> setwd('C:/Rdirectory/data\_mining/data\_mining\_covid');

> covid\_train = read.csv("covid\_train.csv", header=T);

> covid\_train$sex = as.factor(covid\_train$sex);

> covid\_train$patient\_type = as.factor(covid\_train$patient\_type);

> covid\_train$pneumonia = as.factor(covid\_train$pneumonia);

> covid\_train$age = as.numeric(covid\_train$age);

> covid\_train$diabetes = as.factor(covid\_train$diabetes);

> covid\_train$copd = as.factor(covid\_train$copd);

> covid\_train$asthma = as.factor(covid\_train$asthma);

> covid\_train$inmsupr = as.factor(covid\_train$inmsupr);

> covid\_train$hypertension = as.factor(covid\_train$hypertension);

> covid\_train$other\_disease = as.factor(covid\_train$other\_disease);

> covid\_train$cardiovascular = as.factor(covid\_train$cardiovascular);

> covid\_train$obesity = as.factor(covid\_train$obesity);

> covid\_train$renal\_chronic = as.factor(covid\_train$renal\_chronic);

> covid\_train$tobacco = as.factor(covid\_train$tobacco);

> covid\_train$contact\_other\_covid = as.factor(covid\_train$contact\_other\_covid);

> covid\_train$is\_dead = as.factor(covid\_train$is\_dead);

> str(covid\_train);

'data.frame': 32356 obs. of 16 variables:

$ sex : Factor w/ 1 level "1": 1 1 1 1 1 1 1 1 1 1 ...

$ patient\_type : Factor w/ 1 level "2": 1 1 1 1 1 1 1 1 1 1 ...

$ pneumonia : Factor w/ 2 levels "1","2": 2 2 1 1 1 2 1 1 1 2 ...

$ age : num 25 52 51 67 59 52 54 78 80 40 ...

$ diabetes : Factor w/ 2 levels "1","2": 2 2 2 1 1 1 2 2 1 2 ...

$ copd : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ asthma : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ inmsupr : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ hypertension : Factor w/ 2 levels "1","2": 2 2 2 1 2 1 2 1 1 2 ...

$ other\_disease : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ cardiovascular : Factor w/ 2 levels "1","2": 2 2 2 2 2 1 2 2 2 2 ...

$ obesity : Factor w/ 2 levels "1","2": 2 1 2 1 2 2 2 1 1 2 ...

$ renal\_chronic : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ tobacco : Factor w/ 2 levels "1","2": 2 1 2 2 2 2 2 2 2 2 ...

$ contact\_other\_covid: Factor w/ 2 levels "1","2": 1 1 1 1 1 2 2 1 1 2 ...

$ is\_dead : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 1 2 2 ...

> head(covid\_train);

sex patient\_type pneumonia age diabetes copd asthma inmsupr hypertension other\_disease cardiovascular obesity renal\_chronic tobacco

1 1 2 2 25 2 2 2 2 2 2 2 2 2 2

2 1 2 2 52 2 2 2 2 2 2 2 1 2 1

3 1 2 1 51 2 2 2 2 2 2 2 2 2 2

4 1 2 1 67 1 2 2 2 1 2 2 1 2 2

5 1 2 1 59 1 2 2 2 2 2 2 2 2 2

6 1 2 2 52 1 2 2 2 1 2 1 2 2 2

contact\_other\_covid is\_dead

1 1 2

2 1 2

3 1 2

4 1 2

5 1 2

6 2 2

> covid\_test = read.csv("covid\_test.csv", header=T);

> covid\_test$sex = as.factor(covid\_test$sex);

> covid\_test$patient\_type = as.factor(covid\_test$patient\_type);

> covid\_test$pneumonia = as.factor(covid\_test$pneumonia);

> covid\_test$age = as.numeric(covid\_test$age);

> covid\_test$diabetes = as.factor(covid\_test$diabetes);

> covid\_test$copd = as.factor(covid\_test$copd);

