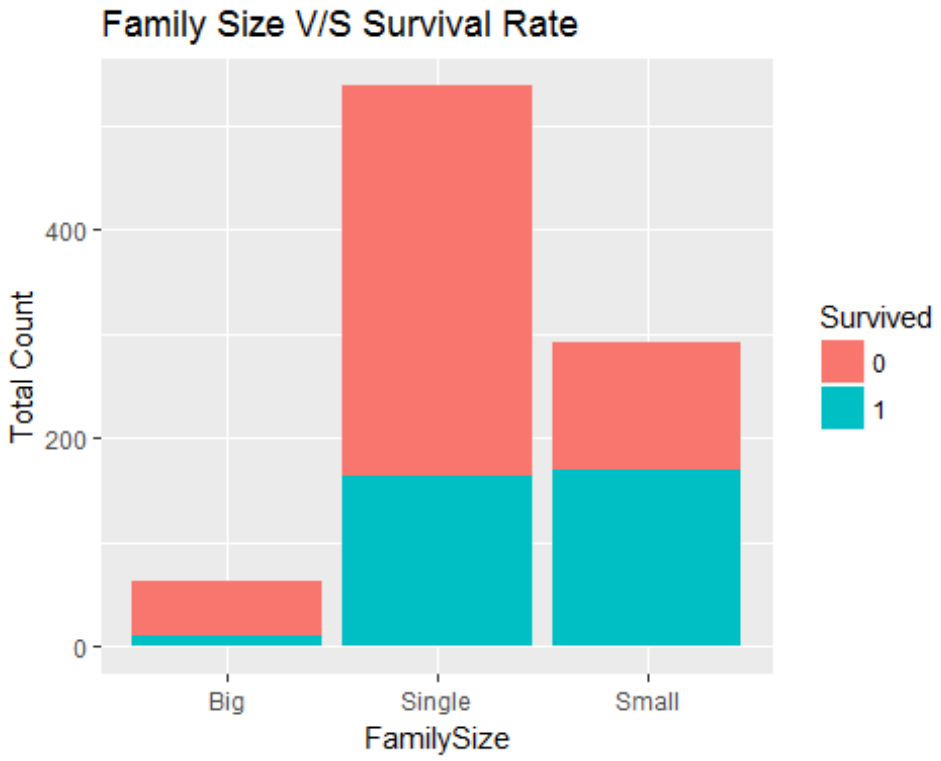


위의 그래프를 보면 Mr 는 아주 낮은 생존율을 갖는다. 반면, Miss 와 Mrs 는 Master 와 Officer 보다 높은 생존율을 갖는다.

```
### Title, Pclass, Survival 3 변수에 대한 시각화

ggplot(full_titanic[1:891,], aes(x = title, fill = Survived)) +
    geom_bar() +
    facet_wrap(~Pclass) +
    ggtitle("3-way relationship of Title, Pclass, and Survival") +
    xlab("Title") +
    ylab("Total Count") +
    labs(fill = "Survived")
```



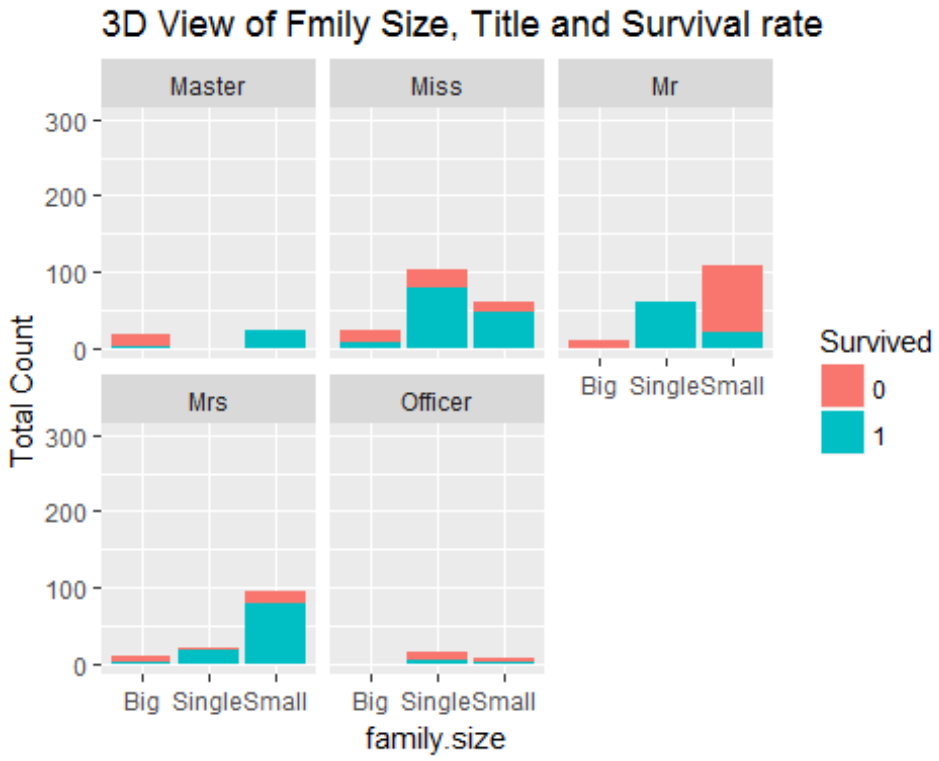

```
### Sibsp 와 Parch 를 이용해 Family Size 생성하기

full_titanic$FamilySize <-full_titanic$SibSp + full_titanic$Parch + 1

full_titanic$FamilySized[full_titanic$FamilySize == 1]   <- 'Single'
full_titanic$FamilySized[full_titanic$FamilySize < 5 & full_titanic$FamilySiz
e >= 2]   <- 'Small'
full_titanic$FamilySized[full_titanic$FamilySize >= 5]   <- 'Big'

full_titanic$FamilySized=as.factor(full_titanic$FamilySized)



### Family Size 로 생존율 시각화
ggplot(full_titanic[1:891,],aes(x = FamilySized,fill=factor(Survived))) +
  geom_bar() +
  ggtitle("Family Size V/S Survival Rate") +
  xlab("FamilySize") +
  ylab("Total Count") +
  labs(fill = "Survived")
```



