balance_data.R

SANGHOOJEFFREY

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```
if(!require(rpart)) install.packages("rpart", repos = "http://cran.us.r-project.org"); library(rpart)
```

```
## Loading required package: rpart
```

```
# randomforest, svm, decision tree 등의 machine learning(기계학습)을 현실적으로 적용시키는데
# 가장 많이 발생하는 문제는 클래스의 불균형이다.

# 분류에 해당하는 데이터의 비율이 반반이 아닌 경우 훈련 데이터 내 비율이 높은 분류 쪽으로 결과를 내놓는 모델을 만든다.
# 예) 돌발홍수가 발생한 자료 50, 발생되지 않은 자료 950 개인 경우
# 모형에서 모두 돌발홍수가 발생되지 않는다로 예측하더라도 예측정확도는 95%임.
# 따라서 분류를 잘하는 모형을 개발하기 위해선 데이터의 비율을 비슷하게 만들 필요가 있다.

if(!require(mlbench)) install.packages("mlbench", repos = "http://cran.us.r-project.org"); library(mlbench)
```

```
## Loading required package: mlbench
```

```
data(BreastCancer)

table(BreastCancer$Class)
```

```
##
##    benign malignant
##       458       241
```

```
# 양성 benign 이 458 개, 악성 malignant 가 241 개
# 그냥 모형을 세우게 되면 benign 을 잘 예측하는 모형을 만들 가능성이 높다.

# 클래스 불균형을 해결하기 위한 방법은 관찰 데이터가 적은 쪽에 더 큰 가중치(Weight)를 주는 방버
# 데이터가 적은 쪽으로 잘못 불류했을 때 더 많은 비용(cost 또는 loss)을 부과하는 방
```

```
법 등이 있다.

# 또 방법으로 훈련데이터를 동일하게 만드는 방법이 있다.

# 업샘플링, 다운샘플링
if(!require(caret)) install.packages("caret", repos = "http://cran.us.r-proje
ct.org"); library(caret)

## Loading required package: caret

## Warning: package 'caret' was built under R version 3.4.4

## Loading required package: lattice

## Loading required package: ggplot2

x <- upSample(subset(BreastCancer, select= -Class),BreastCancer$Class)
table(x$Class)

##
##    benign malignant
##       458       458

# x 내의 행의 상당수는 중복되어 생성되어 있다.

y <- downSample(subset(BreastCancer, select= -Class),BreastCancer$Class)
table(y$Class)

##
##    benign malignant
##       241       241

# y 의 Class 가 benign 인 경우 일부가 임의로 제거되었다.

# UpSample 으로 자료를 생성한 경우와 그냥 사용했을 경우 모형성능은 정말 차이가 날까?

data <- subset(BreastCancer, select=-Id)
set.seed(124)
parts <- createDataPartition(data$Class, p=0.8) # 80%는 훈련, 20%는 테스트 데이
터
data.train <- data[parts$Resample1,]
data.test <- data[-parts$Resample1,]
m.rpart <- rpart(Class ~., data=data.train)
confusionMatrix(data.test$Class, predict(m.rpart, newdat=data.test, type="cla
ss"))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  benign malignant
##   benign        86         5
##   malignant      5        43
##
##                Accuracy : 0.9281
##                  95% CI : (0.8717, 0.965)
##     No Information Rate : 0.6547
##     P-Value [Acc > NIR] : 2.775e-14
##
##                   Kappa : 0.8409
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9451
##             Specificity : 0.8958
##          Pos Pred Value : 0.9451
##          Neg Pred Value : 0.8958
##              Prevalence : 0.6547
##          Detection Rate : 0.6187
##    Detection Prevalence : 0.6547
##       Balanced Accuracy : 0.9204
##
##        'Positive' Class : benign
##
```

```
data2 <- upSample(subset(data.train, select= -Class),data.train$Class)
m.rpart2 <- rpart(Class ~., data=data2)
confusionMatrix(data.test$Class, predict(m.rpart2, newdat=data.test, type="cl
ass"))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  benign malignant
##   benign        86         5
##   malignant      2        46
##
##                Accuracy : 0.9496
##                  95% CI : (0.899, 0.9795)
##     No Information Rate : 0.6331
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.8902
##  Mcnemar's Test P-Value : 0.4497
##
##             Sensitivity : 0.9773
##             Specificity : 0.9020
```

```
##          Pos Pred Value : 0.9451
##          Neg Pred Value : 0.9583
##              Prevalence : 0.6331
##          Detection Rate : 0.6187
##    Detection Prevalence : 0.6547
##       Balanced Accuracy : 0.9396
##
##        'Positive' Class : benign
##
```

