This project aims at developing a machine-learning algorithm and predict if a certain mushroom is edible or poisonous by its specifications like cap shape, cap color, gill color, etc.

In [1]:
```
# IMPORT ALL THE REQUIRED LIBRARY
import warnings
warnings.filterwarnings('ignore')
```

In [2]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [3]:
```
#Now we will import our data
data=pd.read_csv("D:\mushrooms.csv")
```

In [4]:
```
data
```

Out[4]:

	type	cap_shape	cap_surface	cap_color	bruises	odor	gill_attachment	gill_spacing	gill_
0	p	x	s	n	t	p	f	c	
1	e	x	s	y	t	a	f	c	
2	e	b	s	w	t	l	f	c	
3	p	x	y	w	t	p	f	c	
4	e	x	s	g	f	n	f	w	
...	...	...	...	...	...	...	...	...	
8119	e	k	s	n	f	n	a	c	
8120	e	x	s	n	f	n	a	c	
8121	e	f	s	n	f	n	a	c	
8122	p	k	y	n	f	y	f	c	
8123	e	x	s	n	f	n	a	c	

8124 rows × 23 columns

Data is having 8124 rows and 23 columns.

Attribute Information: (classes: edible=e, poisonous=p)

cap-shape: bell=b,conical=c,convex=x,flat=f, knobbed=k,sunken=s

cap-surface: fibrous=f,grooves=g,scaly=y,smooth=s

cap-color: brown=n,buff=b,cinnamon=c,gray=g,green=r,pink=p,purple=u,red=e,white=w,yellow=y

bruises: bruises=t,no=f

odor: almond=a,anise=l,creosote=c,fishy=y,foul=f,musty=m,none=n,pungent=p,spicy=s

gill-attachment: attached=a,descending=d,free=f,notched=n

gill-spacing: close=c,crowded=w,distant=d

gill-size: broad=b,narrow=n

gill-color: black=k,brown=n,buff=b,chocolate=h,gray=g, green=r,orange=o,pink=p,purple=u,red=e,white=w,yellow=y

stalk-shape: enlarging=e,tapering=t

stalk-root: bulbous=b,club=c,cup=u,equal=e,rhizomorphs=z,rooted=r,missing=? stalk-surface-above-ring: fibrous=f,scaly=y,silky=k,smooth=s stalk-surface-below-ring: fibrous=f,scaly=y,silky=k,smooth=s

stalk-color-above-ring: brown=n,buff=b,cinnamon=c,gray=g,orange=o,pink=p,red=e,white=w,yellow=y

stalk-color-below-ring: brown=n,buff=b,cinnamon=c,gray=g,orange=o,pink=p,red=e,white=w,yellow=y

veil-type: partial=p,universal=u

veil-color: brown=n,orange=o,white=w,yellow=y

ring-number: none=n,one=o,two=t

ring-type: cobwebby=c,evanescent=e,flaring=f,large=l,none=n,pendant=p,sheathing=s,zone=z

spore-print-color: black=k,brown=n,buff=b,chocolate=h,green=r,orange=o,purple=u,white=w,yellow=y

