

A Review of Liver Patient Analysis Methods Using Machine Learning

INTRODUCTION:

The liver is one of the most critical organs of the human body.

It plays an essential role in the body's function.

Primary purposes include removing toxins from the body, fighting against infections, and balancing the hormones and secretion of bile juice (Devikanniga et al., 2020).

If these functions are not performed by the liver correctly,
it will result in several complications and liver diseases.

OVERVIEW:

Liver disease is one of the most chronic and threatening diseases globally that can cause various side effects

if not treated early (Dutta et al., 2022). According to World Health Organization (WHO) report in 2018,

the number of deaths due to liver diseases is around one million and

ranked 11th in the world with a critical number of fatalities (World Total Deaths, n.d.).

As the symptoms of liver diseases cannot be visible until the condition becomes chronic, it is challenging and daunting for medical health professionals to identify liver disease

at its early stages (Devikanniga et al., 2020). In addition,

the traditional testing methods like sonography,

MRI scans and CT scans that are available for detecting liver diseases are expensive and harmful with numerous side effects (Joloudari et al., 2019).

Thus, a significant constraint found by health care workers is to predict liver diseases at an early stage,

at minimal cost and at the same time provide a better health care system to treat liver diseases

PURPOSE

The class distribution of the dataset is imbalanced, with 416 having liver disease and 167 without liver disease.

This class distribution is imbalanced and balanced by applying ROSE using R.

ROSE is a bootstrap method that produces balanced synthetic samples to balance the data (Lunardon et al., 2014).

The reason for choosing ROSE is that the dataset is small, and the most reliable information might be lost if undersampling is conducted.

The other reason for considering ROSE is that it generates samples similar to the rare class samples,

which is also a consideration for an effective method for getting reliable accuracy

from the balanced dataset as this study's main aim is the accuracy metrics of the algorithms (Lunardon et al., 2014).

After applying the ROSE method on the class attribute, the sample generated is 520 having liver disease denoted by '1' and 480 without liver disease

PROBLEM DEFINITION & DESIGN THINKING

Accuracy is the value of correctly classified instances in both classes (Wu et al., 2019).

