PREDICTION AND ANALYSIS OF LIVER PATIENT DATA USING IBM MACHINE LEARNING SERVICE

1. INTRODUCTION

1.1 Overview

Liver diseases averts the normal function of the liver. Mainly due to the large amount of alcohol consumption liver disease arises. Early prediction of liver disease using classification algorithms is an efficacious task that can help the doctors to diagnose the disease within a short duration of time. Discovering the existence of liver disease at an early stage is a complex task for the doctors. The main objective of this project is to analyse the parameters of various classification algorithms and compare their predictive accuracies so as to find out the best classifier for determining the liver disease.

1.2 Purpose

The main objective of this project is to analyse the parameters of various classification algorithms and compare their predictive accuracies so as to find out the best classifier for determining the liver disease.

This Project examines data from liver patients concentrating on relationships between a key list of liver enzymes, proteins, age and gender using them to try and predict the likeliness of liver disease. Here we are building a model by applying various machine learning algorithms find the best accurate model. And integrate to flask based web application. User can predict the disease by entering parameters in the web application.

2. LITERATURE SURVEY

2.1 Existing problem

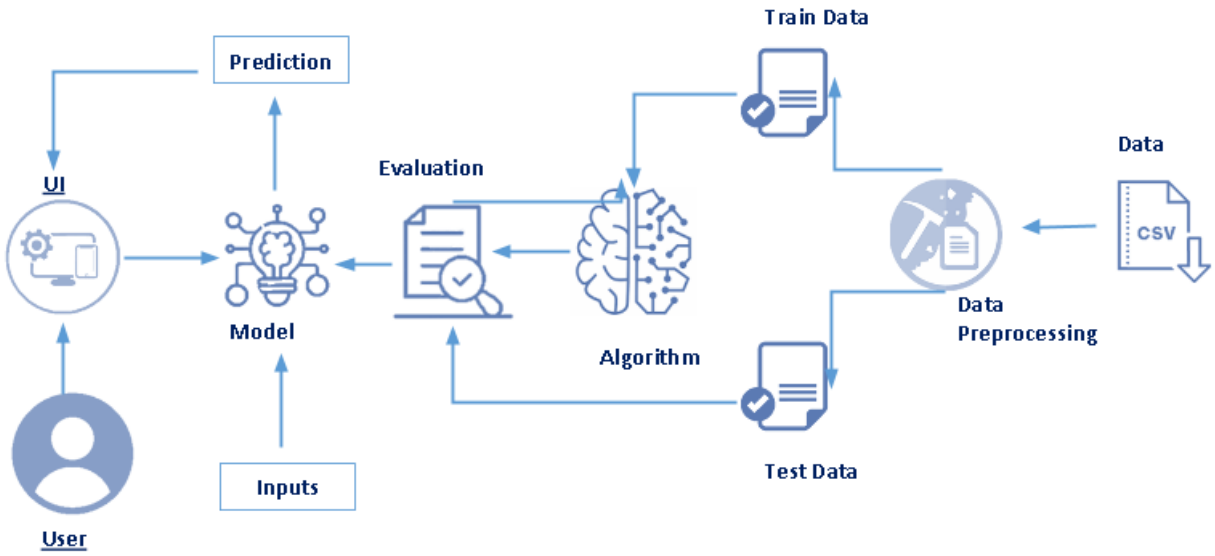
Liver diseases averts the normal function of the liver. Mainly due to the large amount of alcohol consumption liver disease arises. Early prediction of liver disease using classification algorithms is an efficacious task that can help the doctors to diagnose the disease within a short duration of time. Discovering the existence of liver disease at an early stage is a complex task for the doctors.

2.2 Proposed solution

This project treats an evaluation of the analyzed results of classification algorithms selected for better prediction based on the characteristics of data from the data set with liver disease. This Project examines data from liver patients concentrating on relationships between a key list of liver enzymes, proteins, age and gender using them to try and predict the likeliness of liver disease.

