

Decision Tree on diabetes dataset

Code ▾

Install and load libraries : mlr

Hide

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

Install and load libraries : tidyverse and mclust

Hide

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

Load the diabetes data :

Hide

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

Use the installed libs :

Hide

```
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
Normal	97	296	131
1-10 of 145 rows			
Previous 1 2 3 4 5 6 ... 15 Next			

Get some stats of the data :

[Hide](#)

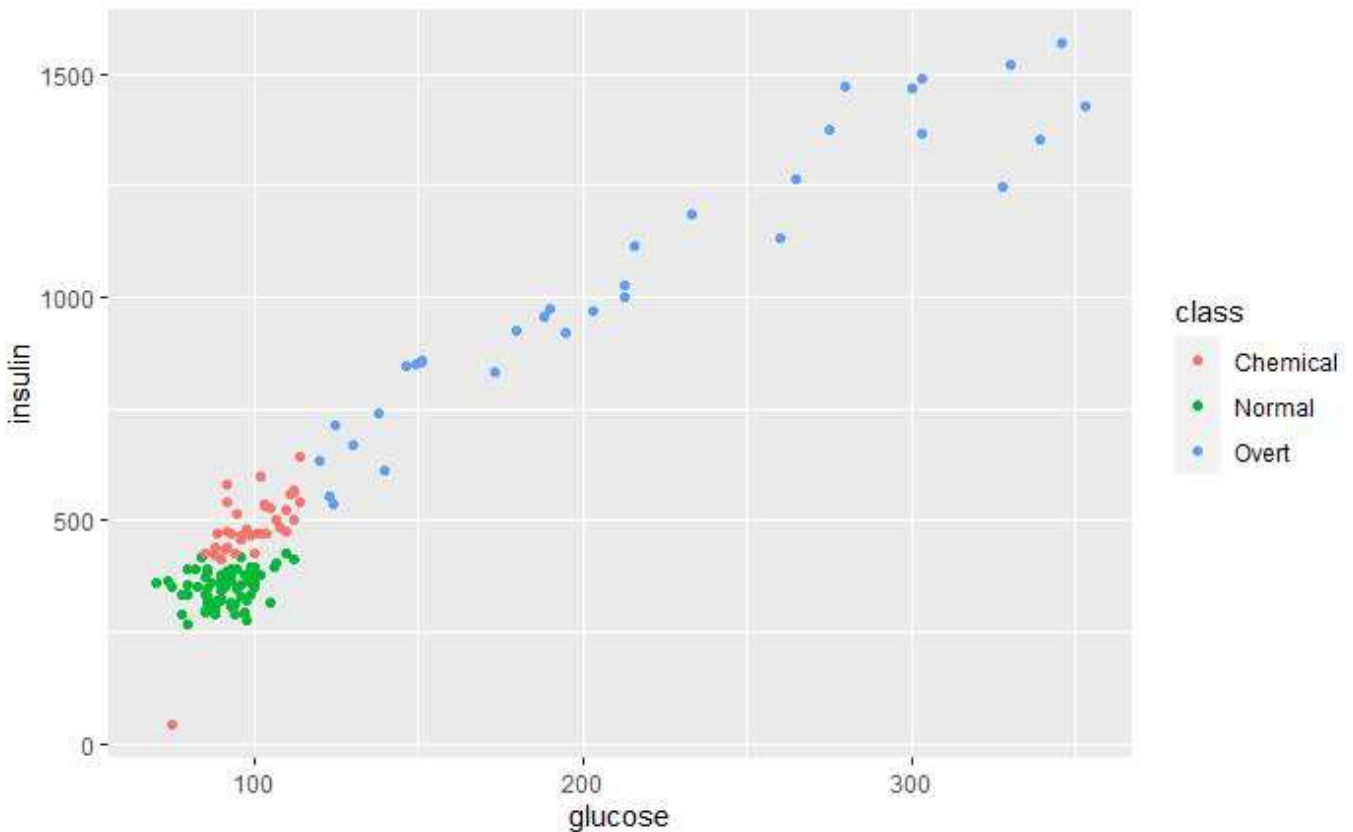
```
summary(diabetesTib)
```

	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

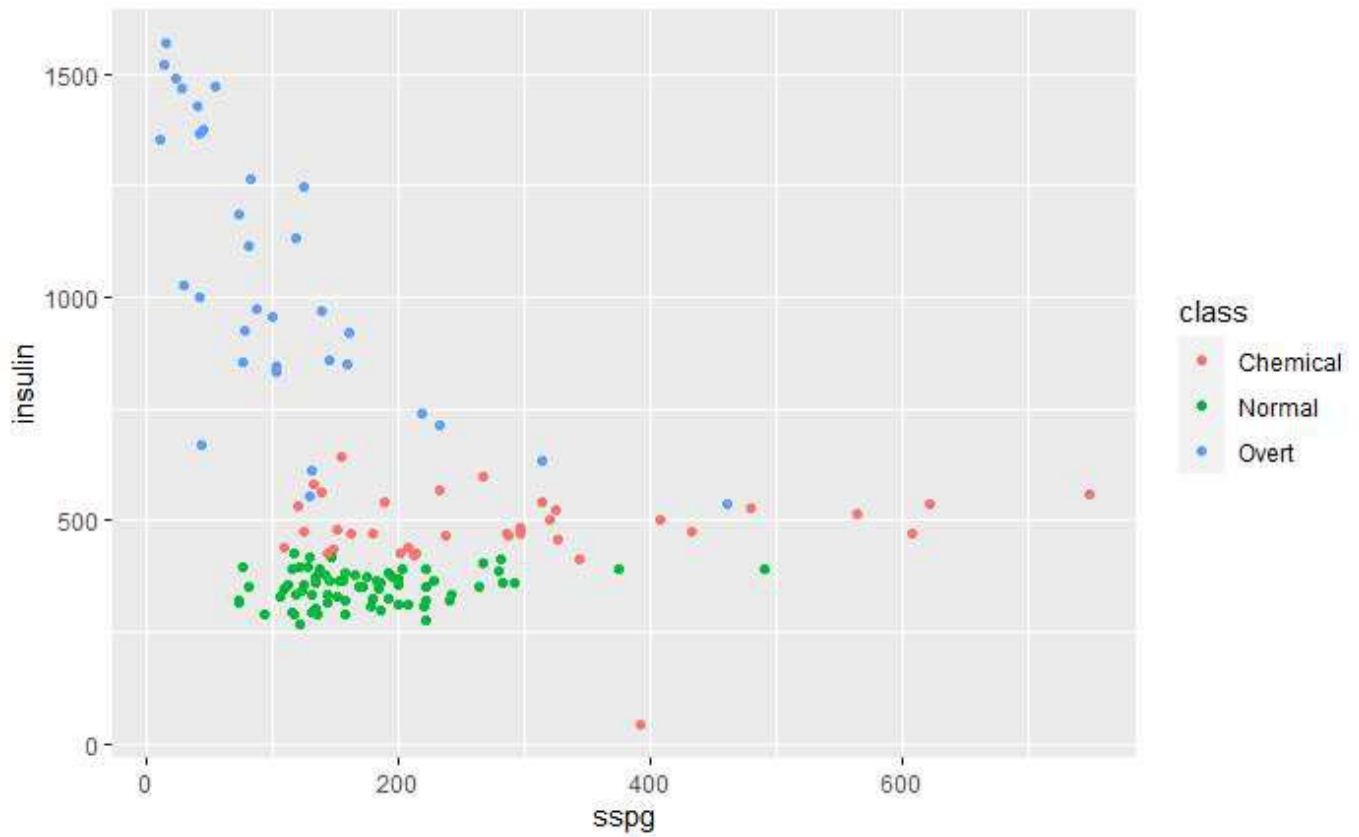