$$\text{Accuracy} = \frac{TN+TP}{(TP+FP+TN+FN)}$$

EMPATHY MAP

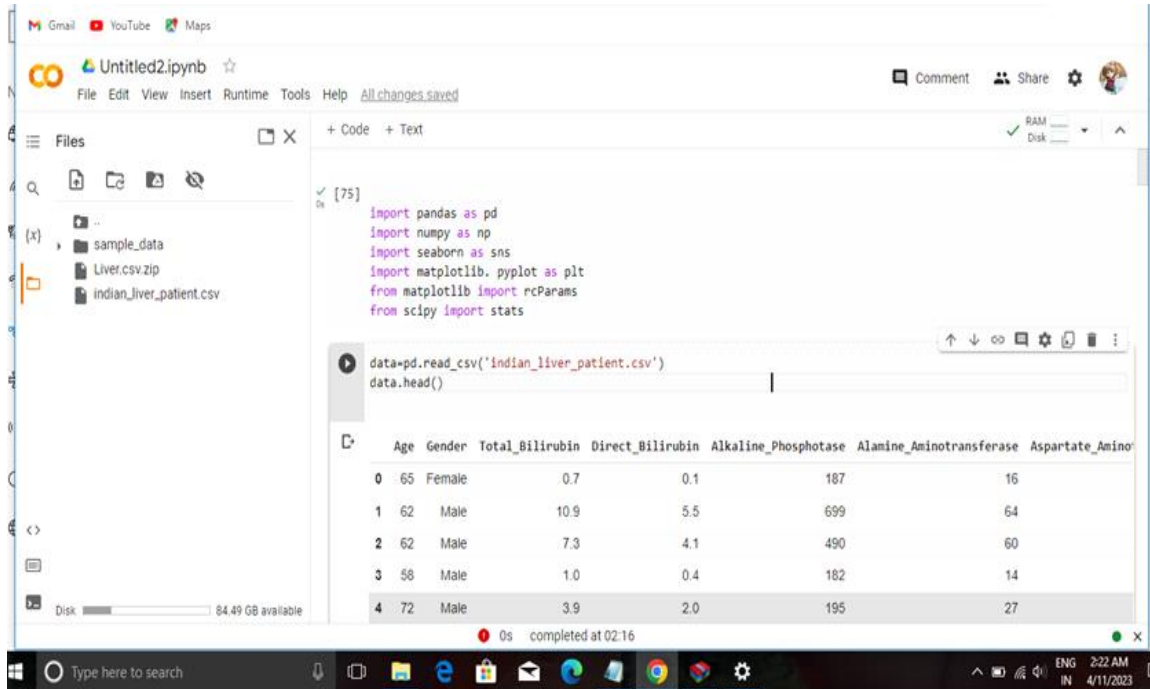


IDEATION & BRINSTORMING MAP



RESULT

The seventh stage of the proposed LDP method is 'Results'. The results stage involves presenting the results after assessing the data. All the results of accuracies and confusion matrix metrics will be described .



The screenshot shows a Jupyter Notebook interface with a file explorer on the left and a code editor on the right. The file explorer shows a directory structure with files like 'sample_data', 'Liver.csv.zip', and 'indian_liver_patient.csv'. The code editor contains the following Python code:

```
[75]: import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from matplotlib import rcParams
from scipy import stats

data=pd.read_csv('indian_liver_patient.csv')
data.head()
```

The output of the code is a table showing the first five rows of the dataset:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Amino
0	65	Female	0.7	0.1	187		16
1	62	Male	10.9	5.5	699		64
2	62	Male	7.3	4.1	490		60
3	58	Male	1.0	0.4	182		14
4	72	Male	3.9	2.0	195		27

The bottom of the screenshot shows the Windows taskbar with the search bar, taskbar icons, and system tray showing the time as 2:22 AM on 4/11/2023.

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Files

- sample_data
- Liver.csv.zip
- indian_liver_patient.csv

Code

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data.head()
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Code

```
[ ] data.info()
```

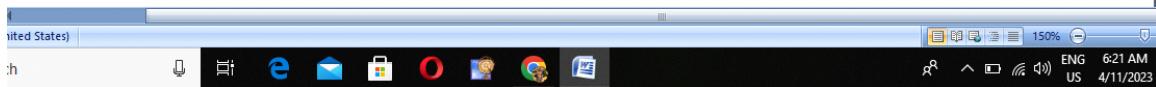
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 583 entries, 0 to 582
Data columns (total 11 columns):
 #   Column              Non-Null Count  Dtype  
---  -
 0   Age                 583 non-null   int64   
 1   Gender              583 non-null   object  
 2   Total_Bilirubin     583 non-null   float64  
 3   Direct_Bilirubin    583 non-null   float64  
 4   Alkaline_Phosphotase 583 non-null   int64   
 5   Alamine_Aminotransferase 583 non-null   int64   
 6   Aspartate_Aminotransferase 583 non-null   int64   
 7   Total_Protiens      583 non-null   float64  
 8   Albumin             583 non-null   float64  
 9   Albumin_and_globulin_ratio 579 non-null   float64  
10   Dataset             583 non-null   int64   
dtypes: float64(5), int64(5), object(1)
memory usage: 50.2+ KB
```

New section

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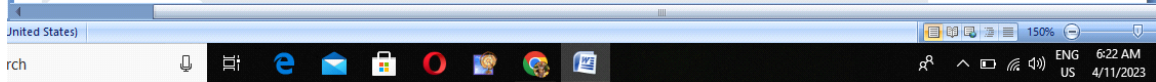
```
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[83]: data.isnull().sum()
Age 0
Gender 0
Total_Bilirubin 0
Direct_Bilirubin 0
Alkaline_Phosphatase 0
Alamine_Aminotransferase 0
Aspartate_Aminotransferase 0
Total_Protiens 0
Albumin 0
Albumin_and_Globulin_Ratio 4
Dataset 0
dtype: int64

