

# Linear Discriminant Analysis

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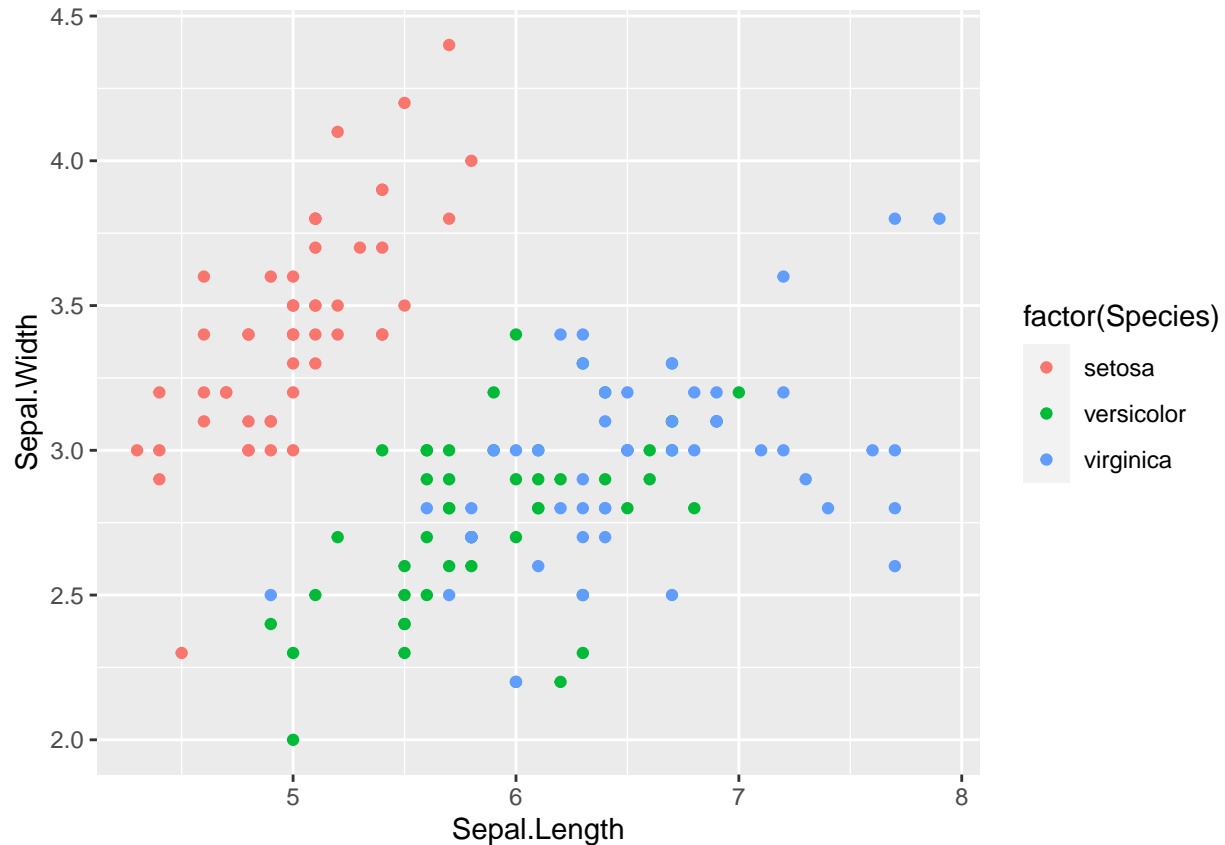
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## Assignment 1. LDA and logistic regression

### 1.

Actually LDA tries to reduce dimensions of the feature set while retaining the information that discriminates output classes. LDA tries to find a decision boundary around each cluster of a class. The goal of a LDA is often to project a feature space (a data-set n-dimensional samples) into a smaller subspace k.

- It is linearly non-separable
- Iris Setosa is linearly separable from the other two classes, so that we can draw a line or hyper-plane to classify each group.



