Assessed Practical III: Can I eat that mushroom?

Anand Samuel Gunti, Student ID: 201687197

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Introduction:

This report aims to investigate and compare the performance of three popular machine learning algorithms, namely logistic regression, decision trees, and random forests, in predicting the edibility of mushrooms based on their visual and olfactory characteristics.

In the given mushroom data set, there are six attributes (variables) that describe the characteristics of mushrooms. These variables are used to predict the edibility of mushrooms. Let's briefly explain each of these variables:

1. Edible: This is the target variable that we aim to predict. It indicates whether a mushroom is edible or poisonous. It is a binary variable, typically represented as "EDIBLE" for edible and "Poisonous" for poisonous.
2. CapShape: This attribute represents the shape of the mushroom's cap. It is a categorical variable with the following possible values:
    - Bell: The cap is shaped like a bell.
    - Conical: The cap is shaped like a cone.
    - Convex: The cap is convex in shape.
    - Flat: The cap is flat.
    - Knobbed: The cap has a knob-like shape.
    - Sunken: The cap is sunken or depressed.
3. CapSurface: This variable describes the surface texture of the mushroom's cap. It is a categorical variable with the following possible values:
    - Fibrous: The cap surface is fibrous.
    - Grooves: The cap surface has grooves.
    - Scaly: The cap surface is scaly.
    - Smooth: The cap surface is smooth.
4. CapColor: This attribute represents the color of the mushroom's cap. It is a categorical variable with the following possible values:
    - brown: The cap is brown.
    - buff: The cap is buff-colored.
    - cinnamon: The cap is cinnamon-colored.
    - gray: The cap is gray.
    - green: The cap is green.
    - pink: The cap is pink.
    - purple: The cap is purple.
    - red: The cap is red.
    - white: The cap is white.
    - yellow: The cap is yellow.

5. Odor: This variable indicates the odor of the mushroom. It is a categorical variable with the following possible values:
    - Almond: The mushroom has an almond-like odor.
    - Anise: The mushroom has an anise-like odor.
    - Fishy: The mushroom has a fishy odor.
    - Foul: The mushroom has a foul odor.
    - None: The mushroom has no odor.
    - Spicy: The mushroom has a spicy odor.
    - Other: The mushroom has a odor other than mentioned above.
6. Height: This attribute represents the height of the mushroom. It is a categorical variable with the following possible values:
    - High: The mushroom has a tall height.
    - Low: The mushroom has a short height.

These variables capture various visual and olfactory characteristics of mushrooms, which are commonly used in determining their edibility. By analyzing the relationships between these variables and the target variable (edible), machine learning models can be trained to predict whether a mushroom is edible or poisonous based on its observed attributes.

Loading required Libraries

```
#library("tinytex")
library(caret)
library(ggplot2)
library(gridExtra)
library(e1071)
library(randomForest)
library(stepPlr)
library(glmnet)
library(wsrf)
library(RRF)
library(tidyr)
library(tidyverse)
library(dplyr)
library(broom)
library(evtree)
library(stringr)
```

Importing the Data

```
data = read.csv("C:\\Users\\anand\\Downloads\\mushrooms.csv")
data_df = data.frame(data)
summary(data_df)
```

```
##      Edible            CapShape          CapSurface         CapColor
##   Length:8124        Length:8124        Length:8124        Length:8124
##   Class :character   Class :character   Class :character   Class :character
##   Mode :character    Mode :character    Mode :character    Mode :character
##       Odor              Height
##   Length:8124        Length:8124
##   Class :character   Class :character
##   Mode :character    Mode :character
```

Converting the variables into factors.

Here are a couple of reasons why converting the variables to factors is beneficial:

Factors in R provide an efficient and convenient way to represent categorical variables. By converting the variables to factors, each unique category within a variable is assigned a numerical value, allowing the machine learning algorithms to work with categorical data effectively.

Many machine learning algorithms in R, such as decision trees and random forests, are specifically designed to handle categorical variables in the form of factors.

```
encoded_mushrooms <- as.data.frame(lapply(data, as.factor))
```

Checking for NULL values

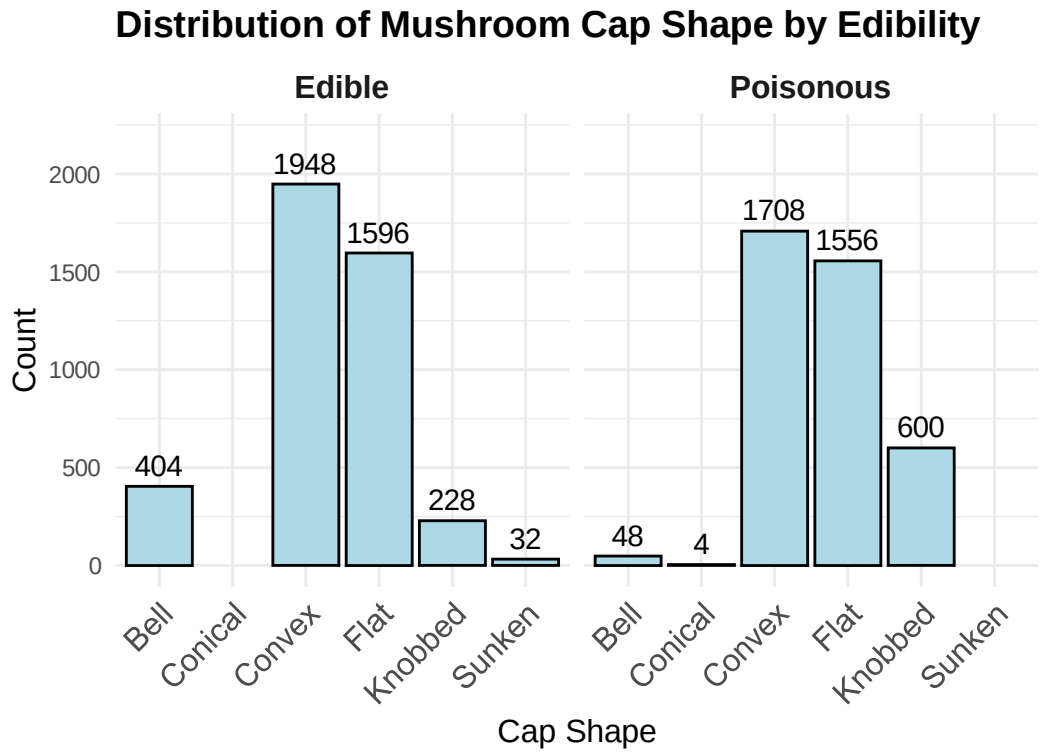
```
map_dbl(encoded_mushrooms, function(.x) {sum(is.na(.x))})
```

```
##      Edible    CapShape  CapSurface    CapColor        Odor      Height
##           0           0           0           0           0           0
```