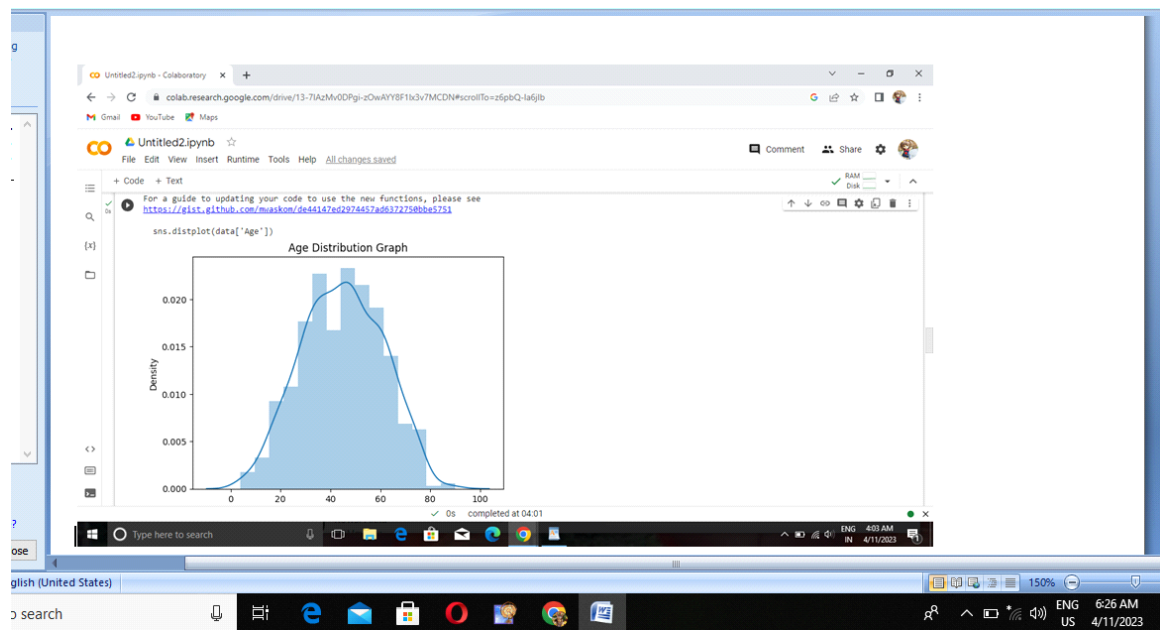
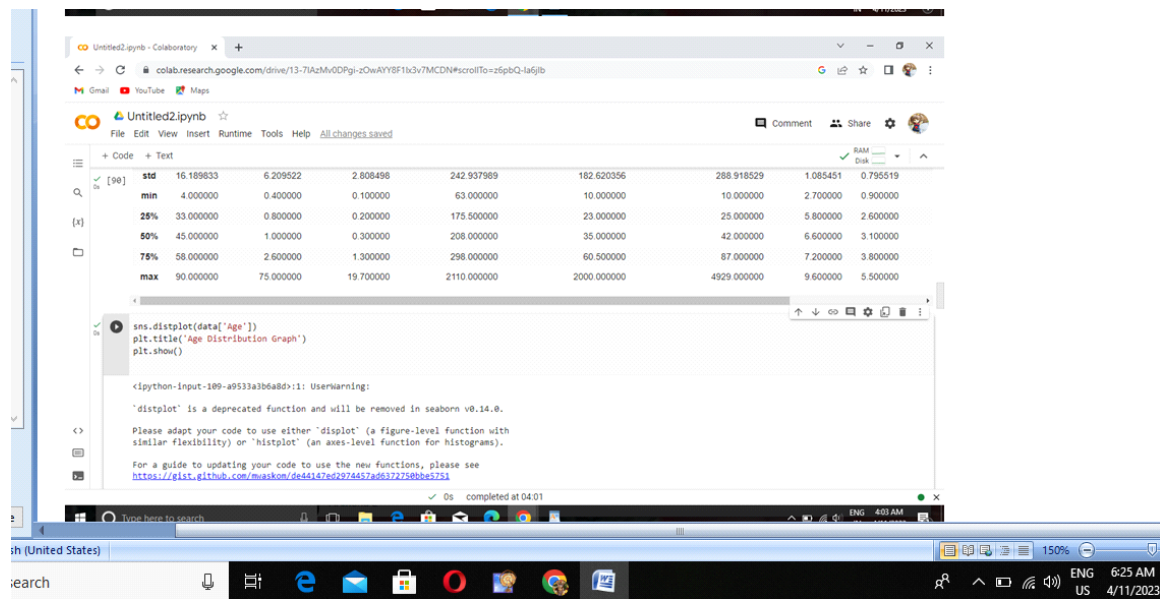
[87]: data['Albumin_and_Globulin_Ratio']
data.isnull().sum()
Age 0
Gender 0
Total_Bilirubin 0
Direct_Bilirubin 0
Alkaline_Phosphatase 0
Alamine_Aminotransferase 0
Aspartate_Aminotransferase 0
Total_Protiens 0
Albumin 0
```



