

Statistical_Mechine_Learning_Final

Hyeonho Lee

2018년 9월 9일

Question 1

It is well-known that ridge regression tends to give similar coefficient values to correlated variables, whereas the lasso may give quite different coefficient values to correlated variables. We will now explore this property in a very simple setting.

Suppose that $n = 2, p = 2, x_{11} = x_{12}, x_{21} = x_{22}$. Furthermore, suppose that $y_1 + y_2 = 0$ and $x_{11} + x_{21} = 0$ and $x_{12} + x_{22} = 0$, so that the estimate for the intercept in a least squares, ridge regression, or lasso model is zero: $\hat{\beta}_0$.

1. Write out the ridge regression optimization problem in this setting.

Answer :

A general form of Ridge regression optimization looks like :

$$\sum_{i=1}^n (y_i - \hat{\beta}_0 - \sum_{j=1}^p \hat{\beta}_j x_{ij})^2 + \lambda \sum_{j=1}^p \hat{\beta}_j^2$$

In this case, $\hat{\beta}_0 = 0$ and $n = p = 2$.

So, the optimization looks like *Minimize* : $(y_1 - \hat{\beta}_1 x_{11} - \hat{\beta}_2 x_{12})^2 + (y_2 - \hat{\beta}_1 x_{21} - \hat{\beta}_2 x_{22})^2 + \lambda(\hat{\beta}_1^2 + \hat{\beta}_2^2)$

2. Argue that in this setting, the ridge coefficient estimates satisfy $\hat{\beta}_1 = \hat{\beta}_2$

Answer :

Argue that in this setting, the ridge coefficient estimates satisfy $\hat{\beta}_1 = \hat{\beta}_2$. Given the situations that $x_{11} = x_{12} = x_1, x_{21} = x_{22} = x_2$, take the derivatives of the expression in (a) with respect to both $\hat{\beta}_1$ and $\hat{\beta}_2$ and setting them equal zero, then we get

$$\hat{\beta}_1^* = \frac{x_1 y_1 + x_2 y_2 - \hat{\beta}_2^* (x_1^2 + x_2^2)}{\lambda + x_1^2 + x_2^2}$$

$$\hat{\beta}_2^* = \frac{x_1 y_1 + x_2 y_2 - \hat{\beta}_1^* (x_1^2 + x_2^2)}{\lambda + x_1^2 + x_2^2}$$

The symmetry form in the above formula suggests that $\hat{\beta}_1 = \hat{\beta}_2$

3. Write ou the lasso optimization problem in this setting.

Answer :

The optimization looks like

Minimize : $(y_1 - \hat{\beta}_1 x_{11} - \hat{\beta}_2 x_{12})^2 + (y_2 - \hat{\beta}_1 x_{21} - \hat{\beta}_2 x_{22})^2 + \lambda(|\hat{\beta}_1| + |\hat{\beta}_2|)$

4. Argue that in this setting, the lasso coefficients $\hat{\beta}_1$ and $\hat{\beta}_2$ are not unique—in other words, there are many possible solutions to the optimization problem in 3. Describe these solutions.

Answer : The Lasso constraint takes the form $|\hat{\beta}_1| + |\hat{\beta}_2| < s$ which plotted takes the shape of a diamond centered at origin (0,0). Next consider the squared optimization constraint $(y_1 - \hat{\beta}_1 x_{11} - \hat{\beta}_2 x_{12})^2 + (y_2 - \hat{\beta}_1 x_{21} - \hat{\beta}_2 x_{22})^2$. We use the facts $x_{11} = x_{12}$, $x_{21} = x_{22}$, $x_{11} + x_{21} = 0$, $x_{12} + x_{22} = 0$, and $y_1 + y_2 = 0$ to simplify is to minimize: $2(y_1 - (\hat{\beta}_1 + \hat{\beta}_2)x_{11})^2$.

This optimization problem has a simple solution: $\hat{\beta}_1 + \hat{\beta}_2 = \frac{y_1}{x_{11}}$. This is a line parallel to the edge of Lasso-diamond $\hat{\beta}_1 + \hat{\beta}_2 = s$. Now the solutions to the original Lasso optimization problem are contours of the function $(y_1 - (\hat{\beta}_1 + \hat{\beta}_2)x_{11})^2$ that touch the Lasso-diamond $\hat{\beta}_1 + \hat{\beta}_2 = s$. Finally, as $\hat{\beta}_1$ and $\hat{\beta}_2$ vary along the line $\hat{\beta}_1 + \hat{\beta}_2 = \frac{y_1}{x_{11}}$, these contours touch the Lasso-diamond edge $\hat{\beta}_1 + \hat{\beta}_2 = s$ at different points. As a result, the entire edge $\hat{\beta}_1 + \hat{\beta}_2 = s$ is a potential solution to the Lasso optimization problem!

Similar argument can be made for the opposite Lasso-diamond edge: $\hat{\beta}_1 + \hat{\beta}_2 = -s$.

Thus, the Lasso problem does not have a unique solution. The general form of solution is

$$\hat{\beta}_1 + \hat{\beta}_2 = s; \hat{\beta}_1 \geq 0; \hat{\beta}_2 \geq 0; \text{ and } \hat{\beta}_1 + \hat{\beta}_2 = -s; \hat{\beta}_1 \leq 0; \hat{\beta}_2 \leq 0.$$

Question 2

Suppose we have a data set with five predictors, $X_1 = GPA$, $X_2 = IQ$, $X_3 = Gender$ (1 for Female and 0 for Male), $X_4 = \text{Interaction between } GPA \text{ and } IQ$, and $X_5 = \text{Interaction between } GPA \text{ and } Gender$. The response is starting salary after graduation (in thousands of dollars). Suppose we use least squares to fit the model, and get $\hat{\beta}_0 = 50$, $\hat{\beta}_1 = 20$, $\hat{\beta}_3 = 35$, $\hat{\beta}_4 = 0.01$, $\hat{\beta}_5$

1. Which answer is correct, and why?

- For a fixed value of IQ and GPA , males earn more on average than females.
 - For a fixed value of IQ and GPA , females earn more on average than males.
 - For a fixed value of IQ and GPA , males earn more on average than females provided that the GPA is high enough.
 - For a fixed value of IQ and GPA , females earn more on average than males provided that the GPA is high enough.
- c. For a fixed value of IQ and GPA , males earn more on average than females provided that the GPA is high enough.

The least squares regression line is :

$$Y = 50 + 20GPA + 0.07IQ + 35Gender + 0.01(GPA * IQ) - 10(GPA * Gender) \\ (35 - 10GPA)Gender$$

If Male = 0 is our baseline, we find that males with a GPA higher than 3.5 will earn more on average than females.

2. Predict the salary of a female with *IQ* of 110 and a *GPA* of 4.0.

$$Y = 50 + 20(4) + 0.07(110) + 35(1) + 0.01(4 \times 110) - 10(4 \times 1) = 137.1$$

The predicted salary would be \$137,100.

3. True or false: Since the coefficient for the *GPA/IQ* interaction term is very small, there is very little evidence of an interaction effect. Justify your answer.

False - The size of the coefficient for the interaction term does not necessarily imply little evidence of an interaction effect. The p value will help us determine significance of the term in the model, and the size of the coefficients of the *GPA* and *IQ* main effects will give us a relative scale of which we will see the actual effects of the interaction.

```
library(caret)
library(randomForest)
library(mice)
library(dplyr)
library(VIM)
library(varhandle)
library(factoextra)
library(ape)
library(fpc)
```