Visualizing the Data

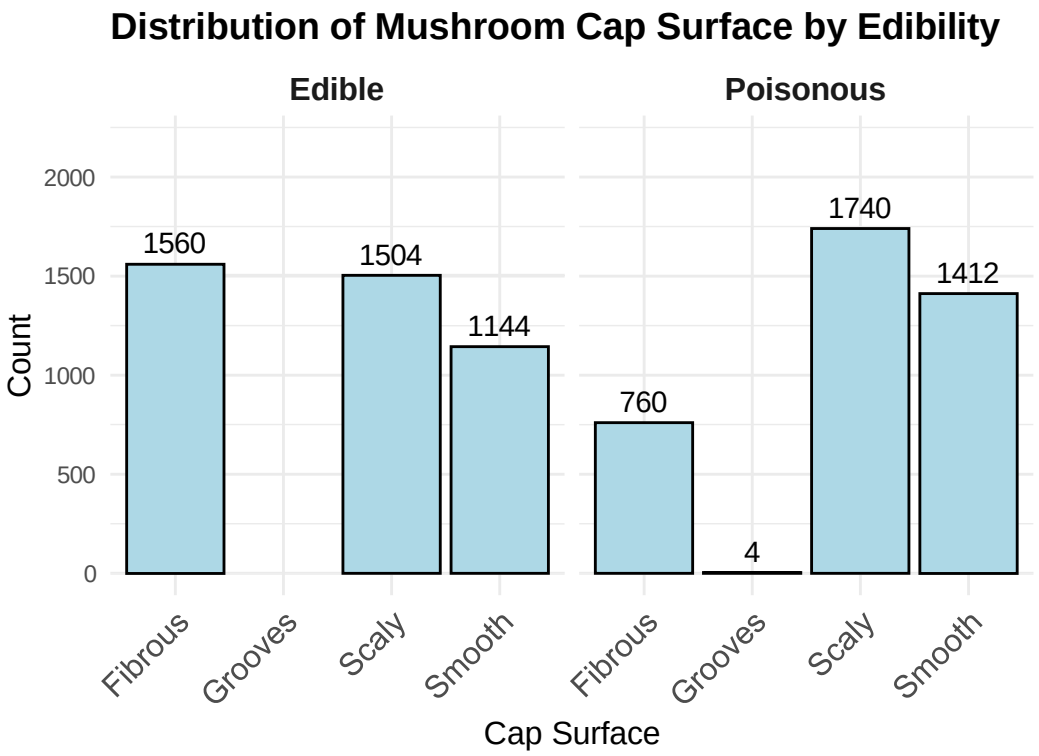
h1

```
## Warning: The dot-dot notation (`..count..`) was deprecated in ggplot2 3.4.0.
## ℹ Please use `after_stat(count)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



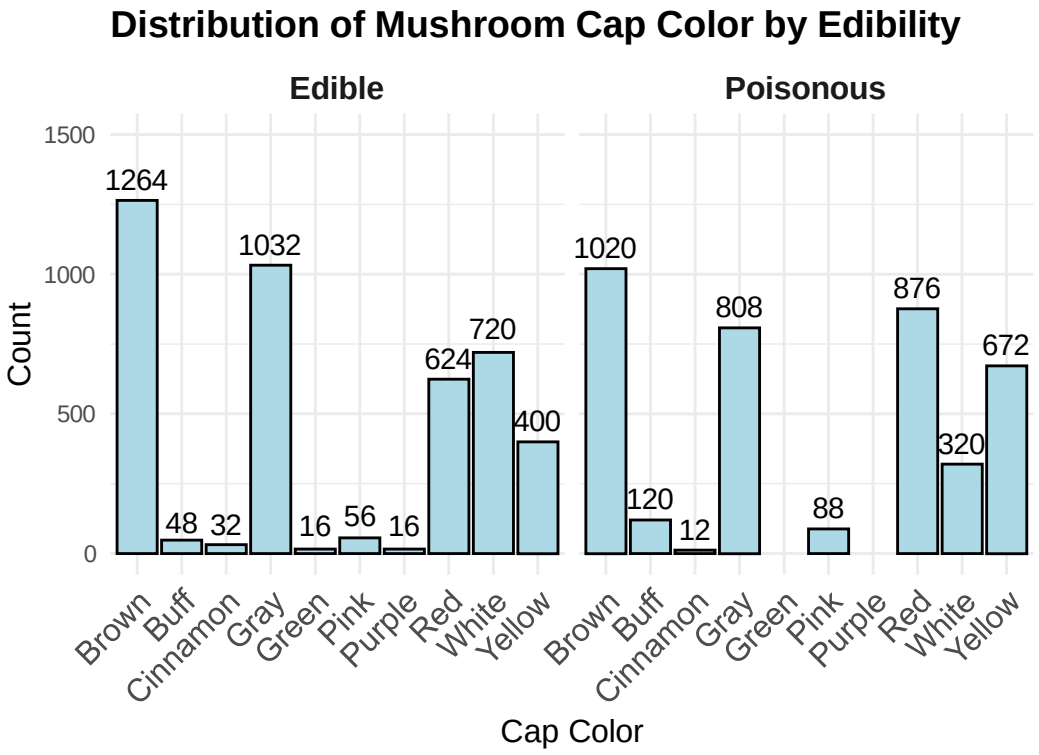
Insights: When the cap shape of mushrooms is conical, they are classified as poisonous. On the other hand, when the cap shape is sunken, mushrooms are categorized as edible. However, there is ambiguity in determining the edibility of mushrooms with a convex or flat cap shape.

h2



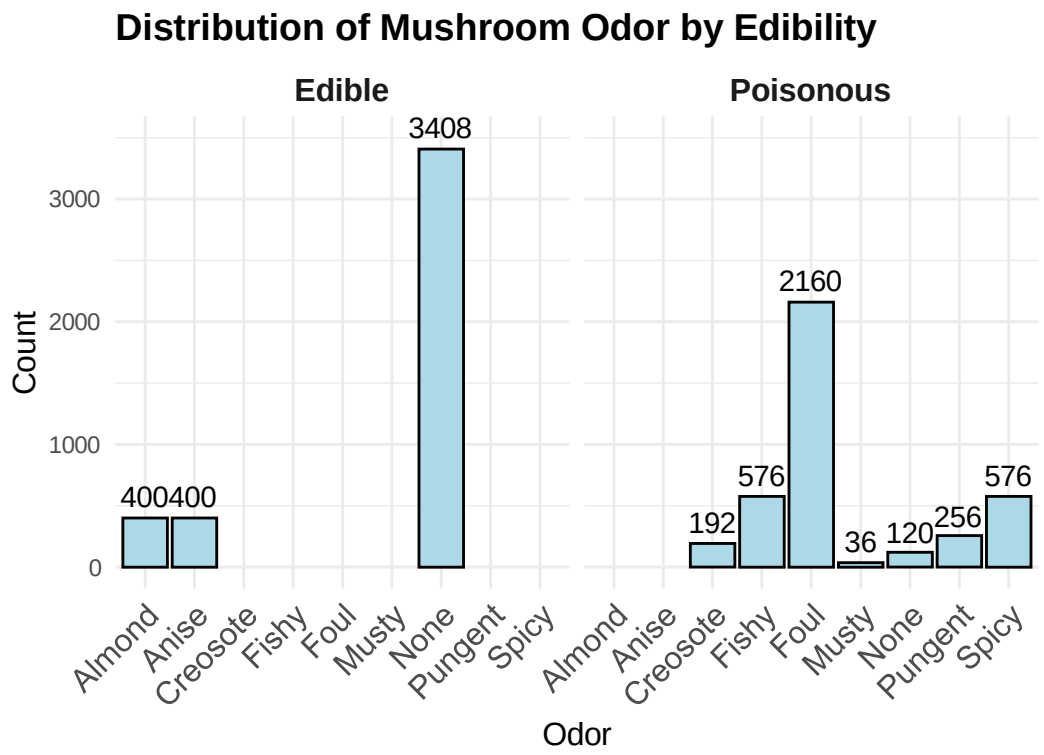
Insights: When the cap surface of mushrooms is Groove, they are classified as poisonous.The rest are kind of ambigious.

h3



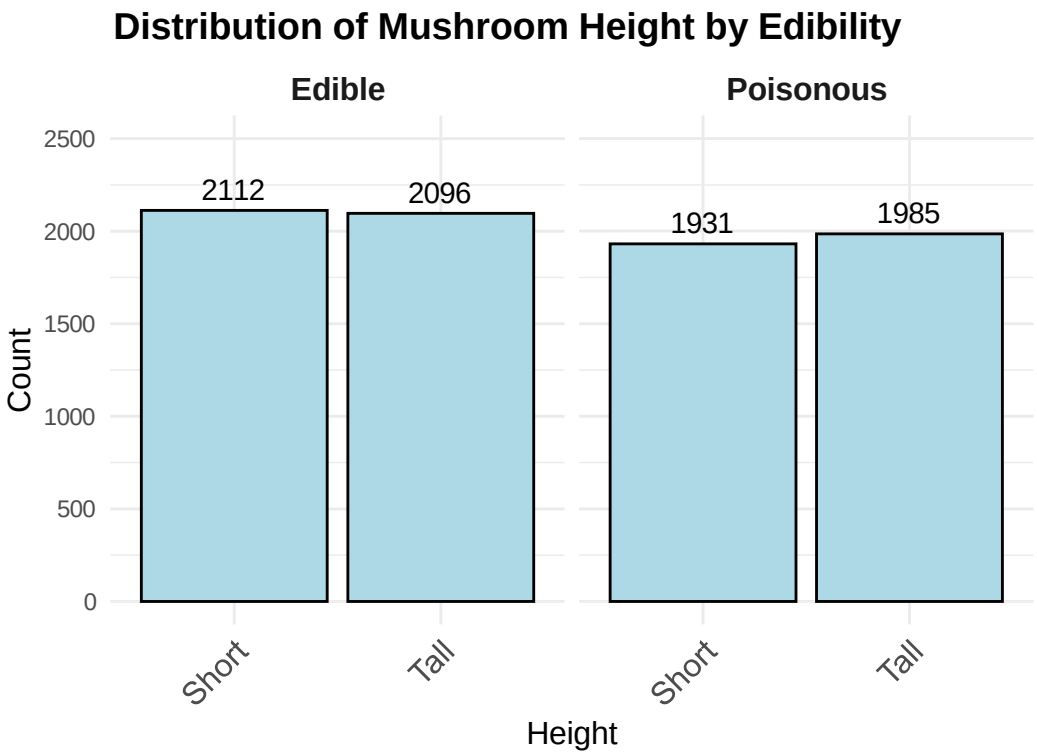
Insights: When the cap color of mushrooms is either green or purple, then we can classify them as Edible.The rest are kind of ambigious we cant clearly classify.

h4



Insights: When the odor of mushrooms is identified as Almond or Anise, we can confidently classify the mushroom as edible. However, if the odor is any other than Almond or Anise, we can classify the mushroom as poisonous.If there is no Odor or None we can say that mushroom is most likley Edible

h5



Insights: This particular variable is ambiguous and does not provide clear classification of mushrooms as either edible or poisonous. It does not offer a definitive distinction between the two categories.

Based on the analysis, we can conclude that the "Odor" variable is the most influential in the classification of mushrooms. It provides valuable information for classfication between edible and poisonous mushrooms. On the other hand, the "Height" variable appears to be the least influential in the classification process. Its contribution to accurately classifying mushrooms as edible or poisonous is relatively limited compared to the other variables.

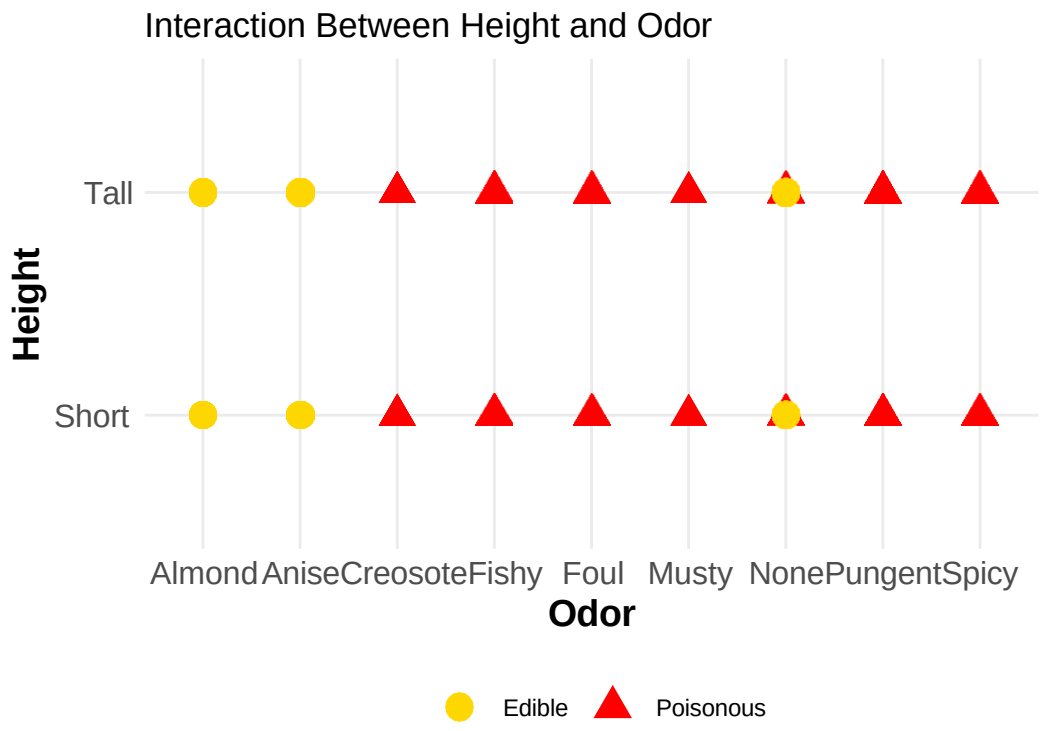
From this we can infer that when considering the characteristics of mushrooms, focusing on the odor attribute is crucial for making accurate classifications. Other variables, such as cap shape, cap surface, and cap color, also provide valuable information but to a lesser extent. The "Height" variable, however, seems to have less impact on the classification outcome.

It's important to note that this conclusion is based on the analysis conducted in this specific context and dataset. The relative influence of variables may vary in different datasets or when applying different classification algorithms. Nonetheless, in the context of this analysis, the findings suggest that Odor is the most influential variable while Height has less impact on the classification of mushrooms.

However, it is important to acknowledge that while "Height" may not provide standalone valuable information, there is a possibility that when combined with other variables, it could potentially offer some valuable insights for classification purposes. Therefore, we need to consider its potential interactions with other variables.

Interaction of Other Variables with Height.

```
i1
```



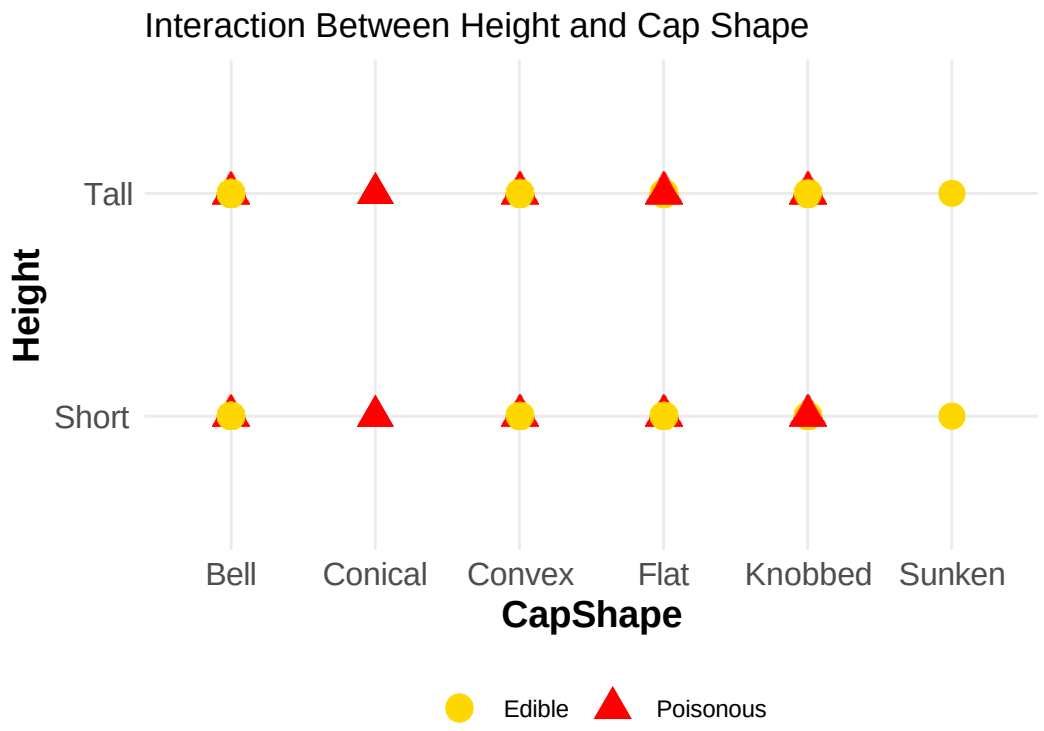
When we combine the variables "Height" and "Odor" in our analysis, we observe that they provide a clearer indication of whether a mushroom is edible or poisonous, with one exception: when the odor is "none".

when considering the combination of "Height" and "Odor", we can confidently classify mushrooms as edible or poisonous based on the following observations:

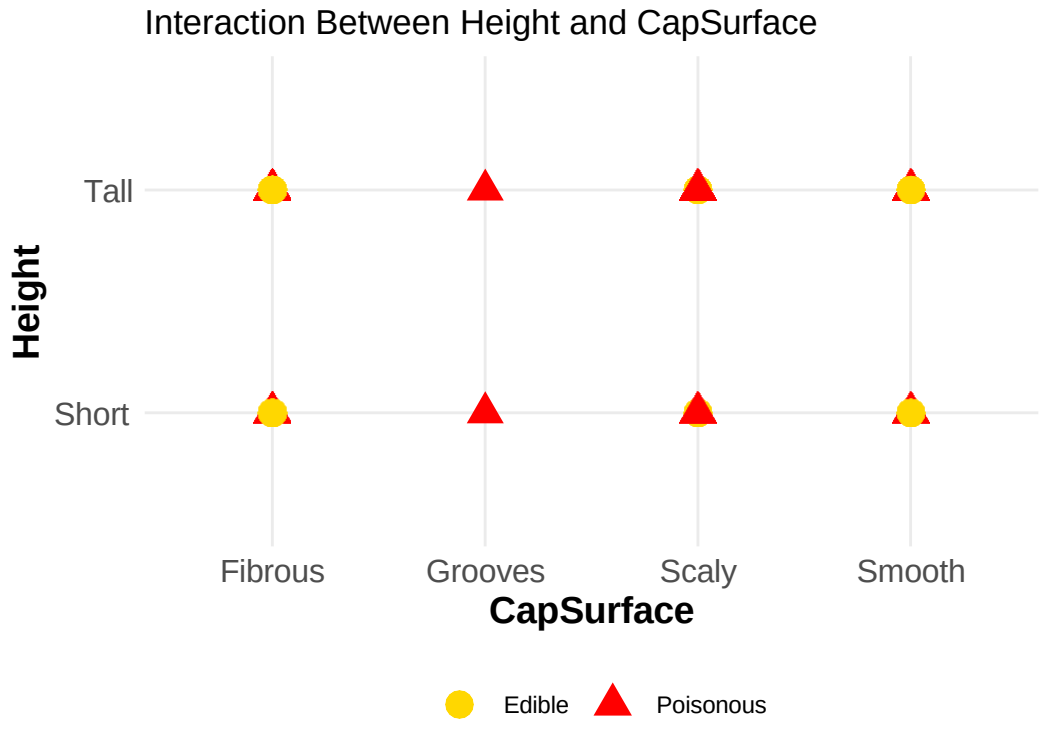
1. When the odor is identified as "almond" or "anise", the mushroom is consistently classified as edible irrespective of the Height. This clear association between specific odors and edible mushrooms allows for accurate classification which is consistent with our previous observation for Odor.
2. For all other odor types, excluding "none", the mushrooms are typically classified as poisonous. This indicates that these odors are strongly correlated with poisonous mushrooms.

However, when the odor is identified as "none", the classification becomes ambiguous. In such cases, it is challenging to determine the edibility of the mushroom based solely on the combination of "Height" and "Odor".

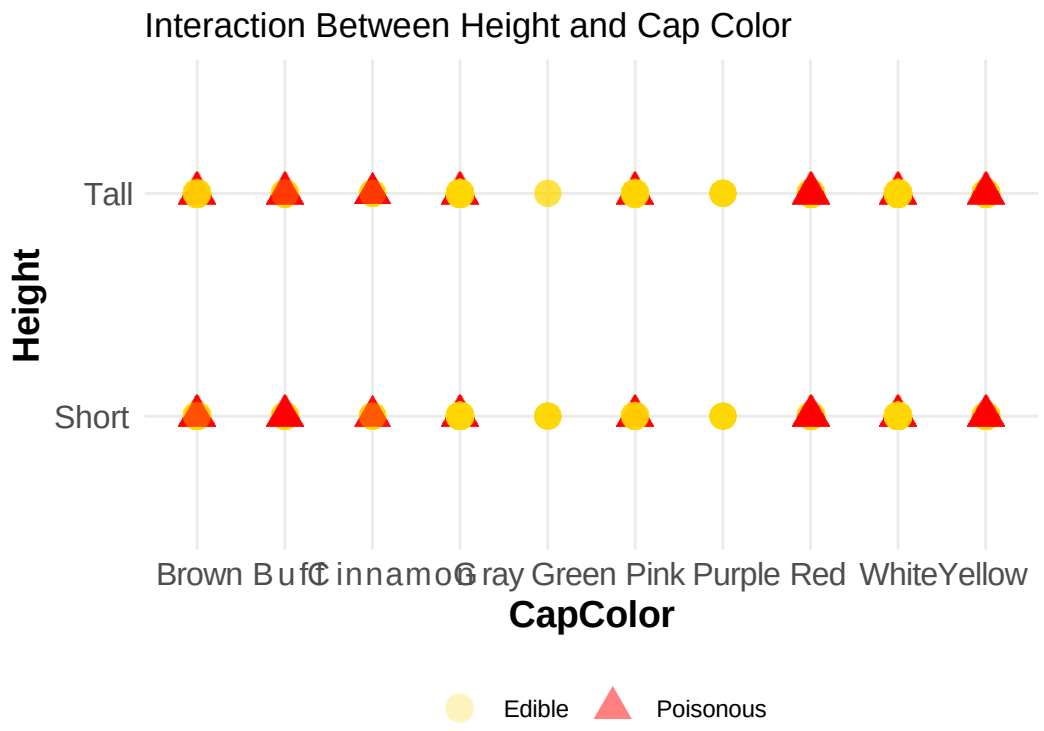
```
i2
```


Interaction Between Height and Cap Shape
Tall
Short
Height
Bell
Conical
Convex
Flat
Knobbed
Sunken
CapShape
Edible
Poisonous

```
i3
```


Interaction Between Height and CapSurface
Tall
Short
Height
Fibrous
Grooves
Scaly
Smooth
CapSurface
Edible
Poisonous

```
i4
```



From the analysis of the interactions between variables, it can be observed that there is no clear classification when considering the combination of variables with certain attributes. For example, when examining the interaction between "Cap Color" and "Height," as well as the interactions of other variables other than odor, there is a significant amount of overlap in the graphs.

This overlapping indicates that the classification of mushrooms is ambiguous and not easily discernible. For Example, the "Cap Color" variable, except for the distinct colors of green and yellow, there is a lack of clear boundaries or patterns that can be used to classify mushrooms. The same ambiguity can be observed when considering other variables in conjunction with "Height."

```
#Representing the interaction between Height and Odor
encoded_mushrooms$Height_Odor <- interaction(encoded_mushrooms$Odor, encoded_mushrooms$Height)
```

Preparing the dataset for cross validation :we would split the data in 80% for training and 20% for testing

```
# Split the dataset into features and target variable

features <- encoded_mushrooms[, -1]
target <- encoded_mushrooms$Edible

set.seed(107)
inTrain <- createDataPartition(
  y = target,
  p = .80, ## The percentage of data in the training set
  list = FALSE
)

training <- encoded_mushrooms[ inTrain,]
testing  <- encoded_mushrooms[-inTrain,]

cat("\nTotal rows in the Data set:", nrow(encoded_mushrooms))
```

```
##
## Total rows in the Data set: 8124
```

```
cat("\n\nThe number of rows in the training set after 80% split:", nrow(training))
```

```
##
##
## The number of rows in the training set after 80% split: 6500
```

```
cat("\n\nThe number of rows in the testing set after 20% split:", nrow(testing))
```

```
##
##
## The number of rows in the testing set after 20% split: 1624
```

LOGISTIC REGRESSION MODEL:

```
head(training)
```

```
##          Edible CapShape CapSurface CapColor     Odor Height    Height_Odor
## 1  Poisonous      Convex       Smooth     Brown Pungent     Tall    Pungent.Tall
## 2       Edible     Convex       Smooth    Yellow  Almond    Short   Almond.Short
## 3       Edible       Bell       Smooth     White   Anise     Tall     Anise.Tall
## 4 Poisonous  Convex              Scaly     White Pungent    Short   Pungent.Short
## 5       Edible     Convex       Smooth      Gray    None    Short     None.Short
## 6       Edible     Convex        Scaly    Yellow  Almond    Short   Almond.Short
```

Feature Selction:

After analyzing the results, we have determined that the best set of features for our model includes CapShape, CapSurface, CapColor, Odor, and Height_Odor. This conclusion was verified using logistic regression, which resulted in an accuracy of 99.45% when using only these selected variables.

On the other hand, if we were to include all the variables in the model, the accuracy drops significantly to 83.32%. This suggests that the additional variables may introduce noise or irrelevant information, negatively impacting the model's predictive performance.

In summary, selecting the specific features mentioned above leads to the highest accuracy of 99.45%, while including all variables decreases the accuracy to 83.32%.

```
# Train the model using logistic regression
ctrl <- trainControl(method = "none")

model <- train(Edible ~ CapShape+CapSurface+CapColor+Odor+Height_Odor, data = training,
               method = "glm", trControl = ctrl,family = "binomial")

modelClasses <- predict(model, newdata = testing)

modelProbs <- predict(model, newdata = testing, type = "prob")

confusionMatrix(data = modelClasses, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction    Edible Poisonous
##    Edible        838         6
```

```
##    Poisonous          3          777
##
##                   Accuracy : 0.9945
##                     95% CI : (0.9895, 0.9975)
##    No Information Rate :  0.5179
##    P-Value [Acc > NIR] :  <2e-16
##
##                      Kappa : 0.9889
##
##   Mcnemar's Test P-Value : 0.505
##
##               Sensitivity : 0.9964
##               Specificity : 0.9923
##            Pos Pred Value : 0.9929
##            Neg Pred Value : 0.9962
##                Prevalence : 0.5179
##            Detection Rate :  0.5160
##    Detection Prevalence  :  0.5197
##         Balanced Accuracy : 0.9944
##
##          'Positive' Class : Edible
##
```

As per this basic model we are getting accuracy of **99.45**. we would try to tune this model further to improve accuracy.

Logistic regression model Fine tuning using the Caret package:

Now we have seen what the GLM model has to offer and we will try to fine tune the model using different methods.

Method:

GLMNET

glmnet is an R package that provides functions for fitting regularized generalized linear models. It is particularly useful for variable selection and regularization.

Hypertuning parameters :

alpha: This parameter controls the elastic net mixing parameter. It determines the balance between L1 (Lasso) and L2 (Ridge) regularization. A value of 1 corresponds to Lasso regression, while 0 corresponds to Ridge regression. Values between 0 and 1 represent a combination of Lasso and Ridge regularization.

lambda: This parameter controls the amount of regularization applied to the model. Larger values of lambda result in stronger regularization, leading to more shrinkage and potentially fewer selected predictors.

We will also

Here we will take a range of values for aplha and lambda and then calculate accuracy for every combination and then with that we will select the best possible alpha and Lambda values.

To facilitate our analysis, we will utilize the caret package, specifically the **trainControl** function. This function allows us to specify the resampling method for model evaluation. Throughout our analysis, we will utilize resampling methods such as bootstrapping (boot) and cross-validation(cv)

The **trainControl** function provides flexibility in selecting the resampling method through its **method** attribute. By specifying "boot", we can apply bootstrapping, which involves sampling with replacement from the original dataset. This method allows us to estimate model performance and assess its variability.

Additionally, we can employ cross-validation, a widely-used resampling technique. By setting the **method** attribute to "cv", we partition the dataset into multiple folds and iteratively train and validate the model on different subsets. This approach provides a robust evaluation of model performance.

By incorporating these resampling methods using the **trainControl** function from the caret package, we can effectively evaluate the performance of our models and make informed decisions based on their results.

After experimenting with different sets of values, the range of lambda and alpha values are adjusted based on the results provided. These final range values are chosen to encompass a reasonable range of regularization and mixing parameters that are expected to yield good model performance.

To begin our analysis, we will use the **cv** method.Here we have run with different k values.we will use accuracy metric for selecting the best k value and also consider False Positives (FP).we would ideally like the FP to be as low as possible in this case.(No of mushrooms classified as edible when they are actually poisonous)

When k = 5 Accuracy is 99.57%

When k=10 Accuracy is 99.57%

when k = 15 Accuracy is 99.57%

After evaluating the models with different values of k, it is observed that the accuracy remains consistent across different values. Specifically, when k = 5, k = 10, and k = 15, the accuracy achieved is 99.57% in all cases. Therefore, based on these findings, it can be concluded that there is no significant difference in accuracy between these values of k. As a result, the most preferable option would be to select **k = 5** for the model.