## 2.

R functions only to implement Linear Discriminant Analysis between the three species based on variables Sepal Length and Sepal Width: Setosa -1 Versicolor-2 Virginica -3

### 2a. Mean, Covariance matrices (use cov() ) and Prior probabilities per class

```
## [1] "Prior probabilities of groups:"
```

```
## [1] 0.3333333 0.3333333 0.3333333
```

```
## [1] "Group means:"
```

```
##      [,1] [,2] [,3]
```

```
## x1 5.006 5.936 6.588
```

```
## x2 3.428 2.770 2.974
```

```
## [1] "covariance matrix of group 1"
```

```
##           x1           x2
```

```
## x1 0.12424898 0.09921633
```

```
## x2 0.09921633 0.14368980
```

```
## [1] "covariance matrix of group 2"
```

```
##           x1           x2
```

```
## x1 0.26643265 0.08518367
```

```
## x2 0.08518367 0.09846939
```

```
## [1] "covariance matrix of group 3"
```

```
##           x1           x2
```

```
## x1 0.40434286 0.09376327
```

```
## x2 0.09376327 0.10400408
```

### 2b. Pooled Covariance Matrix

```
## [1] "Pooled covariance matrix of groups"
```

```
##           x1           x2
```

```
## x1 0.26500816 0.09272109
```

```
## x2 0.09272109 0.11538776
```

### 2c. Probabilistic Model for LDA

$$x|y = C_i, \mu_i, \Sigma \sim N(\mu_i, \Sigma)$$

$$y|\pi \sim Multinomial(\pi_1, \dots, \pi_k)$$

### 2d. Discriminant Function

```
# Discriminant function

disc_fn<-function(v,p_cv,m_g,p_g)
{
  v<-as.matrix(v)
  p_cv<-solve(p_cv)
  d1<-((v%*%p_cv)%*%(m_g))
  d2<-(0.5*t(m_g))%*%(p_cv)%*%(m_g)
  t_d<-d1-(as.numeric(d2))+log(p_g)
  return(t_d)
}
```

## 2e. Decision Boundary

```
## Coefficients

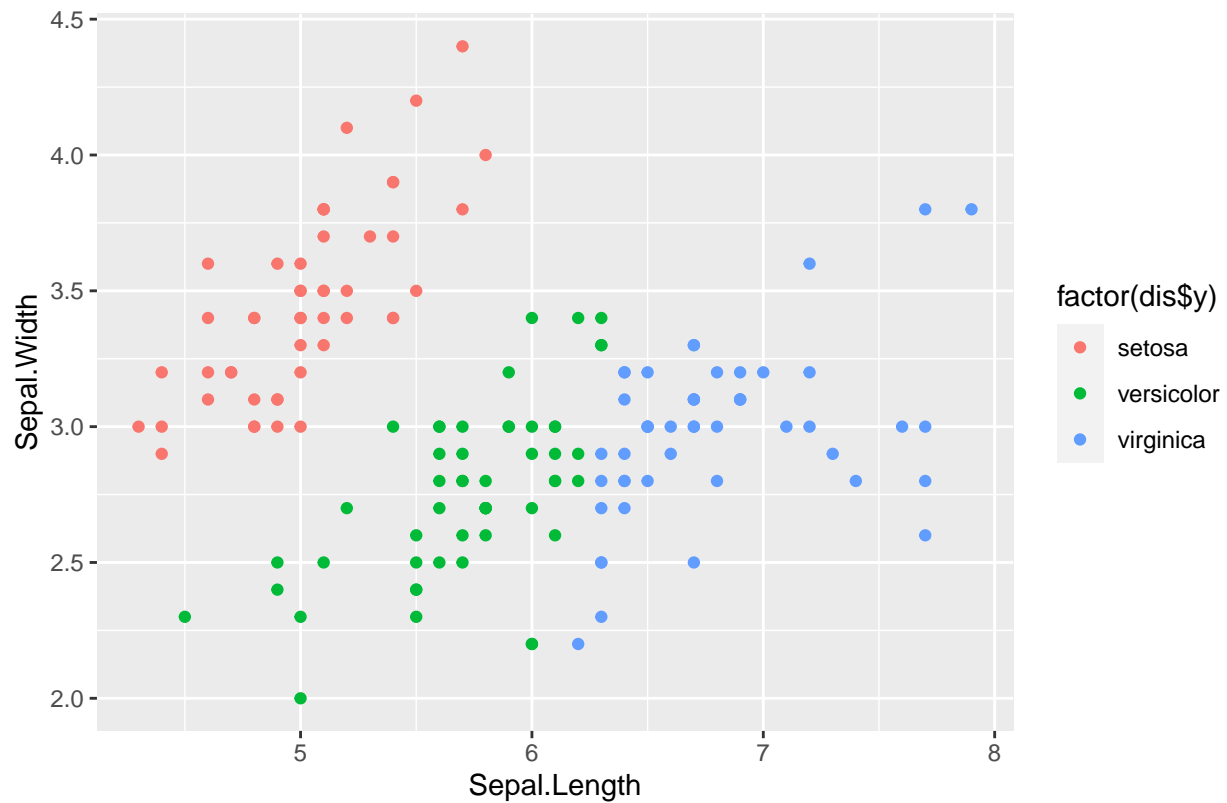
##      Setosa Versicolor Virginica
## x1 47.343881   18.36513   12.21604
## x2 -8.833515   12.24331   17.58185
```