Plot the data around some of its classes :

[Hide](#)

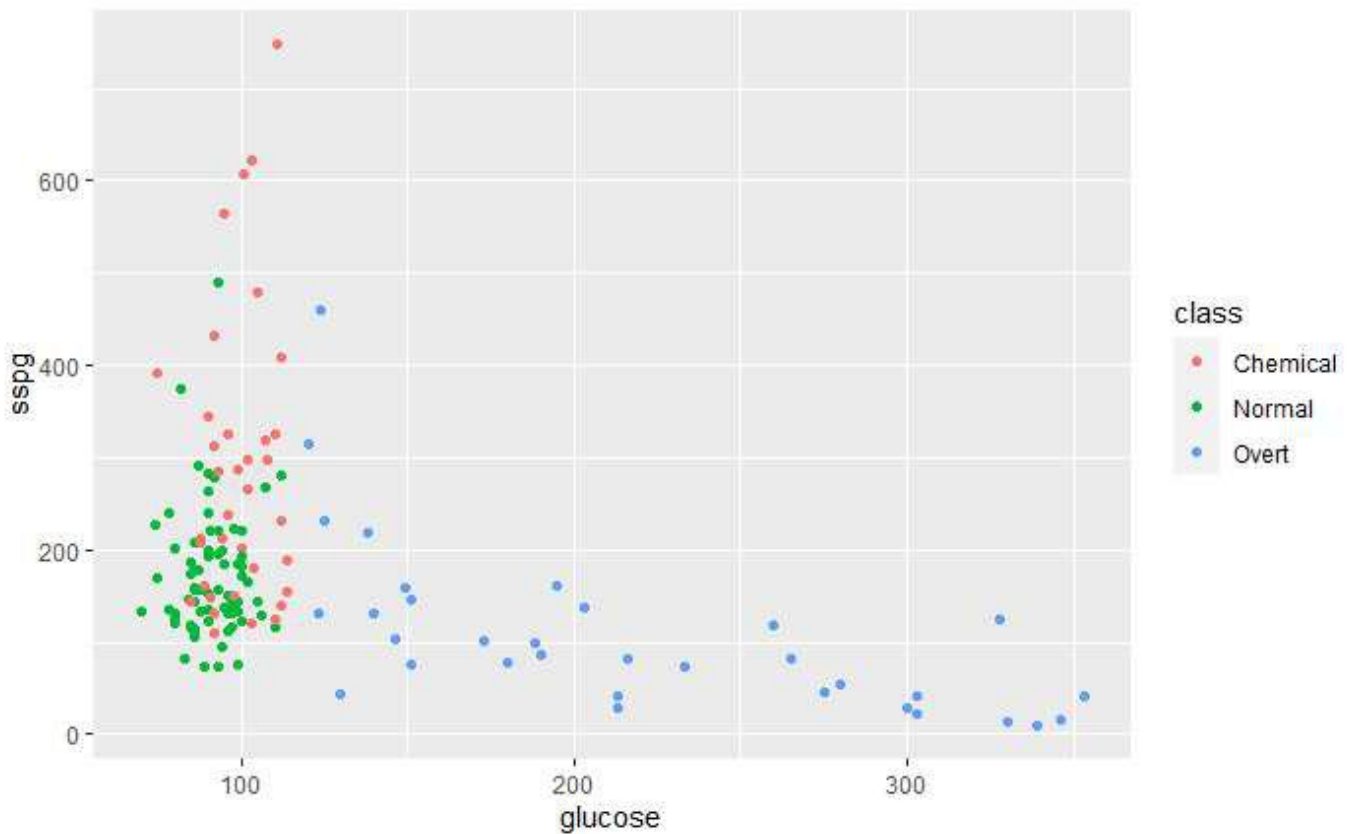
```
ggplot(diabetesTib, aes(glucose, insulin, col = class)) +  
  geom_point()
```

[Hide](#)

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

[Hide](#)

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



Define a Task :

[Hide](#)

```
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 : Recursive Partitioning Decision Tree

[Hide](#)

```
rpart <- makeLearner('classif.rpart', predict.type="prob")
```

Train the model :

[Hide](#)

```
rpartModel <- train(rpart, diabetesTask)
```

Use hold-out crossval :

[Hide](#)

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

[Hide](#)

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

Resampling: repeated cross-validation

Measures:	mmce
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Aggregated Result: mmce.test.mean=0.0264095

Display the confusion matrix :

Hide

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

	predicted			
true	Chemical	Normal	Overt	-err.-
Chemical	1674	126	0	126
Normal	66	3734	0	66
Overt	0	0	1650	0
-err.-	66	126	0	192

We can plot the decision tree :

```
library("rpart.plot")  
rpart.plot(getLearnerModel(rpartModel))
```

Cannot retrieve the data used to build the model (so cannot determine roundint and is.binary for the variables).

To silence this warning:

Call `rpart.plot` with `roundint=FALSE`,
or rebuild the `rpart` model with `model=TRUE`.

