

SVM (Support Vector Machine) on diabetes dataset

Code ▾

Install and load libraries : mlr

Hide

```
# install.packages("mlr", dependencies = TRUE)
```

Install and load libraries : tidyverse and mclust

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```
# install.packages("tidyverse")  
# install.packages("mclust")
```

Load the diabetes data :

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```
data(diabetes, package = "mclust")
```

Use the installed libs :

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```
library(mlr)  
library(tidyverse)
```

Format and display data :

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```
diabetesTib <- as_tibble(diabetes)  
diabetesTib
```

class <fctr>	glucose <dbl>	insulin <dbl>	sspg <dbl>
Normal	80	356	124
Normal	97	289	117
Normal	105	319	143
Normal	90	356	199
Normal	90	323	240
Normal	86	381	157
Normal	100	350	221
Normal	85	301	186
Normal	97	379	142

class	glucose	insulin	sspg
<fctr>	<dbl>	<dbl>	<dbl>
Normal	97	296	131

1-10 of 145 rows

Previous123456...15Next

Get some stats of the data :

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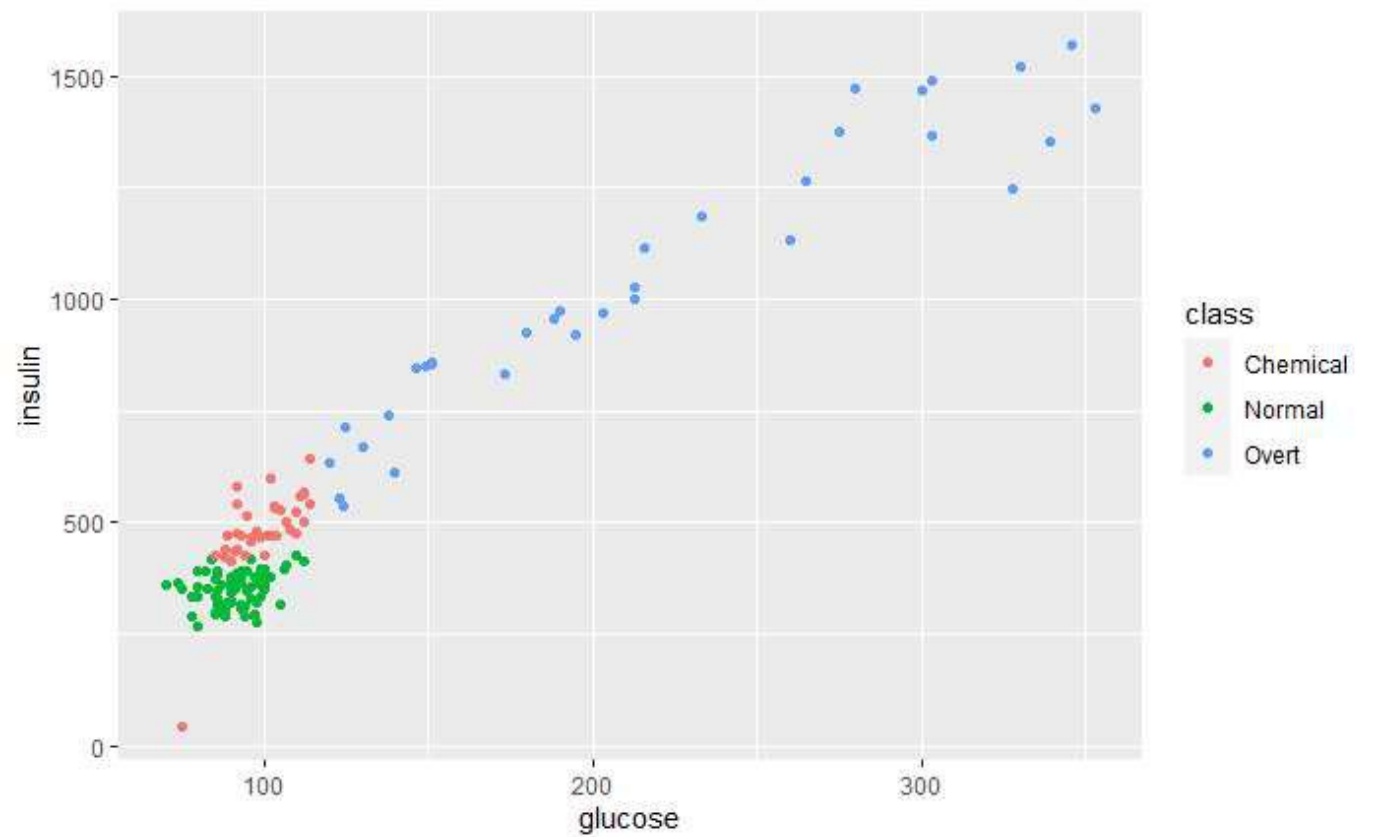
summary(diabetesTib)

class	glucose	insulin	sspg
Chemical:36	Min. : 70	Min. : 45.0	Min. : 10.0
Normal :76	1st Qu.: 90	1st Qu.: 352.0	1st Qu.:118.0
Overt :33	Median : 97	Median : 403.0	Median :156.0
	Mean :122	Mean : 540.8	Mean :186.1
	3rd Qu.:112	3rd Qu.: 558.0	3rd Qu.:221.0
	Max. :353	Max. :1568.0	Max. :748.0