타이타닉에서 많은 가족수를 갖고 있는 사람들은 혼자이거나 작은 가족수를 갖는 사람들보다 생존율이 낮다.

시각화를 통해 대가족의 생존율을 확인한다.

```
ggplot(full_titanic[1:891,], aes(x = FamilySized, fill = Survived)) +
  geom_bar() +
  facet_wrap(~title) +
  ggtitle("3D View of Fmily Size, Title and Survival rate") +
  xlab("family.size") +
  ylab("Total Count") +
  ylim(0,300) +
  labs(fill = "Survived")
```

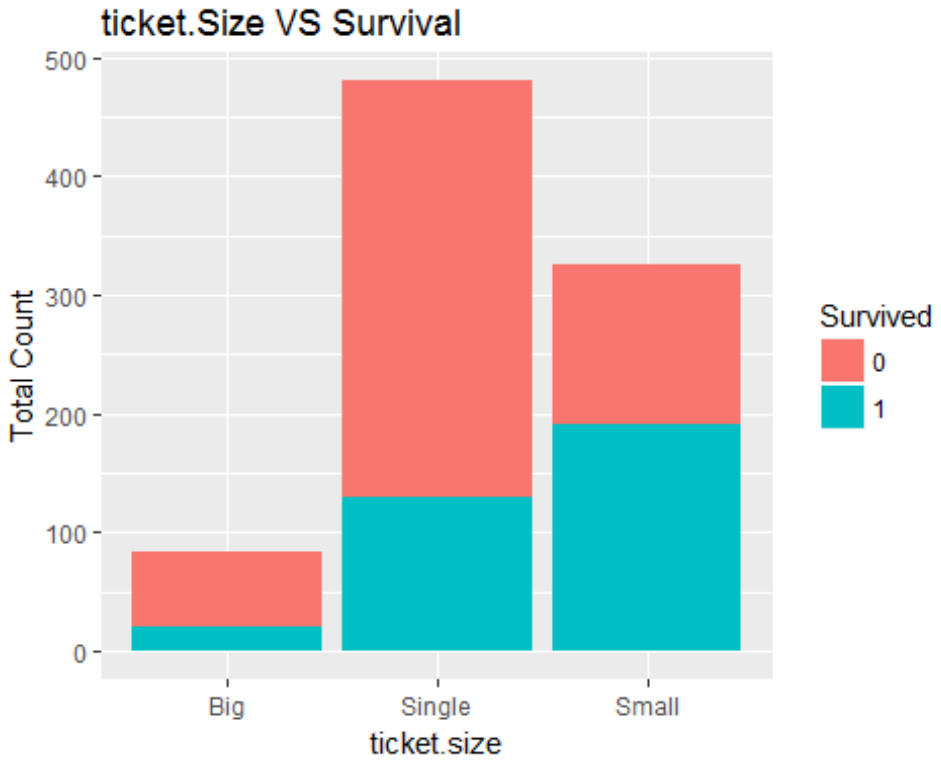


Family Size, Title, Survived 에 대한 그래프이다. 대가족인 경우 생존율이 보다 작은 가족 구성원 보다 훨씬 낮은 것을 알 수 있다.