population: abundant=a,clustered=c,numerous=n,scattered=s,several=v,solitary=y

habitat: grasses=g,leaves=l,meadows=m,paths=p,urban=u,waste=w,woods=d

In [5]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 8124 entries, 0 to 8123
Data columns (total 23 columns):
 #   Column                    Non-Null Count  Dtype 
---  ------                    --------------  ----- 
 0   type                      8124 non-null   object
 1   cap_shape                 8124 non-null   object
 2   cap_surface               8124 non-null   object
 3   cap_color                 8124 non-null   object
 4   bruises                   8124 non-null   object
 5   odor                      8124 non-null   object
 6   gill_attachment           8124 non-null   object
 7   gill_spacing              8124 non-null   object
 8   gill_size                 8124 non-null   object
 9   gill_color                8124 non-null   object
 10  stalk_shape               8124 non-null   object
 11  stalk_root                8124 non-null   object
 12  stalk_surface_above_ring  8124 non-null   object
 13  stalk_surface_below_ring  8124 non-null   object
 14  stalk_color_above_ring    8124 non-null   object
 15  stalk_color_below_ring    8124 non-null   object
 16  veil_type                 8124 non-null   object
 17  veil_color                8124 non-null   object
 18  ring_number               8124 non-null   object
 19  ring_type                 8124 non-null   object
 20  spore_print_color         8124 non-null   object
 21  population                8124 non-null   object
 22  habitat                   8124 non-null   object
dtypes: object(23)
memory usage: 1.4+ MB
```

Here we can see, all the columns having object data type. As the data is object type we will use encoder to encode the value.

In [6]:
```
data.isnull().sum()
```

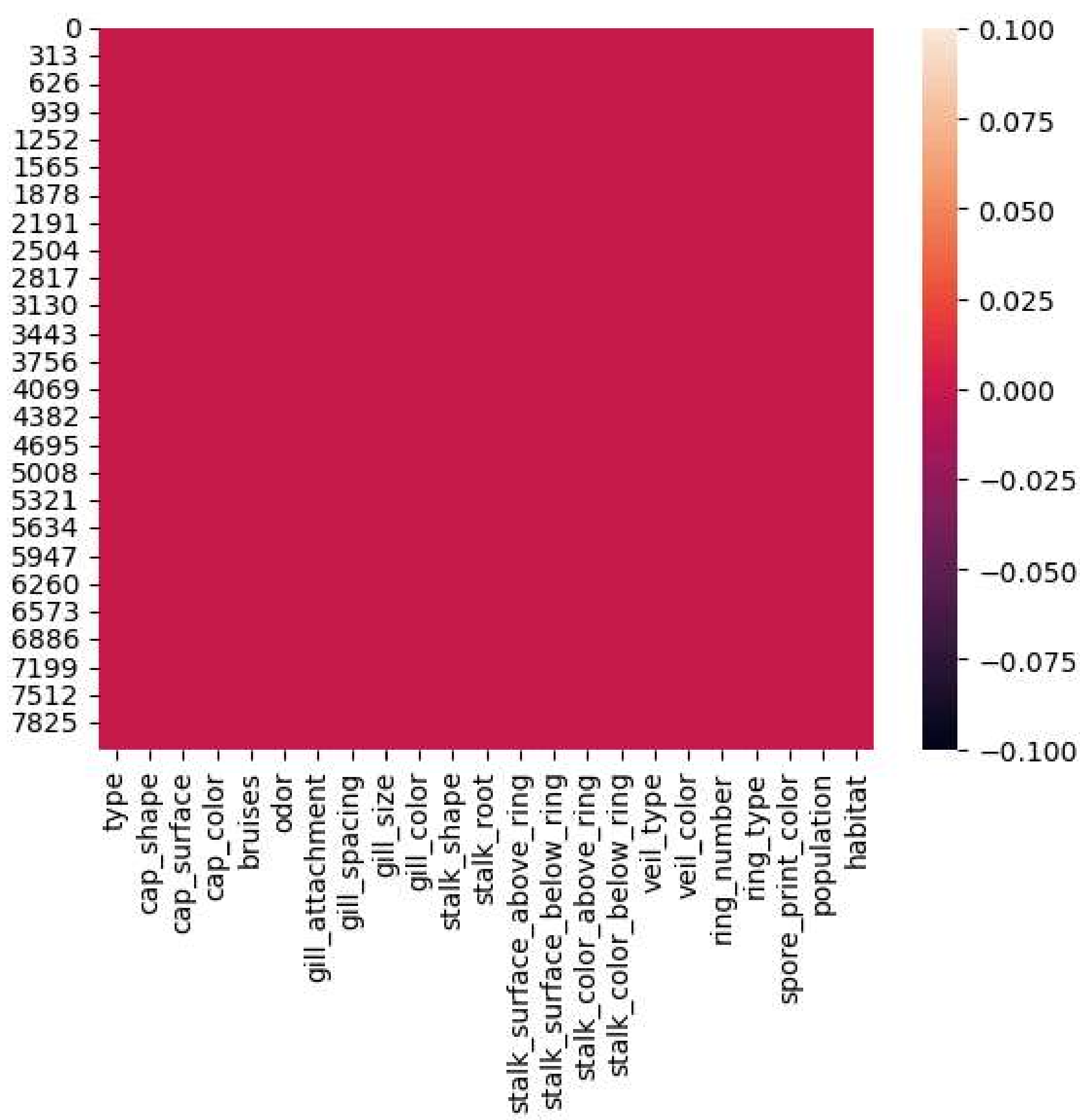
Out[6]:
```
type                        0
cap_shape                   0
cap_surface                 0
cap_color                   0
bruises                     0
odor                        0
gill_attachment             0
gill_spacing                0
gill_size                   0
gill_color                  0
stalk_shape                 0
