

Lab_7

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Dataset: Cleaned-data Design a Support Vector Machine (for the given Dataset) - Binary Classifier using Linear and Radial Kernel and Cross validation to determine optimized values for the hyper-parameters of the model.

The task is to develop a binary classifier to predict each of the severity levels of i) mild ii) moderate iii) severe

```
Cleaned.Data=read.csv("/Users/tarunsidhu/Desktop/Sem 4/ML/ML(Lab)/Data Sets/Cleaned-Data.csv")
summary(Cleaned.Data)
```

```

##      Fever      Tiredness      Dry.Cough      Difficulty.in.Breathing
## Min.    :0.0000    Min.    :0.0      Min.    :0.0000    Min.    :0.0
## 1st Qu.:0.0000    1st Qu.:0.0      1st Qu.:0.0000    1st Qu.:0.0
## Median :0.0000    Median :0.5      Median :1.0000    Median :0.5
## Mean   :0.3125    Mean   :0.5      Mean   :0.5625    Mean   :0.5
## 3rd Qu.:1.0000    3rd Qu.:1.0      3rd Qu.:1.0000    3rd Qu.:1.0
## Max.   :1.0000    Max.   :1.0      Max.   :1.0000    Max.   :1.0
##      Sore.Throat      None_Sympton      Pains      Nasal.Congestion
## Min.    :0.0000    Min.    :0.0000    Min.    :0.0000    Min.    :0.0000
## 1st Qu.:0.0000    1st Qu.:0.0000    1st Qu.:0.0000    1st Qu.:0.0000
## Median :0.0000    Median :0.0000    Median :0.0000    Median :1.0000
## Mean   :0.3125    Mean   :0.0625    Mean   :0.3636    Mean   :0.5455
## 3rd Qu.:1.0000    3rd Qu.:0.0000    3rd Qu.:1.0000    3rd Qu.:1.0000
## Max.   :1.0000    Max.   :1.0000    Max.   :1.0000    Max.   :1.0000
##      Runny.Nose      Diarrhea      None_Experiencing      Age_0.9
## Min.    :0.0000    Min.    :0.0000    Min.    :0.00000    Min.    :0.0
## 1st Qu.:0.0000    1st Qu.:0.0000    1st Qu.:0.00000    1st Qu.:0.0
## Median :1.0000    Median :0.0000    Median :0.00000    Median :0.0
## Mean   :0.5455    Mean   :0.3636    Mean   :0.09091    Mean   :0.2
## 3rd Qu.:1.0000    3rd Qu.:1.0000    3rd Qu.:0.00000    3rd Qu.:0.0
## Max.   :1.0000    Max.   :1.0000    Max.   :1.00000    Max.   :1.0
##      Age_10.19      Age_20.24      Age_25.59      Age_60.      Gender_Female
## Min.    :0.0      Min.    :0.0      Min.    :0.0      Min.    :0.0      Min.    :0.0000
## 1st Qu.:0.0      1st Qu.:0.0      1st Qu.:0.0      1st Qu.:0.0      1st Qu.:0.0000
## Median :0.0      Median :0.0      Median :0.0      Median :0.0      Median :0.0000
## Mean   :0.2      Mean   :0.2      Mean   :0.2      Mean   :0.2      Mean   :0.3333
## 3rd Qu.:0.0      3rd Qu.:0.0      3rd Qu.:0.0      3rd Qu.:0.0      3rd Qu.:1.0000
## Max.   :1.0      Max.   :1.0      Max.   :1.0      Max.   :1.0      Max.   :1.0000
##      Gender_Male      Gender_Transgender      Severity_Mild      Severity_Moderate
## Min.    :0.0000    Min.    :0.0000    Min.    :0.00    Min.    :0.00
## 1st Qu.:0.0000    1st Qu.:0.0000    1st Qu.:0.00    1st Qu.:0.00
## Median :0.0000    Median :0.0000    Median :0.00    Median :0.00
## Mean   :0.3333    Mean   :0.3333    Mean   :0.25    Mean   :0.25
## 3rd Qu.:1.0000    3rd Qu.:1.0000    3rd Qu.:0.25    3rd Qu.:0.25
## Max.   :1.0000    Max.   :1.0000    Max.   :1.00    Max.   :1.00
##      Severity_None      Severity_Severe      Contact_Dont.Know      Contact_No
## Min.    :0.00    Min.    :0.00    Min.    :0.0000    Min.    :0.0000
## 1st Qu.:0.00    1st Qu.:0.00    1st Qu.:0.0000    1st Qu.:0.0000
## Median :0.00    Median :0.00    Median :0.0000    Median :0.0000
## Mean   :0.25    Mean   :0.25    Mean   :0.3333    Mean   :0.3333
## 3rd Qu.:0.25    3rd Qu.:0.25    3rd Qu.:1.0000    3rd Qu.:1.0000
## Max.   :1.00    Max.   :1.00    Max.   :1.0000    Max.   :1.0000
##      Contact_Yes      Country
## Min.    :0.0000      Length:316800
## 1st Qu.:0.0000      Class :character
## Median :0.0000      Mode  :character
## Mean   :0.3333
## 3rd Qu.:1.0000
## Max.   :1.0000

```

```
Cleaned_Data_1 <- Cleaned.Data[1:10000,]  
attach(Cleaned_Data_1)  
plot(Fever,Sore.Throat)  
library(e1071)  
svm.fit <- svm(Severity_Mild ~ Fever+Sore.Throat, data = Cleaned_Data_1, type='C-c  
lassification', kernel='linear', cost=10, scale=FALSE)  
plot(svm.fit, Cleaned_Data_1)
```

```
## Error in plot.svm(svm.fit, Cleaned_Data_1): missing formula.
```

```
summary(svm.fit)
```

```
##  
## Call:  
## svm(formula = Severity_Mild ~ Fever + Sore.Throat, data = Cleaned_Data_1,  
##      type = "C-classification", kernel = "linear", cost = 10, scale = FALSE)  
##  
##  
## Parameters:  
##      SVM-Type:  C-classification  
##      SVM-Kernel: linear  
##              cost: 10  
##  
## Number of Support Vectors: 5004  
##  
## ( 2502 2502 )  
##  
##  
## Number of Classes: 2  
##  
## Levels:  
## 0 1
```

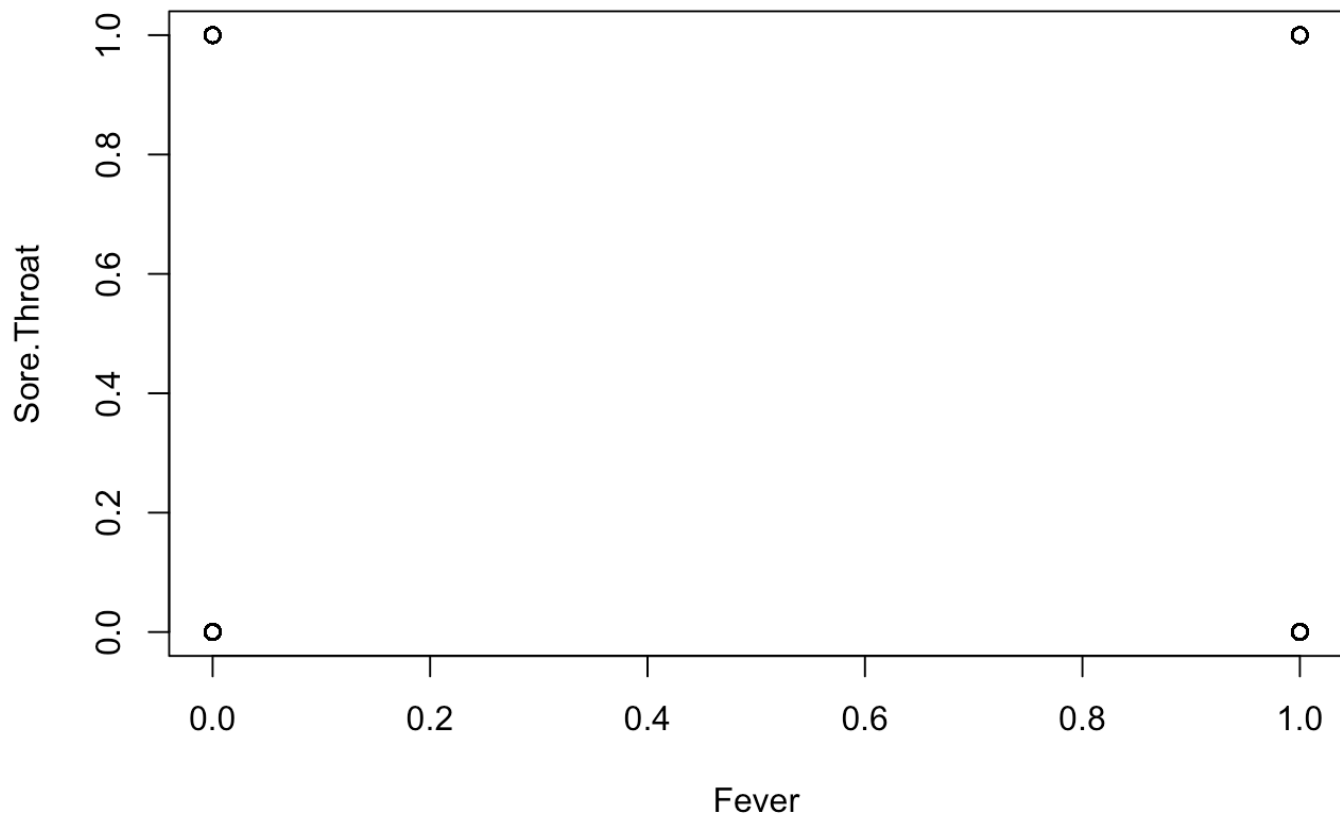
```
yhat <- predict(svm.fit, Cleaned_Data_1)  
table(predict=yhat, truth=Severity_Mild)
```

```
##      truth  
## predict    0    1  
##      0 7498 2502  
##      1     0     0
```

```
library(caret)
```

```
## Loading required package: lattice
```

```
## Loading required package: ggplot2
```



```
confusionMatrix(yhat, as.factor(Cleaned_Data_1$Severity_Mild))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##           0 7498 2502
##           1     0     0
##
##           Accuracy : 0.7498
##           95% CI : (0.7412, 0.7583)
##           No Information Rate : 0.7498
##           P-Value [Acc > NIR] : 0.5054
##
##           Kappa : 0
##
## Mcnemar's Test P-Value : <2e-16
##
##           Sensitivity : 1.0000
##           Specificity : 0.0000
##           Pos Pred Value : 0.7498
##           Neg Pred Value :      NaN
##           Prevalence : 0.7498
##           Detection Rate : 0.7498
##           Detection Prevalence : 1.0000
##           Balanced Accuracy : 0.5000
##
##           'Positive' Class : 0
##
```