Plot the data around some of its classes :

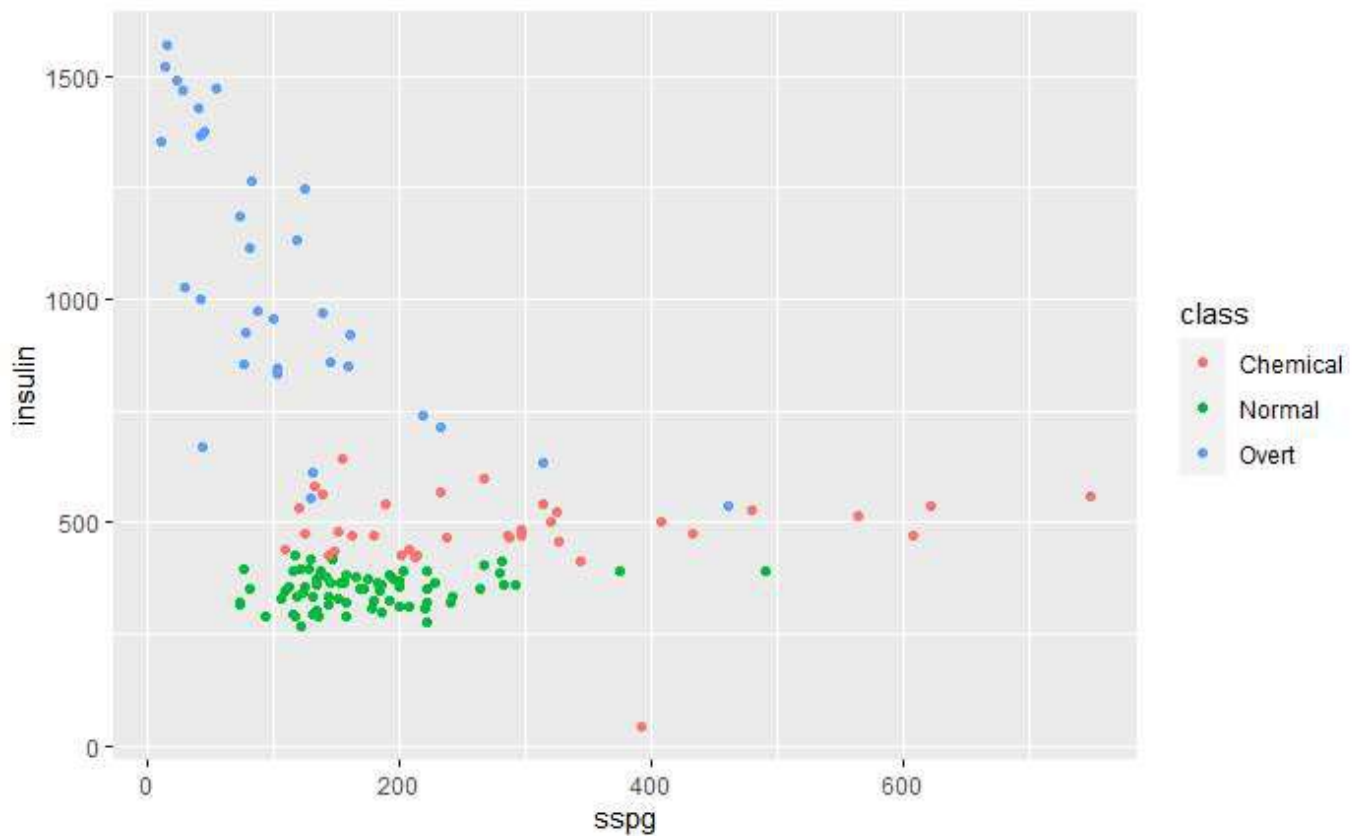
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```
ggplot(diabetesTib, aes(glucose, insulin, col = class)) +  
  geom_point()
```

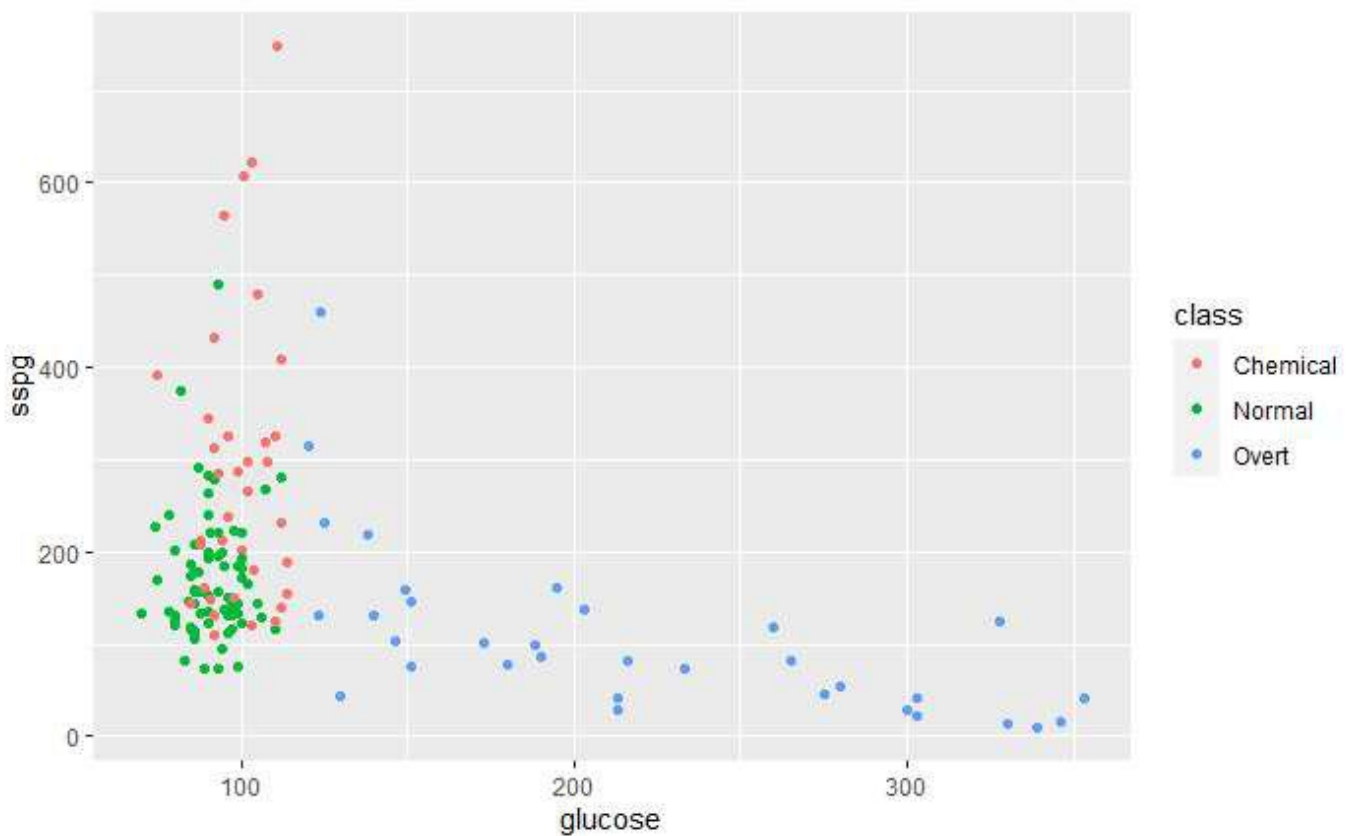


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```
ggplot(diabetesTib, aes(sspg, insulin, col = class)) +  
  geom_point()
```