stalk_root                  0
stalk_surface_above_ring    0
stalk_surface_below_ring    0
stalk_color_above_ring      0
stalk_color_below_ring      0
veil_type                   0
veil_color                  0
ring_number                 0
ring_type                   0
spore_print_color           0
population                  0
habitat                     0
dtype: int64
```

All the columns filled with the data, no column have null value. so we can proceed futher analysis.

We can Visualize it using heatmap.

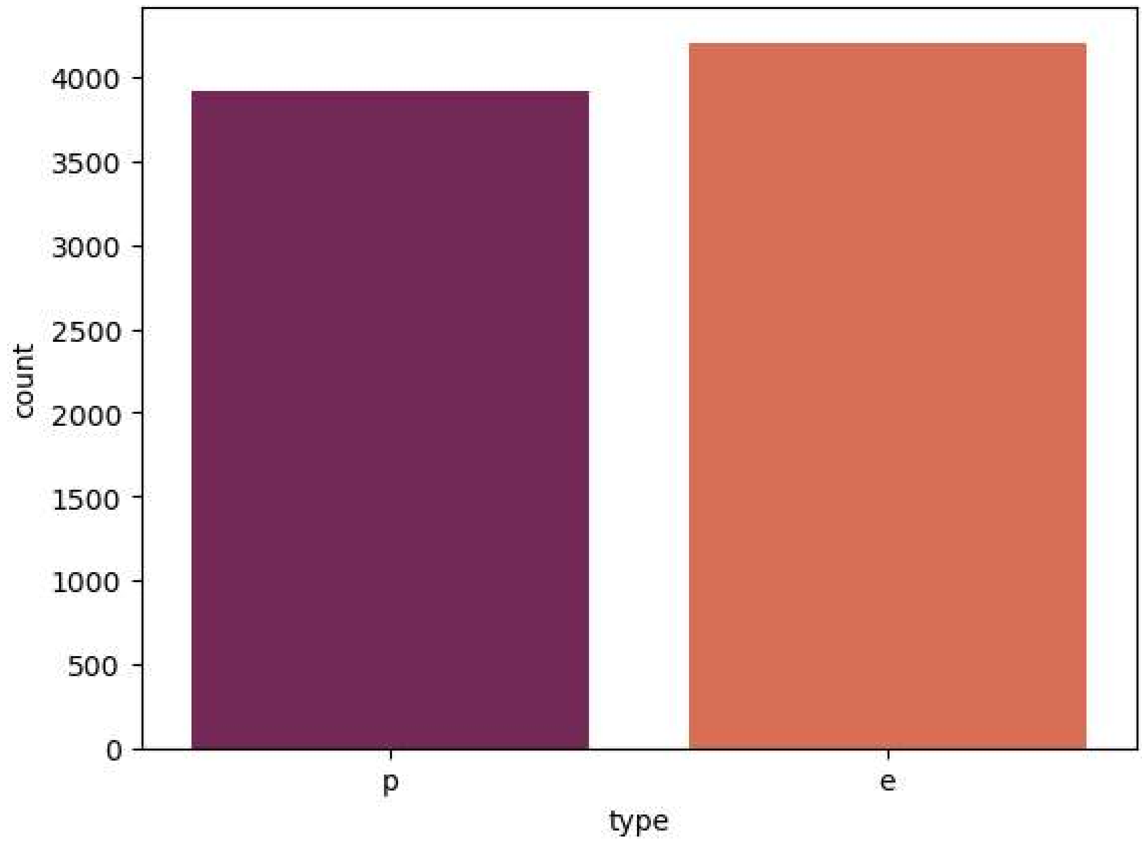
In [7]:
```
sns.heatmap(data.isnull())
```

Out[7]:
```
<Axes: >
```



In [8]:

Out[8]: <Axes: xlabel='type', ylabel='count'>



In [9]:
```
data.value_counts(['type'])
```

Out[9]:
```
type
e       4208
p       3916
Name: count, dtype: int64
```

As our data is almost Balanced. So no need to balance the data.

In [10]:
```
data.dtypes
```

Out[10]:
```
type                        object
cap_shape                   object
cap_surface                 object
cap_color                   object
bruises                     object
odor                        object
gill_attachment             object
gill_spacing                object
gill_size                   object
gill_color                  object
stalk_shape                 object
stalk_root                  object
stalk_surface_above_ring    object
stalk_surface_below_ring    object
stalk_color_above_ring      object
stalk_color_below_ring      object
veil_type                   object
veil_color                  object
ring_number                 object
ring_type                   object
spore_print_color           object
population                  object
habitat                     object
dtype: object
```

here we can see our data type is objective we need to encode the data before going for futher steps of analysis.

In [11]:
```
from sklearn.preprocessing import LabelEncoder
def label_encoded(x):
    le = LabelEncoder()
    le.fit(x)
    print(x.name, le.classes_)
    return le.transform(x)
```

Here we used made the funtion for encoding out data. We used LabelEncoder for this.

In [12]:
```
for col in data.columns:
    data[str(col)] = label_encoded(data[str(col)])
```