```
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Gmail YouTube Maps
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[90]: data.describe()
Age Total_Bilirubin Direct_Bilirubin Alkaline_Phosphatase Alamine_Aminotransferase Aspartate_Aminotransferase Total_Protiens Albumin Album
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

[100]: sns.distplot(data['age'])
plt.title('age Distribution Graph')
plt.show()
```

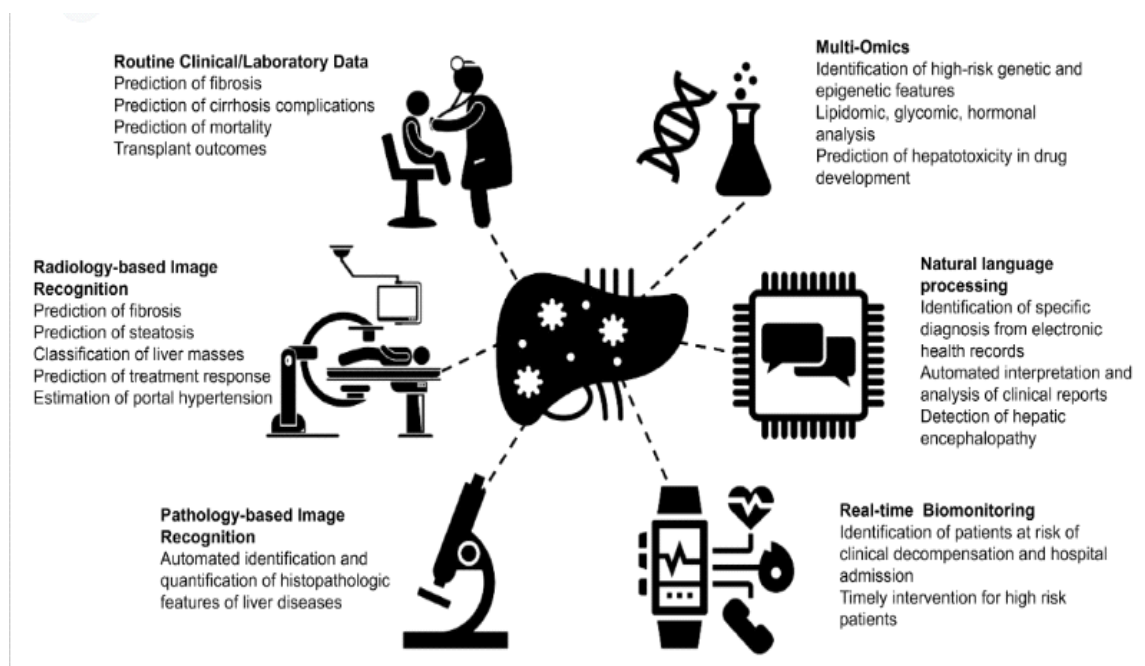




ADVANTAGES & DISADVANTAGES

Advantages	Disadvantages
Diagnostic criterion standard	
Confirmed diagnostic value	Highly invasive test
Etiologic suggestion	
Differential diagnosis	The potential complications include death
Grade and stage evaluation	
Therapeutic decision (eligibility)	Significant sampling error
Treatment evaluation (effectiveness)	High cost
Follow-up comparison of treated and untreated patients	Inter-observer variation

APPLICATION:



CONCLUSION

Since the liver disease is not easy to diagnose, given the delicate nature of its signs, this research is pertinent in determining the algorithms that have better accuracy in predicting this dreadful

disease. The stages in the proposed LDP method provide a better alignment of each phase. Once the dataset is selected, the preprocessing step is conducted by replacing the missing values and balancing the dataset. After that, using R, five different supervised learning methods are applied (i.e., SVM, Naïve Bayes, K-NN, LDA, and CART), and the accuracy with confusion matrix metrics are recorded. The result shows that K-NN has a better accuracy of 91.7% for liver disease prediction

FUTURE SCOPE

To conclude, the approach of the predicting analysis helps in predicting future possibilities by current data. The proposed model improved by applying a combination of three classifiers, Logistic regression, Random forest, and KNN algorithm. The python is employed for the implementation of the suggested model and the result proved regarding accuracy that is achieved 77.58 percent. For the future, the execution of the clustering algorithm is performed with the hybrid classifier technique for the division of data

APPENDIX

SOURCE CODE

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Initiating

New section

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[ ] data.info()

<class 'pandas.core.frame.DataFrame'>
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Data columns (total 11 columns):
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 1   Gender              583 non-null    object
 2   Total_Bilirubin     583 non-null    float64
 3   Direct_Bilirubin    583 non-null    float64
 4   Alkaline_Phosphatase 583 non-null    int64
 5   Alamine_Aminotransferase 583 non-null    int64
 6   Aspartate_Aminotransferase 583 non-null    int64
 7   Total_Protiens      583 non-null    float64
 8   Albumin             583 non-null    float64
 9   Albumin_and_Globulin_Ratio 579 non-null    float64
10   Dataset             583 non-null    int64
dtypes: float64(5), int64(5), object(1)
memory usage: 50.2+ KB
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Disk

