20BDS0146

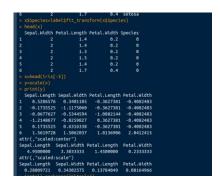
VENNELA G

PROGRAMMING FOR DATA SCIENCE

LAB ASSESSMENT 3

1. Perform Label encoding on IRIS Dataset

```
#label encoding
x=iris[-c(1,33)]
sum(is.na(x))
colSums(is.na(x))
install.packages("superml")
library(superml)
label=LabelEncoder$new()
x$Species=label$fit_transform(x$Species)
head(x)
```



2. Perform One-hot encoding on IRIS Dataset

#one hot encoding

```
install.packages("mltools")
library(mltools)
install.packages("data.table")
library(data.table)
x=iris[c(10,30,50,70,5,8),]
y=one_hot(as.data.table(x))
print(y)
```

3. Feature scaling or standardization

a. Normalization

#normalization

install.packages("BBmisc")
library(BBmisc)
y=normalize(x,method="standardize")
print(y)

```
> y=normalize(x,method="standardize")
> print(y)
Sepal.Length Sepal.Width Petal.Length Petal.Width Species
10 -0.4428074 -0.22140372 -0.3868963 -0.6177539 setosa
30 -1.1070186 0.04428074 -0.2859668 -0.3530023 setosa
50 -0.1107019 0.30996521 -0.4878258 -0.3530023 setosa
70 1.8819316 -1.81551052 2.0354109 2.0297630 versicolor
5 -0.1107019 1.10701861 -0.4878258 -0.3530023 setosa
8 -0.1107019 0.57564968 -0.3868963 -0.3530023 setosa
```

b.Z-scale

#Z-scale

names(x)

x=iris[-5]

z=sapply(x,function(x)((x-mean(x))/sd(x)))print(head(z))

```
Sepal.Length Sepal.Width Petal.Length Petal.Width
  -0.8976739 1.01560199
                             -1.335752
                                           -1.311052
                             -1.335752
  -1.1392005 -0.13153881
                                           -1.311052
  -1.3807271 0.32731751
                             -1.392399
                                           -1.311052
  -1.5014904 0.09788935
                             -1.279104
                                           -1.311052
 -1.0184372 1.24503015
-0.5353840 1.93331463
                             -1.335752
                                           -1.311052
                              -1.165809
                                           -1.048667
```

4. Find the principal components of IRIS dataset

#principal components of iris data set

```
x=iris[-5]
my_pca=prcomp(x, scale = TRUE,center = TRUE, retx = T)
names(iris)
summary(iris)
my_pca$rotation
my_pca$sdev
```

```
> names(iris)
[1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"

> summary(iris)
Sepal.Length Sepal.Width Petal.Length Petal.Width Species
Min. :4.300 Min. :2.000 Min. :1.000 Min. :0.100 setosa :50
1st Qu.:5.100 1st Qu.:2.800 1st Qu.:1.600 1st Qu.:0.300 versicolor:50
Median :5.803 Mean :3.057 Mean :3.758 Mean :1.300 virginica :50
Mean :5.843 Mean :3.057 Mean :3.758 Mean :1.199
3rd Qu.:6.400 3rd Qu.:3.300 3rd Qu.:5.100 3rd Qu.:1.800
Max. :7.900 Max. :4.400 Max. :6.900 Max. :2.500

> my_pcasrotation
PC1 PC2 PC3 PC4
Sepal.Length 0.5210659 -0.37741762 -0.7195664 0.2612863
Sepal.Width -0.26393474 -0.92329566 -0.2443818 -0.1235096
Petal.Length 0.5804131 -0.02449161 -0.1421264 -0.8014492
Petal.Width 0.5648565 -0.06694199 -0.6342727 0.5235971

> my_pcassdev
[1] 1.7083611 0.9560494 0.3830886 0.1439265
```

5. House rent prediction using linear regression

#house rent prediction

```
#Read Dataset
install.packages("mlbench")
library(mlbench)
data(BostonHousing)
x=BostonHousing
str(x)
names(x)
```

#Check NA in dataset sum(is.na(x))

```
#split dataset
install.packages('caTools')
library(caTools)
split=sample.split(x,SplitRatio =0.7)
train=subset(x,split==TRUE)
test=subset(x,split==FALSE)
#The General Linear regression model in R:
#Univariate Model : model < -lm(y \sim x, data)
# Multivariate Model : model < -lm(y~.,data)
#medv is the target variable, predicted using crim,rm,tax,lstat
model=lm(medv \sim crim + rm + tax + lstat, data = train)
summary(model)
#Prediction
test$predicted.medv= predict(model,test)
print(test$medv)
print(test$predicted.medv)
# Error and rmse
error=test$medv-test$predicted.medv
rmse=sqrt(mean(error)^2)
cat("RMSE",rmse)
```

6. Medical diagnosis for disease spread pattern Using SVM

#medical diagnosis

 $x = read.csv("C:\|\Vennela\|\Downloads\|\Cancer_Data.csv") \\ names(x)$

```
names(x)

> names(x)

[1] "id" | "texture_mean" | "perimeter_mean" | "concavity_mean" | "fractal_dimension_mean" | "fractal_dimension_worst" | "smoothness_mean" | "concavity_wean" | "fractal_dimension_mean" | "fractal_dimension_worst" | "smoothness_worst" | "concavity_mean | "concavity_mean | "texture_mean | "tex
```

```
#Check NA in dataset
sum(is.na(x))
colSums(is.na(x))
```

#Label Encoder library(superml) label=LabelEncoder\$new() x\$diagnosis=label\$fit_transform(x\$diagnosis) head(x)

```
#Train-test split
library(caTools)
split=sample.split(x$diagnosis,SplitRatio =0.7)
train=subset(x,split==TRUE)
test=subset(x,split==FALSE)
#SVM
install.packages('e1071')
library(e1071)
train[-1]=scale(train[-1])
test[-1]=scale(test[-1])
names(train)
classifier = svm(formula = diagnosis ~ .,
          data = train,
          type = 'C-classification',
          kernel = 'linear')
#Prediction
```

Diag_pred = predict(classifier, newdata = test[-1])