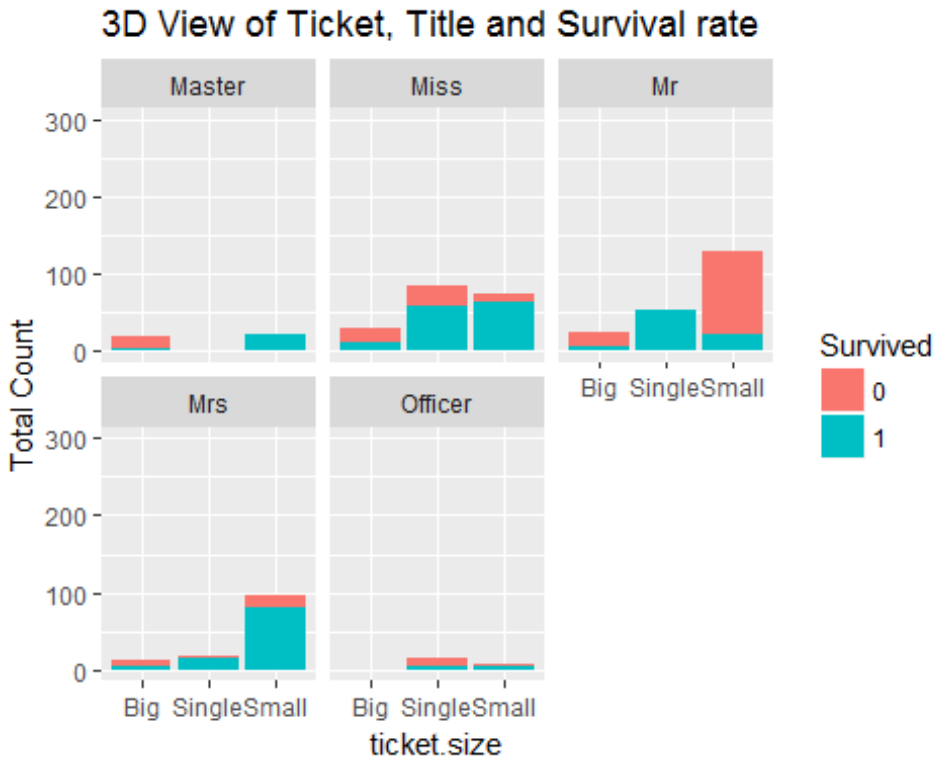
동일한 Ticket 을 가진 승객을 기반으로 한 분석

```
ticket.unique <- rep(0, nrow(full_titanic))
tickets <- unique(full_titanic$Ticket)

for (i in 1:length(tickets)) {
  current.ticket <- tickets[i]
  party.indexes <- which(full_titanic$Ticket == current.ticket)


  for (k in 1:length(party.indexes)) {
    ticket.unique[party.indexes[k]] <- length(party.indexes)
  }
}

full_titanic$ticket.unique <- ticket.unique


full_titanic$ticket.size[full_titanic$ticket.unique == 1]   <- 'Single'
full_titanic$ticket.size[full_titanic$ticket.unique < 5 & full_titanic$ticket.
```

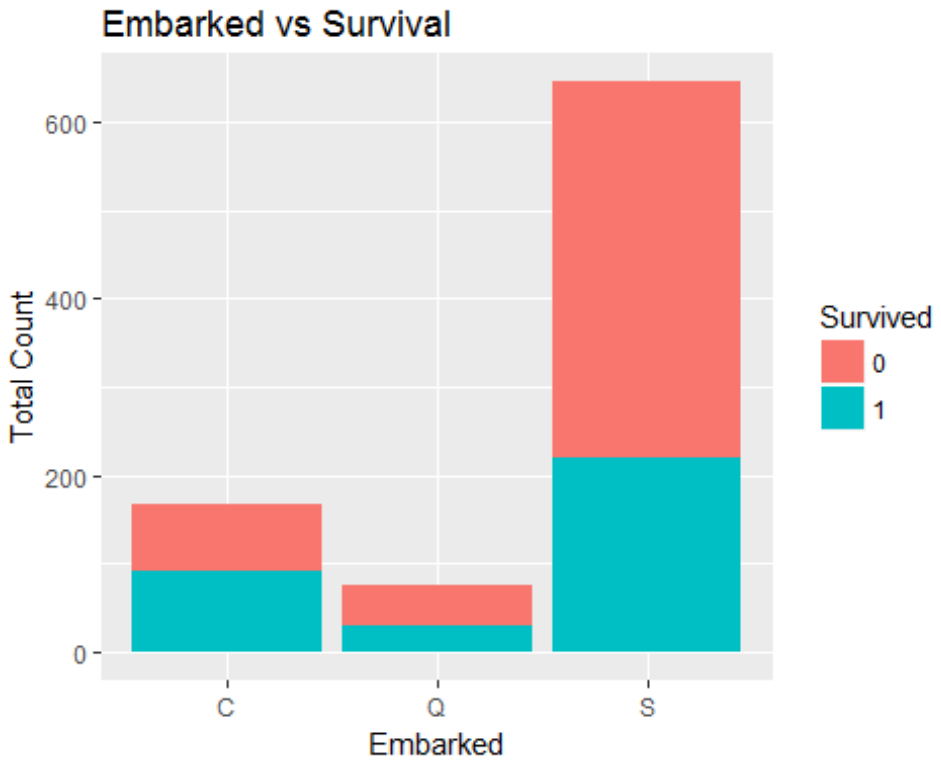
```
unique>= 2]   <- 'Small'
full_titanic$ticket.size[full_titanic$ticket.unique >= 5]   <- 'Big'

## 그래프를 통해 Ticket 사이즈를 확인한다.
ggplot(full_titanic[1:891,],aes(x = ticket.size,fill=factor(Survived))) +
  geom_bar() +
  ggtitle("ticket.Size VS Survival")+
  xlab("ticket.size") +
  ylab("Total Count") +
  labs(fill = "Survived")
```