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```
ggplot(diabetesTib, aes(glucose, sspg, col = class)) +  
  geom_point()
```



Define a Task :

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```
diabetesTask <- makeClassifTask(data = diabetesTib, target = "class")
```

Provided data is not a pure data.frame but from class tbl_df, hence it will be converted.

[Hide](#)

```
diabetesTask
```

```
Supervised task: diabetesTib
Type: classif
Target: class
Observations: 145
Features:
  numerics    factors ordered functionals
        3         0         0         0
Missings: FALSE
Has weights: FALSE
Has blocking: FALSE
Has coordinates: FALSE
Classes: 3
Chemical    Normal    Overt
        36         76         33
Positive class: NA
```

Define a learner : K Nearest Neighbours

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```
svm <- makeLearner("classif.svm")
```

Train the model :

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```
svmModel <- train(svm, diabetesTask)
```

Use hold-out crossval :

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```
kfold <- makeResampleDesc("RepCV", folds = 10, reps = 50)
```

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```
kFoldCV <- resample(learner = svm, task = diabetesTask, resampling = kfold)
```

Resampling: repeated cross-validation

Measures:	mmce
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[Resample] iter 497: 0.0666667
[Resample] iter 498: 0.1428571
[Resample] iter 499: 0.1428571
[Resample] iter 500: 0.0000000
```

Aggregated Result: mmce.test.mean=0.1346667

Display the confusion matrix :

Hide

```
calculateConfusionMatrix(kFoldCV$pred)
```

	predicted			
true	Chemical	Normal	Overt	-err.-
Chemical	1223	577	0	577
Normal	170	3630	0	170
Overt	229	0	1421	229
-err.-	399	577	0	976

We can plot the svm model :

```
plotLearnerPrediction(learner = svm, task = diabetesTask)
```