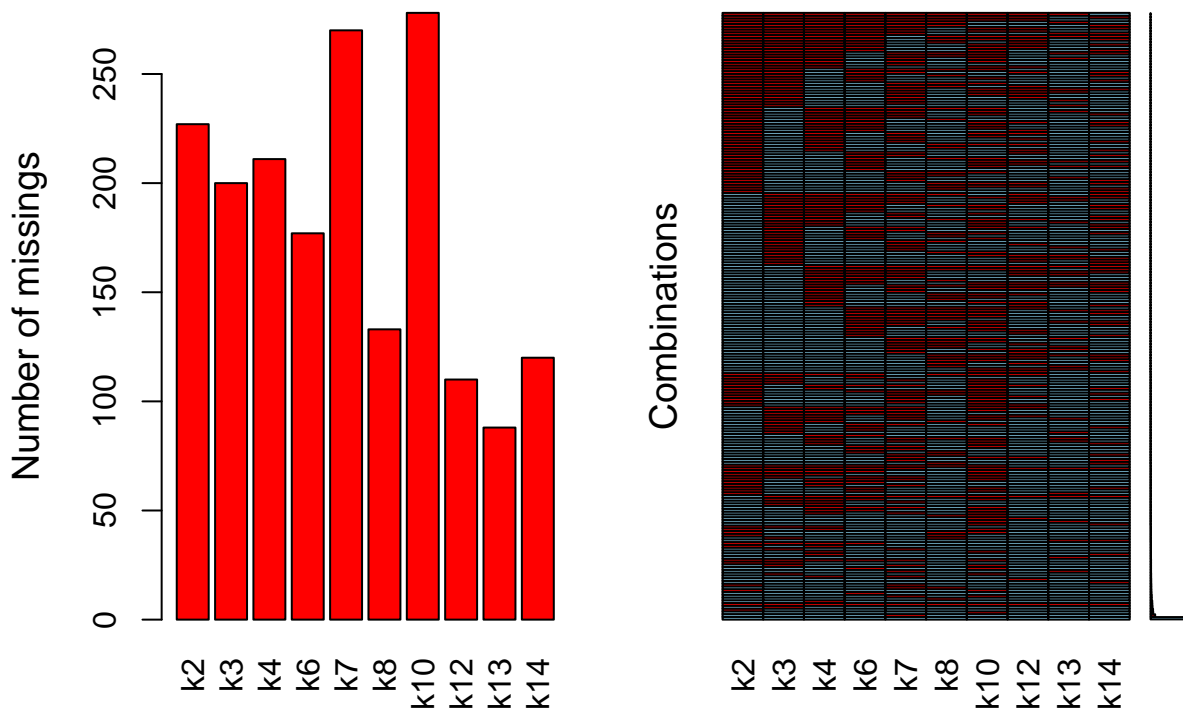
Question 3

강의 후에 제공된 'data3.xlsx'에 대하여 다른 변수들을 이용하여 'ideo_self'를 예측하는 모델을 구축하고자 한다. 본인이 찾은 최적의 예측모형을 서술하고 10-fold cross-validation을 이용한 시험오차 (testing error)에 대해 혼동행렬 (confusion matrix)을 계산하여라

```
dat = read.csv('data3.csv')
dat = dat[,-c(1,3)]
for (i in c(1,3:17))
{
  dat[,i] = as.factor(dat[,i])
}
```

변수의 성격에 맞게 str을 변환하였다.

```
aggr(dat[,7:16], prop=FALSE, numbers=TRUE)
```



결측치의 개수와 결측치의 패턴을 보기 위해 위의 함수를 사용하였다. 패턴은 없다고 판단하였다. 결측치를 모두 채운 후 `ideo_self`를 예측하는 모델링을 할 것이기 때문에, 결측치가 가장 적은 K13부터 가장 많은 K10순서대로 값을 채울 것을 결정하였다.

```
miceresult <- mice(dat, seed = 123, m = 5)

a=complete(miceresult, 1)
b=complete(miceresult, 2)
c=complete(miceresult, 3)
d=complete(miceresult, 4)
e=complete(miceresult, 5)
dat_t=complete(miceresult, 5)

for (j in 7:(ncol(a)-1))
{
  dat_t[,j] <- unfactor(dat_t[,j])
  for (i in 1:nrow(a))
  {
    dat_t[i,j] = round(mean(unfactor(a[i,j]),unfactor(b[i,j]),unfactor(c[i,j]),
                           unfactor(d[i,j]),unfactor(e[i,j])))
  }
  dat_t[,j] <- as.factor(dat_t[,j])
}

completedData <- dat_t
```

결측치의 값을 처리하기 위해 2가지 방법을 사용하였는데, 그 중 첫번째이다. `mice`패키지를 사용하여 결측값을 대체하였다.

5번을 반복한 결과의 평균을 내고 반올림하는 식으로 5개의 값을 모두 이용하여 결측값을 대체하였다.

```
miceresult$method
```

```
##      sex      age1      age      area      edu      income      k2
##      ""      ""      ""      ""      ""      ""      "logreg"
##      k3      k4      k6      k7      k8      k10      k12
## "logreg" "logreg" "logreg" "logreg" "logreg" "logreg" "logreg"
##      k13      k14 ideo_self
## "logreg" "logreg"      ""
```

각각의 변수에 대해 어떤 함수를 사용하여 결측치를 채웠는 지 확인 할 수 있다.

```
Fold_index <- createFolds(1:nrow(completedData), k = 10)
```

```
result = c()
result_acc = c()
result_flex = c()
for(k in 1:10){
  Train <- completedData[-Fold_index[[k]],]
  Test <- completedData[Fold_index[[k]],]

  out <- randomForest(ideo_self~., data = Train)
  pred <- predict(out, Test)

  result[[k]] = table(pred, Test$ideo_self)
  print(result[[k]])

  result_acc[[k]] = sum(diag(result[[k]]))/sum(result[[k]])

  pred_flex <- matrix(result[[k]], 11, 11)
  acc = rep(0, 11)

  for(i in 1:ncol(pred_flex))
  {
    if(i == 1)
    {
      acc[i] <- pred_flex[i,i] + pred_flex[i, i+1]
    }
    else if(i == 11)
    {
      acc[i] <- pred_flex[i,i] + pred_flex[i, i-1]
    }
    else
    {
      acc[i] <- pred_flex[i,i] + pred_flex[i, i-1] + pred_flex[i, i+1]
    }
  }
  result_flex[[k]] = sum(acc)/sum(pred_flex)
}
```

```
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 1 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0 0
```

```

## 3 0 0 0 2 2 4 2 0 0 0 0
## 4 0 1 1 1 2 3 1 0 0 0 0
## 5 3 2 3 6 7 24 6 6 2 1 3
## 6 0 0 0 1 0 0 3 1 0 1 1
## 7 0 0 0 0 0 1 0 3 2 0 2
## 8 0 0 0 0 1 1 0 0 2 1 1
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 1 0 0 0 0 1
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0
## 1 1 0 0 0 0 0 0 0 0 0
## 2 0 0 0 1 0 0 0 0 0 0
## 3 0 0 2 1 1 3 3 0 0 0
## 4 0 0 1 0 1 1 2 0 0 0
## 5 2 2 1 9 8 30 7 6 2 1
## 6 0 0 0 1 0 1 0 1 1 0
## 7 0 0 0 0 0 1 2 2 2 0
## 8 0 0 0 0 0 0 0 1 1 2
## 9 0 0 0 0 0 1 0 0 0 0
## 10 0 0 0 0 0 0 1 0 0 1
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 1 0 0 0
## 2 0 0 1 0 0 0 0 0 0 0
## 3 0 1 0 4 1 4 0 1 2 0
## 4 0 0 0 2 3 0 0 0 0 0
## 5 1 3 4 4 7 24 5 7 1 4
## 6 0 0 0 0 0 3 1 1 0 1
## 7 0 0 0 1 0 1 1 2 3 0
## 8 0 0 0 0 0 0 1 2 2 1
## 9 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 1 2 0 0 0 0
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0
## 3 1 0 0 0 2 2 0 1 0 0
## 4 0 1 1 0 2 1 0 1 0 0
## 5 2 1 3 9 6 25 9 7 3 1
## 6 0 0 0 0 0 2 2 0 1 0
## 7 0 0 0 0 0 1 0 3 2 0
## 8 0 0 0 0 0 0 0 1 4 0
## 9 0 0 0 0 0 0 0 0 0 1
## 10 0 0 0 0 1 0 0 2 0 1
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 1 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0
## 3 0 0 3 4 6 6 0 0 0 0
## 4 0 0 1 3 0 5 0 0 0 0

```

```

## 5 3 3 2 4 6 19 3 7 1 0 4
## 6 0 0 0 1 1 0 0 0 0 0 1
## 7 0 0 0 0 0 1 0 3 1 0 2
## 8 0 0 0 0 0 2 2 2 0 1 3
## 9 0 0 0 0 0 1 0 0 0 0 0
## 10 0 0 0 0 0 2 1 0 0 1 0
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 1 0 0 0 0
## 2 0 0 0 1 0 0 0 0 0 0 0
## 3 3 0 1 3 0 4 1 3 1 0 0
## 4 0 0 1 0 0 2 0 0 0 0 0
## 5 3 4 1 8 8 20 6 7 5 0 1
## 6 0 0 0 1 0 1 4 1 0 0 0
## 7 0 0 0 0 0 0 3 0 1 0 0
## 8 0 0 0 0 0 1 1 1 2 1 1
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 1 0 0 0 0 2 1 0 1 0 0
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 1 0 1 1 0 0 0 0 0
## 2 1 0 0 0 0 0 0 0 0 0 0
## 3 0 0 2 2 1 2 0 0 0 0 0
## 4 0 1 1 2 1 1 1 0 1 0 0
## 5 2 0 3 10 9 17 10 2 2 1 6
## 6 0 0 0 1 1 1 1 1 1 0 0
## 7 0 0 0 0 0 2 2 1 1 0 1
## 8 0 0 0 0 0 1 1 2 1 2 1
## 9 0 0 0 0 0 0 0 0 0 0 1
## 10 0 0 0 0 0 0 0 0 0 0 2
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 1 0 0 0 0 0
## 3 0 1 1 1 2 5 0 0 1 0 0
## 4 0 1 0 4 2 2 0 0 0 0 0
## 5 2 4 2 7 10 18 7 2 3 1 3
## 6 0 0 0 3 0 0 2 1 0 0 0
## 7 0 0 0 0 1 2 0 3 1 0 1
## 8 0 0 0 0 0 2 0 1 1 1 0
## 9 0 0 0 0 0 1 0 0 0 0 0
## 10 0 0 0 1 0 1 1 0 0 0 3
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 2 0 0 0 0 0 0 0
## 3 1 0 1 2 3 3 1 1 0 0 0
## 4 1 0 2 2 0 1 1 0 0 0 0
## 5 4 1 2 3 5 26 6 4 1 0 3
## 6 0 0 0 0 2 1 2 1 0 0 0