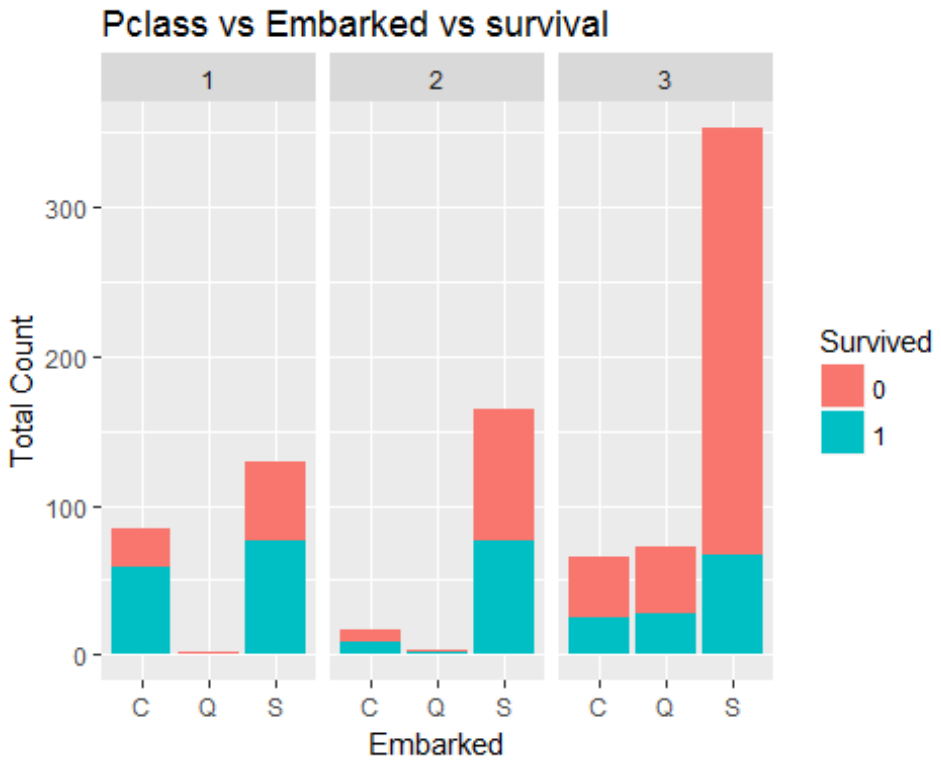

```
## 그래프를 통해 Ticket 와 Title 의 규모를 확인한다.
ggplot(full_titanic[1:891,], aes(x = ticket.size, fill = Survived)) +
  geom_bar() +
  facet_wrap(~title) +
  ggtitle("3D View of Ticket, Title and Survival rate") +
  xlab("ticket.size") +
  ylab("Total Count") +
  ylim(0,300) +
  labs(fill = "Survived")
```




```
Family Size 와 Ticket Size 에 대한 큰 차이점은 없다.

### 승선 위치에 따른 생존율에 관계를 확인한다.
ggplot(full_titanic[1:891,],aes(x = Embarked,fill=factor(Survived))) +
  geom_bar() +
  ggtitle("Embarked vs Survival") +
  xlab("Embarked") +
  ylab("Total Count") +
  labs(fill = "Survived")
```




```
## Pclass 별 Embardedd 위치를 나눈 시각화
ggplot(full_titanic[1:891,], aes(x = Embarked, fill = Survived)) +
  geom_bar() +
  facet_wrap(~Pclass) +
  ggtitle("Pclass vs Embarked vs survival") +
  xlab("Embarked") +
  ylab("Total Count") +
  labs(fill = "Survived")
```



Embarked 와 Survived 와의 관계는 별로 없어 보인다.

Cabin 에는 결측값들이 많아 사용하기 좋지 않아 보인다.

Age 를 대신해 Title 을 사용한다.

그리고, Fare 와 Pclass 와는 관계가 높음으로 분석대상으로 선정한다.

```
full_titanic$ticket.size <- as.factor(full_titanic$ticket.size)
full_titanic$title <- as.factor(full_titanic$title)
```

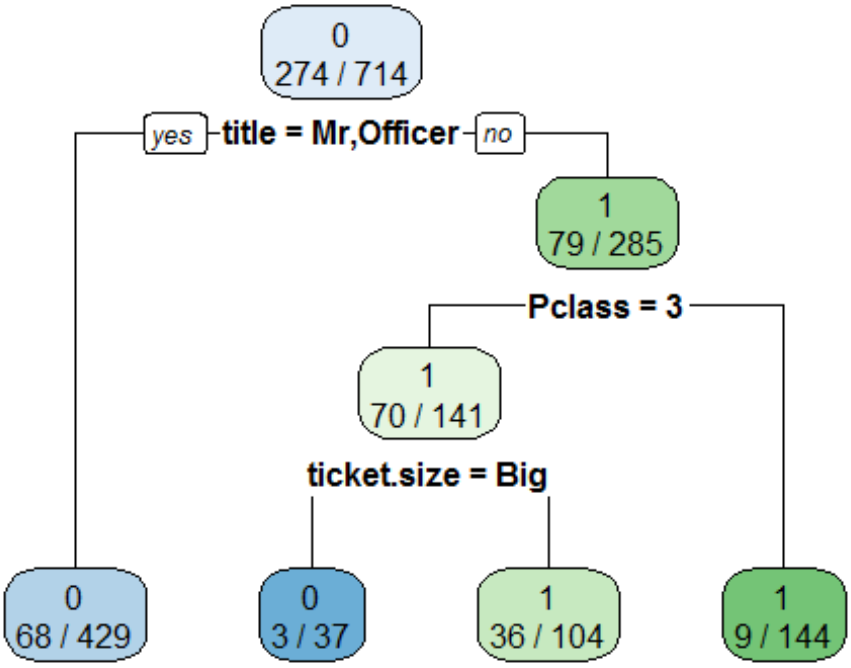
3. 변수 선정

```
## 지금까지 분석한 내용을 바탕으로 모델에 사용할 변수를 정리한다.

##"Pclass", "title","Sex","Embarked","FamilySized","ticket.size"

## 중복된 변수들은 삭제하고 적당한 형식으로 데이터를 변경한다.

feauter1<-full_titanic[1:891, c("Pclass", "title","Sex","Embarked","FamilySized","ticket.size")]
```

```
response <- as.factor(train.tit$Survived)
feauter1$Survived=as.factor(train.tit$Survived)


### 데이터 검증을 위해 원본 데이터에서 20%를 사용하지 않고 남겨둔다.

set.seed(500)
ind=createDataPartition(feauter1$Survived,times=1,p=0.8,list=FALSE)
train_val=feauter1[ind,]
test_val=feauter1[-ind,]

#### 원본 training 데이터, train 와 test 데이터의 생존율 비율을 확인한다.

round(prop.table(table(train.tit$Survived)*100),digits = 1)

##
##   0   1
## 0.6 0.4

round(prop.table(table(train_val$Survived)*100),digits = 1)

##
##   0   1
## 0.6 0.4

round(prop.table(table(test_val$Survived)*100),digits = 1)

##
##   0   1
## 0.6 0.4
```

