

A Comprehensive Guide To Random Forest In R

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Random Forest In R:

With the demand for more complex computations, we cannot rely on simplistic algorithms. Instead, we must utilize algorithms with higher computational capabilities and one such algorithm is the Random Forest. In this blog post on Random Forest In R, you'll learn the fundamentals of Random Forest along with its implementation by using the [R Language](#).

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Here's a list of topics that I'll be covering in this Random Forest In R blog:

1. [What is Classification?](#)
2. [What is Random Forest?](#)
3. [Why use Random Forest?](#)
4. [How does Random Forest work?](#)
5. [Creating a Random Forest](#)
6. [Practical Implementation of Random Forest In R](#)

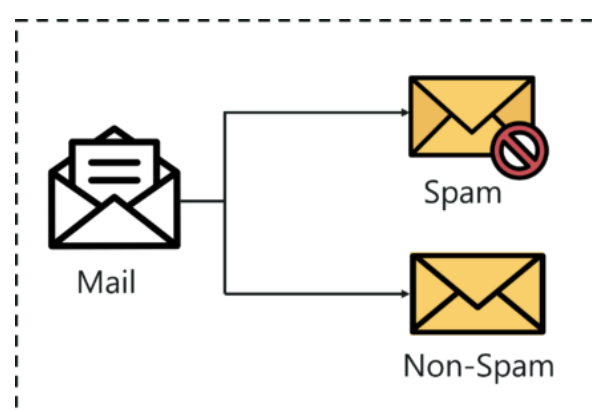
What Is Classification?

Classification is the method of predicting the class of a given input data point. Classification problems are common in machine learning and they fall under the Supervised learning method.

Let's say you want to classify your emails into 2 groups, spam and non-spam emails. For this kind of problems, where you have to assign an input data point into different classes, you can make use of classification algorithms.

Under classification we have 2 types:

- Binary Classification
- Multi-Class Classification



Classification – Random Forest In R – Edureka

The example that I gave earlier about classifying emails as spam and non-spam is of binary type because here we're classifying emails into 2 classes (spam and non-spam).

But let's say that we want to classify our emails into 3 classes:



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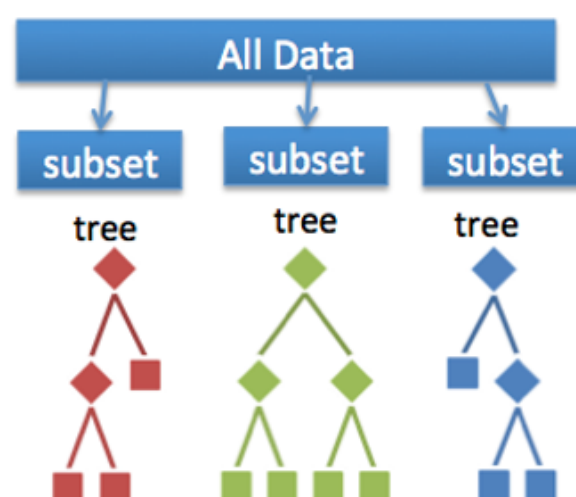
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2. [K Nearest Neighbor \(KNN\)](#)
3. [Decision Tree](#)
4. Support Vector Machine
5. [Naive Bayes](#)
6. Random Forest

What Is Random Forest?

Random forest algorithm is a supervised classification and regression algorithm. As the name suggests, this algorithm randomly creates a forest with several trees.

Generally, the more trees in the forest the more robust the forest looks like. Similarly, in the random forest classifier, the higher the number of trees in the forest, greater is the accuracy of the results.



Random Forest – Random Forest In R – Edureka

In simple words, Random forest builds multiple decision trees (called the forest) and glues them together to get a more accurate and stable prediction. The forest it builds is a collection of Decision Trees, trained with the bagging method.

Before we discuss Random Forest in depth, we need to understand how Decision Trees work.

Many of you have this question in mind:

What Is The Difference Between Random Forest And Decision Trees?

Let me explain.

Let's say that you're looking to buy a house, but you're unable to decide which one to buy. So, you consult a few agents and they give you a list of parameters that you should consider before buying a house. The list includes:

- Price of the house
- Locality
- Number of bedrooms
- Parking space
- Available facilities

These parameters are known as *predictor variables*, which are used to find the response variable. Here's a diagrammatic illustration of how you can represent the above problem statement using a decision tree.

