Iris_KNN

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```
library(corrgram)
library(corrplot)

## corrplot 0.92 loaded

library(caTools)
library(Amelia)

## Loading required package: Rcpp

## ##
## ## Amelia II: Multiple Imputation
## ## (Version 1.8.2, built: 2024-04-10)
## ## Copyright (C) 2005-2024 James Honaker, Gary King and Matthew Blackwell
## ## Refer to http://gking.harvard.edu/amelia/ for more information
## ##

library(ggplot2)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

#### Getting the data

library(ISLR)

head(iris)

##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

```r
####
var(iris[,1])
```

```
## [1] 0.6856935
```

```r
var(iris[,2])
```

```
## [1] 0.1899794
```

```r
#### Making standardization

library(class)

standard.iris <- scale(iris[1:4])

## Binding both standard.iris and species

final.iris <- cbind(standard.iris,iris[5])

View(final.iris)

## Testing variance, it should now show us 1 for every one

var(standard.iris[,1])
```

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

```r
var(standard.iris[,2])
```

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

```r
### Making test and train

sample <- sample.split(final.iris,SplitRatio = 0.7)
train <- subset(final.iris,sample == TRUE)
test <- subset(final.iris,sample==FALSE)

#### KNN Model

model.species <- knn(train[1:4],test[1:4],train$Species,k=1)

print(model.species)
```

```
##  [1] setosa     setosa     setosa     setosa     setosa     setosa
##  [7] setosa     setosa     setosa     setosa     setosa     setosa
## [13] setosa     setosa     setosa     setosa     setosa     setosa
## [19] setosa     setosa     versicolor versicolor versicolor versicolor
## [25] versicolor versicolor versicolor versicolor virginica  virginica
## [31] versicolor versicolor versicolor versicolor versicolor versicolor
## [37] versicolor versicolor versicolor versicolor virginica  virginica
## [43] virginica  virginica  virginica  virginica  virginica  virginica
```

```
## [49] virginica  virginica  virginica  virginica  virginica  virginica
## [55] virginica  virginica  virginica  virginica  virginica  virginica
## Levels: setosa versicolor virginica
```

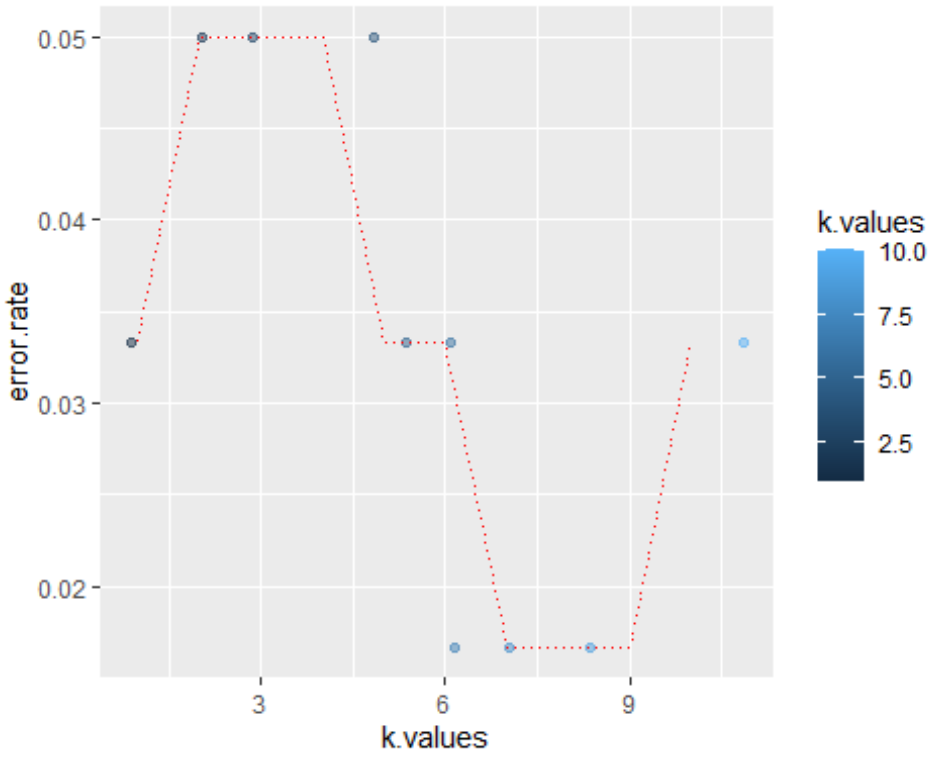
```
#### Mean error

meanerror <- mean(test$Species != model.species)

print(meanerror)
```

```
## [1] 0.03333333
```

```
### Elbow method or graph to see the k values and when it stabilizes

model.species <- NULL
error.rate <- NULL

for (i in 1:10){
  model.species <- knn(train[1:4],test[1:4],train$Species,k=i)
  error.rate[i] <- mean(test$Species != model.species)
}

k.values <- 1:10

df <- data.frame(error.rate,k.values)

print(df)
```

```
##    error.rate k.values
## 1  0.03333333        1
## 2  0.05000000        2
## 3  0.05000000        3
## 4  0.05000000        4
## 5  0.03333333        5
## 6  0.03333333        6
## 7  0.01666667        7
## 8  0.01666667        8
## 9  0.01666667        9
## 10 0.03333333       10
```

```
ggplot(df,aes(k.values,error.rate)) + geom_point(position=position_jitter(w=1
, h=0),aes(color=k.values),alpha=0.5) + geom_line(lty='dotted',color='red')
```




```
## although the error value starts high but as the k value increases the erro
r rate goes down significantly
## also this data set is too small to really implement elbow method
```