> covid\_test$asthma = as.factor(covid\_test$asthma);

> covid\_test$inmsupr = as.factor(covid\_test$inmsupr);

> covid\_test$hypertension = as.factor(covid\_test$hypertension);

> covid\_test$other\_disease = as.factor(covid\_test$other\_disease);

> covid\_test$cardiovascular = as.factor(covid\_test$cardiovascular);

> covid\_test$obesity = as.factor(covid\_test$obesity);

> covid\_test$renal\_chronic = as.factor(covid\_test$renal\_chronic);

> covid\_test$tobacco = as.factor(covid\_test$tobacco);

> covid\_test$contact\_other\_covid = as.factor(covid\_test$contact\_other\_covid);

> covid\_test$is\_dead = as.factor(covid\_test$is\_dead);

> str(covid\_test);

'data.frame': 5920 obs. of 16 variables:

$ sex : Factor w/ 1 level "1": 1 1 1 1 1 1 1 1 1 1 ...

$ patient\_type : Factor w/ 1 level "2": 1 1 1 1 1 1 1 1 1 1 ...

$ pneumonia : Factor w/ 2 levels "1","2": 2 2 1 1 1 1 2 2 2 1 ...

$ age : num 52 36 0 85 75 19 46 60 62 39 ...

$ diabetes : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 1 2 ...

$ copd : Factor w/ 2 levels "1","2": 2 2 2 1 2 2 2 2 2 2 ...

$ asthma : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ inmsupr : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ hypertension : Factor w/ 2 levels "1","2": 2 2 2 1 1 2 2 2 2 1 ...

$ other\_disease : Factor w/ 2 levels "1","2": 1 2 2 2 2 2 2 2 2 2 ...

$ cardiovascular : Factor w/ 2 levels "1","2": 2 2 2 1 2 2 2 2 2 2 ...

$ obesity : Factor w/ 2 levels "1","2": 2 2 2 1 2 2 2 2 2 2 ...

$ renal\_chronic : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ tobacco : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ contact\_other\_covid: Factor w/ 2 levels "1","2": 2 2 2 2 2 2 1 2 2 2 ...

$ is\_dead : Factor w/ 2 levels "1","2": 2 2 1 2 2 2 2 2 2 2 ...

> head(covid\_test);

sex patient\_type pneumonia age diabetes copd asthma inmsupr hypertension other\_disease cardiovascular obesity renal\_chronic tobacco

1 1 2 2 52 2 2 2 2 2 1 2 2 2 2

2 1 2 2 36 2 2 2 2 2 2 2 2 2 2

3 1 2 1 0 2 2 2 2 2 2 2 2 2 2

4 1 2 1 85 2 1 2 2 1 2 1 1 2 2

5 1 2 1 75 2 2 2 2 1 2 2 2 2 2

6 1 2 1 19 2 2 2 2 2 2 2 2 2 2

contact\_other\_covid is\_dead

1 2 2

2 2 2

3 2 1

4 2 2

5 2 2

6 2 2

> covid\_dead\_train = read.csv("covid\_dead\_train.csv", header=T);

> covid\_dead\_train$sex = as.factor(covid\_dead\_train$sex);

> covid\_dead\_train$patient\_type = as.factor(covid\_dead\_train$patient\_type);

> covid\_dead\_train$pneumonia = as.factor(covid\_dead\_train$pneumonia);

> covid\_dead\_train$age = as.numeric(covid\_dead\_train$age);

> covid\_dead\_train$diabetes = as.factor(covid\_dead\_train$diabetes);

> covid\_dead\_train$copd = as.factor(covid\_dead\_train$copd);

> covid\_dead\_train$asthma = as.factor(covid\_dead\_train$asthma);

> covid\_dead\_train$inmsupr = as.factor(covid\_dead\_train$inmsupr);

> covid\_dead\_train$hypertension = as.factor(covid\_dead\_train$hypertension);

> covid\_dead\_train$other\_disease = as.factor(covid\_dead\_train$other\_disease);