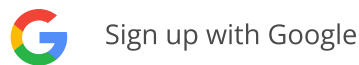


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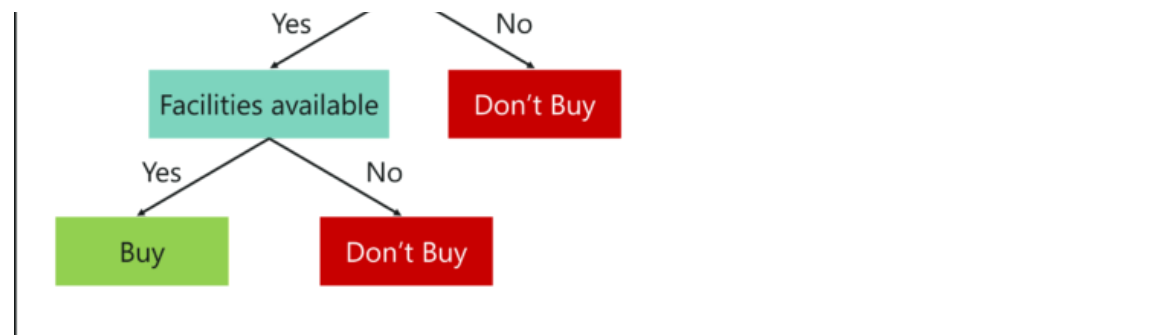
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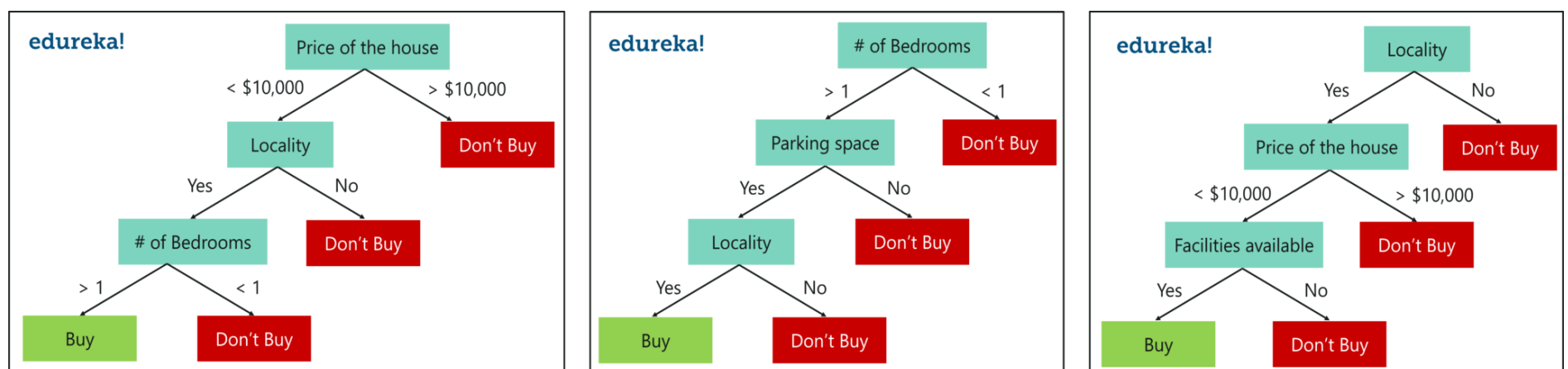


Decision Tree Example – Random Forest In R – Edureka

An important point to note here is that Decision trees are built on the entire data set, by making use of all the predictor variables. Now let's see how Random Forest would solve the same problem.

Like I mentioned earlier Random forest is an ensemble of decision trees, it randomly selects a set of parameters and creates a decision tree for each set of chosen parameters.

Take a look at the below figure.



Random Forest With 3 Decision Trees – Random Forest In R – Edureka

Here, I've created 3 Decision Trees and each Decision Tree is taking only 3 parameters from the entire data set. Each decision tree predicts the outcome based on the respective predictor variables used in that tree and finally takes the average of the results from all the decision trees in the random forest.

In simple words, after creating multiple Decision trees using this method, each tree selects or votes the class (in this case the decision trees will choose whether or not a house is bought), and the class receiving the most votes by a simple majority is termed as the predicted class.

To conclude, Decision trees are built on the entire data set using all the predictor variables, whereas Random Forests are used to create multiple decision trees, such that each decision tree is built only on a part of the data set.

