Yangzhou University

Software Data Analysis 2022

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Random Forest Classifier(Wine quality testing)

dataset link : https://archive.ics.uci.edu/ml/datasets/Wine+Quality

In [3]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

%matplotlib inline
```

In [4]:
```
df = pd.read_csv("winequality-red.csv",sep=";")
```

In [5]:
```
df
```

Out[5]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	9.4	5
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	9.8	5
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	9.8	5
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	9.8	6
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	9.4	5
...	...	...	...	...	...	...	...	...	...	...	...	...
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	10.5	5
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	11.2	6
1596	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	11.0	6
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	10.2	5
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	11.0	6

1599 rows × 12 columns

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

Out[6]:
```
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    0
density                 0
pH                      0
sulphates               0
alcohol                 0
quality                 0
dtype: int64
```

In [7]:
```
df.duplicated().sum()
```

Out[7]:
```
240
```

In [8]:
```
df = df.drop_duplicates()
```

In [9]:
```
df
```

Out[9]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	9.4	5
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	9.8	5
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	9.8	5
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	9.8	6
5	7.4	0.660	0.00	1.8	0.075	13.0	40.0	0.99780	3.51	0.56	9.4	5
...	...	...	...	...	...	...	...	...	...	...	...	...
1593	6.8	0.620	0.08	1.9	0.068	28.0	38.0	0.99651	3.42	0.82	9.5	6
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	10.5	5
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	11.2	6
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	10.2	5
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	11.0	6

1359 rows × 12 columns

In [10]:
```
df['quality'].value_counts()
```

Out[10]:
```
5    577
6    535
7    167
4     53
8     17
3     10
Name: quality, dtype: int64
```

In [11]:
```
df.columns
```

Out[11]:
```
Index(['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar',
       'chlorides', 'free sulfur dioxide', 'total sulfur dioxide', 'density',
       'pH', 'sulphates', 'alcohol', 'quality'],
      dtype='object')
```

In [12]:
```
df["quality"].unique()
```

Out[12]:
```
array([5, 6, 7, 4, 8, 3], dtype=int64)
```

In [13]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 1359 entries, 0 to 1598
Data columns (total 12 columns):
 #   Column                Non-Null Count  Dtype  
---  ------                --------------  -----  
 0   fixed acidity         1359 non-null   float64
 1   volatile acidity      1359 non-null   float64
 2   citric acid           1359 non-null   float64
 3   residual sugar        1359 non-null   float64
 4   chlorides             1359 non-null   float64
 5   free sulfur dioxide   1359 non-null   float64
 6   total sulfur dioxide  1359 non-null   float64
 7   density               1359 non-null   float64
 8   pH                    1359 non-null   float64
 9   sulphates             1359 non-null   float64
 10  alcohol               1359 non-null   float64
 11  quality               1359 non-null   int64  
dtypes: float64(11), int64(1)
memory usage: 138.0 KB
```

In [14]:
```
df.describe()
```

Out[14]:

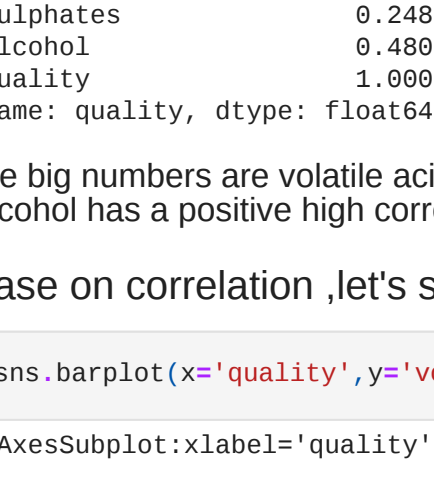
	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
count	1359.000000	1359.000000	1359.000000	1359.000000	1359.000000	1359.000000	1359.000000	1359.000000	1359.000000	1359.000000	1359.000000	1359.000000
mean	8.310596	0.529478	0.272333	2.523400	0.088124	15.893304	46.825975	0.996709	3.309787	0.658705	10.432315	5.623252
std	1.736990	0.183031	0.195537	1.352314	0.049377	10.447270	33.408946	0.001869	0.155036	0.170667	1.082065	0.823578
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.990070	2.740000	0.330000	8.400000	3.000000
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.995600	3.210000	0.550000	9.500000	5.000000
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.996700	3.310000	0.620000	10.200000	6.000000
75%	9.200000	0.640000	0.430000	2.600000	0.091000	21.000000	63.000000	0.997820	3.400000	0.730000	11.100000	6.000000
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1.003690	4.010000	2.000000	14.900000	8.000000

so this is a normal distribution as 3 and 8 have less values ans 5,6, 7 are values for middel