> covid\_dead\_train$cardiovascular = as.factor(covid\_dead\_train$cardiovascular);

> covid\_dead\_train$obesity = as.factor(covid\_dead\_train$obesity);

> covid\_dead\_train$renal\_chronic = as.factor(covid\_dead\_train$renal\_chronic);

> covid\_dead\_train$tobacco = as.factor(covid\_dead\_train$tobacco);

> covid\_dead\_train$contact\_other\_covid = as.factor(covid\_dead\_train$contact\_other\_covid);

> covid\_dead\_train$day\_cnt = as.numeric(covid\_dead\_train$day\_cnt);

> str(covid\_dead\_train);

'data.frame': 3600 obs. of 16 variables:

$ sex : Factor w/ 1 level "1": 1 1 1 1 1 1 1 1 1 1 ...

$ patient\_type : Factor w/ 1 level "2": 1 1 1 1 1 1 1 1 1 1 ...

$ pneumonia : Factor w/ 2 levels "1","2": 1 1 2 1 1 1 1 1 1 2 ...

$ age : num 78 65 58 78 92 70 71 65 56 72 ...

$ diabetes : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 1 1 2 2 ...

$ copd : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 1 2 2 2 ...

$ asthma : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ inmsupr : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ hypertension : Factor w/ 2 levels "1","2": 1 2 2 2 1 2 1 1 2 1 ...

$ other\_disease : Factor w/ 2 levels "1","2": 2 2 1 2 2 2 2 2 2 2 ...

$ cardiovascular : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ obesity : Factor w/ 2 levels "1","2": 1 1 2 1 2 1 1 1 2 2 ...

$ renal\_chronic : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 1 ...

$ tobacco : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 1 2 2 2 ...

$ contact\_other\_covid: Factor w/ 2 levels "1","2": 1 2 1 1 2 2 1 2 2 2 ...

$ day\_cnt : num 10 7 1 6 3 16 21 14 30 20 ...

> head(covid\_dead\_train);

sex patient\_type pneumonia age diabetes copd asthma inmsupr hypertension other\_disease cardiovascular obesity renal\_chronic tobacco

1 1 2 1 78 2 2 2 2 1 2 2 1 2 2

2 1 2 1 65 2 2 2 2 2 2 2 1 2 2

3 1 2 2 58 2 2 2 2 2 1 2 2 2 2

4 1 2 1 78 2 2 2 2 2 2 2 1 2 2

5 1 2 1 92 2 2 2 2 1 2 2 2 2 2

6 1 2 1 70 2 2 2 2 2 2 2 1 2 2

contact\_other\_covid day\_cnt

1 1 10

2 2 7

3 1 1

4 1 6

5 2 3

6 2 16

> covid\_dead\_test = read.csv("covid\_dead\_test.csv", header=T);

> covid\_dead\_test$sex = as.factor(covid\_dead\_test$sex);

> covid\_dead\_test$patient\_type = as.factor(covid\_dead\_test$patient\_type);

> covid\_dead\_test$pneumonia = as.factor(covid\_dead\_test$pneumonia);

> covid\_dead\_test$age = as.numeric(covid\_dead\_test$age);

> covid\_dead\_test$diabetes = as.factor(covid\_dead\_test$diabetes);

> covid\_dead\_test$copd = as.factor(covid\_dead\_test$copd);

> covid\_dead\_test$asthma = as.factor(covid\_dead\_test$asthma);

> covid\_dead\_test$inmsupr = as.factor(covid\_dead\_test$inmsupr);

> covid\_dead\_test$hypertension = as.factor(covid\_dead\_test$hypertension);

> covid\_dead\_test$other\_disease = as.factor(covid\_dead\_test$other\_disease);

> covid\_dead\_test$cardiovascular = as.factor(covid\_dead\_test$cardiovascular);

> covid\_dead\_test$obesity = as.factor(covid\_dead\_test$obesity);