```
type ['e' 'p']
cap_shape ['b' 'c' 'f' 'k' 's' 'x']
cap_surface ['f' 'g' 's' 'y']
cap_color ['b' 'c' 'e' 'g' 'n' 'p' 'r' 'u' 'w' 'y']
bruises ['f' 't']
odor ['a' 'c' 'f' 'l' 'm' 'n' 'p' 's' 'y']
gill_attachment ['a' 'f']
gill_spacing ['c' 'w']
gill_size ['b' 'n']
gill_color ['b' 'e' 'g' 'h' 'k' 'n' 'o' 'p' 'r' 'u' 'w' 'y']
stalk_shape ['e' 't']
stalk_root ['?' 'b' 'c' 'e' 'r']
stalk_surface_above_ring ['f' 'k' 's' 'y']
stalk_surface_below_ring ['f' 'k' 's' 'y']
stalk_color_above_ring ['b' 'c' 'e' 'g' 'n' 'o' 'p' 'w' 'y']
stalk_color_below_ring ['b' 'c' 'e' 'g' 'n' 'o' 'p' 'w' 'y']
veil_type ['p']
veil_color ['n' 'o' 'w' 'y']
ring_number ['n' 'o' 't']
ring_type ['e' 'f' 'l' 'n' 'p']
spore_print_color ['b' 'h' 'k' 'n' 'o' 'r' 'u' 'w' 'y']
population ['a' 'c' 'n' 's' 'v' 'y']
habitat ['d' 'g' 'l' 'm' 'p' 'u' 'w']
```

In [13]:
```
data.head()
```

Out[13]:

	type	cap_shape	cap_surface	cap_color	bruises	odor	gill_attachment	gill_spacing	gill_siz
0	1	5	2	4	1	6	1	0	
1	0	5	2	9	1	0	1	0	
2	0	0	2	8	1	3	1	0	
3	1	5	3	8	1	6	1	0	
4	0	5	2	3	0	5	1	1	

5 rows × 23 columns

In [14]:
```
data.columns
```

Out[14]:
```
Index(['type', 'cap_shape', 'cap_surface', 'cap_color', 'bruises', 'odor',
       'gill_attachment', 'gill_spacing', 'gill_size', 'gill_color',
       'stalk_shape', 'stalk_root', 'stalk_surface_above_ring',
       'stalk_surface_below_ring', 'stalk_color_above_ring',
       'stalk_color_below_ring', 'veil_type', 'veil_color', 'ring_number',
       'ring_type', 'spore_print_color', 'population', 'habitat'],
      dtype='object')
```

In [15]:
```
data.corr()
```

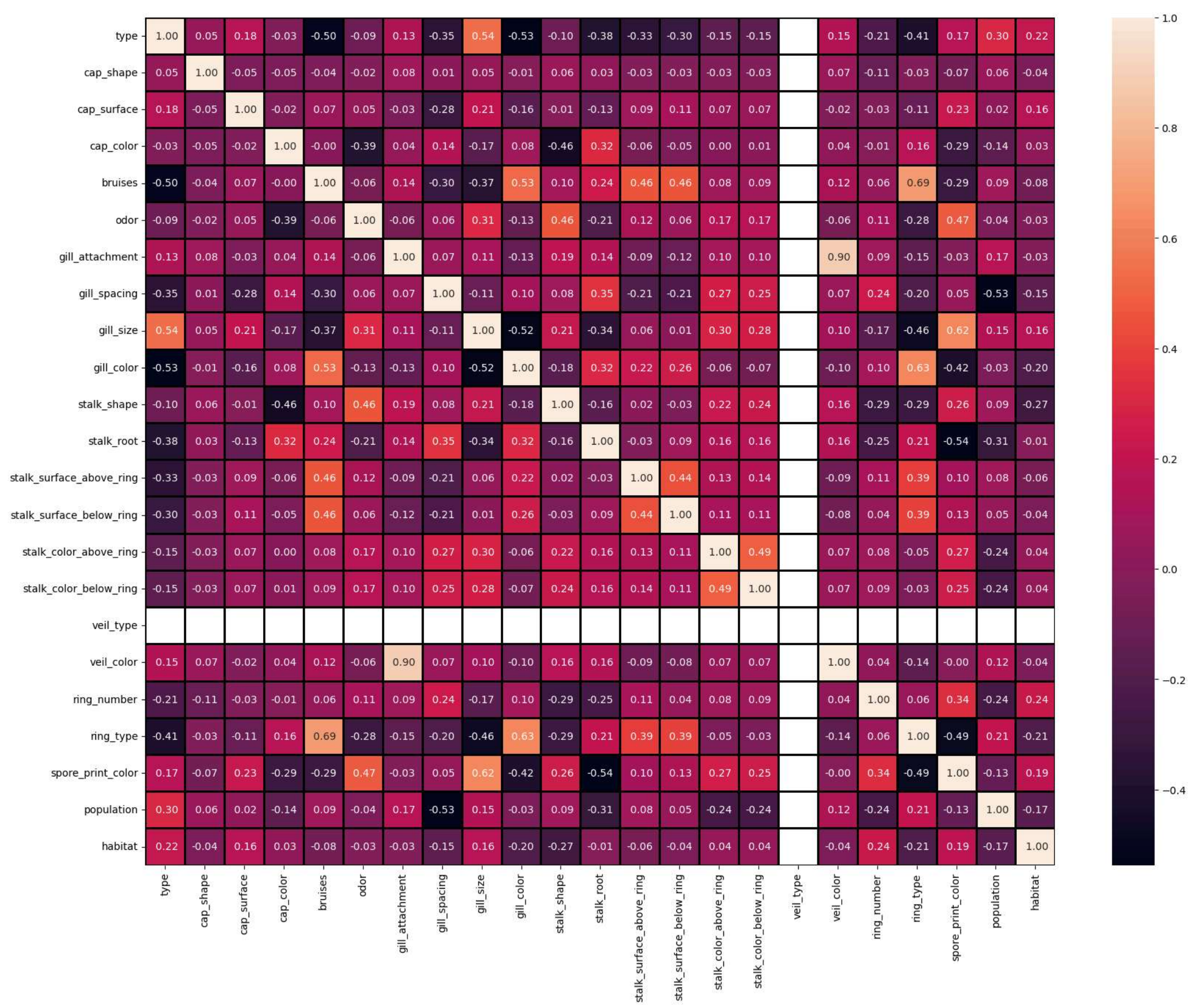
Out[15]:

	type	cap_shape	cap_surface	cap_color	bruises	odor
type	1.000000	0.052951	0.178446	-0.031384	-0.501530	-0.093552
cap_shape	0.052951	1.000000	-0.050454	-0.048203	-0.035374	-0.021935
cap_surface	0.178446	-0.050454	1.000000	-0.019402	0.070228	0.045233
cap_color	-0.031384	-0.048203	-0.019402	1.000000	-0.000764	-0.387121
bruises	-0.501530	-0.035374	0.070228	-0.000764	1.000000	-0.061825
odor	-0.093552	-0.021935	0.045233	-0.387121	-0.061825	1.000000
gill_attachment	0.129200	0.078865	-0.034180	0.041436	0.137359	-0.059590
gill_spacing	-0.348387	0.013196	-0.282306	0.144259	-0.299473	0.063936
gill_size	0.540024	0.054050	0.208100	-0.169464	-0.369596	0.310495
gill_color	-0.530566	-0.006039	-0.161017	0.084659	0.527120	-0.129213
stalk_shape	-0.102019	0.063794	-0.014123	-0.456496	0.099364	0.459766

In [ ]:
```
We can Visualize the correlation using Heatmap. as follow
```

In [16]:
```
plt.figure(figsize=(20,15))
sns.heatmap(data.corr(), annot=True, linewidths=1,linecolor='black',fmt=' .2f'
```

Out[16]: <Axes: >



Here we can see vell-type have no effect on our target column, so we can drop that column.

In [17]:
```
data.head(10)
```

Out[17]:

	type	cap_shape	cap_surface	cap_color	bruises	odor	gill_attachment	gill_spacing	gill_siz
0	1	5	2	4	1	6	1	0	
1	0	5	2	9	1	0	1	0	
2	0	0	2	8	1	3	1	0	
3	1	5	3	8	1	6	1	0	
4	0	5	2	3	0	5	1	1	
5	0	5	3	9	1	0	1	0	
6	0	0	2	8	1	0	1	0	
7	0	0	3	8	1	3	1	0	
8	1	5	3	8	1	6	1	0	
9	0	0	2	9	1	0	1	0	

10 rows × 23 columns

In [18]:
```
data=data.drop(['veil_type'],axis=1)
```

In [19]:
```
data.head(5)
```

Out[19]:

	type	cap_shape	cap_surface	cap_color	bruises	odor	gill_attachment	gill_spacing	gill_siz
0	1	5	2	4	1	6	1	0	
1	0	5	2	9	1	0	1	0	
2	0	0	2	8	1	3	1	0	
3	1	5	3	8	1	6	1	0	
4	0	5	2	3	0	5	1	1	

5 rows × 22 columns

Since the outcome has only two variable we will use binary classification model.

In [20]:
```
# Now split data in dependent and independent variables
x=data.iloc[:,1:]
y=data.iloc[:,-22]
```

In [21]:
```
x.shape
```

Out[21]:
```
(8124, 21)
```

In [22]:
```
y.shape
```

Out[22]:
```
(8124,)
```

In [23]:
```
y.head(10)
```

Out[23]:
```
0    1
1    0
2    0
3    1
4    0
5    0
6    0
7    0
8    1
9    0
Name: type, dtype: int32
```

In [24]:
```
from sklearn.model_selection import train_test_split