```
# Set up control parameters for training repeatedcv
ctrl <- trainControl(method = "cv",number = 5)

lambda_grid <- 10^seq(-6, -1, by = 0.1)
alpha_grid <- seq(0, 1, by = 0.1)


# Perform penalized logistic regression using train function
plsFit1 <- train(
  Edible ~ CapShape+CapSurface+CapColor+Odor+Height_Odor,
  data = training,
  method = "glmnet",
  trControl = ctrl,
  family = "binomial",
  tuneGrid = expand.grid(alpha = alpha_grid,lambda = lambda_grid)
)
plsClasses <- predict(plsFit1, newdata = testing)

plsProbs <- predict(plsFit1, newdata = testing, type = "prob")

confusionMatrix(data = plsClasses, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction    Edible Poisonous
##    Edible        840         6
##    Poisonous       1       777
##
##                   Accuracy : 0.9957
##                     95% CI : (0.9911, 0.9983)
```

```
##    No Information Rate : 0.5179
##    P-Value [Acc > NIR] : <2e-16
##
##                  Kappa : 0.9914
##
##   Mcnemar's Test P-Value : 0.1306
##
##              Sensitivity : 0.9988
##              Specificity : 0.9923
##           Pos Pred Value : 0.9929
##           Neg Pred Value : 0.9987
##               Prevalence : 0.5179
##           Detection Rate : 0.5172
##    Detection Prevalence : 0.5209
##         Balanced Accuracy : 0.9956
##
##          'Positive' Class : Edible
##
```

```
# Set up control parameters for training cv
ctrl <- trainControl(method = "cv",number = 10)

lambda_grid <- 10^seq(-6, -4, by = 0.1)
alpha_grid <- seq(0, 1, by = 0.1)

# Perform penalized logistic regression using train function
logmodel <- train(
  Edible ~ CapShape+CapSurface+CapColor+Odor+Height_Odor,
  data = training,
  method = "glmnet",
  trControl = ctrl,
  family = "binomial",
  tuneGrid = expand.grid(alpha = alpha_grid,lambda = lambda_grid),
  preProc = c("center", "scale")
)

logClasses <- predict(logmodel, newdata = testing)

logProbs <- predict(logmodel, newdata = testing, type = "prob")

confusionMatrix(data = logClasses, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction    Edible Poisonous
##    Edible        840         6
##    Poisonous       1       777
##
##                  Accuracy : 0.9957
##                    95% CI : (0.9911, 0.9983)
##       No Information Rate : 0.5179
##       P-Value [Acc > NIR] : <2e-16
##
##                     Kappa : 0.9914
```

```
##
##   Mcnemar's Test P-Value : 0.1306
##
##               Sensitivity : 0.9988
##               Specificity : 0.9923
##            Pos Pred Value : 0.9929
##            Neg Pred Value : 0.9987
##                Prevalence : 0.5179
##            Detection Rate :  0.5172
##    Detection Prevalence   :  0.5209
##         Balanced Accuracy : 0.9956
##
##          'Positive' Class : Edible
##
```

Additionally, we will also perform the bootstrapping method to compare its results with cross-validation. This will allow us to determine which method is more suitable for our analysis and provide a comprehensive understanding of the data.

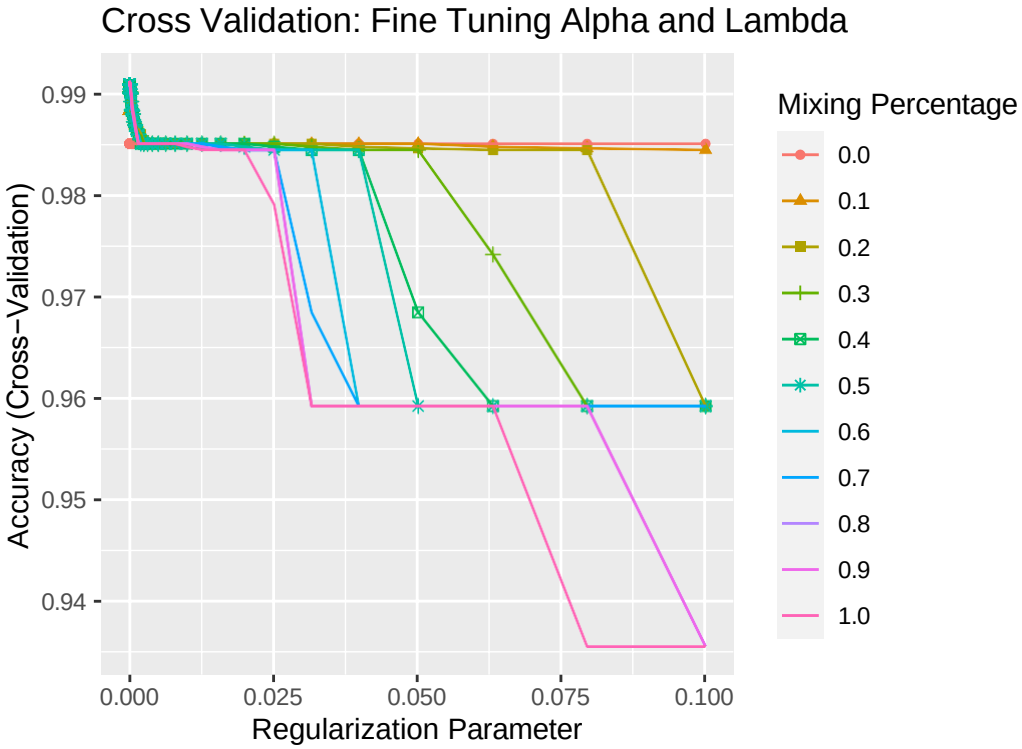
```
# Set up control parameters for training cv
ctrl <- trainControl(method = "boot_all", number = 25)

lambda_grid <- 10^seq(-6, -1, by = 0.1)
alpha_grid <- seq(0, 1, by = 0.1)

# Perform penalized logistic regression using train function
logmodel_boot <- train(
  Edible ~ CapShape+CapSurface+CapColor+Odor+Height_Odor,
  data = training,
  method = "glmnet",
  trControl = ctrl,
  family = "binomial",
  tuneGrid = expand.grid(alpha = alpha_grid,lambda = lambda_grid),
  preProc = c("center", "scale")
)

logClasses <- predict(logmodel_boot, newdata = testing)

logProbs <- predict(logmodel_boot, newdata = testing, type = "prob")

confusionMatrix(data = logClasses, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction    Edible Poisonous
##    Edible         840         6
##    Poisonous        1       777
##
##                   Accuracy : 0.9957
##                     95% CI : (0.9911, 0.9983)
##    No Information Rate :  0.5179
##    P-Value [Acc > NIR] :  <2e-16
##
##                      Kappa : 0.9914
```

```
##
##   Mcnemar's Test P-Value : 0.1306
##
##               Sensitivity : 0.9988
##               Specificity : 0.9923
##            Pos Pred Value : 0.9929
##            Neg Pred Value : 0.9987
##                Prevalence : 0.5179
##            Detection Rate :  0.5172
##    Detection Prevalence   :  0.5209
##         Balanced Accuracy : 0.9956
##
##          'Positive' Class : Edible
##
```

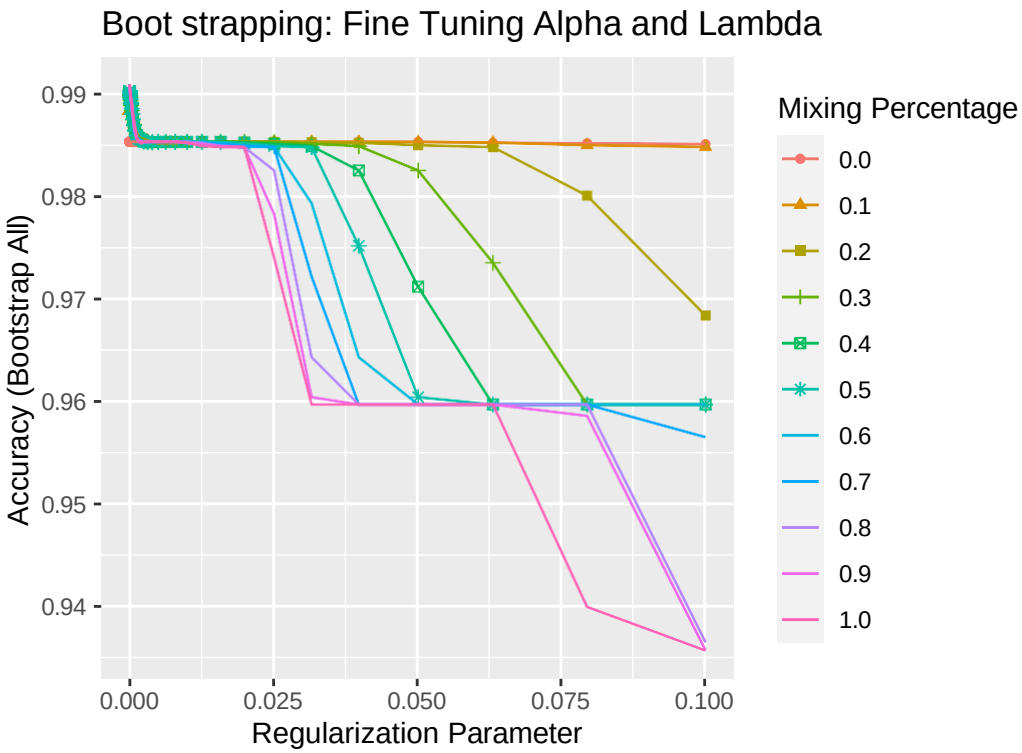
Both the cross-validation and bootstrap methods have yielded identical results in this analysis. Therefore, we will primarily rely on cross-validation for our future evaluations. However, if any discrepancies arise between the results obtained from the two methods, we will address and discuss them in the context of bootstrap analysis.

Let's examine how the fine-tuning parameters are adjusted and determine the optimal tuning parameters.



Note: Mixing percentage is Alpha value

```
p2
```



Note: Mixing percentage is Alpha value

```
cat("Best tuned values  using Cross validation Alpha is:", logmodel$bestTune$alpha,"Lambda is:", logmod
```

```
## Best tuned values  using Cross validation Alpha is: 1 Lambda is: 3.981072e-05
```

```
cat("\n")
```

```
cat("Best tuned values  using Boot strapping Alpha is:", logmodel_boot$bestTune$alpha,"Lambda is:", log
```

```
## Best tuned values  using Boot strapping Alpha is: 1 Lambda is: 5.011872e-05
```

Although both methods have produced similar results, it is worth noting that the values of alpha obtained from the two methods are different. Despite the similarity in overall performance, the specific parameter values differ between the cross-validation and bootstrapping methods.

The accuracy of logistic regression model after fine tuning is **99.57%**

Decision Trees:

A decision tree is a popular and intuitive machine learning algorithm used for classification and regression tasks. It models decisions or predictions based on a sequence of logical rules inferred from the input features.

In R, the caret package provides a convenient and unified framework for training and evaluating decision tree models. It offers different decision tree algorithms, including rpart, C5.0, and ctree, among others. These algorithms provide flexibility in handling various data types, missing values, and other considerations specific to the dataset.

First we need to fix a baseline model and Once the baseline model is set, tuning techniques can be applied to enhance the classification results.To do so we will use above mentoined 3 methods and select baseline model based on accuracy.