4. 모델생성 및 예측

```
의사결정 트리 (Decision tree)


set.seed(1234)
Model_DT=rpart(Survived~.,data=train_val,method="class")

rpart.plot(Model_DT,extra =  3,fallen.leaves = T)
```




```
## Plot 내용을 보면, Single tee 모델에서 Title, Pclass, Ticket.size 변수를 사용하고 있다. 그외 변수들은 사용하지 않는다.

### train 데이터를 Predict 하고 single tree 의 정확성을 확인한다.

PRE_TDT=predict(Model_DT,data=train_val,type="class")
confusionMatrix(PRE_TDT,train_val$Survived)

## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 395  71
##          1  45 203
##
##                Accuracy : 0.8375
##                  95% CI : (0.8084, 0.8639)
##     No Information Rate : 0.6162
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.6502
##  Mcnemar's Test P-Value : 0.02028
##
##             Sensitivity : 0.8977
##             Specificity : 0.7409
```

```
##          Pos Pred Value : 0.8476
##          Neg Pred Value : 0.8185
##              Prevalence : 0.6162
##          Detection Rate : 0.5532
##    Detection Prevalence : 0.6527
##       Balanced Accuracy : 0.8193
##
##        'Positive' Class : 0
##
```

Accuracy 가 0.8375 이다.

그리 나쁜 결과는 아니다. 3 개의 변수만 사용했다.

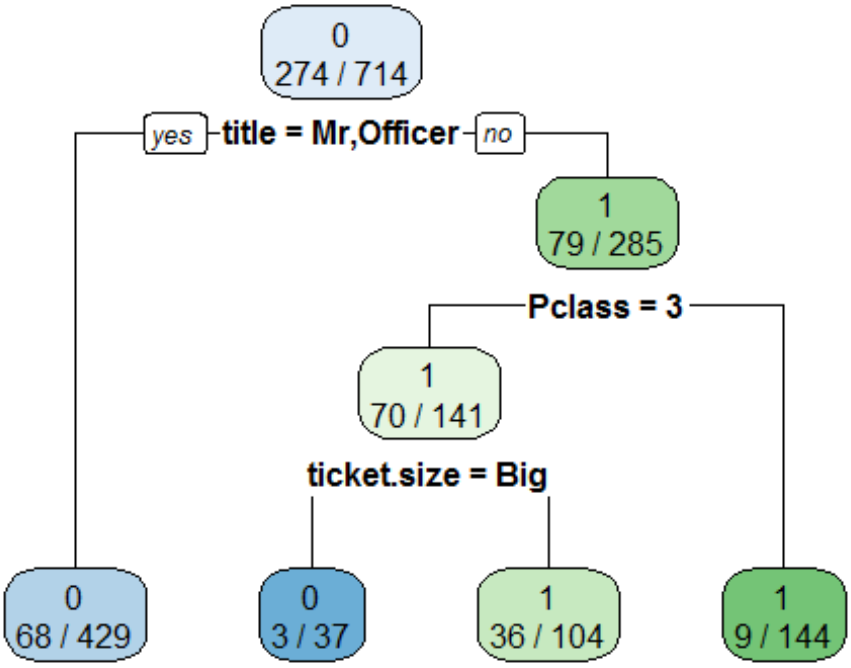
Single tree 는 Overfitting 이 발생할 수 있어, '10 fold 알고리즘'을 사용해 검증한다.

```
set.seed(1234)
cv.10 <- createMultiFolds(train_val$Survived, k = 10, times = 10)

# 조절
ctrl <- trainControl(method = "repeatedcv", number = 10, repeats = 10,
                     index = cv.10)

## 모델생성
Model_CDT <- train(x = train_val[,-7], y = train_val[,7], method = "rpart", t
uneLength = 30, trControl = ctrl)
```

Accuracy 가 0.8139 이다. 앞의 Single tree 에서 Overfitting 된 것으로 보인다.