In [15]:
```
quality_values=df.quality.value_counts().index
quality_count=df.quality.value_counts().values

plt.pie(quality_count,labels=quality_values)
```

Out[15]:
```
([<matplotlib.patches.Wedge at 0x2799ead14c0>,
  <matplotlib.patches.Wedge at 0x2799ead19a0>,
  <matplotlib.patches.Wedge at 0x2799ead1d60>,
  <matplotlib.patches.Wedge at 0x2799eae9280>,
  <matplotlib.patches.Wedge at 0x2799eae9760>,
  <matplotlib.patches.Wedge at 0x2799eae9c40>],
 [Text(0.25821137483255596, 1.0692646472726393, '5'),
  Text(-0.7951496098451692, -0.7600901906767876, '6'),
  Text(0.800401816489204, -0.754557441259963, '7'),
  Text(1.0665207655922797, -0.26932036046399827, '4'),
  Text(1.095978743575482, -0.09397123831634843, '8'),
  Text(1.0997060979325133, -0.0254263282847884, '3')])
```



In [16]:
```
df.corr().quality
```

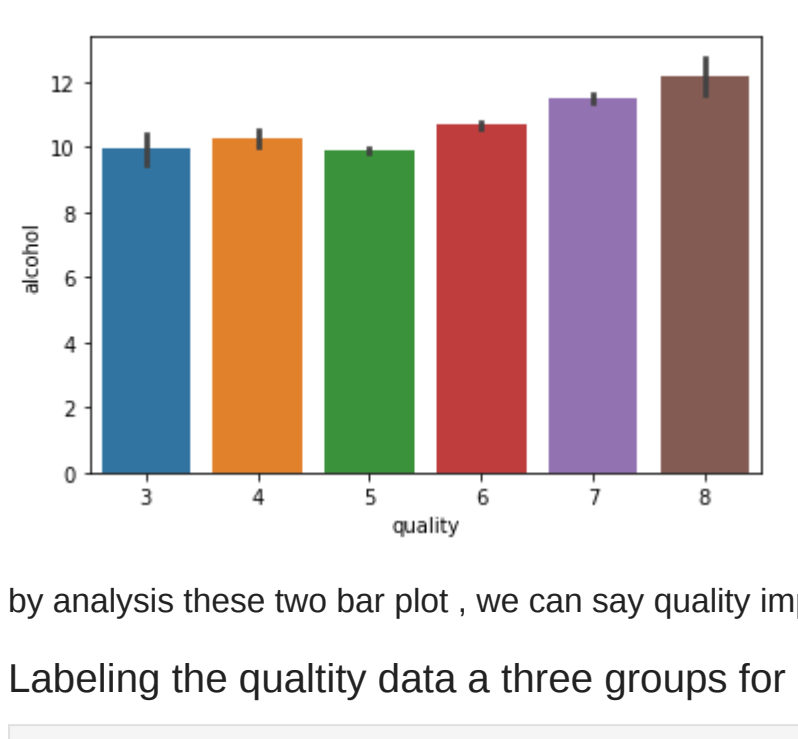
Out[16]:
```
fixed acidity           0.119024
volatile acidity       -0.395214
citric acid             0.228057
residual sugar          0.013640
chlorides              -0.130988
free sulfur dioxide    -0.050463
total sulfur dioxide   -0.177855
density                -0.184252
pH                     -0.055245
sulphates               0.248835
alcohol                 0.480343
quality                 1.000000
Name: quality, dtype: float64
```

the big numbers are volatile acidity (-0.395214), alcohol(0.480343) and quality is the Y means target here. so , volatile acidity has a negative high correlation and alcohol has a positive high correlation.

base on correlation ,let's see the behaviour with quality among alchohol and volatile acidity

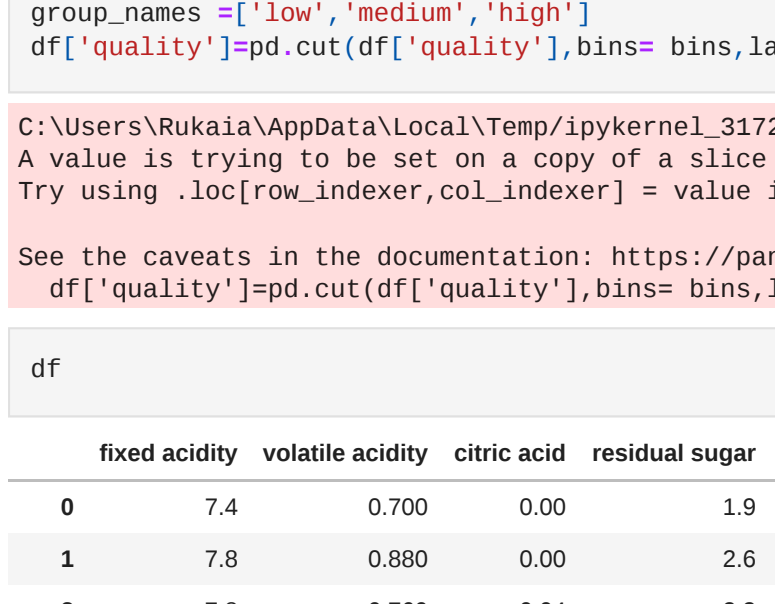
In [17]:
```
sns.barplot(x='quality',y='volatile acidity',data=df)
```