```
dtModel_1 <- train(
  Edible ~ CapShape+CapSurface+CapColor+Odor+Height_Odor,
  data = training,
  method = "ctree"

)

dtClasses_1 <- predict(dtModel_1, newdata = testing)

dtProbs_1 <- predict(dtModel_1, newdata = testing, type = "prob")

confusionMatrix(data = dtClasses_1, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction     Edible Poisonous
##    Edible          841         13
##    Poisonous         0        770
##
##                   Accuracy : 0.992
##                     95% CI : (0.9864, 0.9957)
##       No Information Rate : 0.5179
##       P-Value [Acc > NIR] : < 2.2e-16
##
##                      Kappa : 0.984
##
##  Mcnemar's Test P-Value : 0.0008741
##
##                 Sensitivity : 1.0000
##                 Specificity : 0.9834
##              Pos Pred Value : 0.9848
##              Neg Pred Value : 1.0000
##                  Prevalence : 0.5179
##              Detection Rate : 0.5179
##       Detection Prevalence : 0.5259
##           Balanced Accuracy : 0.9917
##
##           'Positive' Class : Edible
##
```

```
dtModel_2 <- train(
  Edible ~ CapShape+CapSurface+CapColor+Odor+Height_Odor,
  data = training,
  method = "rpart"

)

dtClasses_2 <- predict(dtModel_2, newdata = testing)

dtProbs_2 <- predict(dtModel_2, newdata = testing, type = "prob")

confusionMatrix(data = dtClasses_2, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction     Edible Poisonous
##    Edible          759          19
##    Poisonous        82         764
##
##                    Accuracy : 0.9378
##                      95% CI : (0.9249, 0.9491)
##       No Information Rate : 0.5179
##       P-Value [Acc > NIR] : < 2.2e-16
##
##                       Kappa : 0.8758
##
##  Mcnemar's Test P-Value : 6.862e-10
##
##                 Sensitivity : 0.9025
##                 Specificity : 0.9757
##              Pos Pred Value : 0.9756
##              Neg Pred Value : 0.9031
##                  Prevalence : 0.5179
##              Detection Rate : 0.4674
##       Detection Prevalence : 0.4791
##           Balanced Accuracy : 0.9391
##
##           'Positive' Class : Edible
##
```

```
ctrl <- trainControl(method = "none")

dtModel_3 <- train(
  Edible ~ .,
  data = training,
  method = "C5.0"

)

dtClasses_3 <- predict(dtModel_3, newdata = testing)

dtProbs_3 <- predict(dtModel_3, newdata = testing, type = "prob")

confusionMatrix(data = dtClasses_3, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction     Edible Poisonous
##    Edible          838           9
##    Poisonous         3         774
##
##                    Accuracy : 0.9926
##                      95% CI : (0.9871, 0.9962)
##    No Information Rate :  0.5179
##    P-Value [Acc > NIR] :  <2e-16
##
```

```
##                  Kappa : 0.9852
##
##  Mcnemar's Test P-Value : 0.1489
##
##             Sensitivity : 0.9964
##             Specificity : 0.9885
##          Pos Pred Value : 0.9894
##          Neg Pred Value : 0.9961
##              Prevalence : 0.5179
##          Detection Rate : 0.5160
##    Detection Prevalence : 0.5216
##       Balanced Accuracy : 0.9925
##
##        'Positive' Class : Edible
##
```

Among the three models we have explored, the C5.0 model demonstrates the highest accuracy of 99.26%, outperforming the ctree model with an accuracy of 99.20% and the rpart model with an accuracy of 93.78%. Based on this, we will select the C5.0 model as our baseline model and proceed with fine-tuning it further. By fine-tuning the C5.0 model, we aim to optimize its performance and potentially achieve even better accuracy.

Fine tuning C5.0 model

Here the hyper parameters are

Trials: The number of trials, represented by the trials parameter, determines the number of times the C5.0 algorithm attempts to find an optimal split at each node. Higher values can potentially lead to better performance but may increase computation time.

Model Type: The model parameter specifies the type of model to be used. In C5.0, the default model type is "tree" for decision tree models and in this we will check with "Rules" also.

Winnowing: The winnow parameter controls whether or not the winnowing feature is enabled. Winnowing is a method used in C5.0 to handle attributes with many distinct values efficiently. It allows the algorithm to identify the most relevant attributes for decision-making. Setting winnow to TRUE enables winnowing, while setting it to FALSE disables it.

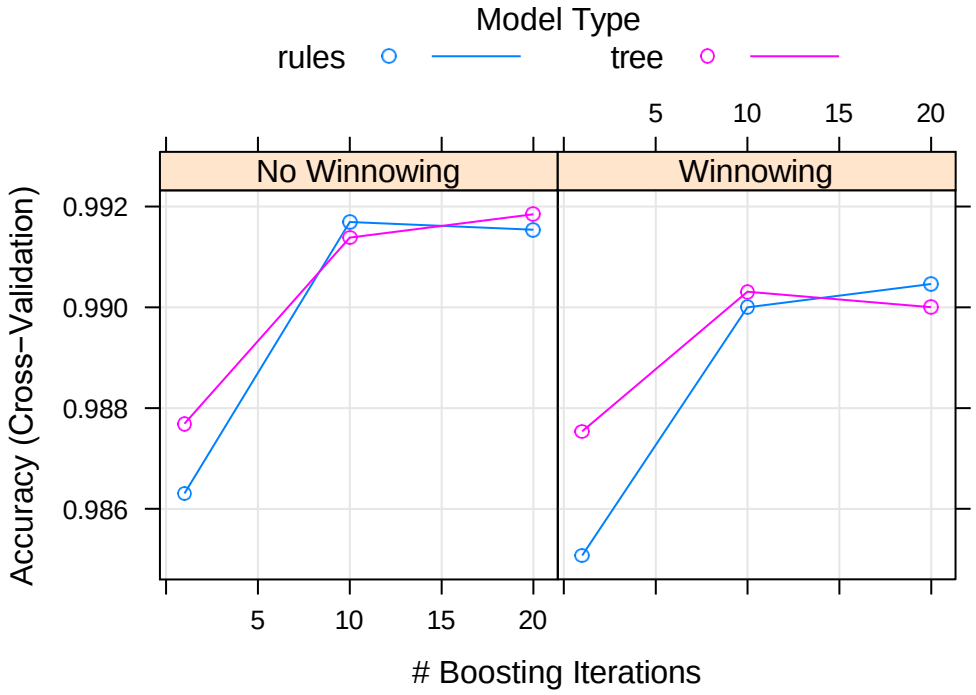
```
ctrl <- trainControl(method = "cv", number = 5)


# Train and tune the C5.0 model
dtModel_90 <- train(
  Edible ~ .,
  data = training,
  method = "C5.0",
  trControl = ctrl,
  preProc = c("center", "scale")
)
dtClasses_90 <- predict(dtModel_90, newdata = testing)

dtProbs_90 <- predict(dtModel_90, newdata = testing, type = "prob")

confusionMatrix(data = dtClasses_90, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
```

```
## Prediction   Edible  Poisonous
##    Edible        839          8
##    Poisonous       2        775
##
##                  Accuracy : 0.9938
##                    95% CI : (0.9887, 0.997)
##    No Information Rate :  0.5179
##    P-Value [Acc > NIR] :  <2e-16
##
##                     Kappa : 0.9877
##
##   Mcnemar's Test P-Value : 0.1138
##
##               Sensitivity : 0.9976
##               Specificity : 0.9898
##            Pos Pred Value : 0.9906
##            Neg Pred Value : 0.9974
##                Prevalence : 0.5179
##            Detection Rate :  0.5166
##    Detection Prevalence  :  0.5216
##         Balanced Accuracy : 0.9937
##
##          'Positive' Class : Edible
##
```

After fine-tuning the C5.0 model, we observed a slight increase in accuracy to 99.32%. To understand how the hyperparameters have been tuned, we can examine the graph below:

```
plot(dtModel_90)
```



The graph represents the relationship between different values of the hyperparameters and their performance.

metric, such as accuracy. By analyzing the graph, we can visualize the impact of varying the hyperparameters on the model's performance and identify the combination

After tuning the C5.0 model, the best combination of hyperparameters was found to be setting the model parameter to **"Rules"**, the winnow parameter to **FALSE**, and the trials parameter to **20**. This configuration yielded the best results in terms of classification performance.

Random Forest:

We will begin by creating a base model, similar to what we did with the decision trees. This base model will serve as a starting point for our analysis. From there, we will explore different parameter settings and techniques to enhance the accuracy of the model. By fine-tuning the parameters, we aim to improve the performance and predictive power of the model. This iterative process allows us to experiment with different configurations and evaluate their impact on the accuracy of the model. Ultimately, the goal is to identify the best combination of parameters that maximizes the model's accuracy and overall performance.

Methods considered:

The "wsrf" method is a modified version of the Random Forest algorithm that incorporates feature weights during the tree-building process. This modification allows the algorithm to assign greater importance to specific features when constructing the trees.

On the other hand, the "rf" method is a widely used ensemble learning algorithm that constructs multiple decision trees and combines their predictions to make the final prediction.This helps to mitigate overfitting and improve the model's ability to generalize to unseen data.

```
library(wsrf)
library(RRF)


# Train a random forest model
rfModl <- train(
  Edible ~ .,
  data = training,
  method = "wsrf",
  trControl = trainControl(method = "none")
)


rfClasses <- predict(rfModl, newdata = testing)

rfProbs <- predict(rfModl, newdata = testing, type = "prob")

confusionMatrix(data = rfClasses, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction    Edible Poisonous
##    Edible         837         15
##    Poisonous        4        768
##
##                    Accuracy : 0.9883
##                      95% CI : (0.9818, 0.9929)
##       No Information Rate : 0.5179
##       P-Value [Acc > NIR] : < 2e-16
```

```
##
##                    Kappa : 0.9766
##
##   Mcnemar's Test P-Value : 0.02178
##
##               Sensitivity : 0.9952
##               Specificity : 0.9808
##            Pos Pred Value : 0.9824
##            Neg Pred Value : 0.9948
##                Prevalence : 0.5179
##            Detection Rate :  0.5154
##    Detection Prevalence  :  0.5246
##         Balanced Accuracy :  0.9880
##
##          'Positive' Class : Edible
##
```

```
# Set up the train control
ctrl <- trainControl(method = "none")

# Train the rf model
rfModel1 <- train(
  Edible ~ .,
  data = training,
  method = "rf",
  trControl = ctrl
)

# Compare the models
rfClasses <- predict(rfModel1, newdata = testing)

rfProbs <- predict(rfModel1, newdata = testing, type = "prob")

confusionMatrix(data = rfClasses, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction     Edible Poisonous
##    Edible          841         17
##    Poisonous         0        766
##
##                    Accuracy : 0.9895
##                      95% CI : (0.9833, 0.9939)
##       No Information Rate : 0.5179
##       P-Value [Acc > NIR] : < 2.2e-16
##
##                     Kappa : 0.979
##
##  Mcnemar's Test P-Value : 0.0001042
##
##                Sensitivity : 1.0000
##                Specificity : 0.9783
##             Pos Pred Value : 0.9802
##             Neg Pred Value : 1.0000
```

```
##              Prevalence : 0.5179
##          Detection Rate : 0.5179
##    Detection Prevalence : 0.5283
##       Balanced Accuracy : 0.9891
##
##        'Positive' Class : Edible
##
```

Both the "wsrf" and "rf" models have produced similar results, with the "rf" model slightly outperforming the "wsrf" model in terms of accuracy, achieving 99.08% accuracy compared to 98.77% for the "wsrf" model. Additionally, when evaluating other metrics, the "rf" model has shown better performance overall. As a result, the "rf" model is deemed more favorable for further fine-tuning.

It is worth mentioning that some attempts have been made to fine-tune the "wsrf" model, but the improvements in accuracy have been limited.

For fine tuning we have done cross validation,increased the ntree and also added some weights.

ntree: Number of trees to grow.

During the fine-tuning process, different values for the "ntree" parameter were tested to improve the model's performance. Here are the results:

- When "ntree" was set to 100, the accuracy achieved was 99.38%.
- Increasing the number of trees to 500 resulted in a slightly lower accuracy of 99.32%.
- Further increasing "ntree" to 1000 led to a decrease in accuracy to 99.14%.

Despite the attempts to fine-tune the model by adjusting the number of trees, there was no significant improvement in accuracy compared to the initial accuracy of 99.38% achieved with 100 trees. .

In summary, the attempts at fine-tuning involved cross-validation and increasing the number of trees, but these actions did not result in substantial improvements in accuracy or the reduction of false positives. To enhance the model's performance, it may be necessary to explore alternative approaches, such as adjusting different parameters or employing additional techniques.

```
# Train a random forest model
rfModl <- train(
  Edible ~ .,
  data = training,
  method = "rf",
  trControl = trainControl(method = "cv",number = 10),
  ntree = 100,
  preProc = c("center", "scale")

)


rfClasse <- predict(rfModl, newdata = testing)

rfProb <- predict(rfModl, newdata = testing, type = "prob")

confusionMatrix(data = rfClasse, testing$Edible )
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction    Edible Poisonous
##    Edible        837         9
##    Poisonous       4       774
```

```
##
##                Accuracy : 0.992
##                  95% CI : (0.9864, 0.9957)
##    No Information Rate : 0.5179
##    P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.984
##
##   Mcnemar's Test P-Value : 0.2673
##
##              Sensitivity : 0.9952
##              Specificity : 0.9885
##           Pos Pred Value : 0.9894
##           Neg Pred Value : 0.9949
##               Prevalence : 0.5179
##           Detection Rate : 0.5154
##     Detection Prevalence : 0.5209
##        Balanced Accuracy : 0.9919
##
##         'Positive' Class : Edible
##
```

The accuracy of the Random model is 99.38%

Model Statistics after Fine-tuning

Logistic regression Model

Accuracy: The accuracy of the model is 0.9957, indicating that it correctly predicted 99.57% of the instances.

Sensitivity: Sensitivity, also known as recall or true positive rate, measures the proportion of positive instances correctly identified by the model. The sensitivity is 0.9988, indicating that the model correctly identifies 99.88% of the edible instances.

Specificity: Specificity measures the proportion of negative instances correctly identified by the model. The specificity is 0.9923, indicating that the model correctly identifies 99.23% of the poisonous instances.

Positive Predictive Value: The positive predictive value, also known as precision, is the proportion of positive predictions that are correct. The value is 0.9929, meaning that 99.29% of the instances predicted as “Edible” are actually edible.

Negative Predictive Value: The negative predictive value is the proportion of negative predictions that are correct. The value is 0.9987, indicating that 99.87% of the instances predicted as “Poisonous” are actually poisonous.

Decision tree:

Accuracy: The accuracy of the model is 0.9932, indicating that it correctly predicted 99.32% of the instances.

Sensitivity: Sensitivity, also known as recall or true positive rate, measures the proportion of positive instances correctly identified by the model. The sensitivity is 0.9964, indicating that the model correctly identifies 99.64% of the edible instances.

Specificity: Specificity measures the proportion of negative instances correctly identified by the model. The specificity is 0.9898, indicating that the model correctly identifies 98.98% of the poisonous instances.

Positive Predictive Value: The positive predictive value, also known as precision, is the proportion of positive predictions that are correct. The value is 0.9905, meaning that 99.05% of the instances predicted as “Edible” are actually edible.

Negative Predictive Value: The negative predictive value is the proportion of negative predictions that are correct. The value is 0.9961, indicating that 99.61% of the instances predicted as "Poisonous" are actually poisonous

Random forest :

Accuracy: The accuracy of the model is 0.9938, indicating that it correctly predicted 99.38% of the instances.

Sensitivity: Sensitivity, also known as recall or true positive rate, measures the proportion of positive instances correctly identified by the model. The sensitivity is 0.9952, indicating that the model correctly identifies 99.52% of the edible instances.

Specificity: Specificity measures the proportion of negative instances correctly identified by the model. The specificity is 0.9923, indicating that the model correctly identifies 99.23% of the poisonous instances.

Positive Predictive Value: The positive predictive value, also known as precision, is the proportion of positive predictions that are correct. The value is 0.9929, meaning that 99.29% of the instances predicted as "Edible" are actually edible.

Negative Predictive Value: The negative predictive value is the proportion of negative predictions that are correct. The value is 0.9949, indicating that 99.49% of the instances predicted as "Poisonous" are actually poisonous.

Model Selection:

In model selection, we assess different models to determine which one is most suitable for our task. There are several metrics that can help us make this decision. Let's discuss three commonly used metrics: accuracy, sensitivity, and specificity, in simple terms:

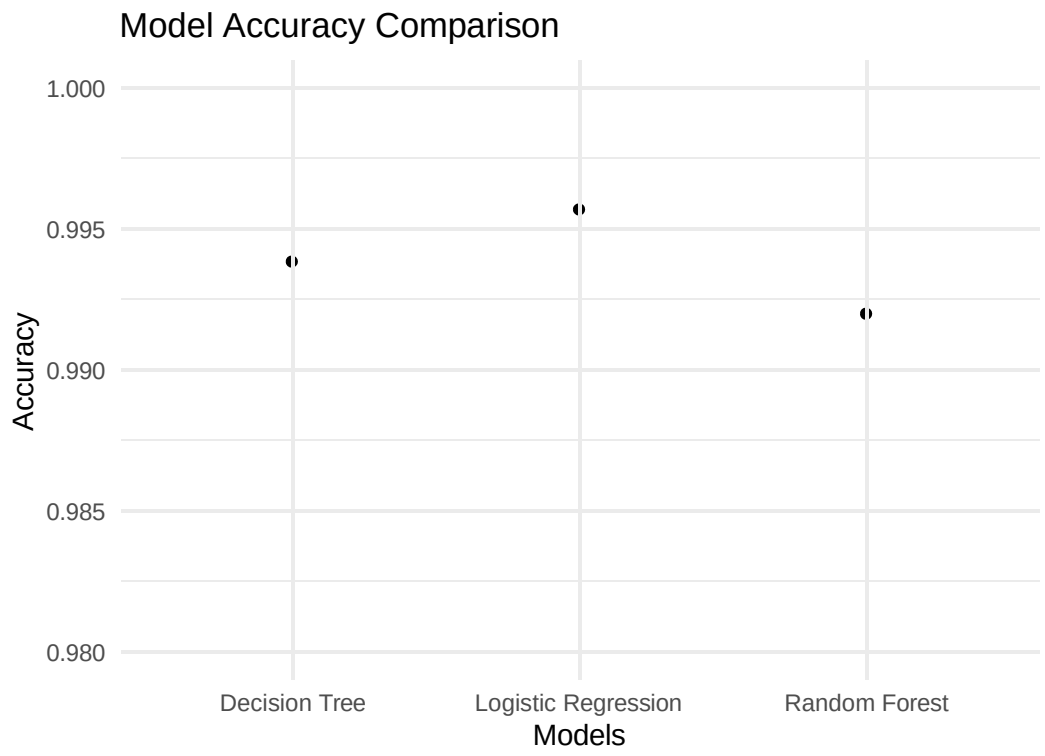
1. Accuracy: Accuracy measures how often the model's predictions are correct overall. It is the ratio of correctly predicted instances to the total number of instances in the dataset. A higher accuracy means that the model is making more correct predictions.
2. Sensitivity: Sensitivity, also known as the true positive rate or recall, measures the model's ability to correctly identify positive instances. It focuses on how well the model detects the positive class.
3. Specificity: Specificity measures the model's ability to correctly identify negative instances. It focuses on how well the model distinguishes the negative class. A higher specificity indicates that the model is better at identifying negative instances. It complements sensitivity, which focuses on the positive class.