중요 변수를 확인한다. Single tree 와 동일한 결과인가?

```
rpart.plot(Model_CDT$finalModel,extra =  3,fallen.leaves = T)
```



사용된 변수에는 차이가 없다.

```
### test 데이터로 정확성을 확인한다.
PRE_VDTS=predict(Model_CDT$finalModel,newdata=test_val,type="class")
confusionMatrix(PRE_VDTS,test_val$Survived)
```

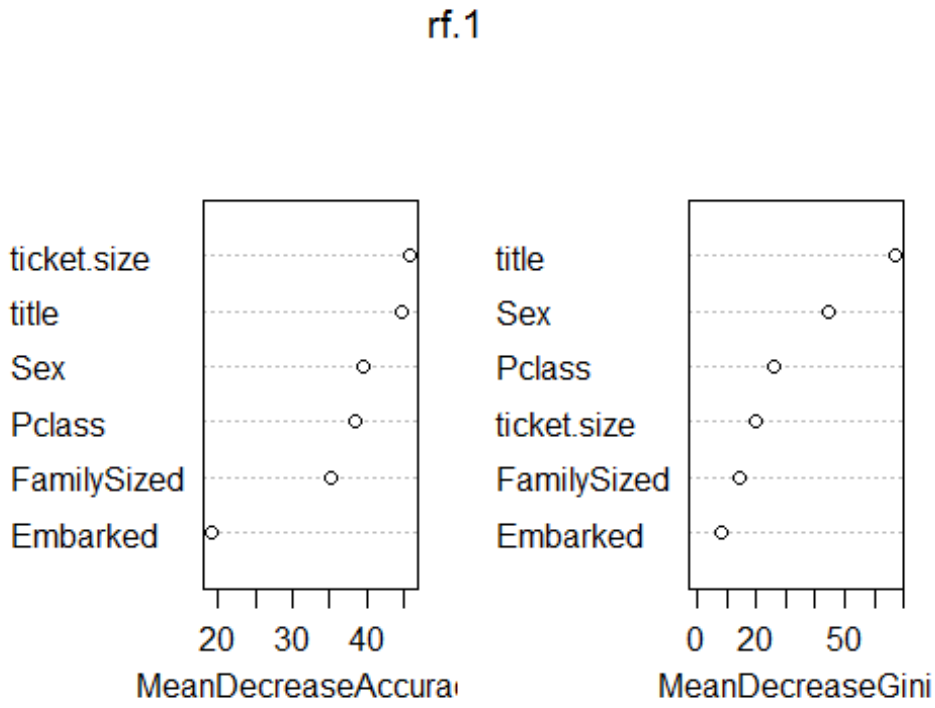
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
##          0 97 20
##          1 12 48
##
##                Accuracy : 0.8192
##                  95% CI : (0.7545, 0.8729)
##     No Information Rate : 0.6158
##     P-Value [Acc > NIR] : 3.784e-09
##
##                   Kappa : 0.6093
##  Mcnemar's Test P-Value : 0.2159
##
##             Sensitivity : 0.8899
##             Specificity : 0.7059
##          Pos Pred Value : 0.8291
##          Neg Pred Value : 0.8000
```

```
##              Prevalence : 0.6158
##          Detection Rate : 0.5480
##    Detection Prevalence : 0.6610
##       Balanced Accuracy : 0.7979
##
##        'Positive' Class : 0
##
```

Accuracy 가 0.8192 이다.

랜덤포레스트 (Random Forest)

```
#install.packages("randomForest")
library(randomForest)
set.seed(1234)
rf.1 <- randomForest(x = train_val[,-7],y=train_val[,7], importance = TRUE, n
tree = 1000)
rf.1

##
## Call:
##  randomForest(x = train_val[, -7], y = train_val[, 7], ntree = 1000,
importance = TRUE)
##                Type of random forest: classification
##                      Number of trees: 1000
## No. of variables tried at each split: 2
##
##         OOB estimate of  error rate: 17.09%
## Confusion matrix:
##     0   1 class.error
## 0 395  45   0.1022727
## 1  77 197   0.2810219