from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.tree import DecisionTreeClassifier
from sklearn.svm import SVC
lr=LogisticRegression()
from sklearn.metrics import accuracy_score, confusion_matrix, classification_r
```

Here we have imported all required training models, we check the best fit model.

In [25]:
```
for i in range(0,1000):
    x_train, x_test, y_train, y_test= train_test_split(x,y,random_state= i,tes
    lr.fit(x_train,y_train)
    pred_train= lr.predict(x_train)
    pred_test= lr.predict(x_test)
    if round (accuracy_score(y_train,pred_train)*100,1)==round(accuracy_score(
        print("At Random state",i, "The model perform very well")
        print("At random State:",i)
        print("Training r2_score",accuracy_score(y_train,pred_train)*100)
        print("testing r2 score ",accuracy_score(y_test,pred_test)*100)
```

```
At Random state 10 The model perform very well
At random State: 10
Training r2_score 95.24542237267272
testing r2 score  95.19999999999999
At Random state 18 The model perform very well
At random State: 18
Training r2_score 95.30697030312356
testing r2 score  95.26153846153846
At Random state 28 The model perform very well
At random State: 28
Training r2_score 94.99923065086936
testing r2 score  95.01538461538462
At Random state 34 The model perform very well
At random State: 34
Training r2_score 95.33774426834898
testing r2 score  95.26153846153846
At Random state 36 The model perform very well
At random State: 36
Training r2_score 94.8915217725804
```

At random State: 210

Training r2_score 95.56854900753962

testing r2 score 95.56923076923077

At random state 210, we are get better r2 score.

In [26]:
```
x_train, x_test, y_train, y_test= train_test_split(x,y,random_state=210,test_s
```

In [27]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test,pred_test))
```

```
              precision    recall  f1-score   support

           0       0.52      0.53      0.53       844
           1       0.48      0.46      0.47       781

    accuracy                           0.50      1625
   macro avg       0.50      0.50      0.50      1625
weighted avg       0.50      0.50      0.50      1625
```