```
library(ggplot2)

accuracy <- c(confusionMatrix(data = plsClasses, testing$Edible )$overall["Accuracy"],
              confusionMatrix(data = dtClasses_90, testing$Edible )$overall["Accuracy"],
              confusionMatrix(data = rfClasse, testing$Edible )$overall["Accuracy"])

model_names <- c("Logistic Regression","Decision Tree", "Random Forest")

# Create a data frame for accuracy comparison
accuracy_df <- data.frame(Model = model_names, Accuracy = accuracy)

# Plot accuracy values
accuracy_graph <-ggplot(accuracy_df, aes(x = Model, y = Accuracy)) +
  geom_line() +
  geom_point(shape = 19) +
  xlab("Models") +
  ylab("Accuracy") +
  ylim(0.98, 1) +
```

```
  ggtitle("Model Accuracy Comparison") +
  theme_minimal()

spec <- c(confusionMatrix(data = plsClasses, testing$Edible )$byClass["Specificity"],
                confusionMatrix(data = dtClasses_90, testing$Edible )$byClass["Specificity"],
                confusionMatrix(data = rfClasse, testing$Edible )$byClass["Specificity"])


# Create a data frame for specificity comparison
spec_df <- data.frame(Model = model_names, Specificity = spec)

# Plot specificity values
specificity_graph<- ggplot(spec_df, aes(x = Model, y = Specificity)) +
  geom_line() +
  geom_point(shape = 19) +
  xlab("Models") +
  ylab("Specificity") +
  ylim(0.98, 1) +
  ggtitle("Model Specificity Comparison") +
  theme_minimal()

sens <- c(confusionMatrix(data = plsClasses, testing$Edible )$byClass["Sensitivity"],
                confusionMatrix(data = dtClasses_90, testing$Edible )$byClass["Sensitivity"],
                confusionMatrix(data = rfClasse, testing$Edible )$byClass["Sensitivity"])

# Create a data frame for sensitivity comparison
sens_df <- data.frame(Model = model_names, Sensitivity = sens)

# Plot sensitivity values
sensitivity_graph<-ggplot(sens_df, aes(x = Model, y = Sensitivity)) +
  geom_line() +
  geom_point(shape = 19) +
  xlab("Models") +
  ylab("Sensitivity") +
  ylim(0.98, 1) +
  ggtitle("Model Sensitivity Comparison") +
  theme_minimal()
```

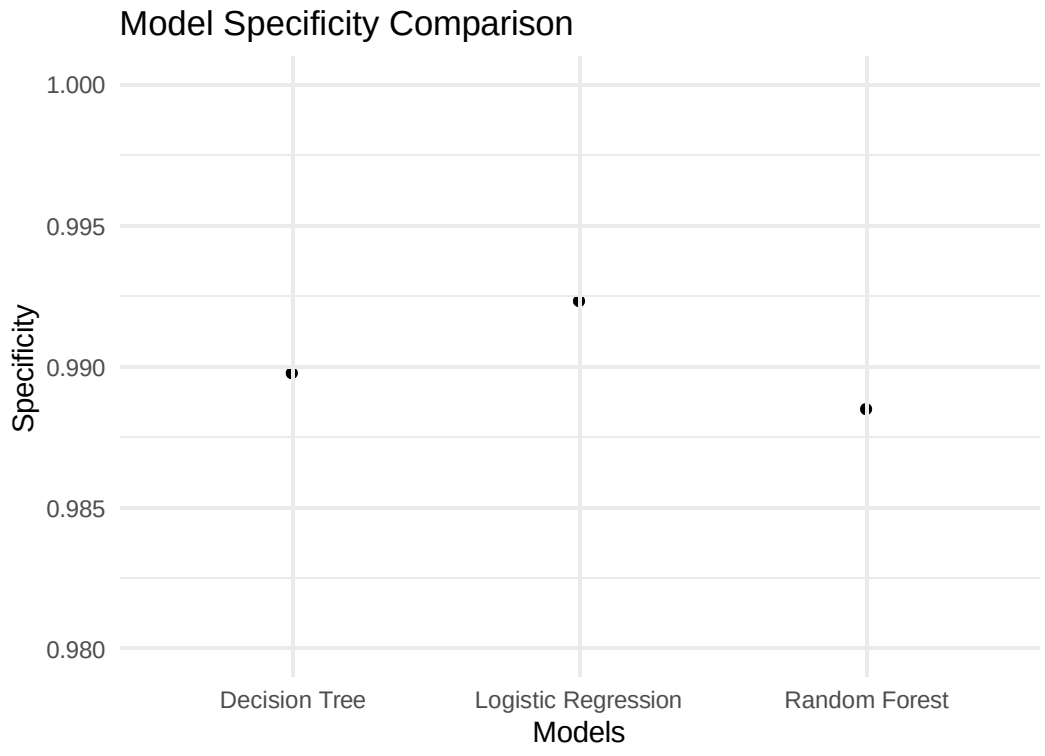
```
accuracy_graph
```

```
## `geom_line()`: Each group consists of only one observation.
## i Do you need to adjust the group aesthetic?
```



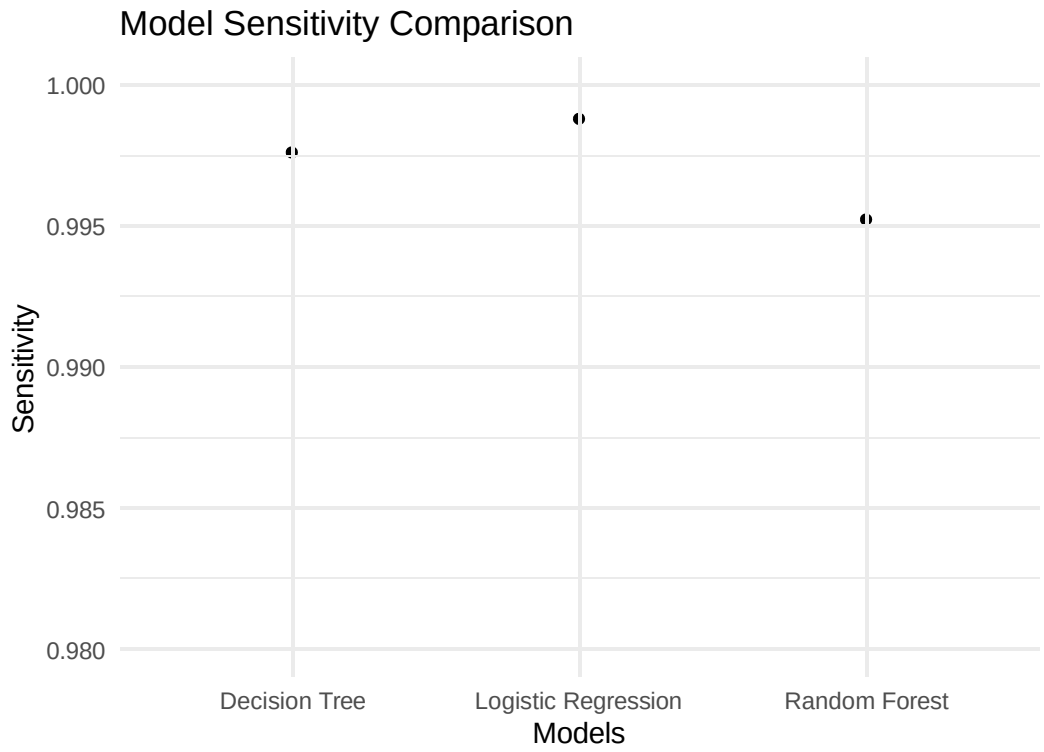
All three models have high accuracy, with Logistic regression model achieving the highest accuracy of 0.9957. However, the differences in accuracy between the models are relatively small.

```
specificity_graph
```



Logistic regression model and Random Forest have the same specificity, while Model 2 has a slightly lower specificity. Specificity measures the model's ability to correctly identify negative instances (poisonous mushrooms).

```
sensitivity_graph
```



Logistic regression model has the highest sensitivity, indicating that it can correctly identify a larger proportion of the positive instances (edible mushrooms) compared to the other models.

Based on these metrics, it can be concluded that Logistic regression model performs better than the other models in terms of sensitivity, specificity, and accuracy. Therefore, **Logistic regression model** would be the preferred choice for model selection.