3. THEORITICAL ANALYSIS

3.1 Block Diagram



3.2 Hardware / Software designing

Software Requirements

- Anaconda Navigator
- Keras
- Flask

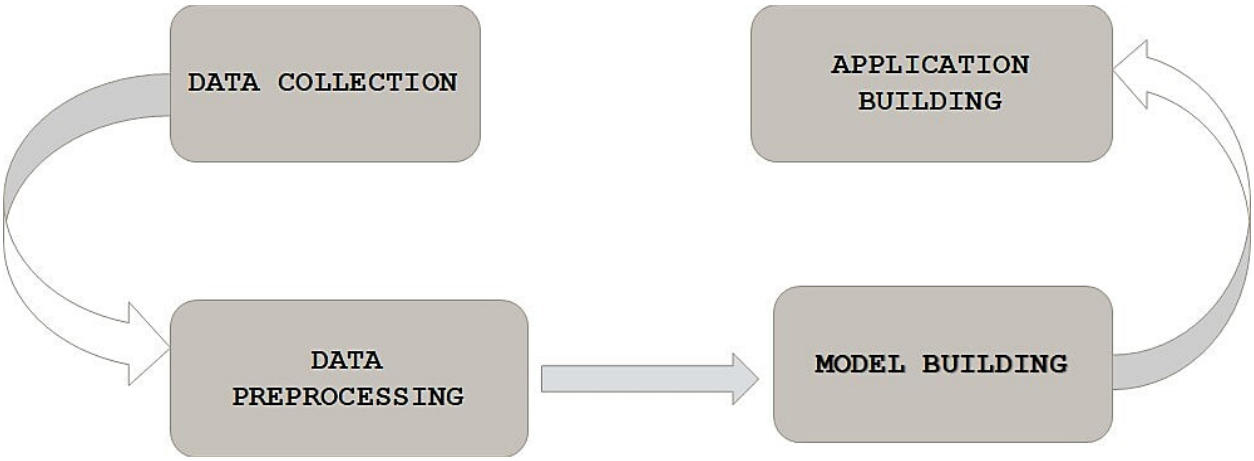
Hardware Requirements

- Processor : Intel Core i3
- Hard Disk Space : Min 100 GB
- Ram : 8 GB

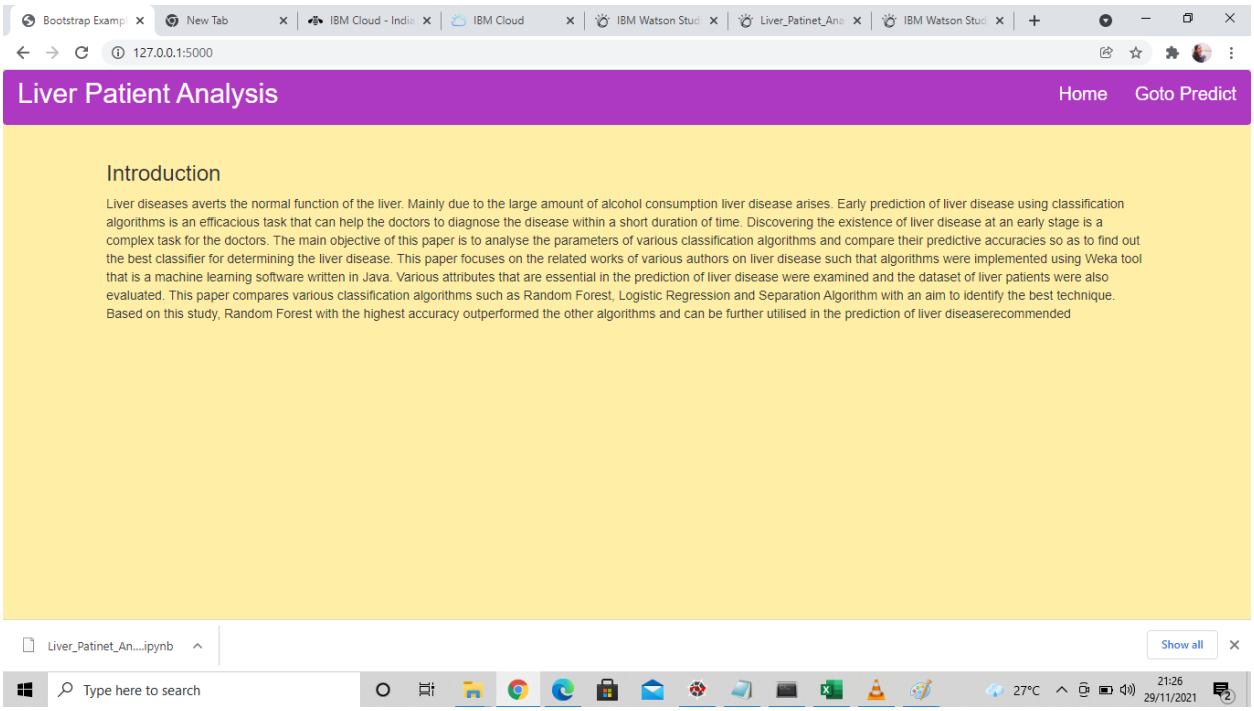
4. EXPERIMENTAL INVESTIGATIONS

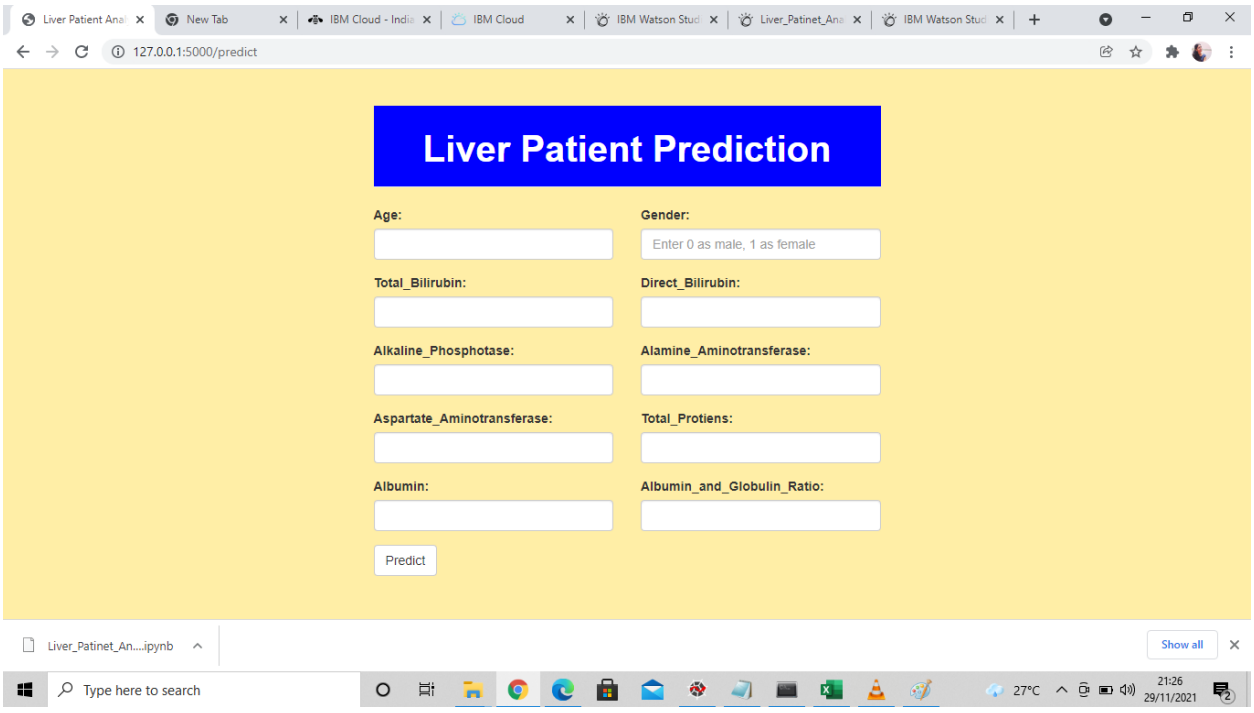
Liver diseases averts the normal function of the liver. Mainly due to the large amount of alcohol consumption liver disease arises. Early prediction of liver disease using classification algorithms is an efficacious task that can help the doctors to diagnose the disease within a short duration of time. Discovering the existence of liver disease at an early stage is a complex task for the doctors. The main objective of this paper is to analyse the parameters of various classification algorithms and compare their predictive accuracies so as to find out the best classifier for determining the liver disease. This paper focuses on the related works of various authors on liver disease such that algorithms were implemented using Weka tool that is a machine learning software written in Java. Various attributes that are essential in the prediction of liver disease were examined and the dataset of liver patients were also evaluated. This paper compares various classification algorithms such as Random Forest, Logistic Regression and Separation Algorithm with an aim to identify the best technique. Based on this study, Random Forest with the highest accuracy outperformed the other algorithms and can be further utilised in the prediction of liver disease.

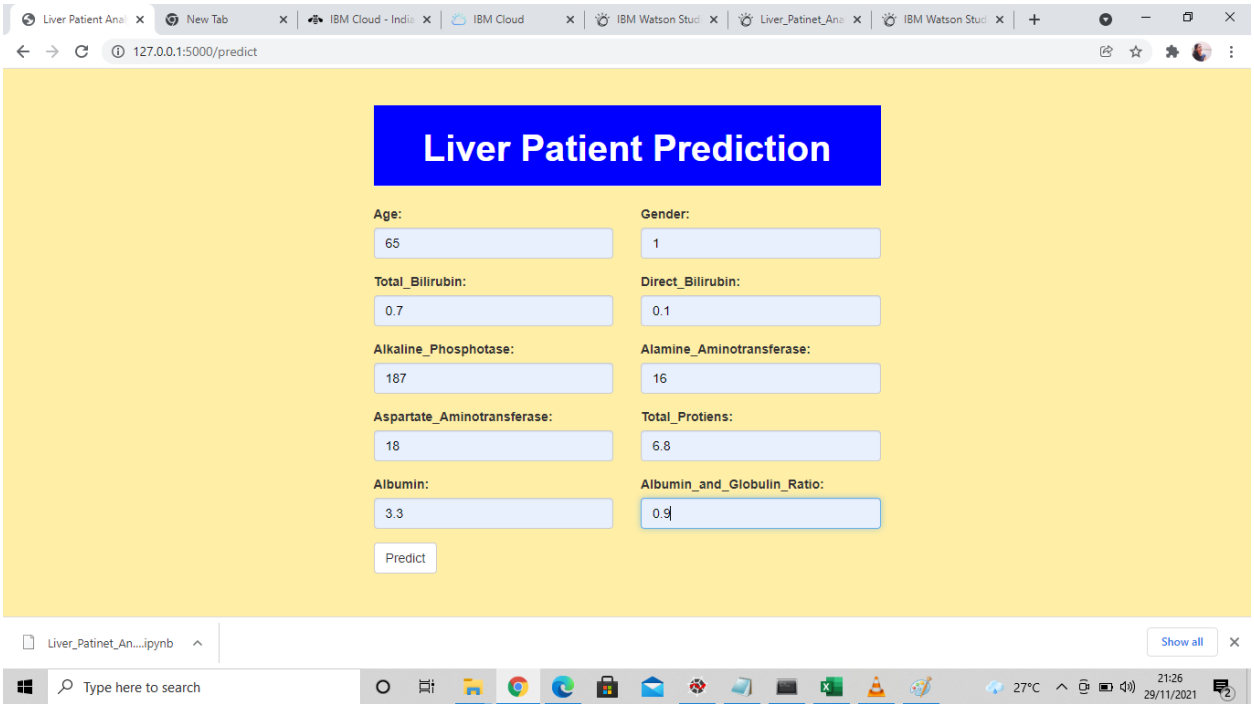
5. FLOWCHART

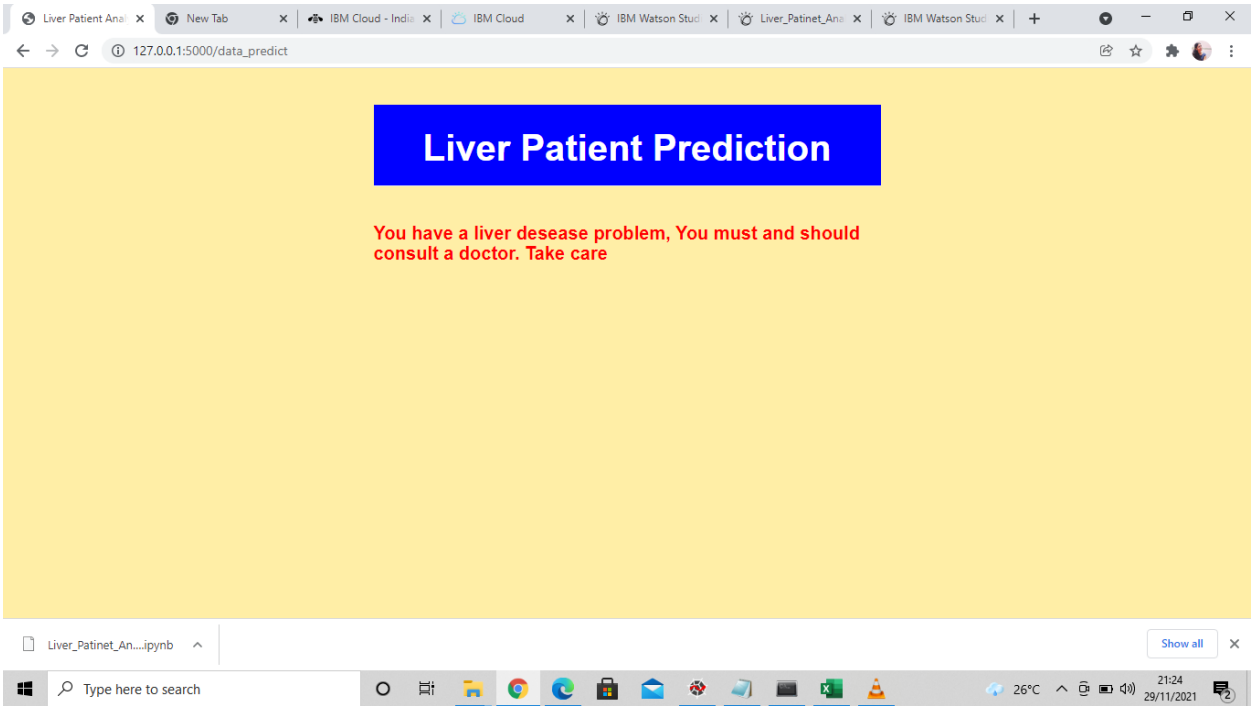


6. RESULT




Liver Patient Prediction
Age:
Gender:
Enter 0 as male, 1 as female
Total_Bilirubin:
Direct_Bilirubin:
Alkaline_Phosphotase:
Alamine_Aminotransferase:
Aspartate_Aminotransferase:
Total_Protiens:
Albumin:
Albumin_and_Globulin_Ratio:
Predict


Liver Patient Prediction
Age:
65
Gender:
1
Total_Bilirubin:
0.7
Direct_Bilirubin:
0.1
Alkaline_Phosphotase:
187
Alamine_Aminotransferase:
16
Aspartate_Aminotransferase:
18
Total_Protiens:
6.8
Albumin:
3.3
Albumin_and_Globulin_Ratio:
0.9
Predict


Liver Patient Ana
New Tab
IBM Cloud - India
IBM Cloud
IBM Watson Stud
Liver_Patinet_Ana
IBM Watson Stud
127.0.0.1:5000/data_predict
Liver Patient Prediction
You have a liver desease problem, You must and should consult a doctor. Take care
Liver_Patinet_An....ipynb
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7. ADVANTAGES & DISADVANTAGES

Advantages

This project helps in earlier prediction. Liver diseases averts the normal function of the liver. Mainly due to the large amount of alcohol consumption liver disease arises. Early prediction of liver disease using classification algorithms is an efficacious task that can help the doctors to diagnose the disease within a short duration of time.