```
[83] data.isnull().sum()

Age                0
Gender             0
Total_Bilirubin    0
Direct_Bilirubin   0
Alkaline_Phosphatase 0
Alamine_Aminotransferase 0
Aspartate_Aminotransferase 0
Total_Protiens     0
Albumin            0
Albumin_and_Globulin_Ratio 4
Dataset            0
dtype: int64

[87] data['Albumin_and_Globulin_Ratio']
data.isnull().sum()

Age                0
Gender             0
Total_Bilirubin    0
Direct_Bilirubin   0
Alkaline_Phosphatase 0
Alamine_Aminotransferase 0
Aspartate_Aminotransferase 0
Total_Protiens     0
Albumin            0
```

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Colab interface showing a Jupyter Notebook with a data summary table and a code cell.

Code cell [90]:

```
data.describe()
```

	Age	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphatase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Proteins	Albumin	Album
count	583.000000	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	

Code cell [100]:

```
sns.distplot(data['age'])  
plt.title('Age Distribution Graph')  
plt.show()
```

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Colab interface showing a Jupyter Notebook with a data summary table and a code cell.

Code cell [90]:

```
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
```

Code cell [100]:

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plt.show()
```

Warning:

<ipython-input-109-a9533a3b6a8d>:1: UserWarning:
"distplot" is a deprecated function and will be removed in seaborn v0.14.0.
Please adapt your code to use either "displot" (a figure-level function with similar flexibility) or "histplot" (an axes-level function for histograms).
For a guide to updating your code to use the new functions, please see
<https://gist.github.com/mwaskon/6e46167e29274637a26372750bb5751>

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