> covid\_dead\_test$renal\_chronic = as.factor(covid\_dead\_test$renal\_chronic);

> covid\_dead\_test$tobacco = as.factor(covid\_dead\_test$tobacco);

> covid\_dead\_test$contact\_other\_covid = as.factor(covid\_dead\_test$contact\_other\_covid);

> covid\_dead\_test$day\_cnt = as.numeric(covid\_dead\_test$day\_cnt);

> str(covid\_dead\_test);

'data.frame': 420 obs. of 16 variables:

$ sex : Factor w/ 1 level "1": 1 1 1 1 1 1 1 1 1 1 ...

$ patient\_type : Factor w/ 1 level "2": 1 1 1 1 1 1 1 1 1 1 ...

$ pneumonia : Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...

$ age : num 66 68 49 61 47 56 68 72 78 64 ...

$ diabetes : Factor w/ 2 levels "1","2": 1 2 2 1 1 2 1 1 1 1 ...

$ copd : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 1 2 2 ...

$ asthma : Factor w/ 2 levels "1","2": 2 2 2 2 1 2 2 2 2 2 ...

$ inmsupr : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ hypertension : Factor w/ 2 levels "1","2": 1 2 2 1 2 2 1 1 2 2 ...

$ other\_disease : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ cardiovascular : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ obesity : Factor w/ 2 levels "1","2": 1 2 1 2 2 2 1 1 1 2 ...

$ renal\_chronic : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ tobacco : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...

$ contact\_other\_covid: Factor w/ 2 levels "1","2": 1 2 2 2 2 2 2 2 2 2 ...

$ day\_cnt : num 3 5 16 4 18 10 9 6 6 8 ...

> head(covid\_dead\_test);

sex patient\_type pneumonia age diabetes copd asthma inmsupr hypertension other\_disease cardiovascular obesity renal\_chronic tobacco

1 1 2 1 66 1 2 2 2 1 2 2 1 2 2

2 1 2 1 68 2 2 2 2 2 2 2 2 2 2

3 1 2 1 49 2 2 2 2 2 2 2 1 2 2

4 1 2 1 61 1 2 2 2 1 2 2 2 2 2

5 1 2 1 47 1 2 1 2 2 2 2 2 2 2

6 1 2 1 56 2 2 2 2 2 2 2 2 2 2

contact\_other\_covid day\_cnt

1 1 3

2 2 5

3 2 16

4 2 4

5 2 18

6 2 10

> # install.packages("C50");

> # install.packages("printr");

> library(C50);

> library(printr);

> C50Fit = C5.0(is\_dead~., data = covid\_train, trials=1);

c50 code called exit with value 1

> plot(C50Fit); text(C50Fit);

Error in 1:which(out == "Decision tree:") : argument of length 0

> print(C50Fit);

Call:

C5.0.formula(formula = is\_dead ~ ., data = covid\_train, trials = 1)

Classification Tree

Number of samples: 32356

Number of predictors: 15

Tree size: 0

Non-standard options: attempt to group attributes

> prediction = predict(C50Fit, newdata=covid\_test[], type="class");

Error in predict.C5.0(C50Fit, newdata = covid\_test[], type = "class") :

either a tree or rules must be provided

> summary(prediction);

1 2

2583 3337

> comparison=cbind(covid\_test,prediction);

> comparison=as.data.frame(comparison);

> print(paste("test 건수 : ",nrow(covid\_test)));

[1] "test 건수 : 5920"

> predictCorrect = comparison[comparison$is\_dead == comparison$prediction,];

> print(paste("사망여부 예측성공 건수 : ", nrow(predictCorrect)));

[1] "사망여부 예측성공 건수 : 5413"

> print(paste("사망여부 예측 정확도 : " ,nrow(predictCorrect)/nrow(covid\_test))); # trials 1 : 91%, 5: 85%, 10 : 80%, 20 : 70%, 30 : 67.8%

[1] "사망여부 예측 정확도 : 0.914358108108108"

>