I hope the difference between Decision Trees and Random Forest is clear.


Why Use Random Forest?

You might be wondering why we use Random Forest when we can solve the same problems using Decision trees. Let me explain.

- Even though Decision trees are convenient and easily implemented, they lack accuracy. Decision trees work very effectively with the training data that was used to build them, but they're not flexible when it comes to classifying the new sample. Which means that the accuracy during testing phase is very low.
- This happens due to a process called Over-fitting.



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- Weight
- Blood flow
- Blocked Arteries
- Chest Pain

Blood Flow	Blocked Arteries	Chest Pain	Weight	Heart Disease
Abnormal	No	No	130	No
Normal	Yes	Yes	195	Yes
Normal	No	Yes	218	No
Abnormal	Yes	Yes	180	Yes

Sample Data Set – Random Forest In R – Edureka

These variables are used to predict whether or not a person has heart disease. We’re going to use this data set to create a Random Forest that predicts if a person has heart disease or not.

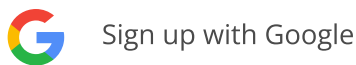
Creating A Random Forest

Step 1: Create a Bootstrapped Data Set

Bootstrapping is an estimation method used to make predictions on a data set by re-sampling it. To create a bootstrapped data set, we must randomly select samples from the original data set. A point to note here is that we can select the same sample more than once.

Blood Flow	Blocked Arteries	Chest Pain	Weight	Heart Disease
Normal	Yes	Yes	195	Yes
Abnormal	No	No	130	No
Abnormal	Yes	Yes	180	Yes
Abnormal	Yes	Yes	180	Yes

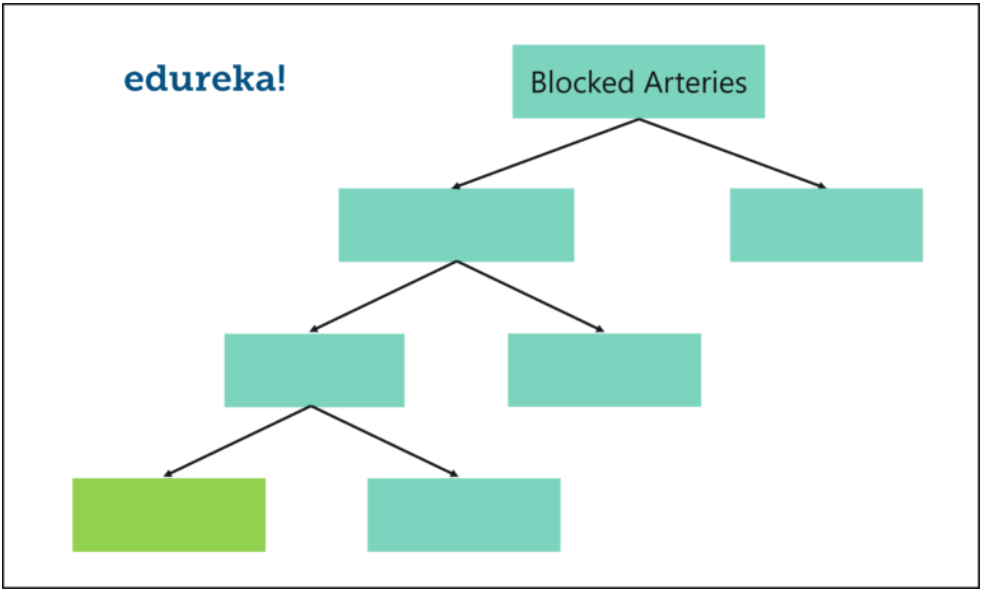
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- Let's say we selected Blood Flow and Blocked arteries. Out of these 2 variables, we must now select the variable that best separates the samples. For the sake of this example, let's say that Blocked Arteries is a more significant predictor and thus assign it as the root node.
- Our next step is to repeat the same process for each of the upcoming branch nodes. Here, we again select two variables at random as candidates for the branch node and then choose a variable that best separates the samples.

Just like this, we build the tree by only considering random subsets of variables at each step. By following the above process, our tree would look something like this:



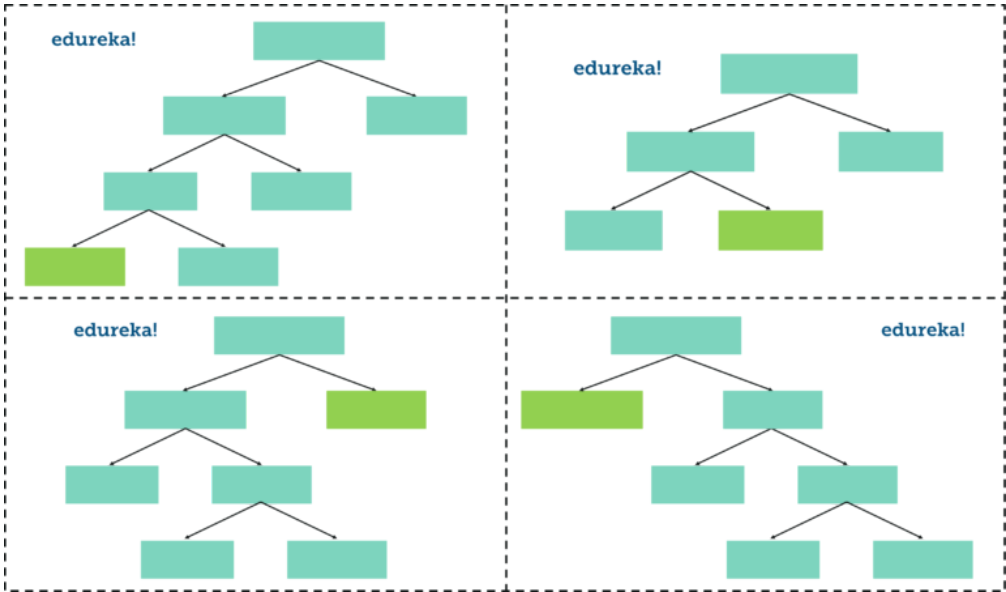
Random Forest Algorithm – Random Forest In R – Edureka

We just created our first Decision tree.

Step 3: Go back to Step 1 and Repeat

Like I mentioned earlier, Random Forest is a collection of Decision Trees. Each Decision Tree predicts the output class based on the respective predictor variables used in that tree. Finally, the outcome of all the Decision Trees in a Random Forest is recorded and the class with the majority votes is computed as the output class.

Thus, we must now create more decision trees by considering a subset of random predictor variables at each step. To do this, go back to step 1, create a new bootstrapped data set and then build a Decision Tree by considering only a subset of variables at each step. So, by following the above steps, our Random Forest would look something like this:



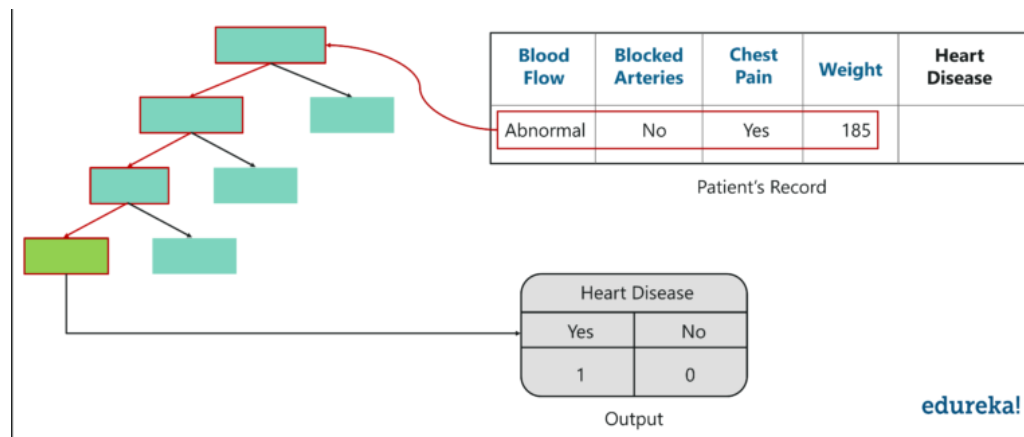
Random Forest – Random Forest In R – Edureka



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Output – Random Forest In R – Edureka

Similarly, we run this data down the other decision trees and keep a track of the class predicted by each tree. After running the data down all the trees in the Random Forest, we check which class got the majority votes. In our case, the class 'Yes' received the most number of votes, hence it's clear that the new patient has heart disease.

To conclude, we bootstrapped the data and used the aggregate from all the trees to make a decision, this process is known as *Bagging*.