Out[17]:
```
<AxesSubplot:xlabel='quality', ylabel='volatile acidity'>
```



In [18]:
```
sns.barplot(x='quality',y='alcohol',data=df)
```

Out[18]:
```
<AxesSubplot:xlabel='quality', ylabel='alcohol'>
```



by analysis these two bar plot , we can say quality improves with the rising amount of alcohol and decreases with the increase of volatile aciidity

Labeling the qualtity data a three groups for improvement of our machine learning model

In [19]:
```
from sklearn.preprocessing import LabelEncoder
```

In [20]:
```
bins=(2,4,6,8)
group_names =['low','medium','high']
df['quality']=pd.cut(df['quality'],bins= bins,labels= group_names)
```

```
C:\Users\Rukaia\AppData\Local\Temp/ipykernel_3172/3421135216.py:3: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  df['quality']=pd.cut(df['quality'],bins= bins,labels= group_names)
```

In [21]:
```
df
```

Out[21]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	9.4	medium
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	9.8	medium
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	9.8	medium
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	9.8	medium
5	7.4	0.660	0.00	1.8	0.075	13.0	40.0	0.99780	3.51	0.56	9.4	medium
...	...	...	...	...	...	...	...	...	...	...	...	...
1593	6.8	0.620	0.08	1.9	0.068	28.0	38.0	0.99651	3.42	0.82	9.5	medium
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	10.5	medium
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	11.2	medium
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	10.2	medium
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	11.0	medium

1359 rows × 12 columns

In [22]:
```
label_encoder = LabelEncoder()
label_encoder
```

Out[22]:
```
▾ LabelEncoder
LabelEncoder()
```

In [23]:
```
df["quality"]= label_encoder.fit_transform(df["quality"])
```

```
C:\Users\Rukaia\AppData\Local\Temp/ipykernel_3172/3683477494.py:1: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  df["quality"]= label_encoder.fit_transform(df["quality"])
```

In [24]:
```
df
```

Out[24]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	9.4	2
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	9.8	2
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	9.8	2
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	9.8	2
5	7.4	0.660	0.00	1.8	0.075	13.0	40.0	0.99780	3.51	0.56	9.4	2
...	...	...	...	...	...	...	...	...	...	...	...	...
1593	6.8	0.620	0.08	1.9	0.068	28.0	38.0	0.99651	3.42	0.82	9.5	2
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	10.5	2
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	11.2	2
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	10.2	2
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	11.0	2

1359 rows × 12 columns

In [25]:
```
df["quality"].value_counts()
```

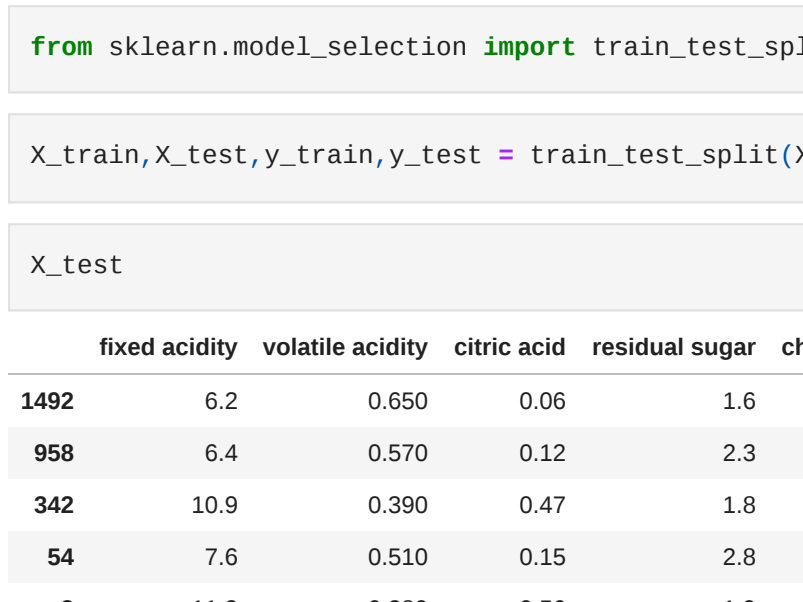
Out[25]:
```
2    1112
0     184
1      63
Name: quality, dtype: int64
```