```

```
## 7 0 0 0 1 0 2 3 2 2 0 0
## 8 0 0 0 1 0 1 1 2 4 0 1
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 0 0 1 0 0 0 1
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0
## 3 2 1 3 3 1 3 2 0 0 0 1
## 4 0 0 0 1 2 0 0 0 0 0 0
## 5 4 0 2 4 9 24 5 6 5 1 0
## 6 0 0 0 1 0 0 2 0 1 0 1
## 7 0 0 0 0 0 0 1 2 4 1 0 0
## 8 0 0 0 0 0 0 0 0 0 3 1 0
## 9 0 0 0 0 0 0 0 0 0 1 0 0
## 10 0 0 0 0 0 0 1 0 1 1 1 3
```

```
mean(result_acc)
```

```
## [1] 0.3180776
```

```
mean(result_flex)
```

```
## [1] 0.58474
```

10-fold결과의 평균값 10-fold결과의 좀더 여유있게 정확도를 보면(예측값의 +-1 정도의 여유치) 좀 더 높게 나오는 것을 알 수 있다.

```
dat_k13 = dat[,c(1:6,15,length(dat))]
model = randomForest(as.factor(k13)~., data = na.omit(dat_k13))
pred = predict(model, newdata = dat_k13[is.na(dat_k13$k13),], type = 'response')
dat[is.na(dat$k13),]['k13'] = as.integer(as.character(pred))
dat$k13 = as.factor(dat$k13)
```

```
dat_k12 = dat[,c(1:6,14,15,length(dat))]
model = randomForest(as.factor(k12)~., data = na.omit(dat_k12))
pred = predict(model, newdata = dat_k12[is.na(dat_k12$k12),], type = 'response')
dat[is.na(dat$k12),]['k12'] = as.integer(as.character(pred))
dat$k12 = as.factor(dat$k12)
```

```
dat_k14 = dat[,c(1:6,14:length(dat))]
model = randomForest(as.factor(k14)~., data = na.omit(dat_k14))
pred = predict(model, newdata = dat_k14[is.na(dat_k14$k14),], type = 'response')
dat[is.na(dat$k14),]['k14'] = as.integer(as.character(pred))
dat$k14 = as.factor(dat$k14)
```

```
dat_k8 = dat[,c(1:6,12,14:length(dat))]
model = randomForest(as.factor(k8)~., data = na.omit(dat_k8))
pred = predict(model, newdata = dat_k8[is.na(dat_k8$k8),], type = 'response')
dat[is.na(dat$k8),]['k8'] = as.integer(as.character(pred))
dat$k8 = as.factor(dat$k8)
```

```
dat_k6 = dat[,c(1:6,10,12,14:length(dat))]
model = randomForest(as.factor(k6)~., data = na.omit(dat_k6))
pred = predict(model, newdata = dat_k6[is.na(dat_k6$k6),], type = 'response')
dat[is.na(dat$k6),]['k6'] = as.integer(as.character(pred))
```



```

dat$k6 = as.factor(dat$k6)

dat_k3 = dat[,c(1:6,8,10,12,14:length(dat))]
model = randomForest(as.factor(k3)~., data = na.omit(dat_k3))
pred = predict(model, newdata = dat_k3[is.na(dat_k3$k3),], type = 'response')
dat[is.na(dat$k3),]['k3'] = as.integer(as.character(pred))
dat$k3 = as.factor(dat$k3)

dat_k4 = dat[,c(1:6,8:10,12,14:length(dat))]
model = randomForest(as.factor(k4)~., data = na.omit(dat_k4))
pred = predict(model, newdata = dat_k4[is.na(dat_k4$k4),], type = 'response')
dat[is.na(dat$k4),]['k4'] = as.integer(as.character(pred))
dat$k4 = as.factor(dat$k4)

dat_k2 = dat[,c(1:10,12,14:length(dat))]
model = randomForest(as.factor(k2)~., data = na.omit(dat_k2))
pred = predict(model, newdata = dat_k2[is.na(dat_k2$k2),], type = 'response')
dat[is.na(dat$k2),]['k2'] = as.integer(as.character(pred))
dat$k2 = as.factor(dat$k2)
dat_k7 = dat[,c(1:12,14:length(dat))]

model = randomForest(as.factor(k7)~., data = na.omit(dat_k7))
pred = predict(model, newdata = dat_k7[is.na(dat_k7$k7),], type = 'response')
dat[is.na(dat$k7),]['k7'] = as.integer(as.character(pred))
dat$k7 = as.factor(dat$k7)
dat_k10 = dat[,c(1:length(dat))]

model = randomForest(as.factor(k10)~., data = na.omit(dat_k10))
pred = predict(model, newdata = dat_k10[is.na(dat_k10$k10),], type = 'response')
dat[is.na(dat$k10),]['k10'] = as.integer(as.character(pred))
dat$k10 = as.factor(dat$k10)

```

각각의 결측치를 가장 적은 k13부터 가장 많은 k10을 randomforest를 사용하여 값을 할당한다.

```

Fold_index <- createFolds(1:nrow(dat), k = 10)

result = c()
result_acc = c()
result_flex = c()
for(k in 1:10){
  Train <- dat[-Fold_index[[k]],]
  Test <- dat[Fold_index[[k]],]

  out <- randomForest(ideo_self~., data = Train)
  pred <- predict(out, Test)

  result[[k]] = table(pred, Test$ideo_self)
  print(result[[k]])

  result_acc[[k]] = sum(diag(result[[k]]))/sum(result[[k]])

  pred_flex <- matrix(result[[k]], 11, 11)

  acc = rep(0, 11)

```

```

for(i in 1:ncol(pred_flex))
{
  if(i == 1)
  {
    acc[i] <- pred_flex[i,i] + pred_flex[i, i+1]
  }
  else if(i == 11)
  {
    acc[i] <- pred_flex[i,i] + pred_flex[i, i-1]
  }
  else
  {
    acc[i] <- pred_flex[i,i] + pred_flex[i, i-1] + pred_flex[i, i+1]
  }
}
result_flex[[k]] = sum(acc)/sum(pred_flex)
}

```

```

##
## pred  0  1  2  3  4  5  6  7  8  9 10
##  0  0  0  0  0  0  0  0  0  0  0
##  1  0  0  0  1  0  0  0  0  0  0
##  2  0  0  0  0  1  1  0  0  0  0
##  3  0  0  1  3  1  3  0  1  0  0
##  4  0  0  0  2  1  1  2  0  1  0
##  5  2  4  1  5  7 26  6  6  0  1
##  6  0  0  0  0  0  0  1  4  1  1
##  7  0  0  0  0  1  1  2  3  1  0
##  8  0  0  0  0  0  0  1  1  3  0
##  9  0  0  0  0  0  0  0  0  0  0
## 10  0  0  0  0  0  0  0  0  2  0
##
## pred  0  1  2  3  4  5  6  7  8  9 10
##  0  0  0  0  1  0  0  0  0  0  0
##  1  1  0  0  1  1  0  0  0  0  0
##  2  0  0  0  2  0  0  0  0  0  0
##  3  0  1  2  1  1  4  1  1  1  0
##  4  0  0  1  0  3  0  0  2  0  0
##  5  5  0  1 10  3 26  4  3  2  7
##  6  0  0  0  0  2  1  1  1  1  0
##  7  0  0  0  1  0  0  1  3  1  1
##  8  0  0  0  1  0  0  0  0  1  0
##  9  0  0  0  0  0  2  0  0  0  0
## 10  0  0  0  0  1  1  1  0  0  0
##
## pred  0  1  2  3  4  5  6  7  8  9 10
##  0  0  0  0  0  0  0  0  0  0  0
##  1  0  0  0  0  0  0  0  0  0  0
##  2  1  0  0  1  0  0  0  0  0  0
##  3  0  0  1  4  0  1  1  1  1  0
##  4  0  0  2  3  0  1  0  1  0  0
##  5  3  1  1  4 10 19 13  4  3  1
##  6  0  0  0  0  0  1  0  1  0  0

```

```

## 7 0 0 0 0 2 0 3 0 2 0 3
## 8 0 0 0 0 0 3 0 1 2 2 0
## 9 0 0 0 0 0 0 0 0 0 1 0
## 10 0 0 0 0 0 1 2 1 0 0 1
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 1 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0
## 2 0 0 1 0 0 0 0 0 0 0
## 3 1 2 1 2 4 2 0 0 0 0
## 4 2 0 1 3 1 2 2 0 0 0
## 5 3 3 5 4 5 16 5 3 2 1 1
## 6 0 0 0 1 0 2 3 0 0 0 1
## 7 0 0 0 0 1 1 2 5 0 1 0
## 8 0 0 0 0 0 0 2 2 1 0 1
## 9 0 0 0 0 0 0 0 0 1 0 2
## 10 0 0 0 0 2 1 1 2 1 0 0
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 1 1 0 0 0 0 0
## 3 0 0 0 4 3 3 0 1 1 0
## 4 0 1 3 1 2 1 0 0 0 0
## 5 2 1 1 7 4 17 4 6 4 1 1
## 6 0 0 0 0 0 7 1 4 2 1 0
## 7 1 0 0 0 1 3 2 1 0 1 1
## 8 0 0 0 0 0 0 0 1 1 1 1
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 1 0 2 1 0 2
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 1 0 0 0 0 0
## 3 0 0 2 7 2 3 2 1 1 0 1
## 4 0 0 0 2 1 2 0 0 0 0 1
## 5 2 1 5 7 6 20 7 7 2 0 1
## 6 0 0 0 0 1 1 4 0 0 0 0
## 7 0 0 0 2 0 1 3 1 1 0 1
## 8 0 0 0 0 0 1 0 0 2 1 0
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 0 0 0 2 0 2
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 1 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0
## 3 0 0 1 0 1 6 2 1 1 0 0
## 4 1 0 0 0 3 3 1 0 0 0 0
## 5 2 3 1 4 6 30 4 8 3 0 3
## 6 0 0 0 0 0 1 3 1 0 0 0
## 7 0 0 0 0 0 1 2 0 2 0 1
## 8 0 0 0 0 0 0 0 0 2 1 1

```

```

## 9 0 0 0 0 1 1 0 0 1 0 0
## 10 0 0 0 0 0 0 1 0 0 0 0 0
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 1 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 1 1 1 1 1 0 1 0 0 0 0
## 3 1 1 0 2 3 7 0 1 0 0 0
## 4 0 2 1 2 2 1 0 0 0 0 0
## 5 2 3 1 5 3 21 2 2 2 1 5
## 6 0 0 2 0 1 3 0 1 0 0 0
## 7 0 0 0 0 0 0 0 1 4 1 0 2
## 8 0 0 0 0 0 0 1 0 1 4 0 1
## 9 0 0 0 0 0 0 1 0 0 0 1 0
## 10 0 0 0 0 0 0 1 1 0 1 1 1
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 1 0 0 0 0 0 0 0 0 0
## 3 0 0 4 1 2 5 2 0 0 0 0
## 4 1 0 2 0 4 1 0 0 0 0 0
## 5 0 0 1 8 5 27 7 5 2 0 2
## 6 0 0 0 1 1 1 3 2 2 0 0
## 7 0 0 0 0 0 0 1 0 1 1 0 1
## 8 0 0 0 0 0 0 1 0 1 2 0 1
## 9 0 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 0 0 1 0 0 0 4
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 1 0 0 0 0 0 0 0
## 3 0 0 0 3 1 2 0 0 0 0 0
## 4 0 1 2 2 4 2 1 0 1 0 0
## 5 4 1 1 7 7 25 8 3 1 2 0
## 6 1 0 0 1 0 2 3 2 1 1 2
## 7 0 0 0 0 0 0 1 1 3 0 0 0
## 8 0 0 0 0 0 0 1 0 1 2 0
## 9 0 0 0 0 0 0 0 0 0 0 0 0
## 10 1 0 0 0 0 0 0 0 1 1 1

```

```
mean(result_acc)
```

```
## [1] 0.3330494
```

```
mean(result_flex)
```

```
## [1] 0.584761
```

10-fold결과의 평균값 10-fold결과의 좀더 여유있게 정확도를 보면(예측값의 +-1 정도의 여유치) 좀 더 높게 나오는 것을 알 수 있다.

결과론적으로 mice함수를 사용한 결과와 랜덤포레스트를 사용하여 직접적으로 변수를 채운 결과는 랜덤포레스트를 사용한 것이 더 높은것을 알 수 있다.

```
Fold_index <- createFolds(1:nrow(dat), k = 10)
```

```

result = c()
result_acc = c()
result_flex = c()
for(k in 1:10){
  Train <- dat[-Fold_index[[k]],]
  Test <- dat[Fold_index[[k]],]

  out <- nnet::multinom(ideo_self~., data = Train[,7:17])
  pred <- predict(out, Test)

  result[[k]] = table(pred, Test$ideo_self)
  print(result[[k]])

  result_acc[[k]] = sum(diag(result[[k]]))/sum(result[[k]])

  pred_flex <- matrix(result[[k]], 11, 11)

  acc = rep(0, 11)

  for(i in 1:ncol(pred_flex))
  {
    if(i == 1)
    {
      acc[i] <- pred_flex[i,i] + pred_flex[i, i+1]
    }
    else if(i == 11)
    {
      acc[i] <- pred_flex[i,i] + pred_flex[i, i-1]
    }
    else
    {
      acc[i] <- pred_flex[i,i] + pred_flex[i, i-1] + pred_flex[i, i+1]
    }
  }
  result_flex[[k]] = sum(acc)/sum(pred_flex)
}

```

```

## # weights: 132 (110 variable)
## initial value 2275.602614
## iter 10 value 1803.357474
## iter 20 value 1727.198704
## iter 30 value 1717.891559
## iter 40 value 1715.995572
## iter 50 value 1715.651171
## iter 60 value 1715.489704
## iter 70 value 1715.429332
## iter 80 value 1715.425082
## iter 90 value 1715.423924
## final value 1715.423679
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0

```

```

## 2 0 0 0 0 0 0 0 0 0 0 0
## 3 0 1 3 4 2 4 1 2 1 0 0
## 4 0 0 0 2 0 0 0 0 0 0 0
## 5 4 3 4 6 6 16 7 7 0 2 3
## 6 0 0 0 1 1 0 0 1 0 0 0
## 7 0 0 0 0 2 1 3 2 0 1 1
## 8 0 0 0 0 1 1 1 3 3 2 1
## 9 0 0 0 0 0 0 1 0 0 0 0
## 10 0 0 0 0 0 0 0 0 1 0 0
## # weights: 132 (110 variable)
## initial value 2275.602614
## iter 10 value 1842.067318
## iter 20 value 1753.011528
## iter 30 value 1742.901743
## iter 40 value 1741.346332
## iter 50 value 1740.886695
## iter 60 value 1740.766888
## iter 70 value 1740.703426
## iter 80 value 1740.682007
## iter 90 value 1740.679465
## final value 1740.679075
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0 0
## 3 1 1 3 5 3 2 0 1 0 0 0
## 4 0 0 0 0 0 0 0 0 0 0 0
## 5 4 1 0 7 5 28 9 4 1 2 5
## 6 0 0 0 1 1 3 0 0 0 0 0
## 7 0 0 0 0 1 0 0 2 4 0 0
## 8 0 0 0 0 0 1 0 3 0 2 2
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 1 0 0 1 0 1
## # weights: 132 (110 variable)
## initial value 2273.204719
## iter 10 value 1805.277079
## iter 20 value 1742.122413
## iter 30 value 1734.193040
## iter 40 value 1731.897393
## iter 50 value 1731.148317
## iter 60 value 1730.768859
## iter 70 value 1730.680554
## iter 80 value 1730.670019
## final value 1730.668897
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0 0
## 3 0 0 0 5 3 1 2 0 1 0 0
## 4 0 0 0 0 0 0 0 0 0 0 0

```

```

## 5 4 1 3 3 6 26 13 7 2 3 4
## 6 0 0 0 0 2 2 0 1 0 0 1
## 7 0 0 0 0 1 1 0 1 0 0 0
## 8 0 0 0 0 0 1 2 3 5 0 1
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 0 1 0 0 0 0
## # weights: 132 (110 variable)
## initial value 2275.602614
## iter 10 value 1821.832094
## iter 20 value 1741.423305
## iter 30 value 1731.627507
## iter 40 value 1729.658922
## iter 50 value 1729.239755
## iter 60 value 1729.068826
## iter 70 value 1729.023280
## iter 80 value 1729.009387
## iter 90 value 1729.007195
## final value 1729.006779
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0 0
## 3 2 1 2 4 2 5 0 1 1 0 2
## 4 0 0 0 2 0 3 2 0 0 0 0
## 5 3 1 0 4 4 21 5 6 7 1 3
## 6 0 0 0 0 0 2 1 0 0 0 0
## 7 0 0 0 0 0 1 1 4 4 0 0
## 8 0 0 0 0 0 1 2 0 2 0 1
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 2 0 0 0 0 2
## # weights: 132 (110 variable)
## initial value 2273.204719
## iter 10 value 1822.208433
## iter 20 value 1748.708765
## iter 30 value 1741.139473
## iter 40 value 1739.124134
## iter 50 value 1738.776535
## iter 60 value 1738.581407
## iter 70 value 1738.534963
## iter 80 value 1738.526903
## iter 90 value 1738.525934
## final value 1738.525715
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 1 0 0 0 0 0 0 0 0 0
## 3 0 0 0 3 0 0 0 0 0 0 0
## 4 0 0 2 3 1 1 0 0 1 0 0
## 5 3 2 5 4 10 30 7 6 1 0 4
## 6 0 0 0 1 0 1 0 1 0 0 0

```

```

## 7 0 0 0 0 0 1 0 2 0 0 0
## 8 0 0 0 0 1 1 4 3 3 2 0
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 0 1 0 1 0 0
## # weights: 132 (110 variable)
## initial value 2273.204719
## iter 10 value 1827.938984
## iter 20 value 1741.550036
## iter 30 value 1731.738556
## iter 40 value 1729.973977
## iter 50 value 1729.655194
## iter 60 value 1729.499103
## iter 70 value 1729.451217
## iter 80 value 1729.445486
## iter 90 value 1729.444567
## final value 1729.444431
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0 0
## 3 1 0 0 4 1 2 0 0 1 0 0
## 4 0 0 1 2 0 1 0 0 0 0 0
## 5 3 2 1 8 14 24 4 6 2 0 4
## 6 0 0 0 0 0 0 0 2 1 0 0
## 7 0 0 0 0 0 2 0 1 1 0 0
## 8 0 0 0 1 0 1 2 3 3 3 1
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 1 0 0 1 0 1 0 0 1
## # weights: 132 (110 variable)
## initial value 2278.000509
## iter 10 value 1841.647889
## iter 20 value 1766.806727
## iter 30 value 1757.801017
## iter 40 value 1756.374855
## iter 50 value 1756.020180
## iter 60 value 1755.870933
## iter 70 value 1755.814422
## iter 80 value 1755.810664
## iter 90 value 1755.809556
## final value 1755.809412
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 1 0 0 0 0 0 0 0
## 3 1 0 0 4 5 1 0 0 0 0 0
## 4 0 0 0 0 0 0 0 0 0 0 0
## 5 1 2 1 4 11 29 6 5 4 0 2
## 6 1 0 0 0 0 3 2 0 0 0 0
## 7 0 0 0 0 0 3 0 4 0 0 1
## 8 0 0 0 0 0 4 2 1 1 2 2

```



```

## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 1 0 0 0 0 0
## # weights: 132 (110 variable)
## initial value 2273.204719
## iter 10 value 1828.740514
## iter 20 value 1747.904328
## iter 30 value 1738.465804
## iter 40 value 1736.763668
## iter 50 value 1736.410225
## iter 60 value 1736.265750
## iter 70 value 1736.207759
## iter 80 value 1736.197172
## iter 90 value 1736.193598
## iter 100 value 1736.192865
## final value 1736.192865
## stopped after 100 iterations
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0 0
## 3 2 0 5 5 2 5 1 1 0 0 0
## 4 0 0 0 1 1 0 0 0 0 0 0
## 5 0 2 4 6 6 30 7 3 4 0 2
## 6 1 0 0 0 0 2 0 2 1 2 1
## 7 1 0 0 0 0 0 0 3 0 0 0
## 8 0 0 0 0 0 0 2 0 2 0 0
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 1 0 0 0 0 1
## # weights: 132 (110 variable)
## initial value 2278.000509
## iter 10 value 1828.729419
## iter 20 value 1757.426467
## iter 30 value 1747.900989
## iter 40 value 1746.037702
## iter 50 value 1745.743042
## iter 60 value 1745.598814
## iter 70 value 1745.543713
## iter 80 value 1745.539794
## iter 90 value 1745.538727
## final value 1745.538645
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 0 0 0 0 0 0 0 0 0 0
## 3 0 2 2 4 2 0 1 0 0 0 0
## 4 0 0 1 1 1 1 1 0 0 0 0
## 5 1 3 2 8 5 24 10 3 2 0 3
## 6 0 0 0 0 0 1 0 1 1 0 0
## 7 0 0 0 0 0 1 1 0 0 0 0
## 8 0 0 0 0 0 3 1 4 5 1 6
## 9 0 0 0 0 0 0 0 0 0 0 0

```

```
## 10 0 0 0 0 0 0 1 0 0 0 1
## # weights: 132 (110 variable)
## initial value 2270.806823
## iter 10 value 1797.770532
## iter 20 value 1729.926496
## iter 30 value 1719.489217
## iter 40 value 1718.071344
## iter 50 value 1717.597903
## iter 60 value 1717.426644
## iter 70 value 1717.361400
## iter 80 value 1717.355943
## iter 90 value 1717.354421
## final value 1717.354347
## converged
##
## pred 0 1 2 3 4 5 6 7 8 9 10
## 0 0 0 0 0 0 0 0 0 0 0 0
## 1 0 0 0 0 0 0 0 0 0 0 0
## 2 0 1 0 0 0 0 0 0 0 0 0
## 3 2 2 1 3 6 4 0 0 1 0 0
## 4 0 0 0 0 1 0 1 0 0 0 0
## 5 1 1 4 11 7 21 10 4 2 0 2
## 6 0 0 0 0 0 0 1 0 0 0 0
## 7 0 0 1 1 0 0 2 0 0 0 1
## 8 1 0 0 0 0 2 2 2 3 2 2
## 9 0 0 0 0 0 0 0 0 0 0 0
## 10 0 0 0 0 0 1 1 0 0 0 0
```

```
mean(result_acc)
```

```
## [1] 0.3321472
```

```
mean(result_flex)
```

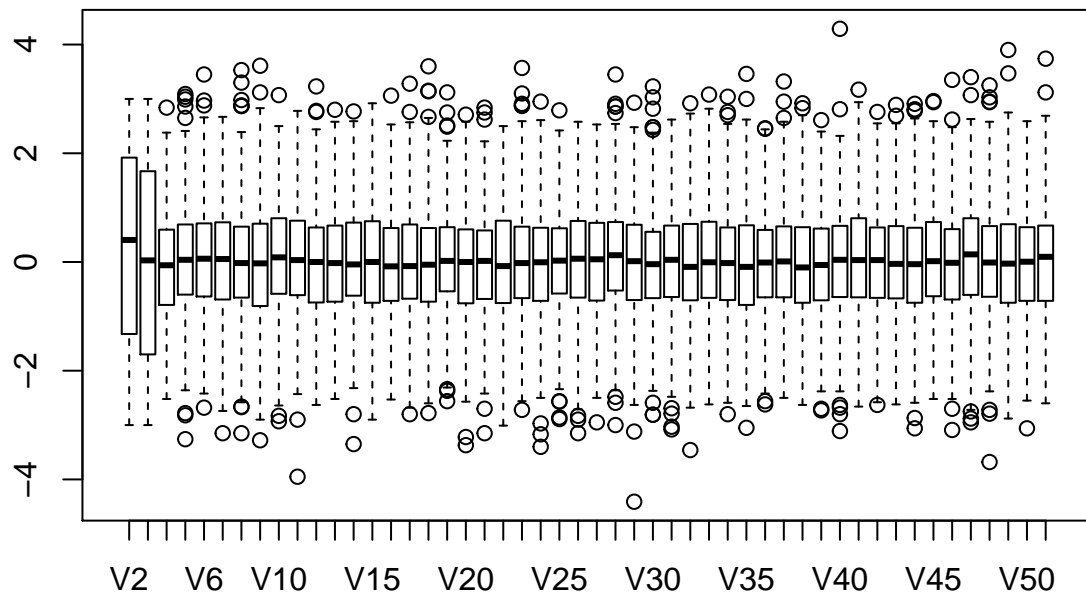
```
## [1] 0.6053969
```

다중클래스로지틱함수와 변수선택을 한 후 모델링을 하였다. 60%가 넘는 (유연한) 결과가 나왔다.

Question 4

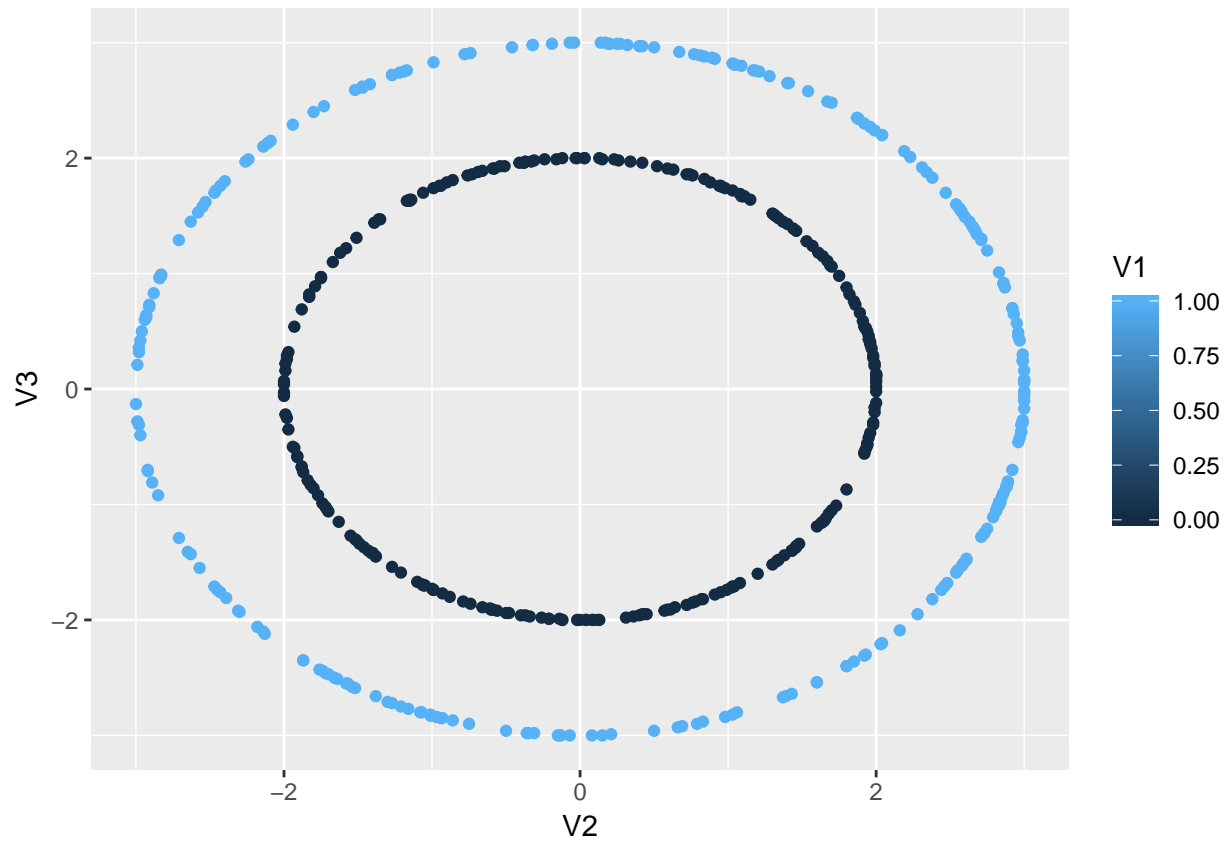
수행한 군집분석을 설명하고 결과를 적어라.

```
boxplot(dat[,2:51])
```



이상치가 없는 V2와 V3를 가지고 군집분석을 수행할 것이다.

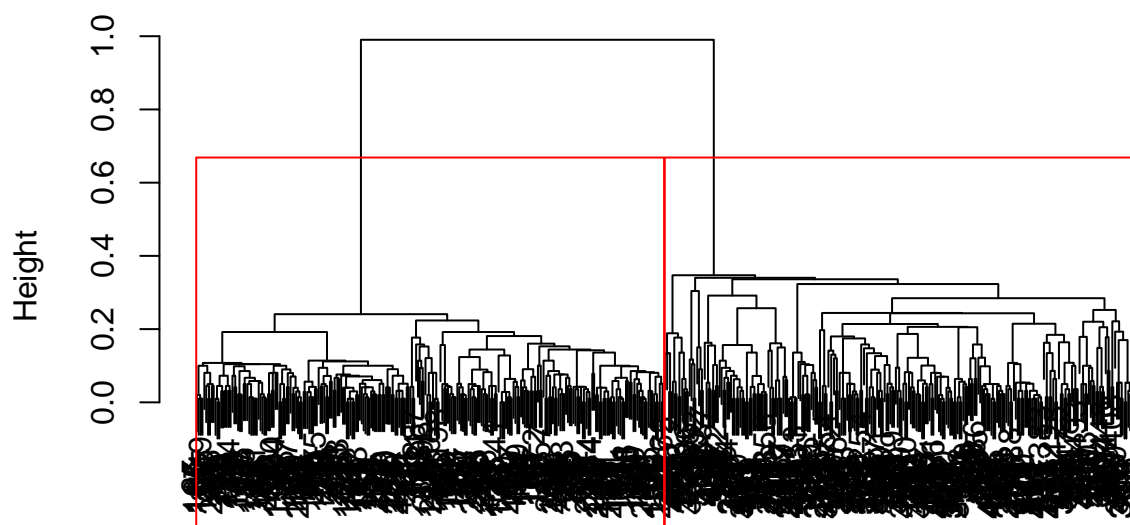
```
ggplot(dat, aes(V2, V3, color = V1)) + geom_point()
```



V2와 V3가 완벽하게 V1을 구분하는 것을 알 수 있다.

```
dat1 = dat[,c(2:3)]
d <- dist(dat1, method="euclidean")
fit <- hclust(d, method="single")
plot(fit)
rect.hclust(fit, k=2, border = 'red')
```

Cluster Dendrogram



d
hclust (*, "single")

계층적 군집을 사용하였고, 거리행렬은 euclidean 거리를 사용하였으며 군집간의 거리계산은 최단연결법을 사용하였다. 그 결과 위의 군집이 형성되었다.

```
confusionMatrix(as.factor(cutree(fit, k=2) - 1), as.factor(dat[,1]))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##           0 250    0
##           1    0 250
##
##           Accuracy : 1
##           95% CI : (0.9926, 1)
##           No Information Rate : 0.5
##           P-Value [Acc > NIR] : < 2.2e-16
##
##           Kappa : 1
##           McNemar's Test P-Value : NA
##
##           Sensitivity : 1.0
##           Specificity : 1.0
##           Pos Pred Value : 1.0
##           Neg Pred Value : 1.0
##           Prevalence : 0.5
##           Detection Rate : 0.5
##           Detection Prevalence : 0.5
```

```
##      Balanced Accuracy : 1.0
##
##      'Positive' Class : 0
##
```

정확도의 경우 100%가 되었다.

binary classification문제를 고려하여 최적의 classifier를 찾고 10-fold cv을 이용한 시험오차에 대한 혼동행렬을 계산하여라

```
result = list()
result_acc = 0
Fold_index <- createFolds(1:nrow(dat), k = 10)

for(k in 1:10){
  Train <- dat[-Fold_index[[k]],]
  Test <- dat[Fold_index[[k]],]

  out <- randomForest(V1~V2+V3, data = Train)
  pred <- round(predict(out, Test))

  result[[k]] = table(Test$V1, pred)
  result_acc[k] = sum(diag(result[[k]]))/sum(result[[k]])
}
```

위의 비지도 학습에서 V2, V3로 100%의 정확도가 나왔기 때문에 두 변수를 사용하였다. 10-fold cv를 실행하였고, 분류기는 randomForest를 사용하였다.

```
for ( i in 1:10)
{
  print(result[[i]])
}
```

```
##      pred
##      0  1
##      0 26  0
##      1  0 24
##      pred
##      0  1
##      0 24  0
##      1  0 25
##      pred
##      0  1
##      0 24  0
##      1  0 26
##      pred
##      0  1
##      0 26  0
##      1  0 25
##      pred
##      0  1
##      0 26  0
##      1  0 25
##      pred
```

```
##      0  1
##    0 24  0
##    1  0 25
##    pred
##      0  1
##    0 24  0
##    1  0 25
##    pred
##      0  1
##    0 26  0
##    1  0 25
##    pred
##      0  1
##    0 24  0
##    1  0 25
##    pred
##      0  1
##    0 26  0
##    1  0 25
```

```
mean(result_acc)
```

```
## [1] 1
```

혼동행렬과 정확도가 모두 100%가 나왔다.

Question 5

```
dat = read.csv('data5.csv')
rownames(dat) = dat[,1]
dat1 = dat[, -c(1, length(dat))]
dat1 = 1455 - dat1
dat1 = scale(dat1)
```

위의 과정은 전처리 과정인데, rownames를 설정해주고, 불필요한 컬럼은 제거하였으며, 거리가 가까움과 멀음이 반대로 되어있으므로 max값에서 빼줌으로써 반대로 바뀌게 되었다. 그 후 분산을 줄여주기 위하여 scaling을 하였다.

```
knitr::kable(table(dat$party), caption = '정당 별 국회의원의 수')
```

Table 1: 정당 별 국회의원의 수

Var1	Freq
국민의당	24
더불어민주당	67
무소속	1
바른정당	7
자유한국당	41
정의당	1

데이터가 주로 3개의 정당이 주를 이루는 걸 알 수 있다.

```

par(mfrow = c(2,2))
d <- dist(dat1, method="euclidean")
fit <- hclust(d, method="ward.D")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')

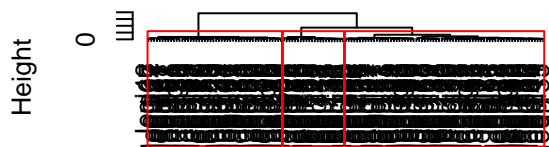
d <- dist(dat1, method="euclidean")
fit <- hclust(d, method="centroid")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')

d <- dist(dat1, method="euclidean")
fit <- hclust(d, method="av")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')

d <- dist(dat1, method="euclidean")
fit <- hclust(d, method="single")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')

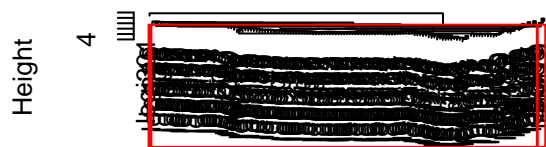
```

Cluster Dendrogram



d
hclust (*, "ward.D")

Cluster Dendrogram



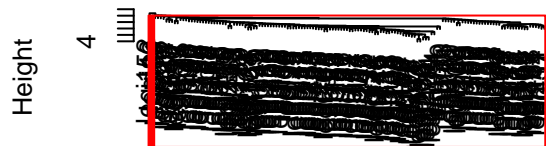
d
hclust (*, "centroid")

Cluster Dendrogram



d
hclust (*, "average")

Cluster Dendrogram



d
hclust (*, "single")

```

par(mfrow = c(2,2))
d <- dist(dat1, method="manhattan")
fit <- hclust(d, method="ward.D")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')

```



```

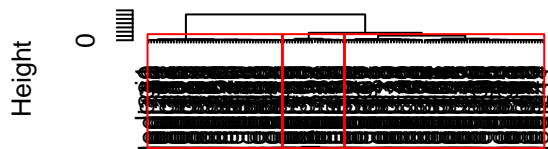
d <- dist(dat1, method="manhattan")
fit <- hclust(d, method="centroid")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')

d <- dist(dat1, method="manhattan")
fit <- hclust(d, method="av")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')

d <- dist(dat1, method="manhattan")
fit <- hclust(d, method="single")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')

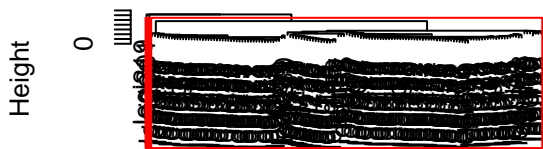
```

Cluster Dendrogram



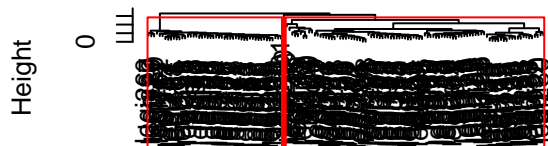
d
hclust (*, "ward.D")

Cluster Dendrogram



d
hclust (*, "centroid")

Cluster Dendrogram



d
hclust (*, "average")

Cluster Dendrogram



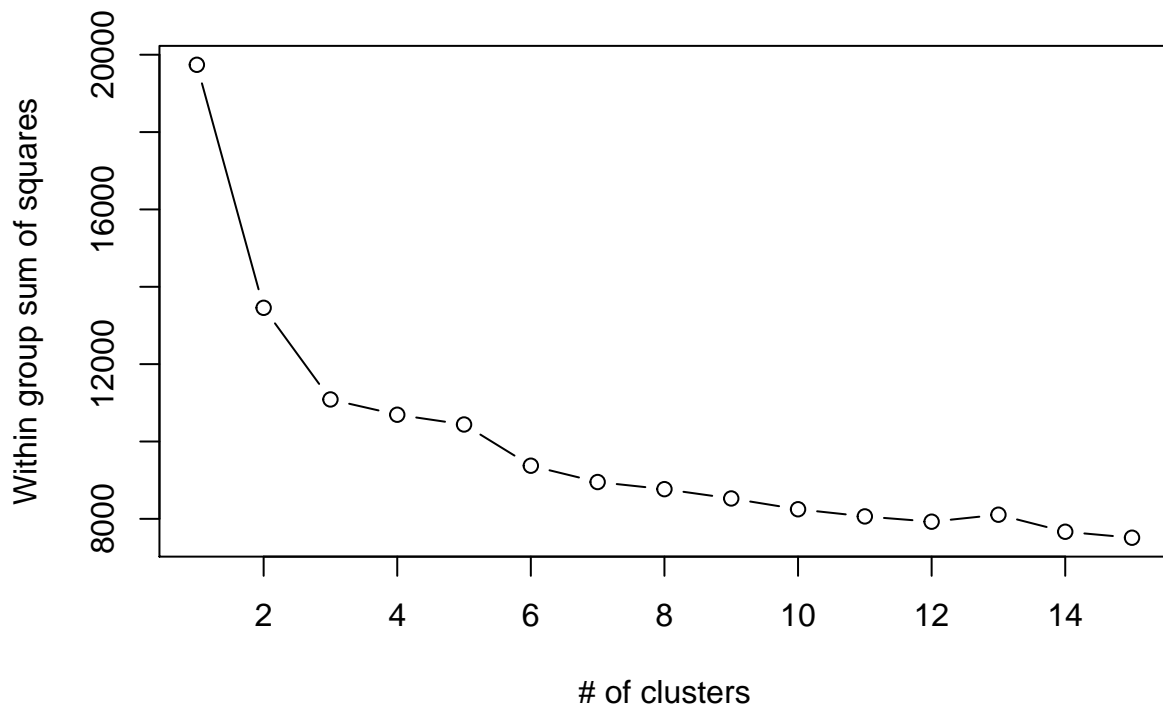
d
hclust (*, "single")

먼저 계층적 군집을 사용하였고, 거리행렬은 euclidean거리와 manhattan거리를 사용하였으며 군집간의 거리계산은 와드연결법, 중심연결법, 평균연결법, 최단연결법을 사용하였다. 그 결과 위의 8가지 군집이 형성되었다. 위의 table에서의 정당 개수와 위의 계층적군집을 보았을 때 3개의 군집이 가장 최적이라고 판단이 되었고, 3개의 군집으로 나뉘보았다. 거리행렬의 거리와는 관계없이 와드연결법이 가장 좋게 나타난 것으로 보인다.

```

wss <- 0; set.seed(1)
for(i in 1:15) wss[i] <- kmeans(dat1, centers=i)$tot.withinss
plot(1:15, wss, type="b", xlab="# of clusters", ylab="Within group sum of squares")

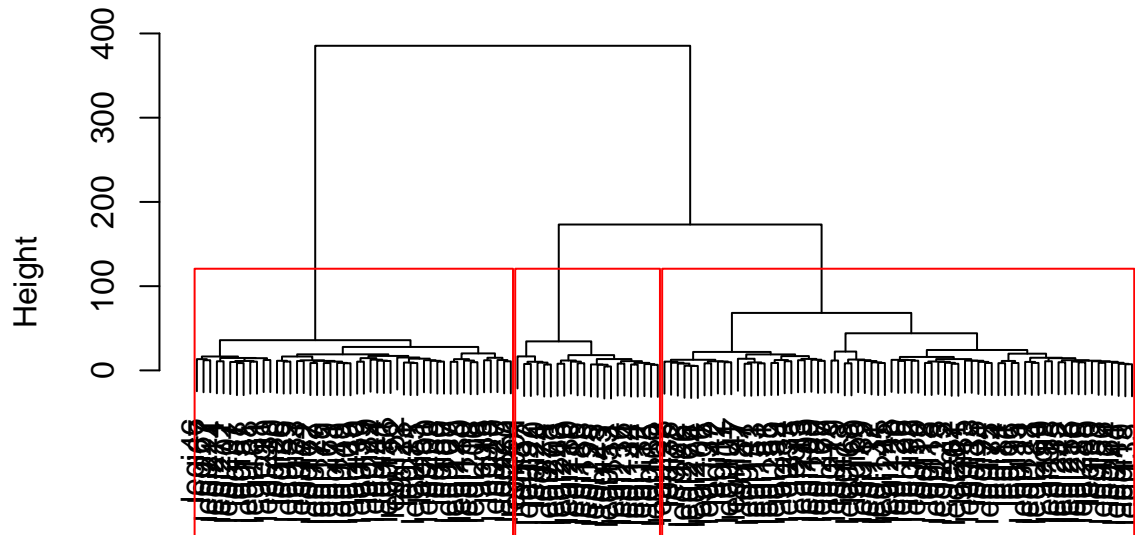
```



군집이 3개가 가장 좋다는 근거를 뒷받침 하기 위해 kmeans를 사용하여 최적의 군집수를 도식화한 결과 분산의 감소량이 군집이 3 개일 때부터 크게 감소하는 것을 볼 수 있다.

```
d <- dist(dat1, method="euclidean")
fit <- hclust(d, method="ward.D")
plot(fit)
rect.hclust(fit, k = 3, border = 'red')
```

Cluster Dendrogram



d
hclust (*, "ward.D")

```
dat2 = data.frame(cbind(rownames(dat1), cutree(fit, k=3)))
dat2 = cbind(dat2, party = dat$party)
dat2 %>% group_by(X2, party) %>% summarise(n = n())
```

```
## # A tibble: 7 x 3
## # Groups:   X2 [?]
##   X2    party      n
##   <fct> <fct>    <int>
## 1 1     바른정당      7
## 2 1     자유한국당    41
## 3 2     국민의당      2
## 4 2     더불어민주당  67
## 5 2     무소속         1
## 6 2     정의당         1
## 7 3     국민의당    22
```

위의 맨해튼과 유클리디안 거리행렬이 따로 차이가 없으므로 유클리디안 거리행렬을 사용하였다. 계층적군집을 3개의 군집을 생성하였고 군집별로 정당이 어떻게 분포되어있는지 볼수 있는 표이다. 보수당인 바른정당과 자유한국당이 한 군집, 진보당인 국민의당 소수, 더불어민주당, 정의당이 한 군집, 국민의당이 한 군집으로 구성되어 있다. 각 정당의 특징별로 잘 군집되었다고 판단된다.

```
km = kmeans(d, 3, nstart = 10)
```

군집의 개수를 3개로 정했으니, 군집이 3개인 kmeans를 실행한다.

```
fviz_cluster(km, data = d,
  palette = c("#2E9FDF", "#00AFBB", "#E7B800", "#FC4E07"),
  ellipse.type = "euclid", # Concentration ellipse
```

```

star.plot = TRUE, # Add segments from centroids to items
repel = TRUE, # Avoid label overplotting (slow)
ggtheme = theme_minimal()
)

```

Cluster plot



주성분 분석이 실행되어, 2개의 변수로 전체 변수의 82%를 설명하였다. 3개지 군집이 이쁘게 잘 형성된 것을 볼 수 있다. 그러나 kmeans의 단점인 가중치와 거리에 대해서 이야기를 하기 어렵다.

```

dat2 = data.frame(cbind(cluster = km$cluster, party = unfactor(dat$party)))
dat2 %>% group_by(cluster, party) %>% summarise(n = n())