varImpPlot(rf.1)
```



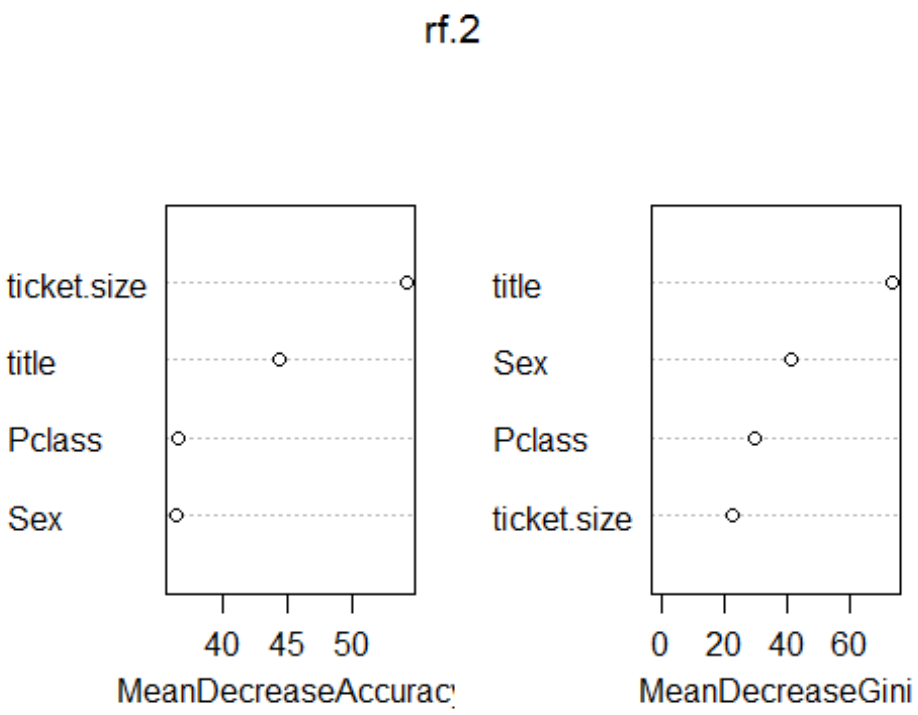
랜덤포레스트 accuracy rate 는 82.91 이다. 의사결정 트리 보다 1% 더 낫다.

중복 변수 2 개를 삭제하고 모델을 재생성한다.

```
train_val1=train_val[,-4:-5]
test_val1=test_val[,-4:-5]

set.seed(1234)
rf.2 <- randomForest(x = train_val1[,-5],y=train_val1[,5], importance = TRUE,
 ntree = 1000)
rf.2

##
## Call:
##  randomForest(x = train_val1[, -5], y = train_val1[, 5], ntree = 1000,
  importance = TRUE)
##                Type of random forest: classification
##                      Number of trees: 1000
## No. of variables tried at each split: 2
##
##         OOB estimate of  error rate: 15.97%
## Confusion matrix:
##     0   1 class.error
```

```
## 0 395  45   0.1022727
## 1  69 205   0.2518248
```

```
varImpPlot(rf.2)
```



2 변수 삭제로 인해, accuracy 가 84.03 으로 증가했다.

교차 검증을 한 후 모델을 선정한다.

```
library(caret)
set.seed(2348)
cv10_1 <- createMultiFolds(train_val1[,5], k = 10, times = 10)

# caret 의 trainControl 를 구성한다.
ctrl_1 <- trainControl(method = "repeatedcv", number = 10, repeats = 10,
                       index = cv10_1)


set.seed(1234)
rf.5<- train(x = train_val1[,-5], y = train_val1[,5], method = "rf", tuneLeng
th = 3,
             ntree = 1000, trControl =ctrl_1)

rf.5
```

```
## Random Forest
##
## 714 samples
##   4 predictor
##   2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 10 times)
## Summary of sample sizes: 642, 643, 642, 643, 643, 643, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##   2     0.8392390  0.6538299
##   3     0.8382551  0.6518851
##   4     0.8368466  0.6489636
##
## Accuracy was used to select the optimal model using  the largest value.
## The final value used for the model was mtry = 2.
```

교차 검증결과 accuracy rate 는 0.8393 이다.

Test data 를 예측한다.

```
pr.rf=predict(rf.5,newdata = test_val1)

confusionMatrix(pr.rf,test_val1$Survived)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
##          0 97 20
##          1 12 48
##
##                Accuracy : 0.8192
##                  95% CI : (0.7545, 0.8729)
##     No Information Rate : 0.6158
##     P-Value [Acc > NIR] : 3.784e-09
##
##                   Kappa : 0.6093
##  Mcnemar's Test P-Value : 0.2159
##
##             Sensitivity : 0.8899
##             Specificity : 0.7059
##          Pos Pred Value : 0.8291
##          Neg Pred Value : 0.8000
##              Prevalence : 0.6158
##          Detection Rate : 0.5480
```

```
##    Detection Prevalence : 0.6610
##       Balanced Accuracy : 0.7979
##
##        'Positive' Class : 0
##
```

accuracy rate 는 0.8192 로 기대 보다 낮았다.

서포트 백터 머신(Support Vector Machine)

```
library(e1071)
set.seed(1274)
liner.tune=tune.svm(Survived~.,data=train_val1,kernel="linear",cost=c(0.01,0.
1,0.2,0.5,0.7,1,2,3,5,10,15,20,50,100))

liner.tune
```

```
##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  cost
##     3
##
## - best performance: 0.1736502
```

Cost=3 일때, 최고의 성능을 낸다. Accuracy rate 가 82.7 이다.