## 3.

Whether the error obtained using discriminant function is not same as error obtained by using LDA model, but the miss-classification rate of the two model are to be same.

- Both the model and function works perfectly for the class1 (setosa) and class3(virginica) , but it confuse with the class2(versicolor)

Plot shows prediction using Discriminant Function



```
## Confusion Matrix of prediction using Discriminant function
```

```
##           y
##           1  2  3
##  setosa    49  0  0
##  versicolor 1 36 15
##  virginica  0 14 35
```

```
## Misclassification Rate using Discriminant function
```

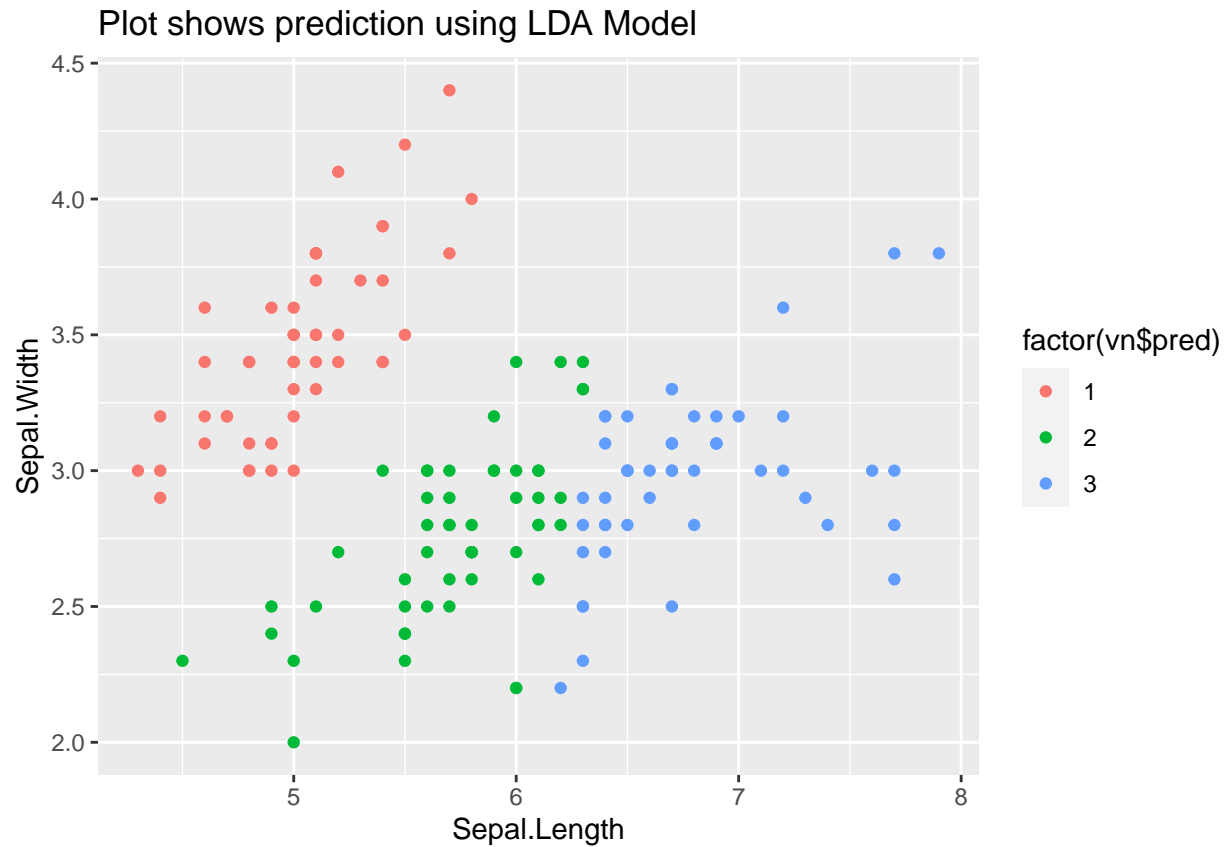
```
## [1] 0.2
```

```
## Confusion Matrix using LDA model
```

```
##
##      1  2  3
##  1 49  0  0
##  2  1 36 15
##  3  0 14 35
```

```
## Misclassification Rate using LDA model
```

```
## [1] 0.2
```