In [28]:
```
pred_lr = lr.predict(x_test)
from sklearn.model_selection import cross_val_score
lss=accuracy_score(y_test,pred_lr)
for j in range(2,10):
    lsscore= cross_val_score(lr,x,y,cv=j)
    lsc=lsscore.mean()
    print("at cv:-", j)
    print("Cross Validation scre is:-",lsc*100)
    print("Accuracy Score:-", lss*100)
    print("\n")
```

```
at cv:- 2
Cross Validation scre is:- 81.29000492368291
Accuracy Score:- 94.95384615384616


at cv:- 3
Cross Validation scre is:- 81.25307730182176
Accuracy Score:- 94.95384615384616


at cv:- 4
Cross Validation scre is:- 82.87789266371246
Accuracy Score:- 94.95384615384616


at cv:- 5
Cross Validation scre is:- 83.93488442591892
Accuracy Score:- 94.95384615384616


at cv:- 6
Cross Validation scre is:- 87.87543082225504
Accuracy Score:- 94.95384615384616


at cv:- 7
Cross Validation scre is:- 88.36851830636915
Accuracy Score:- 94.95384615384616


at cv:- 8
Cross Validation scre is:- 86.70541047670766
Accuracy Score:- 94.95384615384616


at cv:- 9
Cross Validation scre is:- 87.418672586001
Accuracy Score:- 94.95384615384616
```

at cv:- 3

Cross Validation scre is:- 81.12998522895126

Accuracy Score:- 95.19999999999999

In [29]:
```
lssscore_selected=cross_val_score(lr,x,y,cv=3).mean()
print("The cv score is: ", lssscore_selected,"\nThe accuracy score is: ", lss)
```

```
The cv score is:  0.8125307730182176
The accuracy score is:  0.9495384615384616
```

In [30]:
```
from sklearn.model_selection import train_test_split

from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.tree import DecisionTreeClassifier
from sklearn.svm import SVC
```

In [31]:
```
Model= [LogisticRegression(),RandomForestClassifier(),GaussianNB(),DecisionTre

for m in Model:
    m.fit(x_train,y_train)
    m.score(x_train,y_train)
    predm=m.predict(x_test)
    print('Accuracy score of', m, 'is:')
    print (accuracy_score(y_test,predm))
    print (confusion_matrix(y_test,predm))
    print (classification_report(y_test,predm))
    print('\n')
```

```
Accuracy score of LogisticRegression() is:
0.9556923076923077
[[804  40]
 [ 32 749]]
              precision    recall  f1-score   support

           0       0.96      0.95      0.96       844
           1       0.95      0.96      0.95       781

    accuracy                           0.96      1625
   macro avg       0.96      0.96      0.96      1625
weighted avg       0.96      0.96      0.96      1625



Accuracy score of RandomForestClassifier() is:
1.0
[[844   0]
 [  0 781]]
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       844
           1       1.00      1.00      1.00       781

    accuracy                           1.00      1625
   macro avg       1.00      1.00      1.00      1625
weighted avg       1.00      1.00      1.00      1625



Accuracy score of GaussianNB() is:
0.9243076923076923
[[774  70]
 [ 53 728]]
              precision    recall  f1-score   support

           0       0.94      0.92      0.93       844
           1       0.91      0.93      0.92       781

    accuracy                           0.92      1625
   macro avg       0.92      0.92      0.92      1625
weighted avg       0.92      0.92      0.92      1625



Accuracy score of DecisionTreeClassifier() is:
1.0
[[844   0]
 [  0 781]]
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       844
           1       1.00      1.00      1.00       781

    accuracy                           1.00      1625
   macro avg       1.00      1.00      1.00      1625
weighted avg       1.00      1.00      1.00      1625



Accuracy score of SVC() is:
0.9932307692307693
[[844   0]
 [ 11 770]]
              precision    recall  f1-score   support

           0       0.99      1.00      0.99       844
           1       1.00      0.99      0.99       781

    accuracy                           0.99      1625
   macro avg       0.99      0.99      0.99      1625
weighted avg       0.99      0.99      0.99      1625
```

acuracy score [0.9556923076923077, 1.0, 0.9243076923076923, 1.0, 0.9932307692307693]
RandomForestClassifier()=1.0