Step 5: Evaluate the Model

Our final step is to evaluate the Random Forest model. Earlier while we created the bootstrapped data set, we left out one entry/sample since we duplicated another sample. In a real-world problem, about 1/3rd of the original data set is not included in the bootstrapped data set.

The below figure shows the entry that didn't end up in the bootstrapped data set.

Blood Flow	Blocked Arteries	Chest Pain	Weight	Heart Disease
Normal	No	Yes	218	No

Out-Of-Bag Sample – Random Forest In R – Edureka

This sample data set that does not include in the bootstrapped data set is known as the Out-Of-Bag (OOB) data set.

“

The Out-Of-Bag data set is used to check the accuracy of the model, since the model wasn't created using this OOB data it will give us a good understanding of whether the model is effective or not. ”

In our case, the output class for the OOB data set is 'No'. So, in order for our Random Forest model to be accurate, if we run the OOB data down the Decision trees, we must get a majority of 'No' votes. This process is carried out for all the OOB samples, in our case we only had one OOB, however, in most problems, there are usually many more samples.

Therefore, eventually, we can measure the accuracy of a Random Forest by the proportion of OOB samples that are correctly classified.

The proportion of OOB samples that are incorrectly classified is called the *Out-Of-Bag Error*. So that was an example of how Random Forest works.

Now let's get our hands dirty and implement the Random Forest algorithm to solve a more complex problem.



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Practical Implementation Of Random Forest In R

Even people living under a rock would've heard of a movie called Titanic. But how many of you know that the movie is based on a real event? Kaggle assembled a data set containing data on who survived and who died on the Titanic.

Problem Statement: To build a Random Forest model that can study the characteristics of an individual who was on the Titanic and predict the likelihood that they would have survived.

Data Set Description: There are several variables/features in the data set for each person:

- pclass: passenger class (1st, 2nd, or 3rd)
- sex
- age
- sibsp: number of Siblings/Spouses Aboard
- parch: number of Parents/Children Aboard
- fare: how much the passenger paid
- embarked: where they got on the boat (C = Cherbourg; Q = Queenstown; S = Southampton)

We'll be running the below code snippets in R by using RStudio, so go ahead and open up RStudio. For this demo, you need to install the caret package and the randomForest package.

```
1 | install.packages("caret", dependencies = TRUE)
2 | install.packages("randomForest")
```

Next step is to load the packages into the working environment.

```
1 | library(caret)
2 | library(randomForest)
```

It's time to load the data, we will use the read.table function to do this. Make sure you mention the path to the files (train.csv and test.csv)

```
1 | train <- read.table('C:/Users/zulaikha/Desktop/titanic/train.csv', sep="," , header= TRUE)
```

The above command reads in the file "train.csv", using the delimiter ",", (which shows that the file is a CSV file) including the header row as the column names, and assigns it to the R object train.

Now, let's read in the test data:

```
1 | test <- read.table('C:/Users/zulaikha/Desktop/titanic/test.csv', sep = ",", header = TRUE)
```

To compare the training and testing data, let's take a look at the first few rows of the training set:

```
1 | head(train)
```



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1 | head(test)

PassengerId	Pclass	Name
1	892	3 Kelly, Mr. James
2	893	3 Wilkes, Mrs. James (Ellen Needs)
3	894	2 Myles, Mr. Thomas Francis
4	895	3 Wirz, Mr. Albert
5	896	3 Hirvonen, Mrs. Alexander (Helga E Lindqvist)
6	897	3 Svensson, Mr. Johan Cervin

	Sex	Age	SibSp	Parch	Ticket	Fare	Cabin	Embarked
1	male	34.5	0	0	330911	7.8292		Q
2	female	47.0	1	0	363272	7.0000		S
3	male	62.0	0	0	240276	9.6875		Q
4	male	27.0	0	0	315154	8.6625		S
5	female	22.0	1	1	3101298	12.2875		S
6	male	14.0	0	0	7538	9.2250		S

Testing Data – Random Forest In R – Edureka

The main difference between the training set and the test set is that the training set is labeled, but the test set is unlabeled. The train set obviously doesn't have a column called "Survived" because we have to predict that for each person who boarded the titanic.

Before we get any further, the most essential factor while building a model is, picking the best features to use in the model. It's never about picking the best algorithm or using the most sophisticated R package. Now, a "feature" is just a variable.

So, this brings us to the question, how do we pick the most significant variables to use? The easy way is to use cross-tabs and conditional box plots.