```

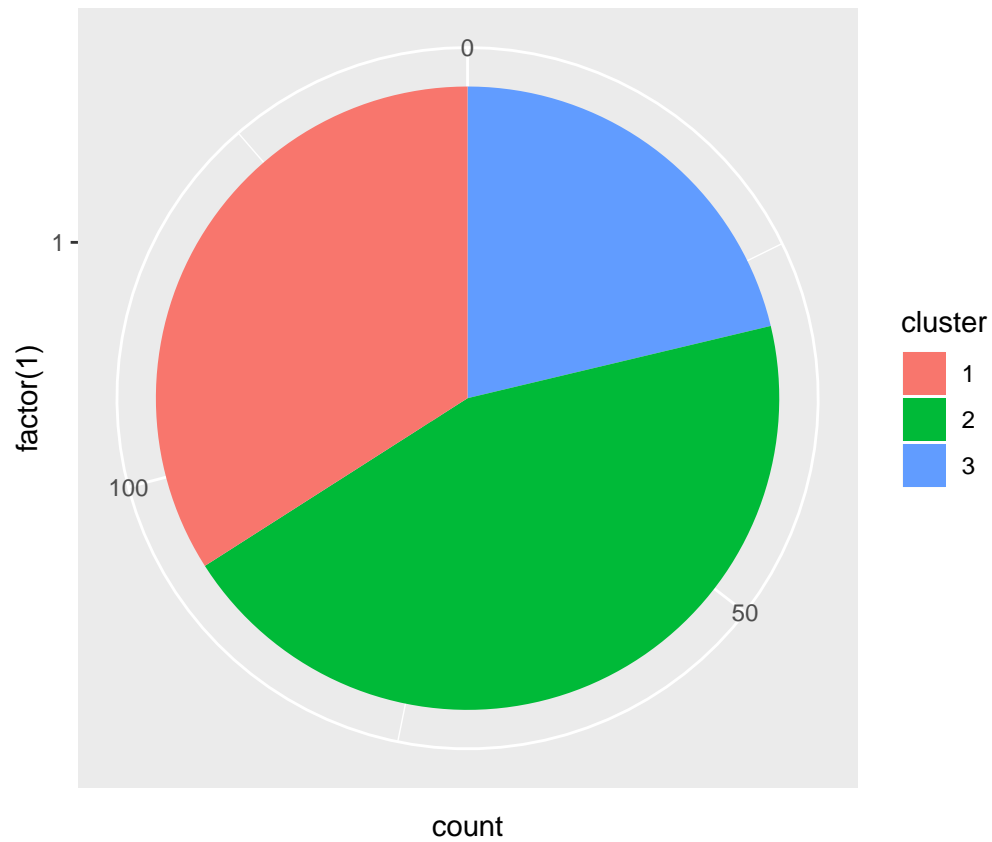
```

## # A tibble: 8 x 3
## # Groups:   cluster [?]
##   cluster party      n
##   <fct>   <fct>   <int>
## 1 1      바른정당       7
## 2 1      자유한국당    41
## 3 2      국민의당     20
## 4 2      더불어민주당  42
## 5 2      정의당        1
## 6 3      국민의당      4
## 7 3      더불어민주당  25
## 8 3      무소속        1

```

k means의 결과이다. 더불어민주당이 2군집으로 나누어 진 것을 볼 수 있다. 정당이 같아도 내부에서의 파벌이라던지, 다른 네트워크가 있다는 사실을 유추할 수 있다.

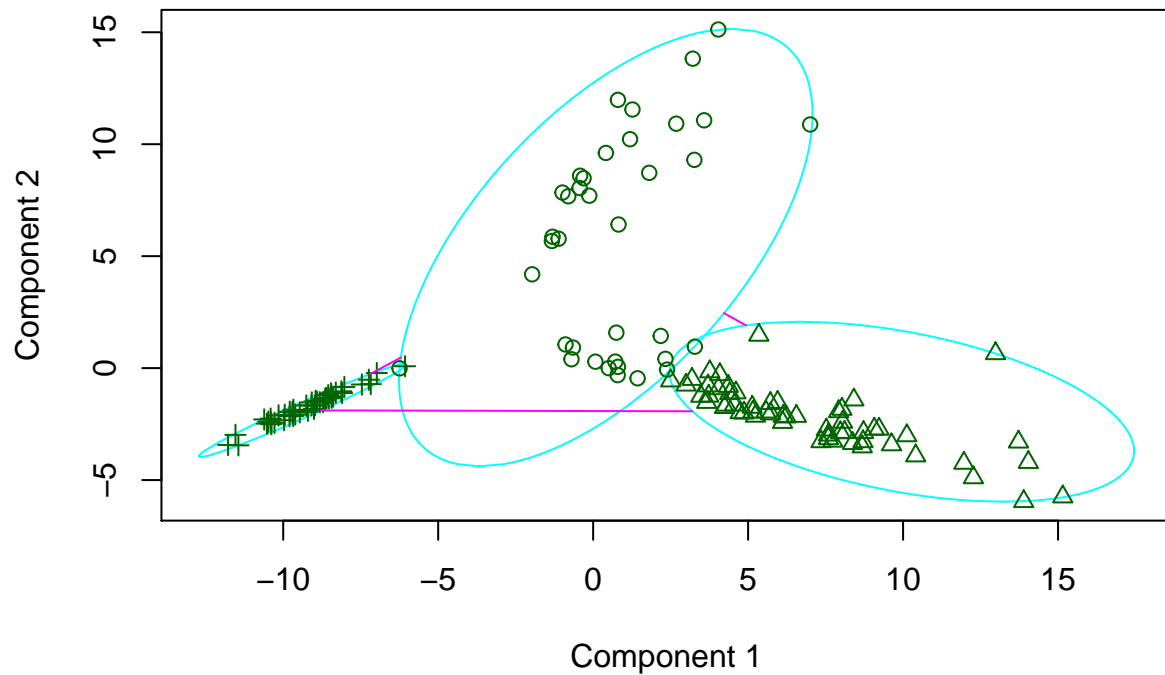
```
x <- ggplot(dat2, aes(x=factor(1), fill=cluster))
x + geom_bar(width=1) + coord_polar(theta="y")
```



k means 의 군집비율을 도식화하였다.

```
pamk.result <- pamk(dat1, 3)
plot(pamk.result$pamobject)
```

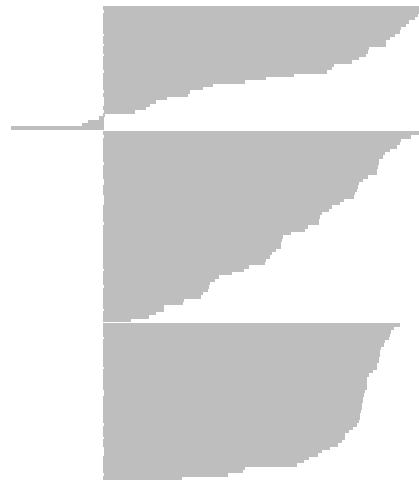
clusplot(pam(x = sdata, k = k, diss = diss))



These two components explain 51.03 % of the point variability.

Silhouette plot of pam(x = sdata, k = k, diss = diss)

n = 141



3 clusters C_j

$j: n_j \mid \text{ave}_{i \in C_j} s_i$

1 : 37 | 0.19

2 : 57 | 0.21

3 : 47 | 0.27

0.0 0.2 0.4 0.6 0.8 1.0

Silhouette width s_i

Average silhouette width : 0.22

추가적으로 k medoid 군집을 실행하였다. PAM은 K-medoid clustering이 가장 일반적으로 실현화된 것이다. 알고리즘은 k-means 알고리즘과 관련된 군집 알고리즘이고 medoidshift 알고리즘이다. k-means 와 k-medoids 알고리즘 둘다 나누는 일을 하고(즉 데이터셋을 군집들로 쪼갬다는 의미) 또한 한 군집 안에 있는 포인트들과 그 군집의 중심점 사이의 거리를 최소화 한다. k-means 알고리즘과는 다르게(한 군집의 평균을 중심점으로 잡음), k-medoids는 데이터 포인트들을 중심점(medoids 또는 exemplars라고 함)으로 선택한다.

```
dat_ta = cbind(cluster = data.frame(pamk.result$pamobject$clustering), party = dat$party)
colnames(dat_ta)[1] = 'cluster'
dat_ta %>% group_by(cluster, party) %>% summarise(n = n())
```

```
## # A tibble: 9 x 3
## # Groups:   cluster [?]
##   cluster party      n
##   <int> <fct>    <int>
## 1      1 국민당      23
## 2      1 더불어민주당 12
## 3      1 바른정당      1
## 4      1 정의당      1
## 5      2 국민당      1
## 6      2 더불어민주당 55
## 7      2 무소속      1
## 8      3 바른정당      6
## 9      3 자유한국당     41
```

이 방법을 사용했을 때에 신기하게 바른정당인원이 진보정당군집으로 보이는 1군집에 속한 것을 볼 수 있다. 그 인원은 legi1로 알 수 있는데, 국민당과 나름 밀접한 관계가 있다고 추정된다.

여러가지 군집분석 방법론을 사용하면서 자유한국당과 더불어민주당은 한 군집으로 좀처럼 섞이지 않는다. 이것은 두 정당의

발의안을 좀처럼 공동발의 하지 않는다는 점을 알 수 있다. 흥미로운 점은 계층적 군집인 경우 더불어 민주당은 군집이 나누어지지 않았지만 비계층적 군집을 시행하였을 경우에 2가지의 군집으로 나누어지는 것을 볼 수 있었다. 이 점으로 보아 더불어민주당은 민주당내에서도 2가지의 그룹으로 나뉜다는 것을 추정 할 수 있다.