Disadvantages

Discovering the existence of liver disease at an early stage is a complex task for the doctors. So realisation of the people who want check by this softwere important task.

8. APPLICATIONS

- Early prediction of liver disease using classification algorithms is an efficacious task that can help the doctors to diagnose the disease within a short duration of time.
- This Project focuses on the related works of various authors on liver disease such that algorithms were implemented using Weka tool that is a machine learning software written in Java.
- This paper compares various classification algorithms such as Random Forest, Logistic Regression and Separation Algorithm with an aim to identify the best technique.

9. CONCLUSION

The project conclude that earlier prediction for the disease. The main objective of this project is to analyse the parameters of various classification algorithms and compare their predictive accuracies so as to find out the best classifier for determining the liver disease.This Project examines data from liver patients concentrating on relationships between a key list of liver enzymes, proteins, age and gender using them to try and predict the likeliness of liver disease. Here we are building a model by applying various machine learning algorithms find the best accurate model. And integrate to flask based web application. User can predict the disease by entering parameters in the web application.

10. FUTURE SCOPE

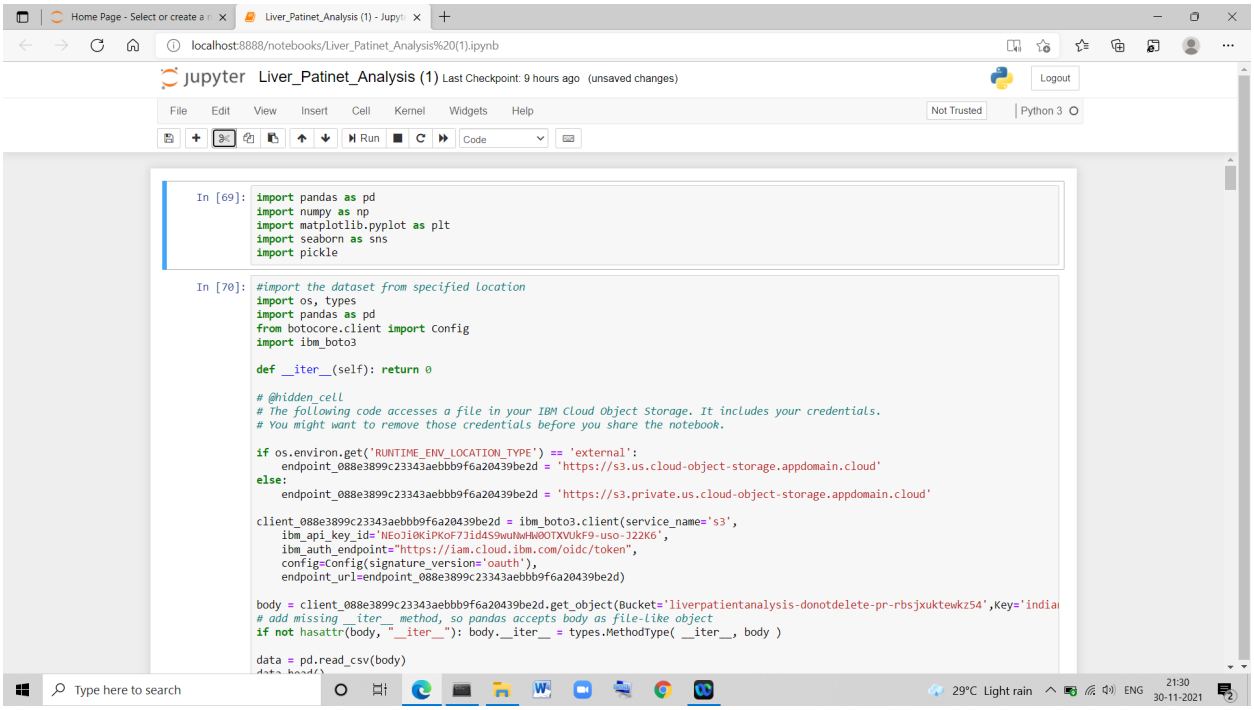
In future, our attempt would be to further improve the predictions using the system with more features. Imparting more features like location, availability of better hospitals and better doctors for the disease.

11. BIBILOGRAPHY

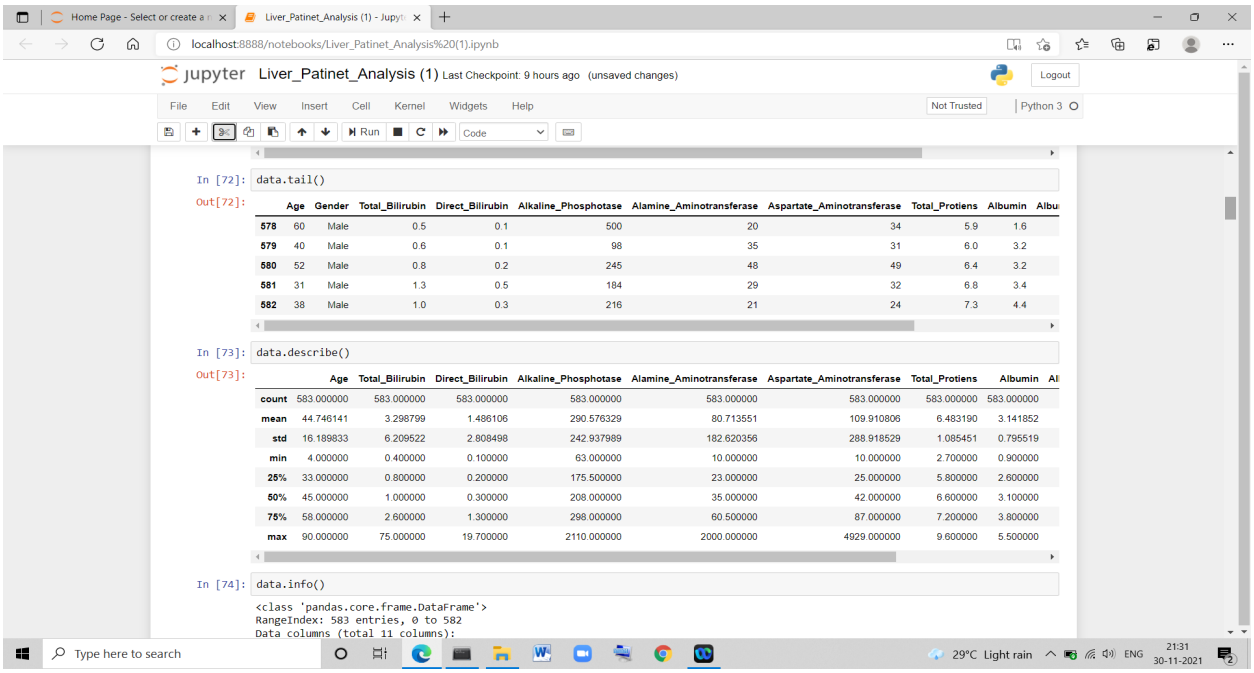
- https://www.kaggle.com//liver_patient
- https://keras.io/api
- https://victorzhou.com/blog/intro-to-cnns-part-1

APPENDIX

Source Code



```
In [69]:
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import pickle

In [70]:
#import the dataset from specified location
import os, types
import pandas as pd
from botocore.client import Config
import ibm_boto3

def __iter__(self): return 0

# @hidden_cell
# The following code accesses a file in your IBM Cloud Object Storage. It includes your credentials.
# You might want to remove those credentials before you share the notebook.

if os.environ.get('RUNTIME_ENV_LOCATION_TYPE') == 'external':
    endpoint_088e3899c23343aebbb9f6a20439be2d = 'https://s3.us.cloud-object-storage.appdomain.cloud'
else:
    endpoint_088e3899c23343aebbb9f6a20439be2d = 'https://s3.private.us.cloud-object-storage.appdomain.cloud'

client_088e3899c23343aebbb9f6a20439be2d = ibm_boto3.client(service_name='s3',
    ibm_api_key_id='NEoJi0KiPKoF7Jid4S9wuNWHW0OTXVUkF9-uso-J22K6',
    ibm_auth_endpoint="https://iam.cloud.ibm.com/oidc/token",
    config=Config(signature_version='oauth'),
    endpoint_url=endpoint_088e3899c23343aebbb9f6a20439be2d)

body = client_088e3899c23343aebbb9f6a20439be2d.get_object(Bucket='liverpatientanalysis-donotdelete-pr-rbsjxuktewkz54',Key='indian
# add missing __iter__ method, so pandas accepts body as file-like object
if not hasattr(body, "__iter__"): body.__iter__ = types.MethodType( __iter__, body )

data = pd.read_csv(body)
```



```
In [72]:
data.tail()
```

Out[72]:

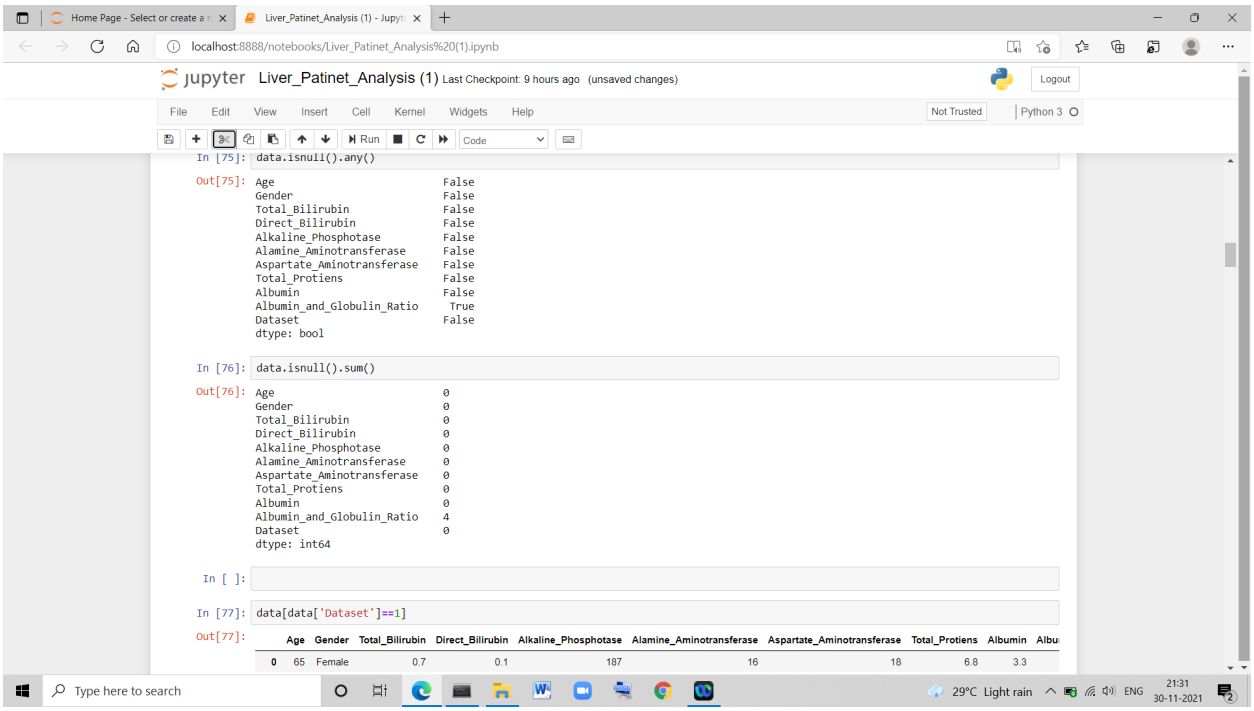
	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Albu
578	60	Male	0.5	0.1	500	20	34	5.9	1.6	
579	40	Male	0.6	0.1	98	35	31	6.0	3.2	
580	52	Male	0.8	0.2	245	48	49	6.4	3.2	
581	31	Male	1.3	0.5	184	29	32	6.8	3.4	
582	38	Male	1.0	0.3	216	21	24	7.3	4.4	

```
In [73]:
data.describe()
```

Out[73]:

	Age	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Al
count	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000	
mean	44.746141	3.298799	1.486106	290.576329	80.713551	109.910806	6.483190	3.141852	
std	16.189833	6.209522	2.808498	242.937989	182.620356	288.918529	1.085451	0.795519	
min	4.000000	0.400000	0.100000	63.000000	10.000000	10.000000	2.700000	0.900000	
25%	33.000000	0.800000	0.200000	175.500000	23.000000	25.000000	5.800000	2.600000	
50%	45.000000	1.000000	0.300000	208.000000	35.000000	42.000000	6.600000	3.100000	
75%	58.000000	2.600000	1.300000	298.000000	60.500000	87.000000	7.200000	3.800000	
max	90.000000	75.000000	19.700000	2110.000000	2000.000000	4929.000000	9.600000	5.500000	

```
In [74]:
data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 583 entries, 0 to 582
Data columns (total 11 columns):
```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Python 3
Run
Code
In [75]: data.isnull().any()
Out[75]:
Age False
Gender False
Total_Bilirubin False
Direct_Bilirubin False
Alkaline_Phosphotase False
Alamine_Aminotransferase False
Aspartate_Aminotransferase False
Total_Protiens False
Albumin False
Albumin_and_Globulin_Ratio True
Dataset False
dtype: bool
In [76]: data.isnull().sum()
Out[76]:
Age 0
Gender 0
Total_Bilirubin 0
Direct_Bilirubin 0
Alkaline_Phosphotase 0
Alamine_Aminotransferase 0
Aspartate_Aminotransferase 0
Total_Protiens 0
Albumin 0
Albumin_and_Globulin_Ratio 4
Dataset 0
dtype: int64
In [ ]:
In [77]: data[data['Dataset']==1]
Out[77]:
Age Gender Total_Bilirubin Direct_Bilirubin Alkaline_Phosphotase Alamine_Aminotransferase Aspartate_Aminotransferase Total_Protiens Albumin Albu
0 65 Female 0.7 0.1 187 16 18 6.8 3.3
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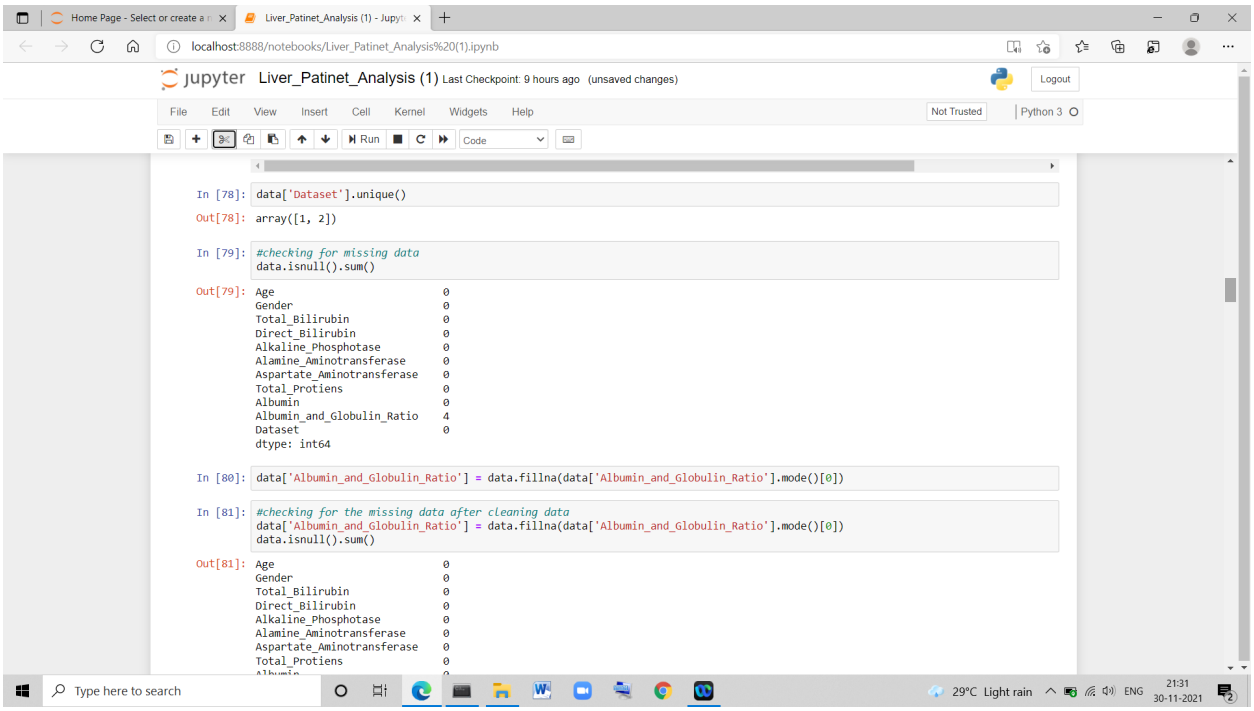
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Python 3
Run
Code
In [78]: data['Dataset'].unique()
Out[78]: array([1, 2])
In [79]:
#checking for missing data
data.isnull().sum()
Out[79]:
Age 0
Gender 0
Total_Bilirubin 0
Direct_Bilirubin 0
Alkaline_Phosphotase 0
Alamine_Aminotransferase 0
Aspartate_Aminotransferase 0
Total_Protiens 0
Albumin 0
Albumin_and_Globulin_Ratio 4
Dataset 0
dtype: int64
In [80]: data['Albumin_and_Globulin_Ratio'] = data.fillna(data['Albumin_and_Globulin_Ratio'].mode()[0])
In [81]:
#checking for the missing data after cleaning data
data['Albumin_and_Globulin_Ratio'] = data.fillna(data['Albumin_and_Globulin_Ratio'].mode()[0])
data.isnull().sum()
Out[81]:
Age 0
Gender 0
Total_Bilirubin 0
Direct_Bilirubin 0
Alkaline_Phosphotase 0
Alamine_Aminotransferase 0
Aspartate_Aminotransferase 0
Total_Protiens 0
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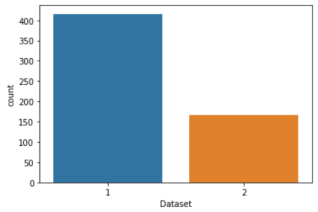
Run | Code

In [82]:
```
# Counting patients who are diagnosed and not diagnoised with liver disease
sns.countplot(data=data, x = 'Dataset')
LD,NLD=data['Dataset'].value_counts()
print("liver disease patinets:",LD)
print("Non-liver disease patinets:",NLD)
```

```
liver disease patinets: 416
Non-liver disease patinets: 167
```



In [83]:
```
# Counting patients who are Male and who are Female
sns.countplot(data=data, x = 'Gender', label='Count')
m,f=data['Gender'].value_counts()
print("No of Males:",m)
print("No of Females:",f)
```

```
No of Males: 441
No of Females: 142
```

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Run | Code

In [84]:
```
# Importing the LabelEncoder libraray from scikit-learn
from sklearn.preprocessing import LabelEncoder
le=LabelEncoder()
# Converting Textual data into numeric data
data['Gender'] = le.fit_transform(data['Gender'])
data.head()
```

Out[84]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Albumi
0	65	0	0.7	0.1	187	16	18	6.8	3.3	
1	62	1	10.9	5.5	699	64	100	7.5	3.2	
2	62	1	7.3	4.1	490	60	68	7.0	3.3	
3	58	1	1.0	0.4	182	14	20	6.8	3.4	
4	72	1	3.9	2.0	195	27	59	7.3	2.4	

In [85]:
```
#Converting Textual data into numeric data
data['Gender'] = le.fit_transform(data['Gender'])
```

In [86]:
```
data.head()
```

Out[86]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Albumi
0	65	0	0.7	0.1	187	16	18	6.8	3.3	
1	62	1	10.9	5.5	699	64	100	7.5	3.2	
2	62	1	7.3	4.1	490	60	68	7.0	3.3	
3	58	1	1.0	0.4	182	14	20	6.8	3.4	
4	72	1	3.9	2.0	195	27	59	7.3	2.4	

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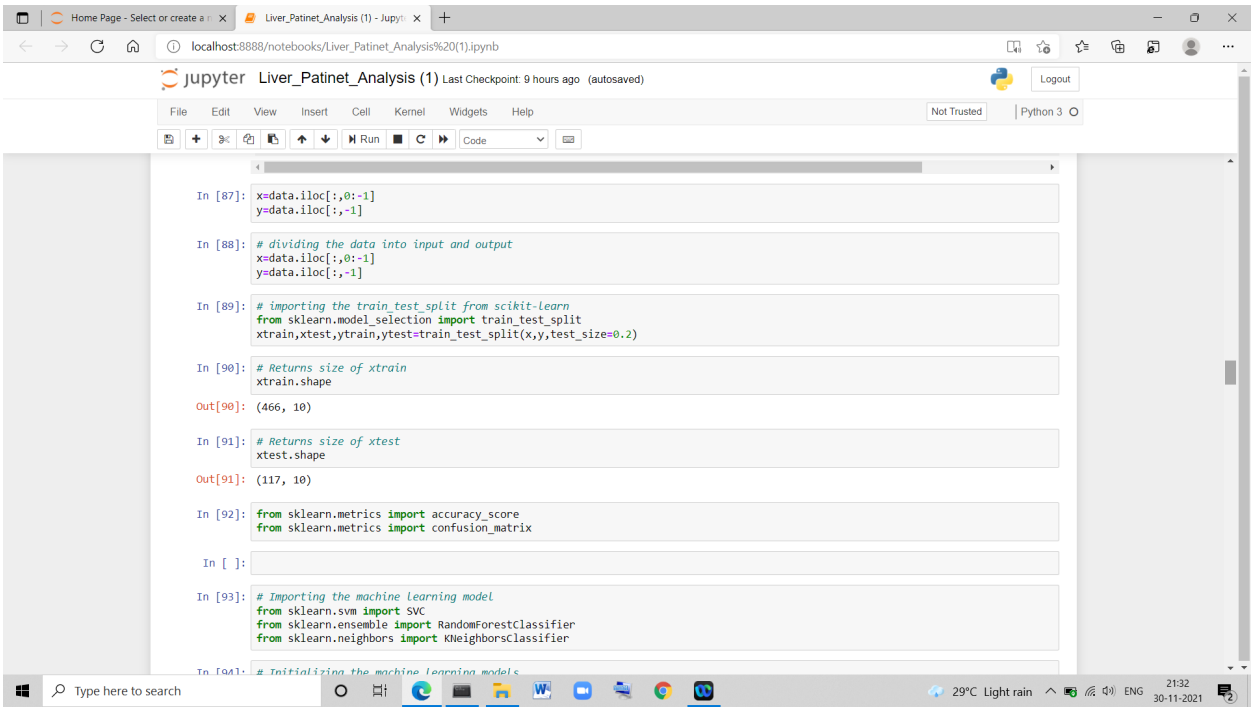
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Python 3
Run
Code
In [87]:
x=data.iloc[:,0:-1]
y=data.iloc[:,-1]
In [88]:
# dividing the data into input and output
x=data.iloc[:,0:-1]
y=data.iloc[:,-1]
In [89]:
# importing the train_test_split from scikit-learn
from sklearn.model_selection import train_test_split
xtrain,xtest,ytrain,ytest=train_test_split(x,y,test_size=0.2)
In [90]:
Returns size of xtrain
xtrain.shape
Out[90]:
(466, 10)
In [91]:
Returns size of xtest
xtest.shape
Out[91]:
(117, 10)
In [92]:
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix
In [ ]:
In [93]:
# Importing the machine learning model
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
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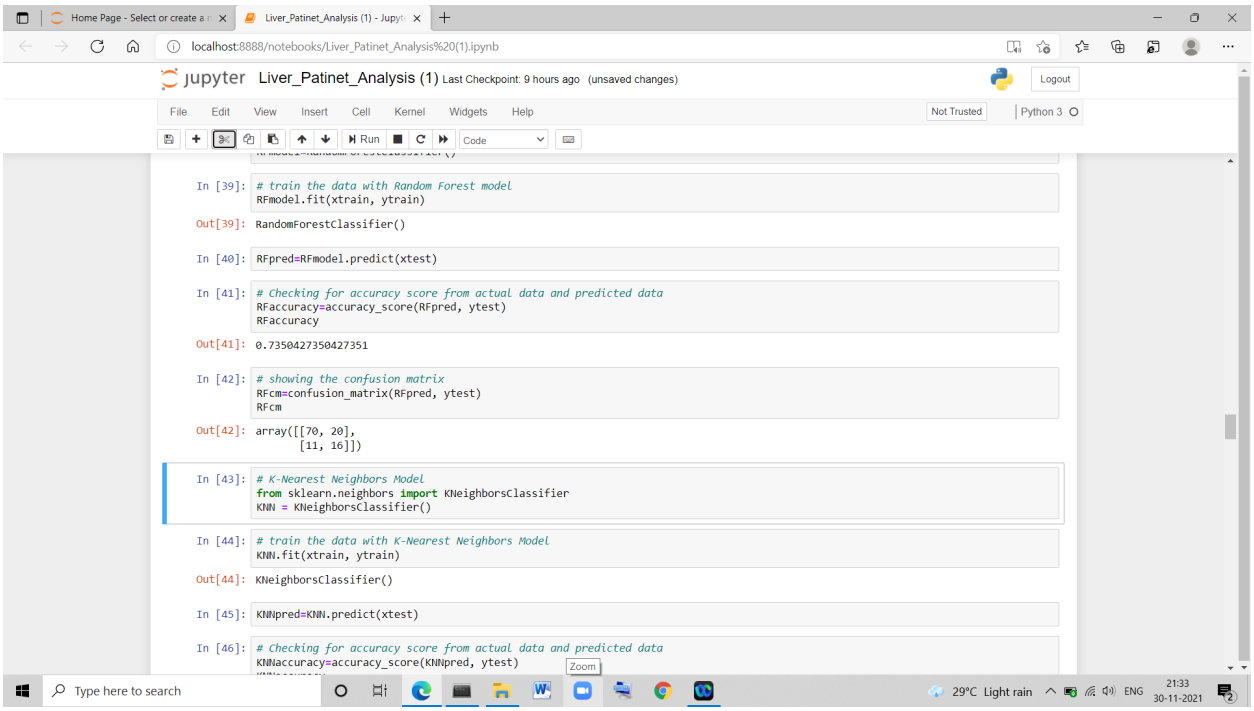
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Python 3
Run
Code
In [39]:
# train the data with Random Forest model
RFmodel.fit(xtrain, ytrain)
Out[39]:
RandomForestClassifier()
In [40]:
RFpred=RFmodel.predict(xtest)
In [41]:
# Checking for accuracy score from actual data and predicted data
RFaccuracy=accuracy_score(RFpred, ytest)
RFaccuracy
Out[41]:
0.7350427350427351
In [42]:
# showing the confusion matrix
RFcm=confusion_matrix(RFpred, ytest)
RFcm
Out[42]:
array([[70, 20],
[11, 16]])
In [43]:
# K-Nearest Neighbors Model
from sklearn.neighbors import KNeighborsClassifier
KNN = KNeighborsClassifier()
In [44]:
# train the data with K-Nearest Neighbors Model
KNN.fit(xtrain, ytrain)
Out[44]:
KNeighborsClassifier()
In [45]:
KNNpred=KNN.predict(xtest)
In [46]:
# Checking for accuracy score from actual data and predicted data
KNNaccuracy=accuracy_score(KNNpred, ytest)
Zoom
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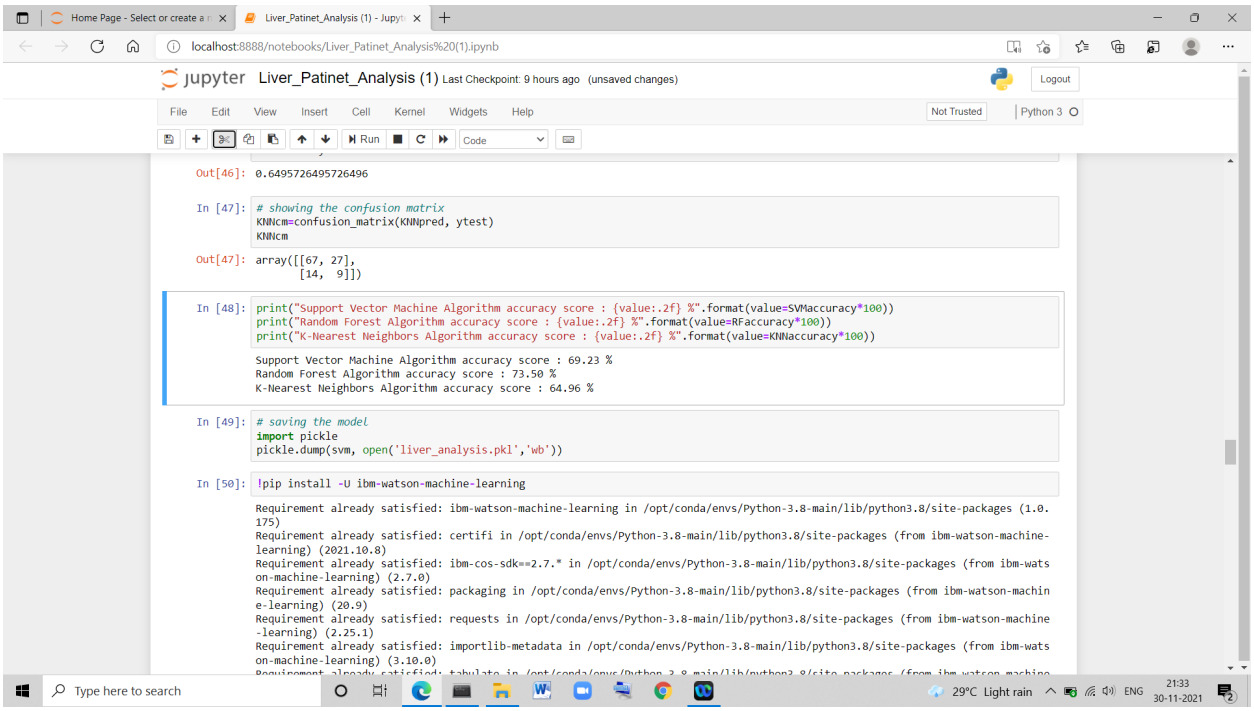

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Run Code

Out[46]: 0.6495726495726496

In [47]:
```
# showing the confusion matrix
KNNcm=confusion_matrix(KNNpred, ytest)
KNNcm
```

Out[47]:
```
array([[67, 27],
       [14,  9]])
```

In [48]:
```
print("Support Vector Machine Algorithm accuracy score : {value:.2f} %".format(value=SVMaccuracy*100))
print("Random Forest Algorithm accuracy score : {value:.2f} %".format(value=RFaccuracy*100))
print("K-Nearest Neighbors Algorithm accuracy score : {value:.2f} %".format(value=KNNaccuracy*100))
```

```
Support Vector Machine Algorithm accuracy score : 69.23 %
Random Forest Algorithm accuracy score : 73.50 %
K-Nearest Neighbors Algorithm accuracy score : 64.96 %
```

In [49]:
```
# saving the model
import pickle
pickle.dump(svm, open('liver_analysis.pkl','wb'))
```

In [50]:
```
!pip install -U ibm-watson-machine-learning
```

```
Requirement already satisfied: ibm-watson-machine-learning in /opt/conda/envs/Python-3.8-main/lib/python3.8/site-packages (1.0.175)
Requirement already satisfied: certifi in /opt/conda/envs/Python-3.8-main/lib/python3.8/site-packages (from ibm-watson-machine-learning) (2021.10.8)
Requirement already satisfied: ibm-cos-sdk==2.7.* in /opt/conda/envs/Python-3.8-main/lib/python3.8/site-packages (from ibm-watson-machine-learning) (2.7.0)
Requirement already satisfied: packaging in /opt/conda/envs/Python-3.8-main/lib/python3.8/site-packages (from ibm-watson-machine-learning) (20.9)
Requirement already satisfied: requests in /opt/conda/envs/Python-3.8-main/lib/python3.8/site-packages (from ibm-watson-machine-learning) (2.25.1)
Requirement already satisfied: importlib-metadata in /opt/conda/envs/Python-3.8-main/lib/python3.8/site-packages (from ibm-watson-machine-learning) (3.10.0)
```

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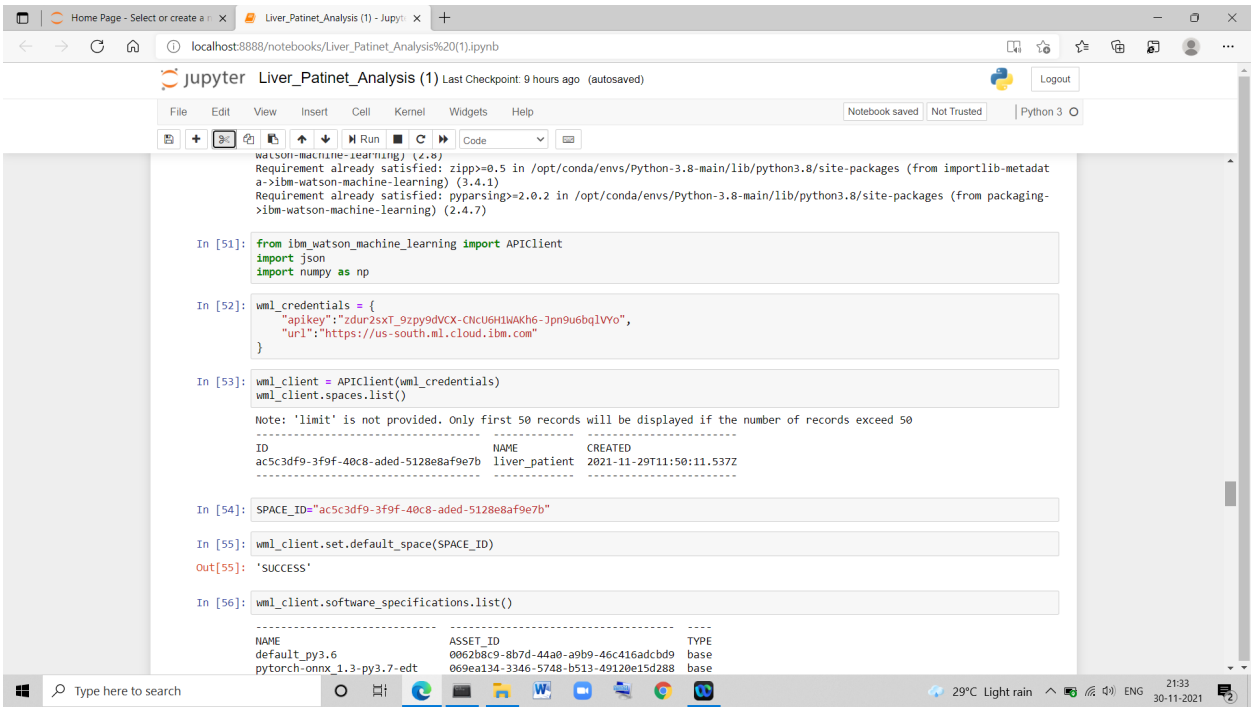

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```
Requirement already satisfied: zipp>=0.5 in /opt/conda/envs/Python-3.8-main/lib/python3.8/site-packages (from importlib-metadata->ibm-watson-machine-learning) (3.4.1)
Requirement already satisfied: pyparsing>=2.0.2 in /opt/conda/envs/Python-3.8-main/lib/python3.8/site-packages (from packaging->ibm-watson-machine-learning) (2.4.7)
```

In [51]:
```
from ibm_watson_machine_learning import APIClient
import json
import numpy as np
```

In [52]:
```
wml_credentials = {
    "apikey":"zdur2sxT_9zpy9dVCX-CNcU6H1WAKh6-Jpn9u6bqlVYo",
    "url":"https://us-south.ml.cloud.ibm.com"
}
```

In [53]:
```
wml_client = APIClient(wml_credentials)
wml_client.spaces.list()
```

```
Note: 'limit' is not provided. Only first 50 records will be displayed if the number of records exceed 50
------------------------------------  -------------  ------------------------
ID                                    NAME           CREATED
ac5c3df9-3f9f-40c8-aded-5128e8af9e7b  liver_patient  2021-11-29T11:50:11.537Z
------------------------------------  -------------  ------------------------
```

In [54]:
```
SPACE_ID="ac5c3df9-3f9f-40c8-aded-5128e8af9e7b"
```

In [55]:
```
wml_client.set.default_space(SPACE_ID)
```

Out[55]: 'SUCCESS'

In [56]:
```
wml_client.software_specifications.list()
```