#### 4.Sample the Data

Sample the data of iris using the multivariate normal distribution .By specifying the mean and sigma in the old dataset. we can generate a new sample from same mean and variance of each groups. so,the scatter plot of the generated data and the original data is looks similar.

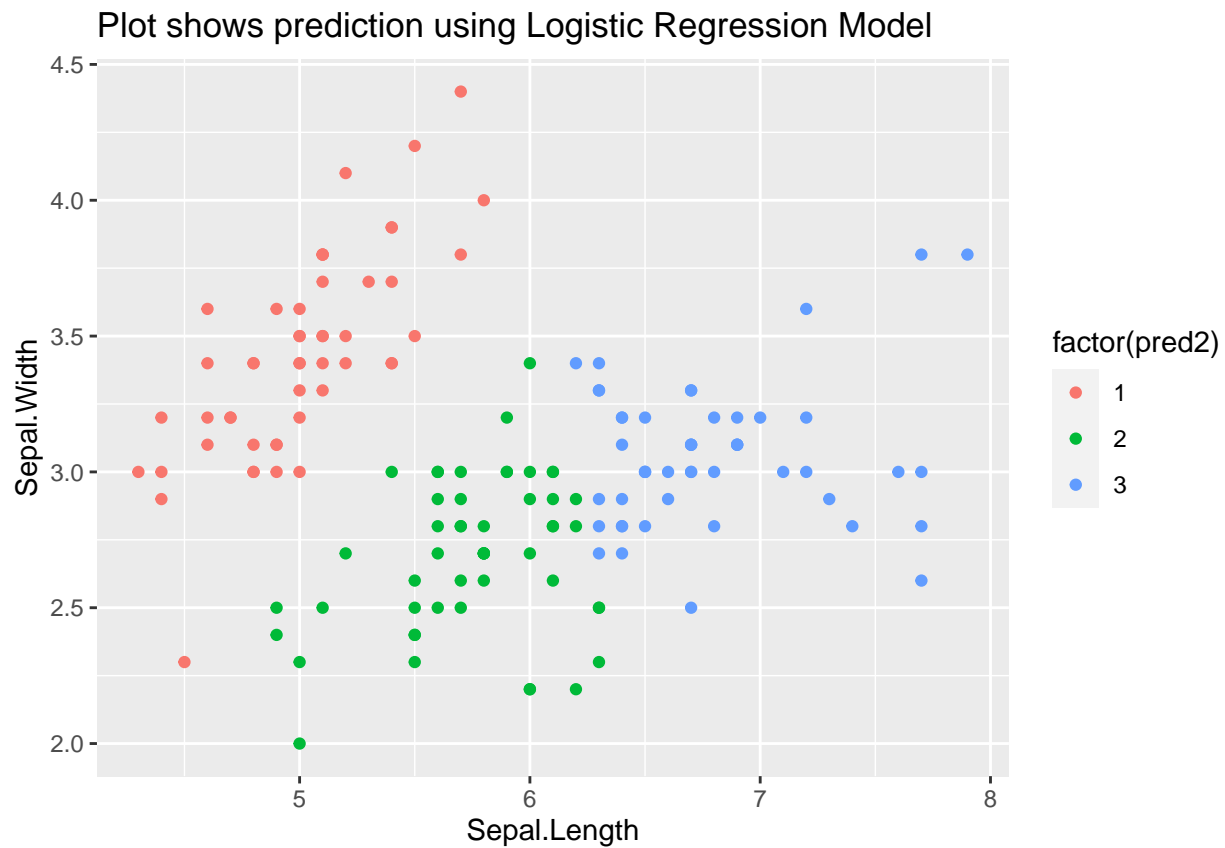
A scatter plot showing the relationship between sepal.length (x-axis) and sepal.width (y-axis) for three species (factor(y) = 1, 2, 3). The x-axis ranges from 4 to 7.5, and the y-axis ranges from 2.0 to 3.5. The plot shows distinct clusters for each species, with species 1 (red) having the highest sepal.length, species 2 (green) having intermediate values, and species 3 (blue) having the lowest sepal.length.