2 is for medium, 1 is for low and 0 is for high

In [26]:
```
sns.countplot(df["quality"])
```

```
C:\Users\Rukaia\AppData\Local\Programs\Python\Python39\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following variable as a keyword ar
g: x. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or
misinterpretation.
  warnings.warn(
```

Out[26]:
```
<AxesSubplot:xlabel='quality', ylabel='count'>
```



spliting the dataset , X as independent features and y dependent feature

In [27]:
```
X= df.iloc[:,:-1]
### X =df.drop(df["quality"])
y = df["quality"]
```

spliting the data set into test and train to fit into a ML model

In [28]:
```
from sklearn.model_selection import train_test_split
```

In [29]:
```
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.2)
```

In [30]:
```
X_test
```

Out[30]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol
1492	6.2	0.650	0.06	1.6	0.050	6.0	18.0	0.99348	3.57	0.54	11.95
958	6.4	0.570	0.12	2.3	0.120	25.0	36.0	0.99519	3.47	0.71	11.30
342	10.9	0.390	0.47	1.8	0.118	6.0	14.0	0.99820	3.30	0.75	9.80
54	7.6	0.510	0.15	2.8	0.110	33.0	73.0	0.99550	3.17	0.63	10.20
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	9.80
...	...	...	...	...	...	...	...	...	...	...	...
1000	7.5	0.430	0.30	2.2	0.062	6.0	12.0	0.99495	3.44	0.72	11.50
255	8.0	0.570	0.23	3.2	0.073	17.0	119.0	0.99675	3.26	0.57	9.30
1445	7.4	0.785	0.19	5.2	0.094	19.0	98.0	0.99713	3.16	0.52	9.60
1454	11.7	0.450	0.63	2.2	0.073	7.0	23.0	0.99974	3.21	0.69	10.90
889	10.7	0.900	0.34	6.6	0.112	23.0	99.0	1.00289	3.22	0.68	9.30

272 rows × 11 columns

scaling the data

for useing machine learnign model ,we need to normalize the data, here scale() is used to standardized

before scalling we should split the dataset

In [31]:
```
from sklearn.preprocessing import scale
```

In [32]:
```
X_train=scale(X_train)
X_test=scale(X_test)
```

Implementing Random forest classifier

In [33]:
```
from sklearn.ensemble import RandomForestClassifier
```

In [34]:
```
rfc= RandomForestClassifier(n_estimators=200)
```

In [35]:
```
rfc.fit(X_train,y_train)
```

Out[35]:
```
▾ RandomForestClassifier
RandomForestClassifier(n_estimators=200)
```

In [36]:
```
pred_rfc=rfc.predict(X_test)
```

Checking the accurecy by Classification report and confusion matrix

In [37]:
```
from sklearn.metrics import classification_report
```

In [38]:
```
from sklearn.metrics import confusion_matrix
```

In [39]:
```
classification_report(y_test,pred_rfc)
```

```
C:\Users\Rukaia\AppData\Local\Programs\Python\Python39\lib\site-packages\sklearn\metrics\_classification.py:1327: UndefinedMetricWarning: Precision and F-scor
e are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\Rukaia\AppData\Local\Programs\Python\Python39\lib\site-packages\sklearn\metrics\_classification.py:1327: UndefinedMetricWarning: Precision and F-scor
e are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\Rukaia\AppData\Local\Programs\Python\Python39\lib\site-packages\sklearn\metrics\_classification.py:1327: UndefinedMetricWarning: Precision and F-scor
e are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

Out[39]:
```
'              precision    recall  f1-score   support\n\n           0       0.25      0.18      0.21        28\n           1       0.00      0.00      0.00
15\n           2       0.85      0.93      0.89       229\n\n    accuracy                           0.81       272\n   macro avg       0.37      0.37      0.3
7       272\nweighted avg       0.74      0.81      0.77       272\n'
```

In [40]:
```
confusion_matrix(y_test,pred_rfc)
```

Out[40]:
```
array([[  5,   0,  23],
       [  0,   0,  15],
       [ 15,   0, 214]], dtype=int64)
```

Model report

By the confusion matrix, the accurate values are shaped in diagonally. so among the 28 values for 0 means medium quality wine our model predicted 5 samples correctly,with 17% accuracy. The 15 values for 1 means low quality wine our model predicted 15 samples correctly,with 100% accuracy.The 229 values for 2 means high quality wine our model predicted 214 samples correctly,with 93.44% accuracy

In [ ]: