Liver Cirrhosis Prediction using Machine Learning Approaches

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***Abstract*— Liver cirrhosis is a highly infectious blood-borne illness that is often asymptomatic in its early stages. As a result, diagnosing and treating patients during the early stages of illness is challenging. As the illness progresses to its latter stages, diagnosis and therapy become increasingly challenging. The purpose of this work is to offer an artificial intelligence system based on machine learning algorithms that may assist healthcare practitioners in making an early diagnosis of liver cirrhosis. Various machine learning algorithms are being developed with this in mind to forecast the possibility of a liver cirrhosis infection. In this research, three alternative models for reliable prediction were produced by training three separate models employing a range of physiological parameters and machine learning methods such as Support Vector Machine, Decision Tree Classification, and Random Forest Classification. Random Forest was the best performing algorithm in this challenge, with an accuracy of around 97 percent. The open-access Liver Cirrhosis data dataset was employed in the method's development. The accuracy percentage of the models employed in this study is substantially greater than in earlier research, showing that the models utilized in this study are more dependable. Several model comparisons have shown their robustness, and the scheme may be determined from the research analysis.**

Keywords*— *Liver Cirrhosis, Machine Learning, Health.

I. INTRODUCTION

Liver cirrhosis is a disease that affects the whole human population. It is a blood-borne illness that spreads by direct contact with infected people's blood or blood-containing bodily fluids. Almost 71 million individuals worldwide are chronically unwell as a result of this condition, and an estimated 399,000 people died from it in 2016 [1]. According to the WHO (World Health Organization), liver cirrhosis is a worldwide illness. According to the research conducted by the WHO, 3–4 million individuals get infected with this virus each year. When compared to wealthy nations in Europe and North America, poor developing Asian and African countries have the greatest frequency of this virus. Furthermore, the number of people suffering from chronic illnesses is increasing in countries such as Pakistan, China, and Egypt [2-4]. Liver cirrhosis virus symptoms appear much later in the disease's progression. Approximately 80% of infected patients do not experience any symptoms after contracting an infection in the early stages, resulting in greater liver damage and higher fatality rates. There is no effective vaccination against the liver cirrhosis virus. As a result, determining the extent to which the afflicted patient's liver has been damaged may benefit doctors in the diagnosis and treatment of chronic infection as well as in its effective management. Proper management is critical in disease prevention because it prevents viral transmission between individuals [5–7]. Artificial intelligence (AI) advancements aid doctors in the rapid diagnosis and treatment of patients. There has been research comparing AI to human efficiency in illness diagnosis. This study found that AI was similarly capable of diagnosing as humans and, in fact, excelled at human efficiency when compared to less experienced physicians [8–12]. Because early detection is impossible due to a lack of symptoms, 75 to 80 percent of patients' liver cirrhosis infection progresses to its final stages. Furthermore, people with chronic illnesses may not exhibit symptoms for years. Then, by the end, the liver's functioning has been entirely compromised, making therapy impossible [13]. According to Lok in an article referenced in Michigan Medicine [14], the best therapy with the greatest chance of recovery is only achievable when the illness is detected at an earlier stage. According to Lok, people infected with liver cirrhosis often exhibit symptoms when they develop liver cirrhosis, increasing their chance of developing liver cancer. As a result, a practical and unique liver cirrhosis diagnostic method answers the requirement for early detection, allowing doctors to provide timely therapies to infected patients. Furthermore, early detection reduces the risk of the virus spreading to others [15]. AI-based disease diagnostics and prediction algorithms may aid in the early detection of acute infections and chronic disorders. Keltch, Lin, and Bayrak (2014) used four distinct kinds of AI algorithms on 424 liver cirrhosis patients' publicly accessible data. By comparing the findings of conventional serum indicators to the outcomes of biopsies, their suggested model aids in predicting the stage of fibrosis. Keltch et al. (2014) offered fresh methodologies and other AI techniques that might aid in the prediction of hepatitis B and C in millions of patients globally without the need for biopsies, thereby benefiting the whole healthcare system. In their work, the authors of [16] also indicate that AI approaches might be used for many types of organized and unstructured healthcare information. Machine learning algorithms for structured datasets are included in the most prominent artificial intelligence systems. Both Pietrangelo (2018) and Lok (2016) argue that, in order to minimize difficulties caused by disease development, the best treatment outcomes are only attainable with early diagnosis of the infectious stage. As a result, therapy should begin as soon as feasible. Lok and her colleagues are working on a unique approach that uses machine learning techniques to include many datasets in order to improve accuracy in forecasting the likelihood of acquiring fibrosis and its development from mild to moderate [17–21]. In [22], 29 algorithmic factors representing liver cirrhosis infection symptoms are utilized to construct an AI approach for diagnosing human illness. Kamal et al. (2019) made accessible a dataset including 29 symptom variables from Egyptian patients who had liver cirrhosis virus therapy for 18

months. Researchers, scientists, and health practitioners will be able to forecast infection phases using the suggested diagnostic approach without forcing patients to undergo liver biopsies. In this study, we employed various well-known machine learning algorithms to obtain our findings. The most effective algorithms were Random Forest, Decision Tree, and Support Vector Machine, with 97 percent, 95 percent, and 97 percent of F1-scores, respectively. The accuracy percent of the models used in this study is substantially higher than the accuracy percent of the models used in prior studies, indicating that the models used in this study are more reliable. They have been demonstrated to be robust in several model comparisons, and the scheme may be developed based on the study's analytic findings. The remainder of this paper is arranged as follows. The second section discusses related work, the third section describes procedures and experimental methods, and the fourth and fifth sections look at results analysis and conclusions.

II. Related Work

The research published in [23] used a data mining strategy to create an artificial neural network (ANN) system using a huge socio-medical dataset. This technique is capable of making a successful predictive diagnosis of people who may be infected with the Liver cirrhosis virus. According to research performed at the University of Michigan [24], lowering disease management costs for Liver cirrhosis patients is a significant problem. As a result, Michigan University scientists created a method that uses a predictive analytics algorithm to identify patients who are at high risk. In the event of subsequent difficulties, the authors believe their method might benefit high-risk patients by providing prompt and effective therapy. When compared to previous investigations, the authors believe that their approach is more accurate. Furthermore, the authors of [25] investigated how characteristics like as gender and obesity may influence the frequency of Liver cirrhosis infection in various populations. The research underlines the significance of all of the aforementioned characteristics in constructing any system, whether manual or using AI, in order to get highly accurate findings and gain healthcare experts' most efficient treatment solutions. A substantial difference is reported in patients for contributing variables such as sex, body mass index (BMI), bilirubin, alanine aminotransferase (ALT), and other parameters in comparable study. It has been shown that the mean BMI value for male patients beyond the age of 60 is lower than for female patients under the age of 60. Furthermore, higher BMI values are associated with a greater risk of early development of Liver cirrhosis sequelae in Liver cirrhosis virus patients [26]. The authors in [27] presents a detailed review of three data mining algorithms, namely decision trees, naive Bayes, and neural networks, for predicting Liver cirrhosis virus infection. In [28] authors discuss the progress made in the development of machine learning artificial intelligence systems for predicting esophageal varices (a consequence of the Liver cirrhosis virus) in chronic Liver cirrhosis patients. The researchers of this study also said that 9 factors out of 24 were discovered to be the most relevant for examination using their established approach. Another study [29] underlines the usefulness of decision tree learning algorithms in predicting Liver cirrhosis virus infection in individuals, particularly those who are at high risk of developing severe liver fibrosis as a result of Liver cirrhosis virus infection. It may eventually reduce or perhaps replace liver biopsy, an invasive approach with downsides. Several research investigations on Liver cirrhosis, its prediction, and extensive analysis have been reported [30-36]. Examples of this kind may be found in [37–40]. These instances demonstrate that Liver cirrhosis has a significant effect, and that additional study is needed to successfully tackle this illness. As a result, utilizing a publicly accessible dataset, this paper proposes a prediction model.

III. Procedure and Experimental Methodology

A. Proposed System

Once the data has been analyzed, it may be used to build a model. A preprocessed dataset and machine learning algorithms are required for model creation. Decision Tree Classification, Random Forest Classification, and Support Vector Machine (SVM) are some of the techniques used. The accuracy metrics Accuracy Score, Precision Score, Recall Score, and F1 Score are used to evaluate the four alternative models once they have been created. Figure 1 depicts the proposed system's block diagram.

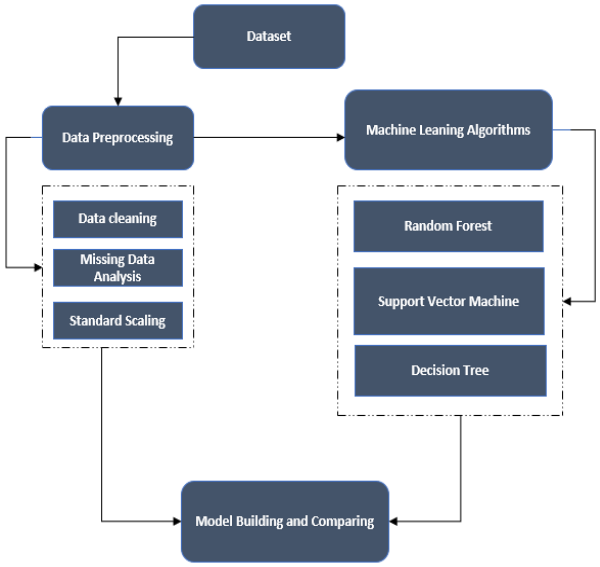


Fig. 1. Proposed Method for Liver Cirrhosis Prediction

Figure 1 depicts the three stages of the suggested paradigm. This is the initial step in the process, in which a raw dataset is obtained from the repository at UCI. There is a lot of noise and junk in the data, which might lead to incorrect predictions by the algorithm. A preprocessing stage is then used to remove any unnecessary data and then look for a feature that may be used as a classifier. Three machine learning algorithms are used to classify the data. The system gets a decision after training.

B. Dataset

The Liver cirrhosis Dataset [41] was utilized to conduct the research. It has 615 rows and 13 columns in this dataset Either '1' or '0' is returned in the 'Category' output field. Values of zero and one reflect the presence or absence of Liver cirrhosis

(LD) in the patient. It is more likely to see a zero in the output column than it is to see a one in the same column. Data pre-processing is used to ensure that the data is evenly distributed. Prior to pre-processing, the total number of LD and healthy data is shown in Figure 2.

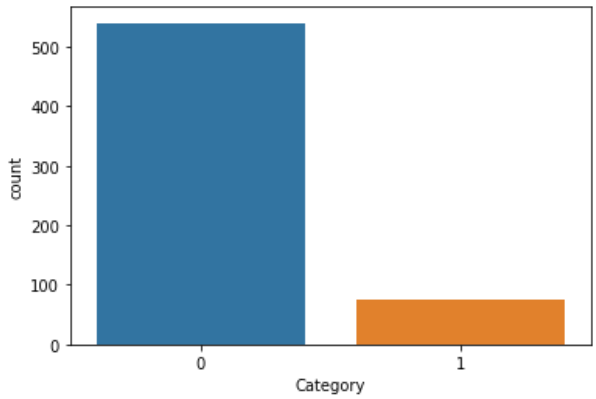


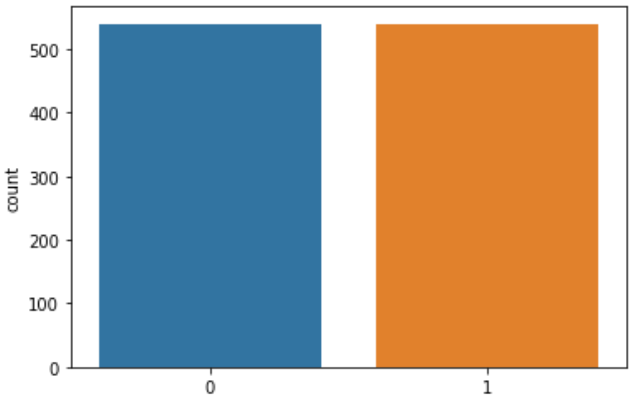
Fig. 2. Visualization of Category Column

C. Preprocessing

It is necessary to do data preprocessing before building a model in order to remove unwanted noise and outliers from the dataset. This step aims to fix any issues that are preventing the model from working more effectively. Cleansing and preparing relevant datasets for model building follows the acquisition of relevant datasets. The dataset utilized has 13 features, as described before. There is no need to include the untitled column in the model since it has no influence on its creation. When any null values are found, they are replaced with the appropriate value. There are no values in the columns "ALT," "CHOL," "PROT," and "ALB" in this case, thus the column data's mean is used to fill the blanks. Using label encoding, a dataset's string literals may be converted to numeric values that the computer can understand. Strings must be converted to integers before they can be used by the machine, which is often trained on numbers. Among the acquired data, there are two columns of the type string. During label encoding, all strings are encoded, and the whole dataset is turned into a collection of numerical values. LD prediction relies on a dataset that is very skewed. 615 rows overall, of which 75 rows indicate the presence of an LD and 540 rows indicate the lack of an LD. The dataset. Machine-level models can be trained using this data, but additional accuracy metrics like as precision and recall are lacking. Unbalanced data must be handled correctly, or the results will be incorrect, making the prediction worthless. So, in order to build an efficient model, the first step is to deal with this imbalanced data. This was done using the SMOTE approach. Figure 3 depicts the dataset's balance output column.

After completing data preparation and balancing the unbalanced dataset, the following step is to build the model. The data for this assignment is divided between training and testing data, with a 70% to 30% split. A number of categorization approaches are used to train the model after splitting. The classification techniques used in this work are Random Forest, Decision Tree Classification Method, and Support Vector Machine.

Fig. 3. Target column after SMOTE applied



D. Applied Algorithms

One of the most often found illnesses in medical research is the ever-increasing occurrence of Liver cirrhosis. Machine learning algorithms for predicting Liver cirrhosis recurrence were evaluated using the publicly available LD prediction dataset. Following algorithms were used in this paper.

- Random Forest
- Support Vector Machine
- Decision Tree

1) Random Forest

Random Forest Classification was used as the algorithm for classification. Multiple decision trees, each trained on a random sampling of data, make form a Random Forest. In training, these trees are built, which yields the trees' outputs. This algorithm uses a procedure known as "vote" to establish its final prediction. To use this method, each decision tree must choose between two possible outcomes (here, 'LD' and 'Healthy'). The class with the highest votes is chosen as the final prediction by the random forest method. a section in Figure 4 depicts a random forest classification diagram.

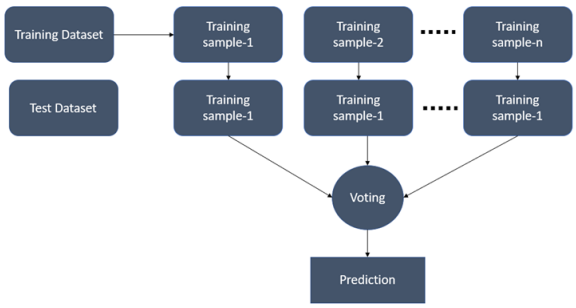


Fig. 4. Working Process of Random Forest Classifier

A major selling point of Random Forest is its adaptability. Both relapse detection and grouping tasks may be accomplished with it. The information features that are given the most weight is easily visible while using it. In addition, the default hyperparameters it utilizes frequently provide clear expectations, making it a good strategy. Understanding the hyperparameters is essential, since there are only a handful of them. Despite the fact that overfitting is a common issue in machine learning, the arbitrary random forest classifier seldom suffers from this problem. The classifier won't overfit the model if there are enough trees in the forest.

2) Decision Tree

The use of Decision Trees can be applied to both regression and classification problems. Because the input variables have a related output variable, this is a supervised learning approach. A tree can be seen in its resemblance. A specific parameter is used to divide the data constantly in this method. Both the Decision and Leaf nodes form the core of a decision tree. Nodes 1 and 2 are responsible for dividing data, whereas nodes 3 and 4 are responsible for producing the final output. Using Figure 5, we can see the Decision Tree Classifier's basic structure and operation.

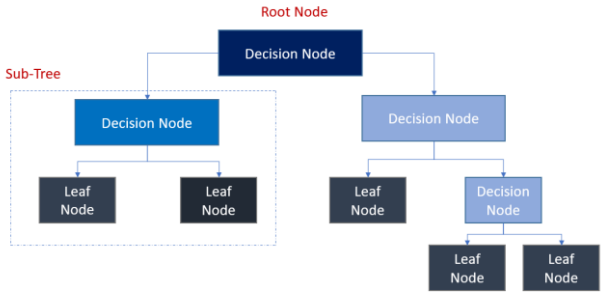


Fig. 5. Structure of Decision Tree Classifier.

As a visual representation of the decision-making process, the Decision Tree is simple to follow and understand. Problems with decision-making may be greatly alleviated. Make a list of all possible solutions to a problem. Compared to other ways, cleaning data isn't necessary as often.

3) Support Vector Machine

An SVM model uses space points to represent the examples so that the examples of individual categories can be broken up into a clear divide as wide as possible. As a result of this mapping, new examples are predicted to fall into a category on one side or another. Figure 6 shows the block diagram of the support vector machine.

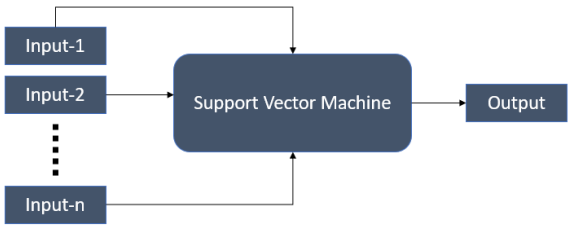


Fig. 6. Structure of Support Vector Machine.

Other classification methods, such as nonlinear classification using the so-called "kernel trick," are as successful, and their inputs are implicitly translated into high-dimensional functional spaces.

E. Evaluation Matrix

The confusion matrix or evaluation matrix is seen in Figure 7. A machine learning classification algorithm's performance may be evaluated using a confusion matrix. All of the models have been tested using the confusion matrix. The confusion matrix shows how accurate our models are and how inaccurate they are. While false positives and false negatives were attributed to incorrectly predicted values, genuine positives and negative values were assigned to correctly predicted values. The model's accuracy, precision-recall trade-off, and AUC were used to assess its performance after grouping all of the predicted values in a matrix.

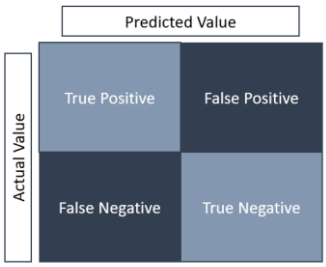


Fig. 7. Confusion Matrix.

IV. Result Analysis

A. Evaluation of The Model

1) Random Forest

Table 1 shows the Random Forest model's assessment report.

```
[ ]  print(classification_report(y_test, y_test_pred_rf))

              precision    recall  f1-score   support

           0       0.98      0.99      0.98       162
           1       0.90      0.83      0.86        23

    accuracy                           0.97       185
   macro avg       0.94      0.91      0.92       185
weighted avg       0.97      0.97      0.97       185
```

Figure 8: Random Forest Classification Report

The final F1 score is 97 percent in this case. Individual F1 scores are at 98 percent for healthy persons and at 86 percent for those who have tested positive for LD. The Random Forest model's forecast is shown in Figure 9. Model performance and expected outcomes are shown in a confusion matrix.

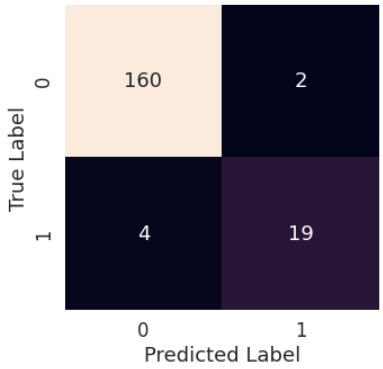


Fig. 9. Confusion Matrix of Random Forest.

Here, TP = 160, TN = 19, FP = 3, and FN = 4, which means there were 179 correct guesses and six wrong ones. This model can predict 160 healthy and 19 LD-affected patient records correctly. But it denoted 2 healthy patient records as LD positive and 4 LD positive patients as healthy.

2) Decision Tree

Figure 10 shows the classification report for the Decision Tree classifier.

```
[ ] y_pred_Clf = Clf.predict(X_test)
    print(classification_report(y_test, y_pred_Clf))
```

	precision	recall	f1-score	support
0	0.97	0.98	0.97	162
1	0.82	0.78	0.80	23
accuracy			0.95	185
macro avg	0.89	0.88	0.89	185
weighted avg	0.95	0.95	0.95	185

Fig. 10. Classification Report of Decision Tree.

The final F1-score is 95 percent in this case. An individual's F1 score is 97 percent for healthy individuals and 80 percent for those who have had an LD positive. Figure 11 depicts the Decision Tree model's prediction.

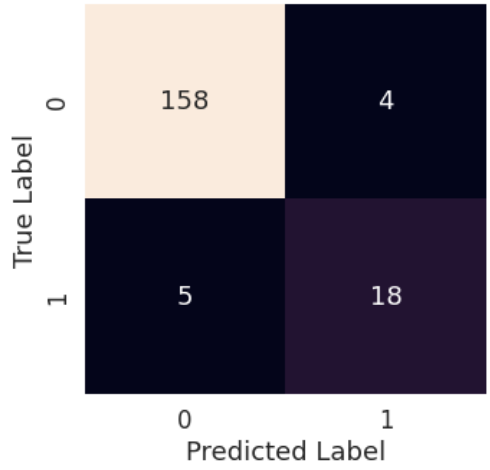


Fig. 11. Confusion Matrix of Decision Tree.

Here, TP = 158, TN = 18, FP = 4, and FN = 5, which means 176 accurate guesses and 9 erroneous predictions. This model can predict 158 healthy and 18 LD-affected patient records correctly. But it denoted 4 healthy patient records as LD positive and 5 LD positive patients as healthy.

3) Support Vector Machine

The classification report for the Voting Classifier is shown in Figure 12.

```
print(classification_report(y_test,y_pred_svm))
```

	precision	recall	f1-score	support
0	0.97	0.99	0.98	162
1	0.95	0.78	0.86	23
accuracy			0.97	185
macro avg	0.96	0.89	0.92	185
weighted avg	0.97	0.97	0.97	185

Fig. 12. Classification Report of SVM.

The total F1-score obtained in this instance is 97 percent. Individual F1-scores is 98 percent for healthy people and 86 percent for those who have had an LD positive. The prediction made by the SVM classifier is shown in Figure 13.

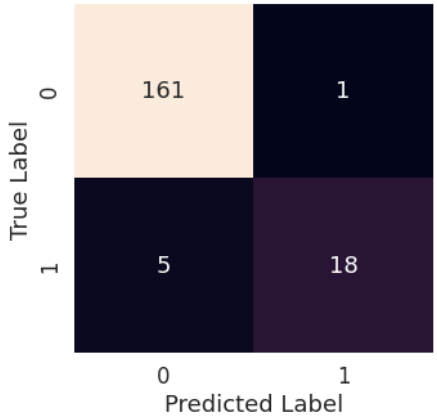


Fig. 13. Confusion Matrix of SVM.

Here, TP = 161, TN = 18, FP = 1, and FN = 5, which means the overall number of accurate guesses is179, while the total number of erroneous predictions is 6. This model can predict 161 healthy and 18 LD-affected patient records correctly. But it denoted 1 healthy patient record as LD positive and 5 LD positive patients as health. Table 1 shows the result comparison with previous reported results.

Table 1: Result comparison

Reference Number	Algorithm Name	Accuracy (%)	Accuracy in this Study (%)
29	Support Vector Machine	75	97
24	Decision Tree	82.5	95
31	Random Forest	80.3	97

The table clearly shows that Random Forest and Support Vector Machine are the best models among the several models in the framework. It is more accurate. Using the same method, ref [29] achieved an accuracy of 75 percent. Also using Decision tree ref [24] achieved 83.5 percent accuracy which is lower than our implemented model's result.

V. Conclusion

LD is a potentially fatal infection that must be treated immediately to avert future complications. The construction of a machine learning model may aid in the detection of LD and may help mitigate its long-term health consequences. Different machine learning algorithms are evaluated for their effectiveness in predicting LD infection based on a variety of physiological factors. Random Forest Classification, on the whole, outperforms the other methodologies tested. The accuracy % of the models used in this investigation is significantly higher than that used in previous studies, indicating that the models used in this study are more reliable. When cross-validation is used to predict brain strokes, a random forest algorithm outperforms previous approaches. There are numerous machine learning models that could be utilized in the future to improve framework models. This improvement will improve the framework's dependability and look. A machine-learning architecture may be able to aid the

general public in determining whether an adult patient is a danger of having a stroke. In an ideal world, LD patients would receive early treatment and rebuild their lives.

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