Logistic regression measures the relationship between one or more independent variables (X) and the categorical dependent variable (Y) by estimating probabilities using a logistic(sigmoid) function[1].

- ```
## # weights: 12 (6 variable)
## initial value 164.791843
## iter 10 value 62.715967
## iter 20 value 59.808291
## iter 30 value 55.445984
## iter 40 value 55.375704
## iter 50 value 55.346472
## iter 60 value 55.301707
## iter 70 value 55.253532
## iter 80 value 55.243230
## iter 90 value 55.230241
## iter 100 value 55.212479
## final value 55.212479
## stopped after 100 iterations

## [1] 1
```

```
## [38] 1 1 1 1 1 1 1 1 1 1 1 1 1 3 3 3 2 3 2 3 2 2 2 2 2 3 2 2 2 2 2 2
## [75] 3 3 3 3 2 2 2 2 2 2 2 2 3 2 2 2 2 2 2 2 2 2 2 2 3 2 3 3 3 2 3 3 3
## [112] 3 3 2 2 3 3 3 3 2 3 2 3 3 3 2 2 3 3 3 3 3 2 3 3 3 2 3 3 3 2 3
## [149] 3 2
## Levels: 1 2 3
```



```
##           Reference
## Prediction  1  2  3
##           1 50  0  0
##           2  0 38 13
##           3  0 12 37
```

```
## Misclassification Rate using Logistic Regression model
```

```
## [1] 0.1666667
```

## References

1.[https://en.wikipedia.org/wiki/Logistic\\_regression](https://en.wikipedia.org/wiki/Logistic_regression)

## Appendix: All code for this report

```
knitr::opts_chunk$set(echo = TRUE)
library(ggplot2)
library(MASS)
library(mvtnorm)
data=iris
x0=c(data$Sepal.Length)
y0=c(data$Sepal.Width)
z=c(data$Species)
x = data.frame(x1=x0,x2=y0)
y=as.factor(z)

# scatter plot for original data with target
ggplot(data = data, aes(x = Sepal.Length,y = Sepal.Width)) +geom_point(aes(color = factor(Species)))
# Grouping the Targets
group1_index = which( y == 1 )
group2_index = which( y == 2 )
group3_index = which( y == 3 )

#priors:
prior_group1 = length(group1_index) / length(y)
prior_group2 = length(group2_index) / length(y)
prior_group3 = length(group3_index) / length(y)
print("Prior probabilities of groups:")
print(c(prior_group1, prior_group2,prior_group3))

#means:
mean_group1 = as.matrix(colMeans(x[group1_index, ]))
mean_group2 = as.matrix(colMeans(x[group2_index, ]))
mean_group3 = as.matrix(colMeans(x[group3_index, ]))

print("Group means:")
print(cbind(mean_group1, mean_group2,mean_group3))

# Covariance Matrix
cv1<-cov(x[group1_index, ])
cv2<-cov(x[group2_index, ])
cv3<-cov(x[group3_index, ])
print("covariance matrix of group 1")
print(cv1)

print("covariance matrix of group 2")
print(cv2)

print("covariance matrix of group 3")
print(cv3)
# Pooled Co-variance Matrix
pooled_cv<-as.matrix((length(group1_index)*cv1)+(length(group2_index)*cv2)+
                      (length(group3_index)*cv3))/length(y)
print("Pooled covariance matrix of groups")
print(pooled_cv)
```



```

# Discriminant function

disc_fn<-function(v,p_cv,m_g,p_g)
{
  v<-as.matrix(v)
  p_cv<-solve(p_cv)
  d1<-((v%*%p_cv)%*%(m_g))
  d2<-(0.5*t(m_g))%*%(p_cv)%*%(m_g)
  t_d<-d1-(as.numeric(d2))+log(p_g)
  return(t_d)
}

# Decision Boundary Function
decision_boundary<-function(x,y,z)
{
  y<-solve(y)
  m<-(-0.5*t(x))%*%(y)%*%(x)
  w_oi<-m+log(z)
  w_i<-y%*%x
  #cat("w_oi",w_oi,"\\n","w_i",w_i,"\\n")
}

dc1<- decision_boundary(mean_group1,cv1,prior_group1) #decision_bndy value of group 1
dc2<- decision_boundary(mean_group2,cv2,prior_group2) #decision_bndy value of group 2
dc3<- decision_boundary(mean_group3,cv3,prior_group3) #decision_bndy value of group 3

dc_b<-data.frame(dc1,dc2,dc3)
colnames(dc_b)<-c("Setosa","Versicolor","Virginica")
cat("Coefficients")
dc_b
#Bind the Discriminant values in the data.frame

d_val1<- disc_fn(x,pooled_cv,mean_group1,prior_group1)
d_val2<- disc_fn(x,pooled_cv,mean_group2,prior_group2)
d_val3<- disc_fn(x,pooled_cv,mean_group3,prior_group3)

disc_val<-cbind(d_val1,d_val2,d_val3)
dis<-as.data.frame(disc_val)

colnames(dis)<-c("setosa","versicolor","virginica")

# Found the target value of this data by max value occurs on the row

m<-colnames(dis)[max.col(dis, ties.method = "first")]

dis$y<-m # add those values as y in the same dataframe

ggplot(data = data, aes(x = Sepal.Length,y = Sepal.Width)) +
  geom_point(aes(color = factor(dis$y))) + ggtitle("Plot shows prediction using Discriminant Function")

#confusion matrix