```
------------------------------  ------------------------------------  ----
NAME                            ASSET_ID                              TYPE
default_py3.6                   0062b8c9-8b7d-44a0-a9b9-46c416adcbd9  base
pytorch-onnx_1.3-py3.7-edt      069ea134-3346-5748-b513-49120e15d288  base
```

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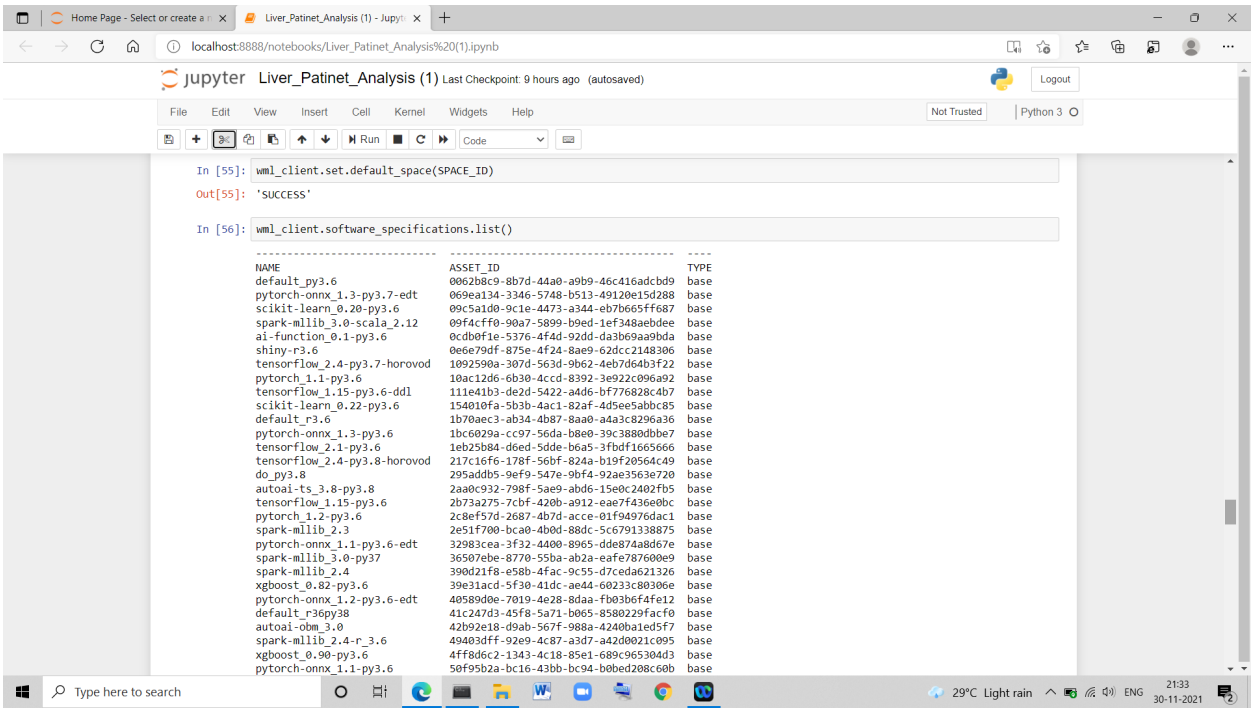

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In [55]:
```
wml_client.set.default_space(SPACE_ID)
```

Out[55]:
```
'SUCCESS'
```

In [56]:
```
wml_client.software_specifications.list()
```

```
------------------------------  ------------------------------------  ----
NAME                            ASSET_ID                              TYPE
default_py3.6                   0062b8c9-8b7d-44a0-a9b9-46c416adcbd9  base
pytorch-onnx_1.3-py3.7-edt      069ea134-3346-5748-b513-49120e15d288  base
scikit-learn_0.20-py3.6         09c5a1d0-9c1e-4473-a344-eb7b665ff687  base
spark-mllib_3.0-scala_2.12      09f4cff0-90a7-5899-b9ed-1ef348aebdee  base
ai-function_0.1-py3.6           0cdb0f1e-5376-4f4d-92dd-da3b69aa9bda  base
shiny-r3.6                      0e6e79df-875e-4f24-8ae9-62dcc2148306  base
tensorflow_2.4-py3.7-horovod    1092590a-307d-563d-9b62-4eb7d64b3f22  base
pytorch_1.1-py3.6               10ac12d6-6b30-4ccd-8392-3e922c096a92  base
tensorflow_1.15-py3.6-ddl       111e41b3-de2d-5422-a4d6-bf776828c4b7  base
scikit-learn_0.22-py3.6         154010fa-5b3b-4ac1-82af-4d5ee5abbc85  base
default_r3.6                    1b70aec3-ab34-4b87-8aa0-a4a3c8296a36  base
pytorch-onnx_1.3-py3.6          1bc6029a-cc97-56da-b8e0-39c3880dbbe7  base
tensorflow_2.1-py3.6            1eb25b84-d6ed-5dde-b6a5-3fbdf1665666  base
tensorflow_2.4-py3.8-horovod    217c16f6-178f-56bf-824a-b19f20564c49  base
do_py3.8                        295addb5-9ef9-547e-9bf4-92ae3563e720  base
autoai-ts_3.8-py3.8             2aa0c932-798f-5ae9-abd6-15e0c2402fb5  base
tensorflow_1.15-py3.6           2b73a275-7cbf-420b-a912-eae7f436e0bc  base
pytorch_1.2-py3.6               2c8ef57d-2687-4b7d-acce-01f94976dac1  base
spark-mllib_2.3                 2e51f700-bca0-4b0d-88dc-5c6791338875  base
pytorch-onnx_1.1-py3.6-edt      32983cea-3f32-4400-8965-dde874a8d67e  base
spark-mllib_3.0-py37            36507ebe-8770-55ba-ab2a-eafe787600e9  base
spark-mllib_2.4                 390d21f8-e58b-4fac-9c55-d7ceda621326  base
xgboost_0.82-py3.6              39e31acd-5f30-41dc-ae44-60233c80306e  base
pytorch-onnx_1.2-py3.6-edt      40589d0e-7019-4e28-8daa-fb03b6f4fe12  base
default_r36py38                 41c247d3-45f8-5a71-b065-8580229facf0  base
autoai-obm_3.0                  42b92e18-d9ab-567f-988a-4240ba1ed5f7  base
spark-mllib_2.4-r_3.6           49403dff-92e9-4c87-a3d7-a42d0021c095  base
xgboost_0.90-py3.6              4ff8d6c2-1343-4c18-85e1-689c965304d3  base
pytorch-onnx_1.1-py3.6          50f95b2a-bc16-43bb-bc94-b0bed208c60b  base
```

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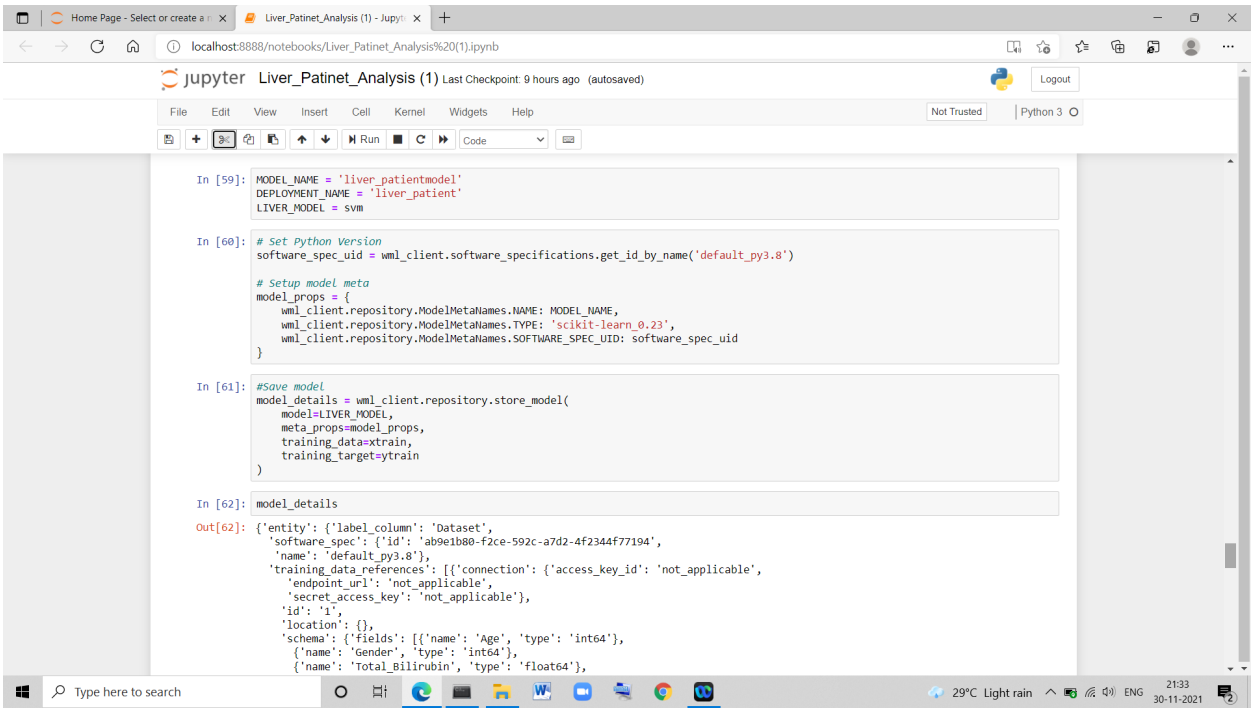

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In [59]:
```
MODEL_NAME = 'liver_patientmodel'
DEPLOYMENT_NAME = 'liver_patient'
LIVER_MODEL = svm
```

In [60]:
```
# Set Python Version
software_spec_uid = wml_client.software_specifications.get_id_by_name('default_py3.8')