```
# SMOTE 함수
# 인접값들을 찾아 추가하는 방법으로, 비율이 낮은 분류의 데이터를 추가로 생성하거나
높은 쪽ㅇ 데이터를 적게 샘플링 해준다.
```

```
if(!require(DMwR)) install.packages("DMwR", repos = "http://cran.us.r-project.
org"); library(DMwR)
```

```
## Loading required package: DMwR
```

```
## Warning in library(package, lib.loc = lib.loc, character.only = TRUE,
## logical.return = TRUE, : there is no package called 'DMwR'
```

```
## Installing package into 'C:/Users/SANGHOOJEFFREY/Documents/R/win-library/3.
4'
## (as 'lib' is unspecified)
```

```
## package 'DMwR' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
##  C:\Users\SANGHOOJEFFREY\AppData\Local\Temp\RtmpIHijIW\downloaded_packages
```

```
## Warning: package 'DMwR' was built under R version 3.4.4
```

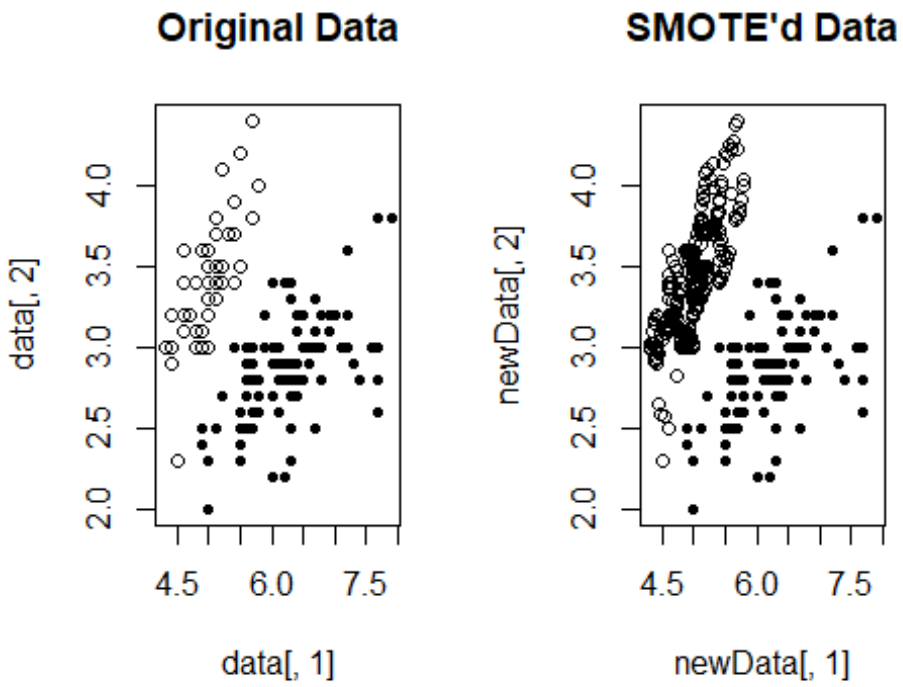
```
## Loading required package: grid
```

```
## A small example with a data set created artificially from the IRIS
## data
data(iris)
data <- iris[, c(1, 2, 5)]
data$Species <- factor(ifelse(data$Species == "setosa","rare","common"))
## checking the class distribution of this artificial data set
table(data$Species)
```

```
##
## common   rare
##    100     50
```

```
## now using SMOTE to create a more "balanced problem"
newData <- SMOTE(Species ~ ., data, perc.over = 600,perc.under=100)
table(newData$Species)
```

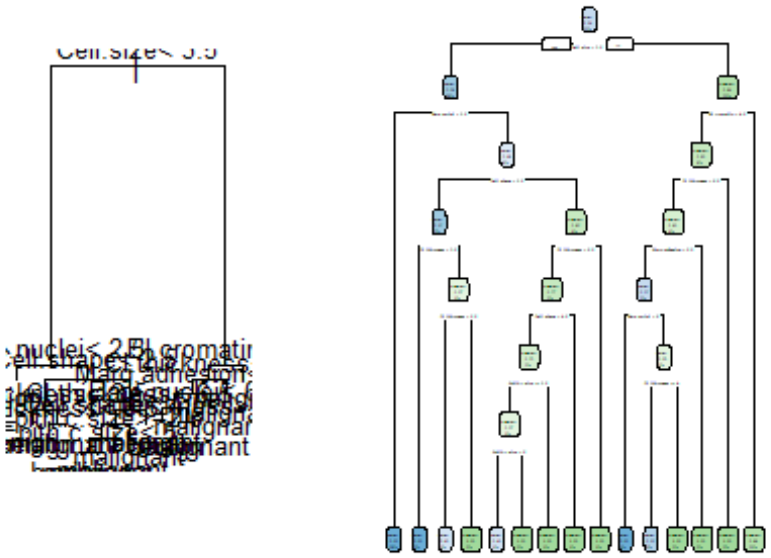
```
##
## common   rare
##    300    350