```
### 최상의 liner 모델을 생성한다.
best.linear=liner.tune$best.model

## test data 를 이용해 Survival rate 을 예측한다.

best.test=predict(best.linear,newdata=test_val1,type="class")
confusionMatrix(best.test,test_val1$Survived)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
```

```
##          0 97 21
##          1 12 47
##
##                Accuracy : 0.8136
##                  95% CI : (0.7483, 0.8681)
##     No Information Rate : 0.6158
##     P-Value [Acc > NIR] : 1.058e-08
##
##                   Kappa : 0.5959
##  Mcnemar's Test P-Value : 0.1637
##
##             Sensitivity : 0.8899
##             Specificity : 0.6912
##          Pos Pred Value : 0.8220
##          Neg Pred Value : 0.7966
##              Prevalence : 0.6158
##          Detection Rate : 0.5480
##    Detection Prevalence : 0.6667
##       Balanced Accuracy : 0.7905
##
##        'Positive' Class : 0
##
```

Linear 모델 accuracy 는 0.8136 이다.

Radial Support vector Machine

```
set.seed(1274)

rd.poly=tune.svm(Survived~.,data=train_val1,kernel="radial",gamma=seq(0.1,5))

summary(rd.poly)
```

```
##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  gamma
##    2.1
##
## - best performance: 0.166608
##
## - Detailed performance results:
```

```
##   gamma     error dispersion
## 1   0.1 0.1680164 0.04245604
## 2   1.1 0.1680164 0.03983673
## 3   2.1 0.1666080 0.04166448
## 4   3.1 0.1666080 0.04166448
## 5   4.1 0.1666080 0.04166448
```

```
best.rd=rd.poly$best.model
```

Non Linear Kerenel 은 높은 accuracy 를 제공한다.

```
## test data 예측하기
pre.rd=predict(best.rd,newdata = test_val1)
```

```
confusionMatrix(pre.rd,test_val1$Survived)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
##          0 97 20
##          1 12 48
##
##                Accuracy : 0.8192
##                  95% CI : (0.7545, 0.8729)
##     No Information Rate : 0.6158
##     P-Value [Acc > NIR] : 3.784e-09
##
##                   Kappa : 0.6093
##  Mcnemar's Test P-Value : 0.2159
##
##             Sensitivity : 0.8899
##             Specificity : 0.7059
##          Pos Pred Value : 0.8291
##          Neg Pred Value : 0.8000
##              Prevalence : 0.6158
##          Detection Rate : 0.5480
##    Detection Prevalence : 0.6610
##       Balanced Accuracy : 0.7979
##
##        'Positive' Class : 0
##
```

Non Liner 모델은 사용한 test data 의 accuracy 는 0.81 이다.

로지스틱 회귀모델 (Logistic Regression)

```
contrasts(train_val1$Sex)
```

```
##        male
## female    0
## male      1
```

```
contrasts(train_val1$Pclass)
```

```
##   2 3
## 1 0 0
## 2 1 0
## 3 0 1
```

```
## 변수가 어떻게 구성되어 있는지 확인한다.


## 로지스틱 회귀 모델을 실행한다.
log.mod <- glm(Survived ~ ., family = binomial(link=logit),
               data = train_val1)
### summary 확인
summary(log.mod)
```

```
##
## Call:
## glm(formula = Survived ~ ., family = binomial(link = logit),
##     data = train_val1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.4187  -0.5944  -0.3937   0.5805   3.0414
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        16.8752   624.0921   0.027 0.978428
## Pclass2            -1.1968     0.3129  -3.824 0.000131 ***
## Pclass3            -2.1324     0.2721  -7.838 4.58e-15 ***
## titleMiss         -16.1021   624.0921  -0.026 0.979416
## titleMr            -3.7422     0.5216  -7.175 7.24e-13 ***
## titleMrs          -16.0186   624.0921  -0.026 0.979523
## titleOfficer       -4.3752     0.8595  -5.090 3.58e-07 ***
## Sexmale           -15.6157   624.0919  -0.025 0.980038
## ticket.sizeSingle   2.0968     0.4082   5.137 2.79e-07 ***
## ticket.sizeSmall    2.0356     0.3870   5.260 1.44e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 950.86  on 713  degrees of freedom
## Residual deviance: 589.82  on 704  degrees of freedom
## AIC: 609.82
##
## Number of Fisher Scoring iterations: 13
```

```r
confint(log.mod)
```

```
## Waiting for profiling to be done...

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

##                         2.5 %     97.5 %
## (Intercept)       -80.363813         NA
## Pclass2            -1.821261 -0.5924824
## Pclass3            -2.676712 -1.6082641
## titleMiss                 NA 81.1580568
## titleMr            -4.806899 -2.7544131
## titleMrs                  NA 81.2072009
## titleOfficer       -6.200669 -2.7777761
## Sexmale                   NA 81.9299127
## ticket.sizeSingle   1.318753  2.9224495
## ticket.sizeSmall    1.294852  2.8160324

###train data 예측하기
train.probs <- predict(log.mod, data=train_val1,type =  "response")
table(train_val1$Survived,train.probs>0.5)

##
##     FALSE TRUE
##   0   395   45
##   1    70  204

(395+204)/(395+204+70+45)

## [1] 0.8389356
```

로지스틱 회귀모델은 train data 에서 accuracy rate 을 0.83 으로 예측했다.

```
test.probs <- predict(log.mod, newdata=test_val1,type =  "response")
table(test_val1$Survived,test.probs>0.5)

##
##     FALSE TRUE
##   0    97   12
##   1    21   47

(97+47)/(97+12+21+47)

## [1] 0.8135593
```

teat data 의 accuracy rate 는 0.8135 이다.

여러 모델을 실행한 결과 대부분 결과가 비슷하게 나온 것을 확인할 수 있었다. 모델 선정도 중요하지만 데이터를 이해하고 변수 분석을 통해 좀더 예측 결과에 효과를 줄 수 있도록 결측치 처리 와 기존 변수를 통한 파생변수를 생성이 더 중요함을 느꼈다.