

Multivariate_HW4

김민국

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```
library("mvtnorm")
library("caret")

## Loading required package: lattice

## Loading required package: ggplot2

library("GGally")

## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg      ggplot2

iris1 <- iris[iris$Species != "setosa",]

iris1_ve <- iris1[iris1$Species == "versicolor",1:4]
iris1_vi <- iris1[iris1$Species == "virginica",1:4]

mean_ve <- sapply(iris1_ve, mean)
mean_vi <- sapply(iris1_vi, mean)

var_ve <- cov(iris1_ve)
var_vi <- cov(iris1_vi)

## dmvnorm(iris1[,1:4], mean_ve, var_ve) ## f_ve = f_p
## dmvnorm(iris1[,1:4], mean_ve, var_vi) ## f_vi = f_n

pi_ve <- nrow(iris1_ve) / nrow(iris1) ## pi_p
pi_vi <- nrow(iris1_vi) / nrow(iris1) ## pi_n

ve_vi <- 1 ## c(p/n)
vi_ve <- 10 ## c(n/p)

predicted <- c()

for(i in 1:nrow(iris1)) {
  if((dmvnorm(iris1[i,1:4],mean_ve,var_ve))/dmvnorm(iris1[i,1:4],mean_vi,var_vi)
```

```

    > ((ve_vi * pi_vi) / (vi_ve * pi_ve)){
      predicted[i] <- "versicolor"
    }
    else predicted[i] <- "virginica"
  }

confusionMatrix(as.factor(predicted),as.factor(iris1$Species))

```

```

## Warning in levels(reference) != levels(data): 두 객체의 길이가 서로 배수관
## 계에 있지 않습니다

```

```

## Warning in confusionMatrix.default(as.factor(predicted),
## as.factor(iris1$Species)): Levels are not in the same order for reference
## and data. Refactoring data to match.

```

```

## Confusion Matrix and Statistics

```

```
##
```

```
##           Reference
```

```
## Prediction  setosa versicolor virginica
```

```
##   setosa      0          0          0
```

```
##   versicolor  0         50          3
```

```
##   virginica   0          0         47
```

```
##
```

```
## Overall Statistics
```

```
##
```

```
##           Accuracy : 0.97
```

```
##           95% CI : (0.9148, 0.9938)
```

```
##   No Information Rate : 0.5
```

```
##   P-Value [Acc > NIR] : < 2.2e-16
```

```
##
```

```
##           Kappa : 0.94
```

```
##
```

```
##   McNemar's Test P-Value : NA
```

```
##
```

```
## Statistics by Class:
```

```
##
```

```
##           Class: setosa Class: versicolor Class: virginica
```

```
## Sensitivity          NA          1.0000          0.9400
```

```
## Specificity          1          0.9400          1.0000
```

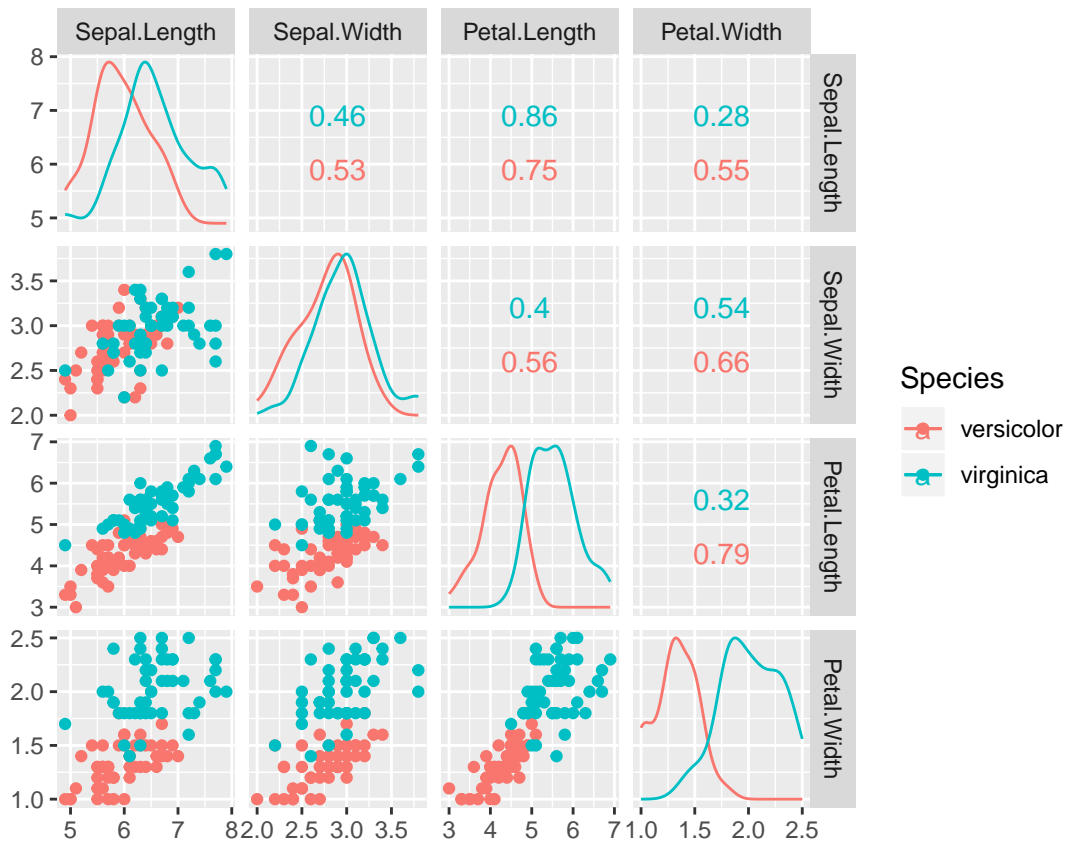
```
## Pos Pred Value       NA          0.9434          1.0000
```

```
## Neg Pred Value       NA          1.0000          0.9434
```

```
## Prevalence           0          0.5000          0.5000
```

```
## Detection Rate      0      0.5000      0.4700
## Detection Prevalence 0      0.5300      0.4700
## Balanced Accuracy   NA      0.9700      0.9700
```

```
iris2 <- cbind(iris1[, -5], predicted)
ggscatmat(iris1, columns = 1:4, color = "Species")
```



```
ggscatmat(iris2, columns = 1:4, color = "predicted")
```