# Setup model meta
model_props = {
    wml_client.repository.ModelMetaNames.NAME: MODEL_NAME,
    wml_client.repository.ModelMetaNames.TYPE: 'scikit-learn_0.23',
    wml_client.repository.ModelMetaNames.SOFTWARE_SPEC_UID: software_spec_uid
}
```

In [61]:
```
#Save model
model_details = wml_client.repository.store_model(
    model=LIVER_MODEL,
    meta_props=model_props,
    training_data=xtrain,
    training_target=ytrain
)
```

In [62]:
```
model_details
```

Out[62]:
```
{'entity': {'label_column': 'Dataset',
  'software_spec': {'id': 'ab9e1b80-f2ce-592c-a7d2-4f2344f77194',
   'name': 'default_py3.8'},
  'training_data_references': [{'connection': {'access_key_id': 'not_applicable',
     'endpoint_url': 'not_applicable',
     'secret_access_key': 'not_applicable'},
    'id': '1',
    'location': {},
    'schema': {'fields': [{'name': 'Age', 'type': 'int64'},
      {'name': 'Gender', 'type': 'int64'},
      {'name': 'Total_Bilirubin', 'type': 'float64'},
```

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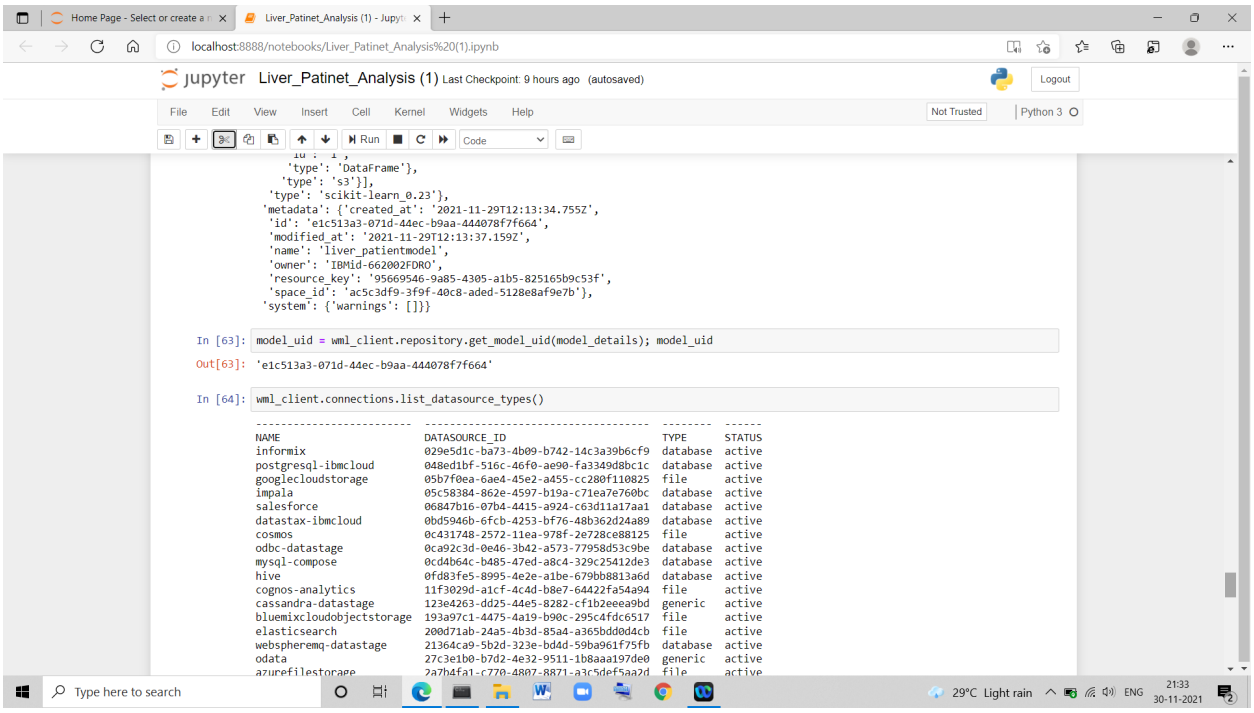
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'type': 'DataFrame'},
'type': 's3'}],
'type': 'scikit-learn_0.23'},
'metadata': {'created_at': '2021-11-29T12:13:34.755Z',
'id': 'e1c513a3-071d-44ec-b9aa-444078f7f664',
'modified_at': '2021-11-29T12:13:37.159Z',
'name': 'liver_patientmodel',
'owner': 'IBMid-662002FDRO',
'resource_key': '95669546-9a85-4305-a1b5-825165b9c53f',
'space_id': 'ac5c3df9-3f9f-40c8-aded-5128e8af9e7b'},
'system': {'warnings': []}}
In [63]: model_uid = wml_client.repository.get_model_uid(model_details); model_uid
Out[63]: 'e1c513a3-071d-44ec-b9aa-444078f7f664'
In [64]: wml_client.connections.list_datasource_types()
NAME DATASOURCE_ID TYPE STATUS
informix 029e5d1c-ba73-4b09-b742-14c3a39b6cf9 database active
postgresql-ibmcloud 048ed1bf-516c-46f0-ae90-fa3349d8bc1c database active
googlecloudstorage 05b7f0ea-6ae4-45e2-a455-cc280f110825 file active
impala 05c58384-862e-4597-b19a-c71ea7e760bc database active
salesforce 06847b16-07b4-4415-a924-c63d11a17aa1 database active
datastax-ibmcloud 0bd5946b-6fcb-4253-bf76-48b362d24a89 database active
cosmos 0c431748-2572-11ea-978f-2e728ce88125 file active
odbc-datastage 0ca92c3d-0e46-3b42-a573-77958d53c9be database active
mysql-compose 0cd4b64c-b485-47ed-a8c4-329c25412de3 database active
hive 0fd83fe5-8995-4e2e-a1be-679bb8813a6d database active
cognos-analytics 11f3029d-a1cf-4c4d-b8e7-64422fa54a94 file active
cassandra-datastage 123e4263-dd25-44e5-8282-cf1b2eeea9bd generic active
bluemixcloudobjectstorage 193a97c1-4475-4a19-b90c-295c4fdc6517 file active
elasticsearch 200d71ab-24a5-4b3d-85a4-a365bdd0d4cb file active
webspheremq-datastage 21364ca9-5b2d-323e-bd4d-59ba961f75fb database active
odata 27c3e1b0-b7d2-4e32-9511-1b8aaa197de0 generic active
azurefilestorage 2a7b4fa1-c770-4807-8871-a3c5def5aa2d file active
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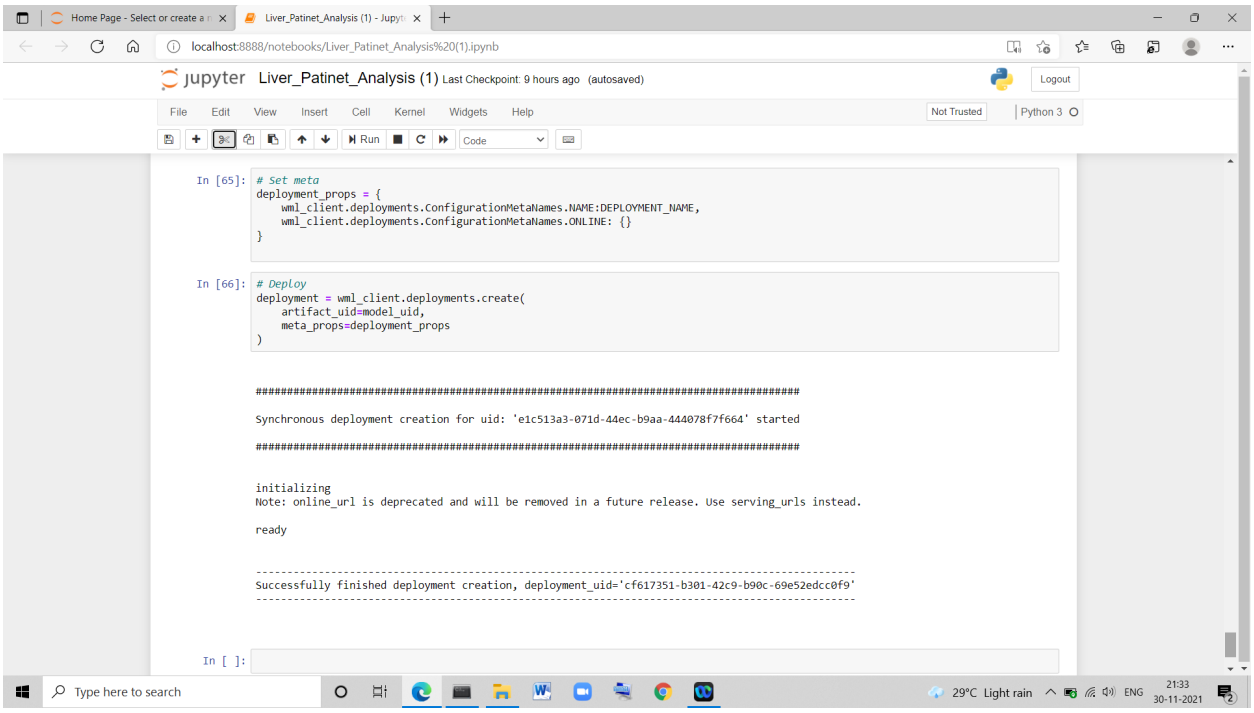
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In [65]:
# Set meta
deployment_props = {
wml_client.deployments.ConfigurationMetaNames.NAME:DEPLOYMENT_NAME,
wml_client.deployments.ConfigurationMetaNames.ONLINE: {}
}
In [66]:
# Deploy
deployment = wml_client.deployments.create(
artifact_uid=model_uid,
meta_props=deployment_props
)
##
Synchronous deployment creation for uid: 'e1c513a3-071d-44ec-b9aa-444078f7f664' started
##
initializing
Note: online_url is deprecated and will be removed in a future release. Use serving_urls instead.
ready
Successfully finished deployment creation, deployment_uid='cf617351-b301-42c9-b90c-69e52edcc0f9'
In [ ]:
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