Cross-tabs represent relations between two variables in an understandable manner. In accordance to our problem, we want to know which variables are the best predictors for "Survived". Let's look at the cross-tabs between "Survived" and each other variable. In R, we use the table function:

```
1 | table(train[,c('Survived', 'Pclass')])
2 |      Pclass
3 | Survived    1    2    3
4 |      0    80   97 372
5 |      1   136   87 119
```

From the cross-tab, we can see that "Pclass" could be a useful predictor of "Survived." This is because, the first column of the cross-tab shows that, of the passengers in Class 1, 136 survived and 80 died (i.e. 63% of first-class passengers survived). On the other hand, in Class 2, 87 survived and 97 died (i.e. only 47% of second class passengers survived). Finally, in Class 3, 119 survived and 372 died (i.e. only 24% of third-class passengers survived). This means that there's an obvious relationship between the passenger class and the survival chances.

Now we know that we must use Pclass in our model because it definitely has a strong predictive value of whether someone survived or not. Now, you can repeat this process for the other categorical variables in the data set, and decide which variables you want to include

To make things easier, let's use the "conditional" box plots to compare the distribution of each continuous variable, conditioned on whether the passengers survived or not. But first we'll need to install the 'fields' package:

```
1 | install.packages("fields")
2 | library(fields)
3 | bplot.xy(train$Survived, train$Age)
```



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Box Plot – Random Forest In R – Edureka

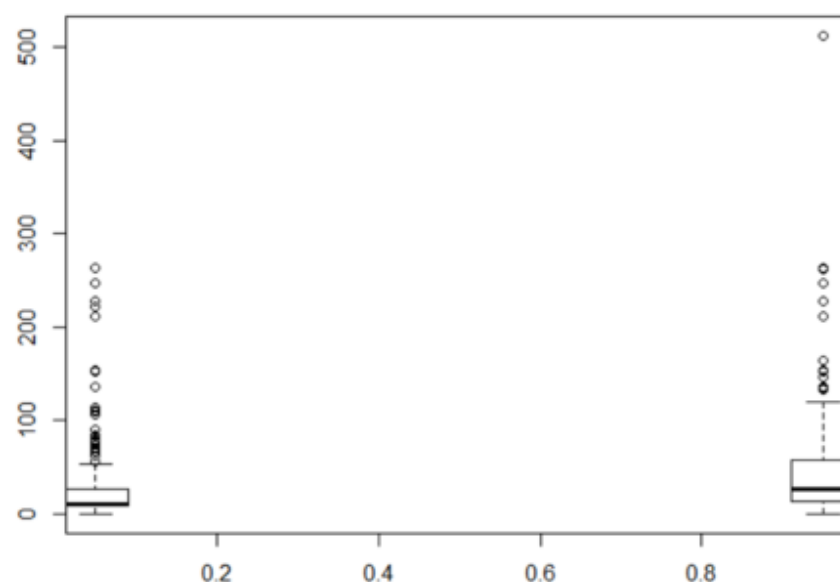
The box plot of age for people who survived and who didn't is nearly the same. This means that Age of a person did not have a large effect on whether one survived or not. The y-axis is Age and the x-axis is Survived.

Also, if you summarize it, there are lots of NA's. So, let's exclude the variable Age, because it doesn't have a big impact on Survived, and because the NA's make it hard to work with.

```
1 summary(train$Age)
2   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
3   0.42  20.12   28.00   29.70  38.00   80.00   177
```

In the below boxplot, the boxplot for Fares are much different for those who survived and those who didn't. Again, the y-axis is Fare and the x-axis is Survived.

```
1 bplot.xy(train$Survived, train$Fare)
```



Box Plot For Fair – Random Forest In R – Edureka

On summarizing you'll find that there are no NA's for Fare. So, let's include this variable.

```
1 summary(train$Fare)
2   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
3   0.00   7.91   14.45   32.20   31.00   512.33
```

The next step is to convert Survived to a Factor data type so that caret builds a classification instead of a regression model. After that, we use a simple train command to train the model.

Now the model is trained using the Random Forest algorithm that we discussed earlier. Random Forest is perfect for such problems because it performs numerous computations and predicts the results with high accuracy.