```

```

cat("Confusion Matrix of prediction using Discriminant function")
table(as.factor(dis$y), y)

#miss-classification rate
missclassrate=function(y,y_i)
{
  n=length(y)
  v<-1-(sum(diag(table(y,y_i)))/n)
  return(v)
}
ms=missclassrate(as.factor(dis$y),y)

cat("Misclassification Rate using Discriminant function","\n")
ms

#LDA Model
fit_lda <- lda(y~., data = x)
# ca("coefficients")
# coef(fit_lda)
pred_lda <- predict(fit_lda, x)
vn<-data.frame(original = y, pred = pred_lda$class)
cat("Confusion Matrix using LDA model")
table(vn$pred,vn$original)
ldms=missclassrate(as.factor(vn$pred),y)
cat("Misclassification Rate using LDA model","\n")
ldms

ggplot(data = data, aes(x = Sepal.Length,y = Sepal.Width)) +
  geom_point(aes(color = factor(vn$pred)))+ ggtitle("Plot shows prediction using LDA Model")
# bind the all groups in a single dataframe
bvn1 <- rmvnorm(50, mean = mean_group1, sigma = cv1 )
bvn2 <- rmvnorm(50, mean = mean_group2, sigma = cv2 )
bvn3 <- rmvnorm(50, mean = mean_group3, sigma = cv3 )

bvn<-rbind(bvn1,bvn2,bvn3)
bvn<-as.data.frame(bvn)
bvn$y<-y

sample_data<-bvn[sample(nrow(bvn), 150), ]

colnames(bvn)<-c("sepal.length","sepal.width","species")

ggplot(data =bvn, aes(x = sepal.length,y = sepal.width)) +
  geom_point(aes(color = factor(y)))+ ggtitle("sampled data of iris")

### 5.Logistic Regression Model

library(nnet)
irisModel<-multinom(y~x1+x2 ,data = x)
m<-summary(irisModel)

```

```

pred2<-predict(irisModel,x)
pred2

ggplot(data = data, aes(x = Sepal.Length,y = Sepal.Width)) +
  geom_point(aes(color = factor(pred2)))+ ggtitle("Plot shows prediction using Logistic Regression Model")

table("Prediction"=as.factor(pred2), "Reference"=y)  # confusion Matrix

lms=missclassrate(as.factor(pred2),y)
cat("Misclassification Rate using Logistic Regression model","\n")
lms

```