## Checking visually the created data
## Not run:
par(mfrow = c(1, 2))
plot(data[, 1], data[, 2], pch = 19 + as.integer(data[, 3]),
     main = "Original Data")
plot(newData[, 1], newData[, 2], pch = 19 + as.integer(newData[,3]),
     main = "SMOTE'd Data")
```




```
## End(Not run)

## Now an example where we obtain a model with the "balanced" data
classTree <- SMOTE(Species ~ ., data, perc.over = 600,perc.under=100,
                   learner='rpartXse',se=0.5)
## check the resulting classification tree
classTree

## n= 650
##
## node), split, n, loss, yval, (yprob)
##       * denotes terminal node
##
##  1) root 650 300 rare (0.46153846 0.53846154)
```

```
##    2) Sepal.Length>=5.499929 305  24 common (0.92131148 0.07868852)
##      4) Sepal.Width< 3.819972 286   5 common (0.98251748 0.01748252)
##        8) Sepal.Width< 3.45 271   0 common (1.00000000 0.00000000) *
##        9) Sepal.Width>=3.45 15   5 common (0.66666667 0.33333333)
##         18) Sepal.Length>=6.45 10   0 common (1.00000000 0.00000000) *
##         19) Sepal.Length< 6.45 5   0 rare (0.00000000 1.00000000) *
##      5) Sepal.Width>=3.819972 19   0 rare (0.00000000 1.00000000) *
##    3) Sepal.Length< 5.499929 345  19 rare (0.05507246 0.94492754)
##      6) Sepal.Width< 2.759635 21   4 common (0.80952381 0.19047619)
##       12) Sepal.Length>=4.7 17   0 common (1.00000000 0.00000000) *
##       13) Sepal.Length< 4.7 4   0 rare (0.00000000 1.00000000) *
##      7) Sepal.Width>=2.759635 324   2 rare (0.00617284 0.99382716) *

## The tree with the unbalanced data set would be
rpartXse(Species ~ .,data,se=0.5)

## n= 150
##
## node), split, n, loss, yval, (yprob)
##       * denotes terminal node
##
##  1) root 150 50 common (0.66666667 0.33333333)
##    2) Sepal.Length>=5.45 98  5 common (0.94897959 0.05102041)
##      4) Sepal.Width< 3.45 90  0 common (1.00000000 0.00000000) *
##      5) Sepal.Width>=3.45 8  3 rare (0.37500000 0.62500000)
##       10) Sepal.Length>=6.5 3  0 common (1.00000000 0.00000000) *
##       11) Sepal.Length< 6.5 5  0 rare (0.00000000 1.00000000) *
##    3) Sepal.Length< 5.45 52  7 rare (0.13461538 0.86538462)
##      6) Sepal.Width< 2.8 7  1 common (0.85714286 0.14285714) *
##      7) Sepal.Width>=2.8 45  1 rare (0.02222222 0.97777778) *

################################################################################
#########
if(!require(rpart)) install.packages("rpart");library(rpart)
if(!require(rpart.plot)) install.packages("rpart.plot");library(rpart.plot)

## Loading required package: rpart.plot

set.seed(42)
index <- createDataPartition(BreastCancer$Class, p = 0.7, list = FALSE)

train_data <- BreastCancer[index, -1]
test_data  <- BreastCancer[-index, -1]

train_data[,1:9] <- apply(train_data[, 1:9], 2, function(x) as.numeric(as.cha
racter(x)))
test_data[,1:9] <- apply(test_data[, 1:9], 2, function(x) as.numeric(as.chara
cter(x)))
```

```r
set.seed(42)
fit <- rpart(Class ~ .,
             data = train_data,
             method = "class",
             control = rpart.control(xval = 10,
                                     minbucket = 2,
                                     cp = 0),
             parms = list(split = "information"))

plot(fit)
text(fit, cex=0.8)

rpart.plot(fit)
```



```r
# logistic regression 으로 세운다면 그리고 그 결과
# randomforest 로 세운다면
# SVM 으로 세운다면

# UpSample 된 자료로 rpart, randomforest 을 돌려보자.
```