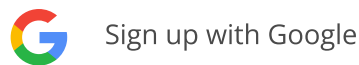
```
1 # Converting 'Survived' to a factor
2 train$Survived <- factor(train$Survived)
3 # Set a random seed
4 set.seed(51)
5 # Training using 'random forest' algorithm
6 model <- train(Survived ~ Pclass + Sex + SibSp +
7 Embarked + Parch + Fare, # Survived is a function of the variables we decided to include
8 data = train, # Use the train data frame as the training data
9 method = 'rf', # Use the 'random forest' algorithm
10 trControl = trainControl(method = 'cv', # Use cross-validation
11 number = 5) # Use 5 folds for cross-validation
```



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```

7
8 No pre-processing
9 Resampling: Cross-Validated (5 fold)
10 Summary of sample sizes: 712, 713, 713, 712, 714
11 Resampling results across tuning parameters:
12
13      mtry  Accuracy   Kappa
14      2      0.8047116 0.5640887
15      5      0.8070094 0.5818153
16      8      0.8002236 0.5704306
17
18 Accuracy was used to select the optimal model using the largest value.
19 The final value used for the model was mtry = 5.
    
```

The first thing to notice is where it says, “The final value used for the model was mtry = 5.” The “mtry” is a hyper-parameter of the random forest model that determines how many variables the model uses to split the trees.

The table shows different values of mtry along with their corresponding average accuracy under cross-validation. Caret automatically picks the value of the hyper-parameter “mtry” that is the most accurate under cross-validation.

In the output, with mtry = 5, the average accuracy is 0.8170964, or about 82 percent. Which is the highest value, hence Caret picks this value for us.

Before we predict the output for the test data, let’s check if there is any missing data in the variables we are using to predict. If Caret finds any missing values, it will not return a prediction at all. So, we must find the missing data before moving ahead:



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```
1 | summary(test)
```

Parch	Ticket	Fare	Cabin
Min. :0.0000	PC 17608: 5	Min. : 0.000	:327
1st Qu.:0.0000	113503 : 4	1st Qu.: 7.896	B57 B59 B63 B66: 3
Median :0.0000	CA. 2343: 4	Median : 14.454	A34 : 2
Mean :0.3923	16966 : 3	Mean : 35.627	B45 : 2
3rd Qu.:0.0000	220845 : 3	3rd Qu.: 31.500	C101 : 2
Max. :9.0000	347077 : 3	Max. :512.329	C116 : 2
	(Other) :396	NA's :1	(Other) : 80

Summary of the Test Data – Random Forest In R – Edureka

Notice the variable “Fare” has one NA value. Let’s fill in that value with the mean of the “Fare” column. We use an if-else statement to do this.

So, if an entry in the column “Fare” is NA, then replace it with the mean of the column and remove the NA’s when you take the mean:

```
1 | test$Fare <- ifelse(is.na(test$Fare), mean(test$Fare, na.rm = TRUE), test$Fare)
```

Now, our final step is to make predictions on the test set. To do this, you just have to call the predict method on the model object you trained. Let’s make the predictions on the test set and add them as a new column.

```
1 | test$Survived <- predict(model, newdata = test)
```



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Here you can see the “Survived” values (either 0 or 1) for each passenger. Where one stands for survived and 0 stands for died. This prediction is made based on the “pclass” and “Fare” variables. You can use other variables too, if they are somehow related to whether a person boarding the titanic will survive or not.

Now that you know how Random Forest works, I’m sure you’re curious to learn more about the various Machine learning algorithms. Here’s a list of blogs that cover the different types of Machine Learning algorithms in depth

- [Linear Regression](#)
- [Logistic Regression](#)
- [Support Vector Machine](#)
- [Decision Trees](#)
- [K-Means](#)

So, with this, we come to the end of this blog. I hope you all found this blog informative. If you have any thoughts to share, please comment them below. Stay tuned for more blogs like these!

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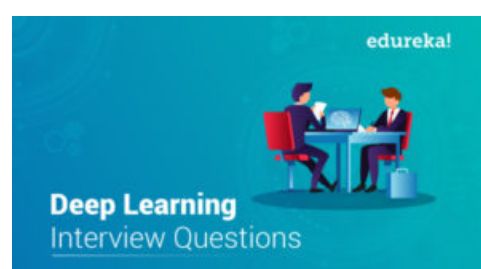
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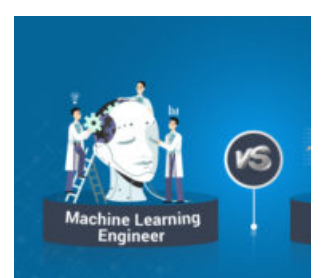
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