```
R version 4.4.2 (2024-10-31 ucrt) -- "Pile of Leaves"
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Platform: x86 64-w64-mingw32/x64
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  Natural language support but running in an English locale
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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
[Previously saved workspace restored]
> x<- read.table("/Users/Simon/Downloads/iris.csv", header = T, sep= ",")
  SepalLength SepalWidth PetalLength PetalWidth Species
               3.5 1.4
         5.1
                                       0.2
                                              setosa
                                          0.2 setosa
2
         4.9
                   3.0
                               1.4
3
         4.7
                   3.2
                              1.3
                                         0.2 setosa
4
         4.6
                   3.1
                               1.5
                                         0.2 setosa
                   3.6
                               1.4
                                         0.2 setosa
         5.0
                   3.9
         5.4
                              1.7
                                         0.4 setosa
> iris original<-data.frame(x)</pre>
> dim(iris_original)
[1] 150
> iris o sample<-iris original[sample(1:nrow(iris original), size = 210), ]</pre>
Error in sample.int(length(x), size, replace, prob) :
  cannot take a sample larger than the population when 'replace = FALSE'
> iris_o_sample<-iris_original[sample(1:nrow(iris_original), size = 150), ]</pre>
> head(iris o sample)
    SepalLength SepalWidth PetalLength PetalWidth
                                                   Species
93
           5.8
                 2.6 4.0
                                      1.2 versicolor
                     3.4
                                 4.5
                                            1.6 versicolor
86
           6.0
           4.6
                     3.6
                                 1.0
2.3
                                            0.2
                                                    setosa
                     2.8
                                 4.8
                                            1.8 virginica
127
           6.2
91
           5.5
                     2.6
                                 4.4
                                            1.2 versicolor
           5.1
                     2.5
                                 3.0
                                            1.1 versicolor
> iris_o_sample<-iris_original[sample(1:nrow(iris_original), size = 150, replace = TRUE), ]</pre>
> head(iris o sample)
   SepalLength SepalWidth PetalLength PetalWidth
                                                  Species
130
         7.2 3.0 5.8 1.6 virginica
80
           5.7
                     2.6
                                 3.5
                                            1.0 versicolor
                     3.4
                                1.5
                                            0.2
8
           5.0
                                                   setosa
                     2.2
                                 4.0
                                            1.0 versicolor
63
           6.0
                     2.3
                                 3.3
           5.0
                                            1.0 versicolor
           5.1
                     3.5
                                 1.4
                                            0.3
                                                    setosa
> dim(iris o sample)
[1] 150
> # Set a random seed so your split is reproducible (optional but good practice)
> set.seed(123)
> # Randomly sample 70% for training
> train index <- sample(1:nrow(iris o sample), size = 0.7 * nrow(iris o sample))
> # Create training and testing datasets
> iris train <- iris o sample[train index, ]</pre>
> iris test <- iris o sample[-train index, ]</pre>
> # Check the size
> dim(iris train) # Should be around 105 rows
[1] 105
> dim(iris_test)  # Should be around 45 rows
```

```
[1] 45 5
> install.packages("rpart") # Only if you don't have it installed
Installing package into 'C:/Users/Simon/AppData/Local/R/win-library/4.4'
(as 'lib' is unspecified)
--- Please select a CRAN mirror for use in this session ---
trying URL 'https://lib.stat.cmu.edu/R/CRAN/bin/windows/contrib/4.4/rpart 4.1.24.zip'
Content type 'application/zip' length 716854 bytes (700 KB)
downloaded 700 KB
package 'rpart' successfully unpacked and MD5 sums checked
The downloaded binary packages are in
        C:\Users\Simon\AppData\Local\Temp\RtmpUz8d0S\downloaded packages
> library(rpart)
Error in value[[3L]](cond) :
  Package 'rpart' version 4.1.23 cannot be unloaded:
 Error in unloadNamespace (package) : namespace 'rpart' is imported by 'ipred' so cannot be unload
In addition: Warning message:
package 'rpart' was built under R version 4.4.3
> # Build the Decision Tree model
> dt model <- rpart(Species ~ ., data = iris train, method = "class")</pre>
Error in rpart(Species ~ ., data = iris train, method = "class") :
 could not find function "rpart"
> # View a simple summary
> summary(dt model)
Error: object 'dt model' not found
> library(rpart)
Error in value[[3L]](cond) :
  Package 'rpart' version 4.1.23 cannot be unloaded:
Error in unloadNamespace(package): namespace 'rpart' is imported by 'ipred' so cannot be unload
In addition: Warning message:
package 'rpart' was built under R version 4.4.3
> # Train the Decision Tree
> dt model <- rpart(Species ~ ., data = iris train, method = "class")</pre>
Error in rpart(Species ~ ., data = iris train, method = "class") :
 could not find function "rpart"
> # View the model
> summary(dt model)
```

Error: object 'dt model' not found