DecisionTreeClassifier() =1.0

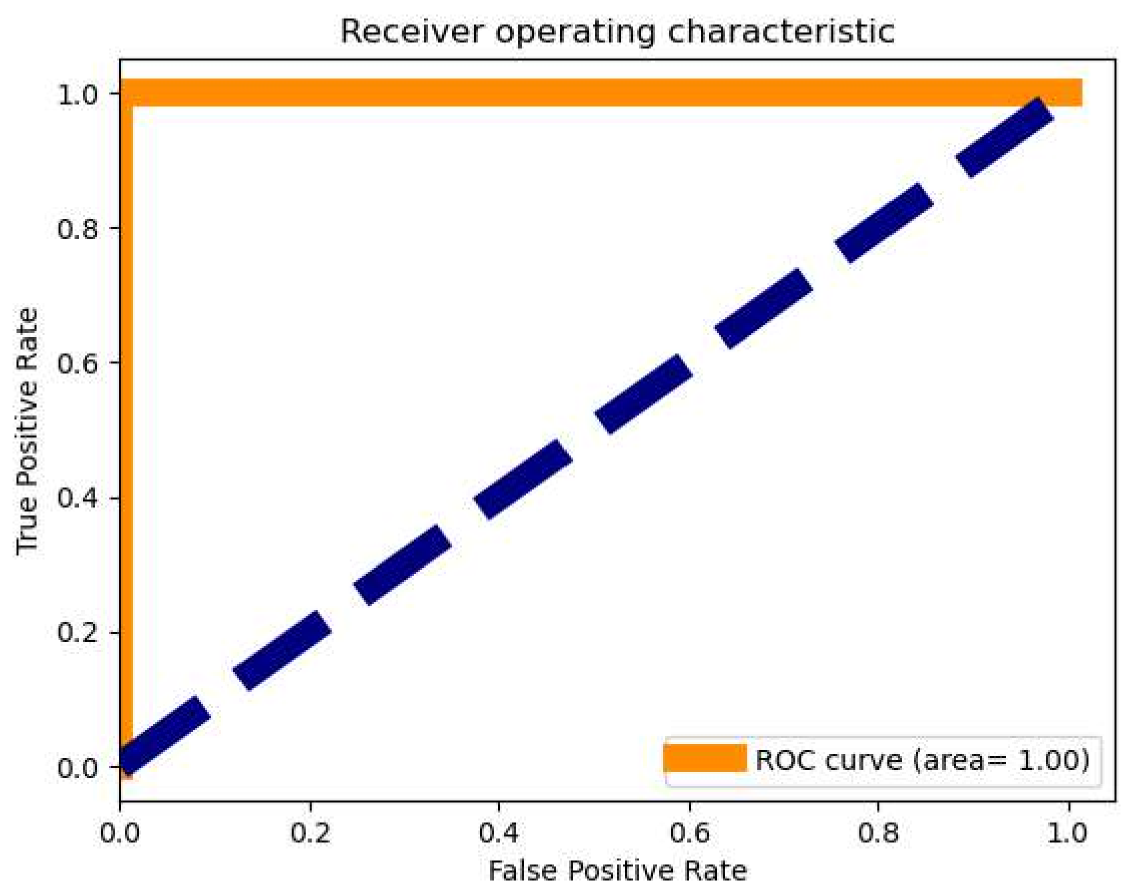
Here all the three performing well so we can save any one model.

In [37]:
```
dtc= DecisionTreeClassifier()
dtc.fit(x_train,y_train)
dtc.score(x_train,y_train)

dtcpred=dtc.predict(x_test)
print(accuracy_score(y_test,dtcpred ))
print(confusion_matrix(y_test,dtcpred ))
print(classification_report(y_test,dtcpred ))
```

```
1.0
[[844   0]
 [  0 781]]
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       844
           1       1.00      1.00      1.00       781

    accuracy                           1.00      1625
   macro avg       1.00      1.00      1.00      1625
weighted avg       1.00      1.00      1.00      1625
```

AUC ROC Curve:

In [38]:
```
from sklearn.metrics import roc_curve, auc
fpr, tpr, thresholds= roc_curve(dtcpred, y_test)
roc_auc= auc(fpr, tpr)

plt.figure()
plt.plot(fpr,tpr, color='darkorange', lw=10,label='ROC curve (area= %0.2f)' %r
plt.plot([0,1],[0,1],color ='navy', lw=10, linestyle= '--')
plt.xlim([0.0, 1.0])
plt.xlim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver operating characteristic')
plt.legend(loc="lower right")
plt.show()
```



Now Saving best Model

In [39]:
```
import pickle
filename='Mushroom_Pred.pkl'
pickle.dump(dtc,open(filename,'wb'))
```

Conclusion

In [40]:

```
import numpy as np
a=np.array(y_test)
predicted= np.array(dtc.predict(x_test))
df_com= pd.DataFrame({'original':a, 'predicted':predicted}, index= range(len(a
df_com
```

Out[40]:

	original	predicted
0	1	1
1	0	0
2	0	0
3	0	0
4	0	0
...	...	...
1620	0	0
1621	0	0
1622	0	0
1623	0	0
1624	0	0

1625 rows × 2 columns

In [ ]: