AN IMPROVED MACHINE LEARNING ALGORITHM FOR LIVER DISEASE DETECTION

A project report submitted to

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In partial fulfillment of the requirements for the award of a degree of

BACHELOR OF TECHNOLOGY

in

COMPUTER SCIENCE & ENGINEERING (AI & ML)

Submitted by

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(Telangana State Private Universities Act No.13 of 2020 and G.O.Ms.No.14, Higher Education (UE) Department)

COLLEGE CERTIFICATE

This is to certify that this is the bonafide record of the Application Development entitled**AN IMPROVED MACHINE LEARNING ALGORITHM FOR LIVER DISEASE DETECTION**Submitted by N MANASA PRIYA (2211CS020366), N SAIKRISHNA (2211CS020369), N RAGHUVARDHAN (2211CS020370), O MOKSHA (2211CS020382), P PRAVEEN KUMAR (2211CS020391) B. Tech II year II semester, Department of CSE (AI&ML) during the year 2023-24. The results embodied in the report have not been submitted to any other university or institute for the award of any degree or diploma.

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PROJECT GUIDE

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ABSTRACT

This project introduces a comprehensive liver disease prediction system integrating machine learning techniques with a user-friendly web interface. Leveraging a Random Forest Classifier trained on a diverse dataset comprising demographic information and key blood biomarkers, the system enables accurate predictions of liver disease presence. Robust preprocessing methods address data irregularities, ensuring the model's reliability. A Flask web application facilitates user interaction, allowing individuals to input health parameters through an intuitive HTML form. Upon submission, the system processes the input, applies the trained model, and provides real time predictions. By seamlessly blending advanced algorithms with accessible user interface design, this project aims to enhance early detection and management of liver-related conditions, ultimately contributing to improved healthcare outcomes..

To facilitate user interaction and promote accessibility, an interactive HTML form interface is developed. This interface allows individuals to input their health parameters conveniently, enabling the system to provide real-time predictions on the likelihood of liver disease. The HTML form is meticulously designed with intuitive features and custom styling to enhance user experience and ensure ease of use. By seamlessly integrating advanced machine learning algorithms with a user friendly interface, this project aims to offer a valuable tool for healthcare professionals and individuals alike. Early detection of liver disease can significantly impact patient outcomes, and this system holds the potential to assist in the early identification and management of liver-related conditions, ultimately contributing to improved healthcare delivery and patient well-being.

1. INTRODUCTION

- **Project Identification / Problem Definition**

The Liver Disease Prediction Web Application is a comprehensive project aimed at developing a user-friendly web-based tool to assist in the early detection and assessment of liver disease. By leveraging advanced machine learning algorithms, the application predicts the likelihood of liver disease based on user inputs such as age, gender, and specific blood test results including total bilirubin, alkaline phosphatase, alamine aminotransferase, aspartate aminotransferase, total proteins, albumin, and the albumin-to-globulin ratio. The project involves designing a clean and intuitive web interface using HTML, CSS, and JavaScript for data input, which seamlessly integrates with a backend server developed with frameworks like Flask or Django to process the input data and return predictions. The model is trained on a comprehensive liver disease dataset to ensure high accuracy and reliability. Once developed, the application is deployed on a scalable and secure platform such as AWS, Google Cloud, or Heroku, ensuring it is accessible to users anytime and anywhere. The primary objective is to provide healthcare professionals and individuals with a reliable tool that can aid in the early diagnosis and timely intervention of liver disease, ultimately contributing to better health outcomes.

In addition to its primary functionality, the Liver Disease Prediction Web Application emphasizes security and performance, ensuring that user data is handled with the utmost confidentiality and processed efficiently. The web application features real-time predictions, allowing users to receive immediate feedback upon data submission. To enhance user experience, the interface is designed to be responsive and accessible across various devices, including desktops, tablets, and smartphones. Continuous monitoring and periodic retraining of the machine learning model are implemented to maintain and improve the model's accuracy over time. Overall, the Liver Disease Prediction Web Application represents a significant advancement in medical technology, providing an innovative solution that empowers users with critical health information and supports healthcare providers in making informed decisions.

1.2 Objective of the Project

- **Machine Learning Model Development:** Implement machine learning algorithms, including Logistic Regression, Support Vector Machine (SVM), Random Forest, and Gradient Boosting, to develop a predictive model. This model will accurately classify the likelihood of liver disease based on input parameters such as age, gender, and various blood test results like bilirubin levels, liver enzymes, and protein levels.
- **Early Detection and Intervention**: Use the predictive model to enable early detection of liver disease, facilitating timely intervention and treatment planning. This objective aims to improve health outcomes by identifying potential cases of liver disease at an early stage.
- **User-Friendly Web Interface**: Design and develop an intuitive web interface where users, including healthcare professionals and individuals, can easily input medical data. The interface will provide clear and immediate predictions regarding the presence of liver disease upon submission of relevant health metrics.
- **Integration of Frontend and Backend Systems**: Ensure seamless communication between the frontend interface and backend server. This integration is critical for efficient data processing, model prediction, and real-time feedback to users.
- **Deployment and Accessibility**: Deploy the web application on a secure and scalable platform (e.g., AWS, Google Cloud) to ensure continuous accessibility. This includes implementing security measures to protect user data and maintaining high performance levels for reliable use.
- **Enhanced Healthcare Decision-Making**: Enable healthcare professionals to make informed decisions by providing reliable predictions based on robust data analysis. The application aims to support medical practitioners in diagnosing liver disease accurately and efficiently.
- **Continuous Improvement and Adaptation**: Implement mechanisms for continuous model monitoring, evaluation, and refinement based on new data patterns and feedback. This iterative process ensures that the predictive model remains accurate and relevant over time.

1.3 Scope of the Project

The scope of the Liver Disease Prediction Web Application project:

- **Data Collection and Preparation:**The project involves gathering a comprehensive dataset of medical parameters relevant to liver disease, including demographic information (age, gender) and specific blood test results (bilirubin levels, liver enzymes, protein levels). Data preprocessing techniques will be applied to clean and format the data for machine learning model training.

- **Machine Learning Model Development:** Implement various machine learning algorithms to build and train a predictive model. Algorithms such as Logistic Regression, Support Vector Machine (SVM), Random Forest, and Gradient Boosting will be explored to determine the most accurate model for predicting the likelihood of liver disease based on input parameters.

- **Web Application Development:** Design and develop a user-friendly web interface using HTML, CSS, and JavaScript for seamless data input and interaction. The interface will allow users to input their medical data through a form and receive real-time predictions regarding the presence of liver disease.

- **Integration of Frontend and Backend Systems:** Ensure smooth integration between the frontend user interface and the backend server, which will handle data processing, model prediction, and result visualization. Technologies like Flask or Django will be utilized for backend development to manage data flow and ensure responsiveness.

- **Deployment and Hosting:** Deploy the web application on a reliable and scalable cloud platform (e.g., AWS, Google Cloud) to ensure accessibility and performance. Security measures will be implemented to protect user data and maintain confidentiality.

- **Testing and Validation:** Conduct thorough testing of the application to verify its functionality, usability, and accuracy in predicting liver disease. This includes unit testing, integration testing, and performance testing to ensure the application meets quality standards.

- **Documentation and Maintenance:** Prepare comprehensive documentation covering system architecture, deployment procedures, user guides, and maintenance protocols. Ongoing maintenance will involve monitoring the application's performance, updating models as necessary based on new data, and addressing any issues or enhancements.

- **User Training and Support:** Provide training sessions and support materials for users, including healthcare professionals and individuals, to effectively use the web application for liver disease prediction. This includes ensuring that users understand how to input data, interpret predictions, and utilize the application for informed decision-making.

2. ANALYSIS

2.1Project Planning and Research

Project planning and research are critical phases in developing the Liver Disease Prediction Web Application, aimed at establishing a solid foundation for the project's success. This phase involves several key activities to ensure the accurate prediction of liver disease based on medical data input.

Understanding Requirements

- **Identifying Stakeholders**: Engage with healthcare professionals, medical researchers, and potential end-users to gather insights into their needs and expectations regarding liver disease prediction.
- **Defining Functionalities:** Outline specific functionalities of the web application, such as input parameters (age, gender, blood test results), real-time prediction capabilities, and integration requirements with existing healthcare systems.
- **Performance Metrics:** Define accuracy benchmarks and performance metrics for the predictive model to ensure reliable diagnosis and early detection of liver disease.
- **Scalability and Accessibility:** Determine scalability requirements to handle potential increases in user traffic and ensure accessibility across different devices and platforms.

Literature Review

- **Research on Liver Disease Diagnosis:** Conduct a comprehensive literature review to understand current methodologies, algorithms, and technologies used in diagnosing liver disease based on medical parameters.
- **Review of Medical Datasets:** Explore existing medical datasets used for training machine learning models in liver disease prediction. Evaluate data quality, diversity, and relevance to ensure robust model development.
- **Best Practices in Machine Learning:** Identify best practices and state-of-the-art techniques in machine learning for healthcare applications, particularly in predictive modeling and disease diagnosis.

Technology Selection

- **Machine Learning Algorithms:** Select appropriate machine learning algorithms (e.g., Logistic Regression, SVM, Random Forest) based on their suitability for classifying liver disease from medical data.
- **Programming Languages and Frameworks:** Choose programming languages (e.g., Python for its extensive libraries) and frameworks (e.g., Scikit-learn, TensorFlow) best suited for model development, training, and deployment.
- **Integration Tools:** Identify tools for integrating frontend (e.g., HTML/CSS, JavaScript) with backend (e.g., Flask, Django) components to ensure seamless data processing and real-time prediction capabilities.

Project Timeline and Milestones

- **Developing a Timeline:** Create a detailed project timeline with milestones and deliverables, including data preprocessing, model training, web interface development, and deployment phases.
- **Task Allocation:** Allocate tasks among team members, specifying roles and responsibilities to streamline development efforts and meet project deadlines.
- **Quality Assurance:** Plan for rigorous testing and validation procedures to ensure the accuracy, reliability, and security of the web application before deployment.

Risk Assessment

- **Identifying Risks:**Conduct a risk assessment to anticipate potential challenges such as data variability, model overfitting, technical constraints, and regulatory compliance issues.
- **Mitigation Strategies:**Develop strategies to mitigate identified risks, including data preprocessing techniques, model validation procedures, and
contingency plans for unexpected setbacks.
- **Continuous Monitoring:**Establish protocols for continuous monitoring of model performance and application security post-deployment to address emerging risks effectively.

Ethical and Legal Considerations

- **Data Privacy and Security:** Ensure compliance with data protection regulations (e.g., GDPR, HIPAA) by implementing robust security measures for handling sensitive medical data.
- **Informed Consent:** Establish protocols for obtaining informed consent from users regarding data usage and ensure transparency in data processing practices.
- **Ethical Guidelines:** Adhere to ethical guidelines in healthcare research and technology development, emphasizing patient confidentiality, fairness in model predictions, and responsible use of predictive analytics.

In conclusion, thorough project planning and research are essential for developing the Liver Disease Prediction Web Application. By defining requirements, conducting a literature review, selecting appropriate technologies, setting timelines, assessing risks, and addressing ethical considerations, the project team can ensure a systematic and efficient development process. This approach aims to deliver a reliable and user-friendly tool that supports healthcare professionals in early detection and intervention for better management of liver disease.

2.2 Software and Hardware Requirement Specifications

2.2.1 Software Requirements

The Liver Disease Prediction Web Application is primarily developed and executed using Python, a versatile programming language known for its efficiency in handling data-intensive tasks and machine learning applications. Python version 3.8 or higher is recommended for compatibility with the required libraries and features utilized in the project.

Flask: Flask is chosen as the web framework for its simplicity and flexibility in building web applications. It facilitates the development of RESTful APIs to handle data input from users, interact with the predictive model, and deliver real-time predictions via the web interface.

Pandas: Pandas is essential for data manipulation and analysis. It provides data structures and functions to preprocess and organize the dataset containing medical parameters such as age, gender, and blood test results. Pandas ensures the data is formatted correctly for model training and prediction.

Scikit-learn: Scikit-learn offers a comprehensive set of tools for machine learning tasks. In this application, it is utilized for implementing various machine learning algorithms such as Logistic Regression, Support Vector Machine (SVM), Random Forest, and Gradient Boosting. These algorithms are crucial for accurately predicting the likelihood of liver disease based on input parameters.

NumPy: NumPy is fundamental for scientific computing in Python. It provides support for large, multi-dimensional arrays and matrices, essential for efficient data handling and numerical computations required by machine learning algorithms implemented using Scikit-learn.

Matplotlib and Seaborn: Matplotlib and Seaborn are used for data visualization within the application. They enable the creation of graphical representations such as histograms, box plots, and ROC curves to visualize model performance metrics, aiding in the evaluation and comparison of different machine learning algorithms.

Flask-WTF and WTForms: Flask-WTF along with WTForms are utilized for form handling and validation within the Flask framework. They provide tools to create and manage web forms where users input their medical data, ensuring data integrity and security before processing by the predictive model.

SQLAlchemy (Optional):SQLAlchemy may be used for database management and integration, allowing the application to store user data securely if persistent storage is required beyond session-based data handling.

To ensure the proper functioning of data preprocessing and machine learning operations, dependencies such as Flask, Pandas, Scikit-learn, NumPy, Matplotlib, and Seaborn must be installed using Python's package manager, pip. It is recommended to create a virtual environment to manage dependencies and isolate the project's environment from other Python installations.

2.2.2 Hardware Requirements

The hardware requirements for the Liver Disease Prediction Web Application are designed to ensure optimal performance and scalability, accommodating both development and deployment phases of the project.

Development Environment:

- **Processor:** A multi-core processor (Intel Core i5 or equivalent) is recommended to handle computational tasks efficiently during development and testing.
- RAM: Minimum 8 GB of RAM is recommended to support simultaneous running of Python scripts, data manipulation, and machine learning model training without performance degradation.
- Storage: Solid-state drive (SSD) with at least 256 GB of storage capacity is preferable for faster data access and handling large datasets used for model training.

Deployment Environment:

- **Processor:** A multi-core processor (Intel Xeon or equivalent) is recommended for handling concurrent user requests and processing predictive model computations in real-time.
- **RAM:** Minimum 16 GB of RAM is recommended to support multiple users accessing the web application simultaneously, ensuring responsiveness and efficient data processing.
- Storage: SSD storage with sufficient capacity (500 GB or more) to store application files, user data, and logs. SSDs offer faster read/write speeds, improving application performance.
- Network: Reliable internet connection with adequate bandwidth to handle incoming and outgoing data traffic from users accessing the web application.

Server Infrastructure:

- **Cloud Platform:** Deploy the web application on a scalable cloud platform such as Amazon Web Services (AWS), Google Cloud Platform (GCP), or Microsoft Azure. Cloud platforms offer scalability, high availability, and robust security features.
- **Virtual Machines (VMs):** Utilize VM instances with configurations matching the recommended hardware specifications for both development and production environments. VMs provide flexibility in resource allocation based on application demand.
- **Load Balancing:** Implement load balancing mechanisms (e.g., AWS Elastic Load Balancing, GCP Load Balancer) to distribute incoming web traffic across multiple instances of the application, ensuring optimal performance and availability during peak usage periods.
- **Backup and Recovery:** Implement regular data backups and disaster recovery plans to protect against data loss and ensure continuity of service in case of hardware failures or unforeseen incidents.

By meeting these hardware requirements, the Liver Disease Prediction Web Application can deliver reliable performance, scalability, and responsiveness, meeting the needs of healthcare professionals and individuals seeking accurate predictions and early detection of liver disease through a secure and accessible web interface.

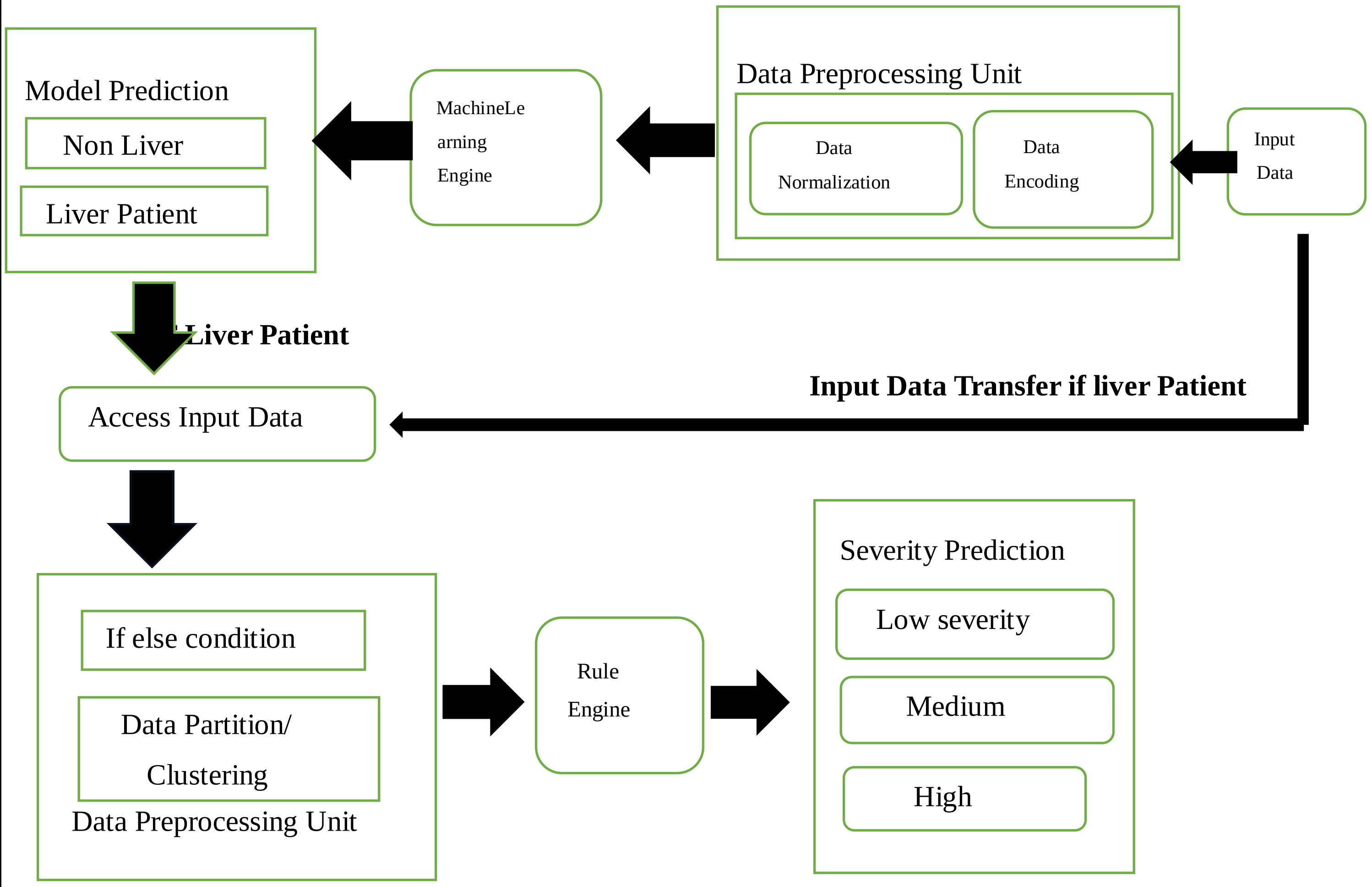
2.3 Model Selection and Architecture

Model Selection

The selection of the machine learning model and its architecture for the Liver Disease Prediction Web Application is crucial to ensure accurate and reliable predictions based on input medical data. This section outlines the approach to model selection and the overall architecture of the predictive system.

- **Logistic Regression:** A straightforward linear model suitable for binary classification tasks, often used as a baseline model for comparison.
- **Support Vector Machine (SVM):** Effective in high-dimensional spaces, SVMs aim to find the hyperplane that best separates classes in the feature space.
- **Random Forest:** Ensemble learning method that constructs multiple decision trees and outputs the class that is the mode of the classes (classification) of the individual trees.
- **Gradient Boosting:** Builds trees sequentially, where each tree corrects the errors of the previous one, aiming to minimize the loss function.
- **Neural Networks :** Deep learning models, such as feedforward neural networks, may be considered for their ability to learn complex patterns in data, although they require more computational resources and data compared to traditional machine learning algorithms.

ARCHITECTURE:

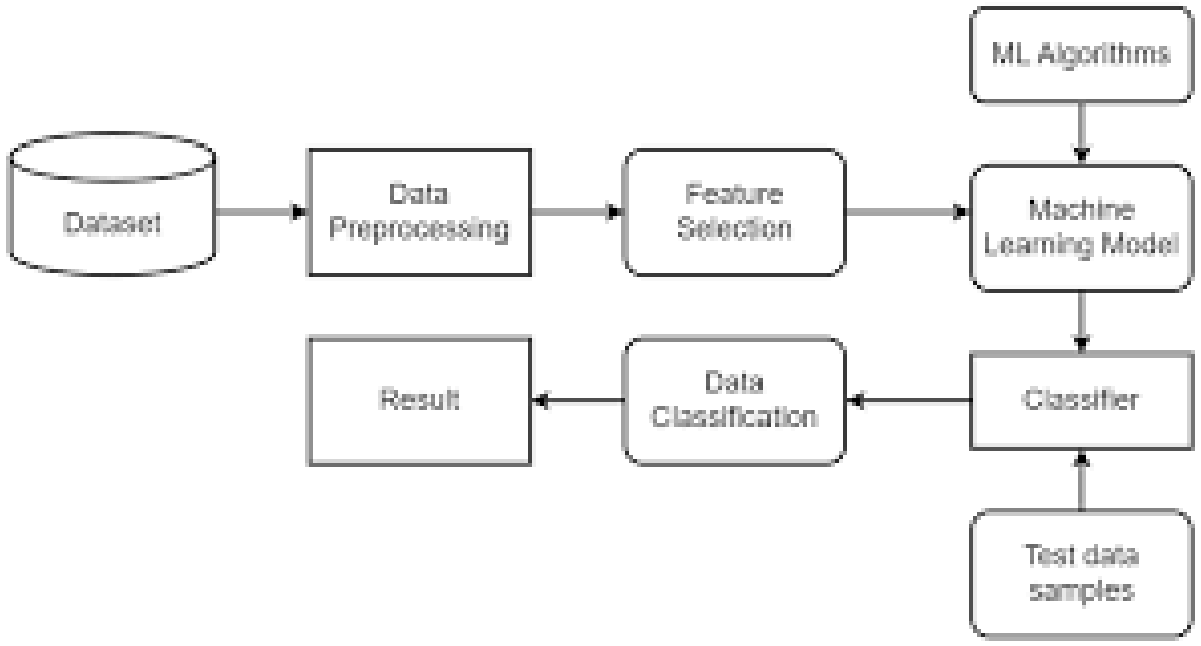


3. DESIGN

3.1 Introduction

This project aims to develop an advanced machine learning system focused on accurate detection of various liver disorders including cirrhosis, hepatitis, and fatty liver disease. By employing robust algorithms such as Random Forest, logistic regression, and SVM, the system will analyze diverse sets of patient data encompassing demographic details and clinical indicators. Special attention will be given to handling data complexities like missing values and class imbalance to ensure the reliability and effectiveness of the models. A key aspect of the project involves integrating these predictive models into clinical practice, supported by intuitive user interfaces that allow healthcare professionals and patients to input parameters and receive real-time predictions. Ultimately, the project seeks to enhance early diagnosis and intervention of liver-related conditions, thereby improving patient outcomes and optimizing healthcare resource utilization.

3.2 Data Flow Diagram:



3.3 Data Set Descriptions

Age: The age of the individual in years (numeric).

Gender: Gender of the individual encoded as a binary value:

- 1 for Male
- 0 for Female

Total Bilirubin: Total amount of bilirubin in the blood (numeric, typically in mg/dL).

Alkaline Phosphotase: Level of alkaline phosphotase in the blood (numeric, typically in IU/L).

Alamine Aminotransferase: Level of alanine aminotransferase (ALT or SGPT) in the blood (numeric, typically in IU/L).

Aspartate Aminotransferase: Level of aspartate aminotransferase (AST or SGOT) in the blood (numeric, typically in IU/L).

Total Protiens: Total protein level in the blood (numeric, typically in g/dL).

Albumin: Albumin level in the blood (numeric, typically in g/dL).

Albumin and Globulin Ratio: Ratio of albumin to globulin in the blood (numeric).

3.4 Data Preprocessing Techniques

Data preprocessing is a critical step in preparing the dataset for training machine learning models in the Liver Disease Prediction Web Application. This section outlines the techniques and methodologies used to clean, transform, and enhance the raw medical data before feeding it into the predictive models.

Data Cleaning:

- **Handling Missing Values:** Identify and handle missing data in the dataset, typically through techniques such as imputation (replacing missing values with a statistical measure like mean, median, or mode) or deletion of rows or columns with missing values if deemed appropriate.
- **Removing Duplicates:** Eliminate duplicate records from the dataset to ensure each data point is unique and prevents bias during model training.

Data Transformation:

- **Normalization:** Scale numerical features to a standard range (e.g., between 0 and 1) to ensure all features contribute equally to model training. Common normalization techniques include Min-Max scaling or Z-score normalization.
- **Encoding Categorical Variables:** Convert categorical variables (e.g., gender) into numerical representations suitable for machine learning algorithms. This can be achieved through techniques like one-hot encoding or label encoding, depending on the nature of the categorical data.

Feature Selection and Engineering:

- **Feature Selection:** Identify and select relevant features (input variables) that have the most significant impact on predicting liver disease. This can be done using statistical methods (e.g., correlation analysis, feature importance scores from models) or domain knowledge.
- **Feature Engineering:** Create new features from existing ones that may enhance the predictive power of the model. For instance, calculating derived features like body

mass index (BMI) from height and weight data can provide additional insights into health status.

Handling Outliers:

- **Identifying Outliers:** Detect outliers in numerical data that may skew statistical analysis and model predictions. Techniques such as visualization (e.g., box plots, scatter plots) and statistical methods (e.g., Z-score, IQR) can be used for outlier detection.
- **Treating Outliers:** Depending on the nature of outliers, they can be removed if they are data entry errors or transformed (e.g., through winsorization) to mitigate their impact on model training without losing valuable information.

Data Integration and Formatting:

- **Data Integration:** Combine and merge datasets from different sources (e.g., demographic data, laboratory test results) into a cohesive dataset suitable for model training.
- **Data Formatting:** Ensure the dataset is formatted correctly according to the input requirements of the machine learning algorithms and libraries being used (e.g., Pandas DataFrame for Scikit-learn).

Validation and Quality Assurance:

- **Cross-Validation:** Split the dataset into training and validation sets to assess model performance and generalize its ability to make predictions on unseen data.
- **Quality Assurance:** Conduct thorough checks and validations to ensure the integrity, consistency, and correctness of the preprocessed dataset before proceeding to model training and deployment.

3.5 Methods and Algorithms

1. Support Vector Machines (SVM)

Support Vector Machines (SVMs) can classify liver conditions by analyzing features from CT or MRI scans to differentiate between healthy and diseased tissues. They find the optimal hyperplane that separates different classes in a high-dimensional space, making them effective for imaging analysis. SVMs can also classify patients based on biomarkers like ALT and AST levels to distinguish between conditions such as hepatitis and cirrhosis.

2. Naive Bayes

Naive Bayes can predict the likelihood of liver diseases by analyzing risk factors such as age, alcohol consumption, and genetic predisposition. It leverages probabilistic modeling to handle clinical features, making it suitable for risk prediction. Additionally, Naive Bayes can analyze text from electronic health records to identify patterns and keywords associated with liver diseases, aiding in early detection.

3. Decision Trees

Decision Trees help in diagnostic decision-making by partitioning patient data based on significant features like lab results and symptoms. They create clear decision rules that highlight key diagnostic criteria, making them interpretable and effective for identifying liver diseases such as cirrhosis. By determining the most relevant features, Decision Trees improve diagnostic accuracy and patient care.

4. Random Forests

Random Forests improve liver disease classification by constructing multiple decision trees and combining their outputs, enhancing accuracy and robustness. They handle large datasets effectively and can classify various liver conditions, such as hepatitis and liver cancer. Random Forests are also used for predicting disease progression by analyzing longitudinal patient data, which is crucial for managing chronic liver diseases.

5. Logistic Regression

Logistic Regression models the probability of a patient having a specific liver disease based on predictors like liver enzyme levels and imaging findings. It is used for binary classification tasks, such as predicting the likelihood of hepatocellular carcinoma. Logistic Regression also helps in assessing the risk of developing liver diseases based on lifestyle factors and genetic predispositions, aiding in preventive healthcare.

6. K-Nearest Neighbors (KNN)

Application in Liver Disease Detection:

K-Nearest Neighbors (KNN) classifies liver diseases by comparing new patient data with historical cases based on feature similarity. It clusters patients with similar lab results and symptoms, identifying those with conditions like hepatitis or cirrhosis. KNN leverages the similarity in feature space to suggest potential diagnoses, making it an intuitive method for detecting liver diseases.

4.DEPLOYMENT AND RESULTS

4.1 Introduction

Deploying machine learning models for liver disease detection involves integrating the developed algorithms into clinical workflows and healthcare systems. This process includes setting up the necessary infrastructure, such as servers and databases, and ensuring data security and patient privacy. The models are then tested and validated using real-world clinical data to assess their performance and reliability. Results from deployment are evaluated based on metrics such as accuracy, sensitivity, specificity, and predictive value, providing insights into the effectiveness of the models in aiding liver disease diagnosis and management. Successful deployment can lead to improved early detection, treatment planning, and overall patient outcomes.

4.2 Source Code

Liver.py

```
import pandas as pd
import numpy as np
import pickle
# for displaying all feature from dataset:
pd.pandas.set_option('display.max_columns', None)
# Reading Dataset:
dataset = pd.read_csv("Dataset/Liver_data.csv")
# Filling NaN Values of "Albumin_and_Globulin_Ratio" feature with Median:
dataset['Albumin_and_Globulin_Ratio'] =
dataset['Albumin_and_Globulin_Ratio'].fillna(dataset['Albumin_and_Globulin_Ratio'].media
n())
# Label Encoding:
dataset['Gender'] = np.where(dataset['Gender']=='Male', 1,0)
# Droping 'Direct_Bilirubin' feature:
dataset = dataset.drop('Direct_Bilirubin', axis=1)
# Independent and Dependent Feature:
X = dataset.iloc[:, :-1]
y = dataset.iloc[:, -1]
```

```
# SMOTE Technique:
from imblearn.combine import SMOTETomek
smote = SMOTETomek()
X_smote, y_smote = smote.fit_resample(X,y)
# Train Test Split:
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test = train_test_split(X_smote,y_smote, test_size=0.3,
random_state=33)
# RandomForestClassifier:
from sklearn.ensemble import RandomForestClassifier
RandomForest = RandomForestClassifier()
RandomForest = RandomForest.fit(X_train,y_train)
# Creating a pickle file for the classifier
filename = 'Liver2.pkl'
pickle.dump(RandomForest, open(filename, 'wb'))
```

Index.html

```
<!DOCTYPE html>
<html lang="en">
<head>
<meta charset="UTF-8">
<title>Liver Prediction Model</title>
</head>
<body>
<div class="container">
<h2 class='container-heading'><span class="heading_font">Liver Disease
Prediction</span></h2>
</div>
<div class="ml-container">
<form action="{{ url_for('predict') }}" method="POST">
<br>
```

```
<h3>Age</h3>
<input id="first" name="Age" placeholder="in Year" required="required">
<br>
<h3>Gender</h3>
<input id="second" name="Gender" placeholder="Male = 1, Female=0"
required="required">
<br>
<h3>Total Bilirubin</h3>
<input id="third" name="Total_Bilirubin" placeholder="Total Bilirubin"
required="required">
<br>
<h3>Alkaline Phosphotase</h3>
<input id="fourth" name="Alkaline_Phosphotase" placeholder="Alkaline Phosphotase"
required="required">
<br>
<h3>Alamine Aminotransferase</h3>
<input id="fifth" name="Alamine_Aminotransferase" placeholder="Alamine
Aminotransferase" required="required">
<br>
<h3>Aspartate Aminotransferase</h3>
<input id="sixth" name="Aspartate_Aminotransferase" placeholder="Aspartate
Aminotransferase" required="required">
<br>
<h3>Total Protiens</h3>
<input id="seventh" name="Total_Protiens" placeholder="Total Protiens"
required="required">
<br>
<h3>Albumin</h3>
<input id="eight" name="Albumin" placeholder="Albumin" required="required">
<br>
<h3>Albumin and Globulin Ratio</h3>
```

```
<input id="ninth" name="Albumin_and_Globulin_Ratio" placeholder="Albumin and
Globulin Ratio" required="required">
<br>
<br>
<br>
<button id="sub" type="submit ">Submit</button>
<br>
<br>
<br>
<br>
</form>
</div>

<style>
/* Background Image */
body
{
background-image:url("https://raw.githubusercontent.com/SagarDhandare/Liver-Disease-
Prediction-Project/main/Images/Liver.jpg");
height: 100%;
/* Center and scale the image nicely */
background-position: center;
background-repeat: no-repeat;
background-size: 100% 100%;
}
/* Color */
body{
font-family: Arial, Helvetica,sans-serif;
    text-align: center;
    margin: 0;
    padding: 0;
    width: 100%;
```

```
height: 100%;
display: flex;
flex-direction: column;
}
/* Heading Font */
.container-heading{
   margin: 0;
}
.heading_font{
color: #black;
font-family: 'Pacifico', cursive;
font-size: 50px;
font-weight: normal;
}
/* Box */
      #first {
         border-radius: 14px;
         height: 25px;
         width: 150px;
         font-size: 20px;
         text-align: center;
      }
      #second {
         border-radius: 14px;
         height: 25px;
         width: 220px;
         font-size: 20px;
         text-align: center;
      }
      #third {
         border-radius: 14px;
         height: 25px;
```

```
    width: 180px;
    font-size: 20px;
    text-align: center;
}
#fourth {
    border-radius: 14px;
    height: 25px;
    width: 250px;
    font-size: 20px;
    text-align: center;
}

#fifth {
    border-radius: 14px;
    height: 25px;
    width: 270px;
    font-size: 20px;
    text-align: center;
}
#sixth {
    border-radius: 14px;
    height: 25px;
    width: 280px;
    font-size: 20px;
    text-align: center;
}
#seventh {
    border-radius: 14px;
    height: 25px;
    width: 170px;
    font-size: 20px;
    text-align: center;
```

```
        }
        #eight {
            border-radius: 14px;
            height: 25px;
            width: 150px;
            font-size: 20px;
            text-align: center;
        }
        #ninth {
            border-radius: 14px;
            height: 25px;
            width: 280px;
            font-size: 20px;
            text-align: center;
        }
/* Submit Button */
#sub {
            width: 120px;
            height: 43px;
            text-align: center;
            border-radius: 14px;
            font-size: 18px;
        }
<linkrel="stylesheet"href="https://cdnjs.cloudflare.com/ajax/libs/font-
awesome/4.7.0/css/font-awesome.min.css">
</style>
</body>
</html>
```

Result.html

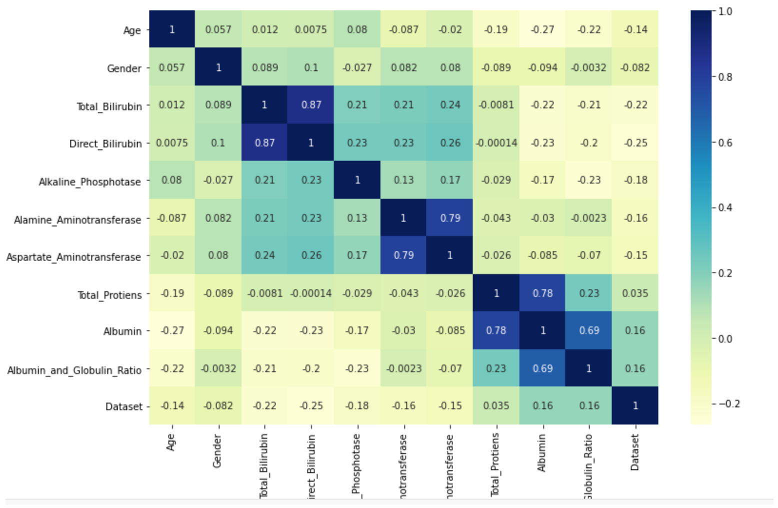
```
<!DOCTYPE html>
<html lang="en">
<head>
<meta charset="UTF-8">
<meta name="viewport" content="width=device-width, initial-scale=1.0">
<title>Liver Disease Result</title>
</head>
<body>
<div class="container">
<form action="{{ url_for('predict')}}" method="post">
<h2 class='container-heading'><span class="heading_font">Liver Disease Prediction</span></h2>
<br><br><br><br><br><br><br>
<!-- Result -->
<div class="results">
{% if prediction==2 %}
<h1><span class='danger'>Oops! ☹<br><br>You have LIVER DISEASE <br><br>Please Consult a Doctor.</span></h1>
<img class="gif" src="{{ url_for('static', filename='dr.gif') }}" alt="LIVER Image">
{% elif prediction==1 %}
<h1><span class='safe'>□ Congratulation! □<br><br>You DON'T have LIVER DISEASE.</span></h1>
<img class="gif1" src="{{ url_for('static', filename='yes.webp') }}" alt="Not LIVER Image">
{% endif %}
</div>
</form>
```

```
</div>
<div>
<br><br><br><br><br><br><br><br><br><br>
</div>
<style>
/* Background Image */
body
{
background-image:url("https://raw.githubusercontent.com/SagarDhandare/Liver-Disease-
Prediction-Project/main/Images/Liver.jpg");
height: 100%;
/* Center and scale the image nicely */
background-position: center;
background-repeat: no-repeat;
background-size: 100% 100%;
}
/* Color */
body{
font-family: Arial, Helvetica,sans-serif;
text-align: center;
margin: 0;
padding: 0;
width: 100%;
height: 100%;
display: flex;
flex-direction: column;
}
```

```
/* Heading Font */
.container-heading{
margin: 0;
}
.heading_font{
color: #black;
font-family: 'Pacifico', cursive;
font-size: 50px;
font-weight: normal;
}

<link  rel="stylesheet"  href="https://cdnjs.cloudflare.com/ajax/libs/font-awesome/4.7.0/css/font-
awesome.min.css">
</style>
</body>
</html>
```

4.3 Model Implementation and Training

To implement and train a simple liver disease prediction application, we first imported essential libraries such as NumPy, Pandas, Matplotlib, Seaborn, and Flask. These libraries facilitate data manipulation, visualization, and web application development. We then utilized the RandomForestClassifier from the Scikit-learn library for building our predictive model. This ensemble learning algorithm is well-suited for classification tasks, making it suitable for predicting liver disease based on given features. Next, we train the RandomForestClassifier model on the training data. Once trained, we evaluate the model's performance on the testing set.



4.4 Model Evaluation Metrics

Evaluating the performance of the trained models is crucial to understanding their effectiveness and making informed decisions about model selection and deployment. Several metrics are used to evaluate the models in this project, each providing a different perspective on the model's performance. The key metrics include accuracy, precision, recall, and F1 score.

Accuracy

Accuracy provides an overall measure of how well the model performs across all classes. It is particularly useful when the classes are balanced, meaning each class has roughly the same number of instances. Mathematically, it can be expressed as:

$$\text{□□□□□□□□□} = \frac{\text{□□□□□□□ □□ □□□□□□□□ □□□□□□□□□□□□}}{\text{□□□□□ □□□□□□□ □□ □□□□□□□□□□□□}}$$

Precision

High precision indicates that the model has a low false positive rate, meaning that when it predicts a positive instance, it is likely to be correct. This metric is particularly important in scenarios where the cost of false positives is high. Precision is defined as:

$$\text{□□□□□□□□□□} = \frac{\text{□□□□ □□□□□□□□□□}}{\text{□□□□ □□□□□□□□□□} +}$$

□□□□□ □□□□□□□□□□

Recall

Recall, also known as Sensitivity or True Positive Rate. High recall indicates that the model has a low false negative rate, meaning it successfully identifies most of the positive instances and is defined as:

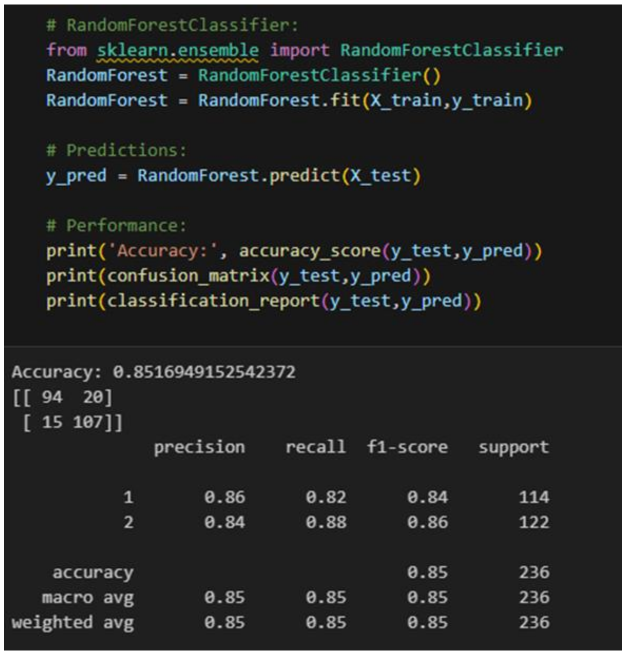
$$\text{□□□□□□□} = \frac{\text{□□□□ □□□□□□□□□□}}{\text{□□□□ □□□□□□□□□□} + \text{□□□□□ □□□□□□□□□□}}$$

F1 Score

The F1 score is the harmonic mean of precision and recall. The F1 score is particularly useful when there is an imbalance between precision and recall. By combining both metrics, the F1 score gives a more comprehensive view of the model's performance. It is defined as:

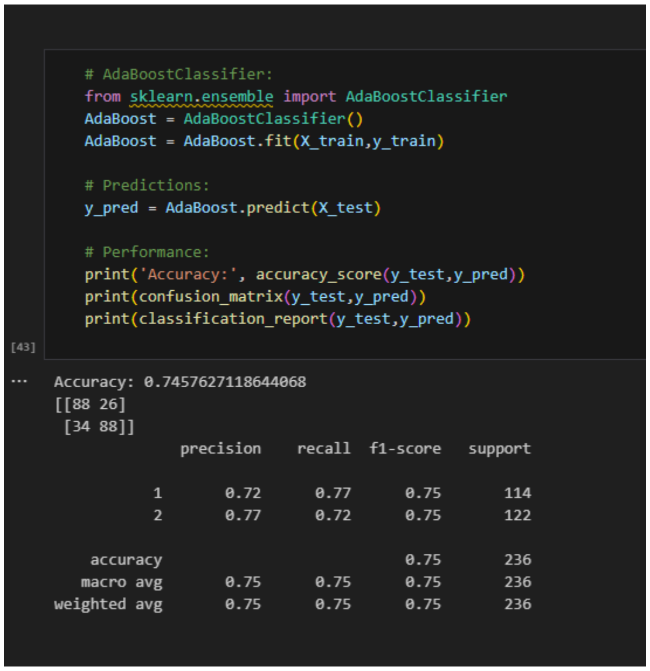
$$F1\ Score = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

In assessing the effectiveness of a simple liver disease prediction application employing machine learning, several key metrics come into play to provide a comprehensive understanding of its performance.



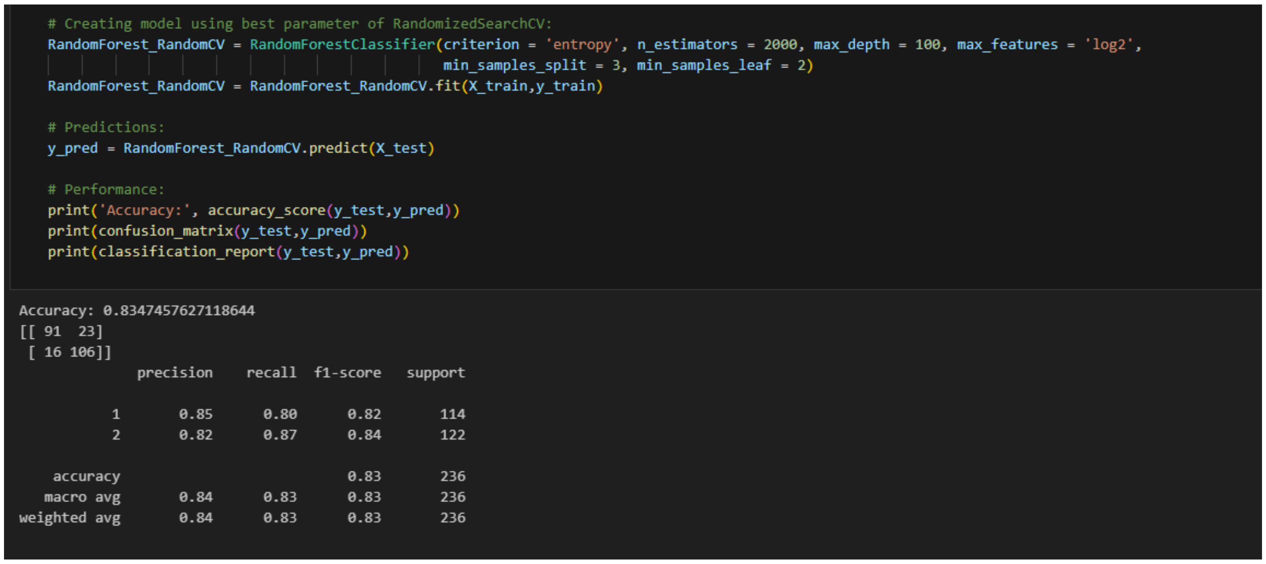
```
# RandomForestClassifier:
from sklearn.ensemble import RandomForestClassifier
RandomForest = RandomForestClassifier()
RandomForest = RandomForest.fit(X_train,y_train)

# Predictions:
y_pred = RandomForest.predict(X_test)

# Performance:
print('Accuracy:', accuracy_score(y_test,y_pred))
print(confusion_matrix(y_test,y_pred))
print(classification_report(y_test,y_pred))
```

```
Accuracy: 0.8516949152542372
[[ 94  20]
 [ 15 107]]
              precision    recall  f1-score   support

           1       0.86      0.82      0.84       114
           2       0.84      0.88      0.86       122

    accuracy                           0.85       236
   macro avg       0.85      0.85      0.85       236
weighted avg       0.85      0.85      0.85       236
```



```
# AdaBoostClassifier:
from sklearn.ensemble import AdaBoostClassifier
AdaBoost = AdaBoostClassifier()
AdaBoost = AdaBoost.fit(X_train,y_train)

# Predictions:
y_pred = AdaBoost.predict(X_test)

# Performance:
print('Accuracy:', accuracy_score(y_test,y_pred))
print(confusion_matrix(y_test,y_pred))
print(classification_report(y_test,y_pred))
```

```
Accuracy: 0.7457627118644068
[[88 26]
 [34 88]]
              precision    recall  f1-score   support

           1       0.72      0.77      0.75       114
           2       0.77      0.72      0.75       122

    accuracy                           0.75       236
   macro avg       0.75      0.75      0.75       236
weighted avg       0.75      0.75      0.75       236
```



```
# Creating model using best parameter of RandomizedSearchCV:
RandomForest_RandomCV = RandomForestClassifier(criterion = 'entropy', n_estimators = 2000, max_depth = 100, max_features = 'log2',
                                               min_samples_split = 3, min_samples_leaf = 2)
RandomForest_RandomCV = RandomForest_RandomCV.fit(X_train,y_train)

# Predictions:
y_pred = RandomForest_RandomCV.predict(X_test)

# Performance:
print('Accuracy:', accuracy_score(y_test,y_pred))
print(confusion_matrix(y_test,y_pred))
print(classification_report(y_test,y_pred))
```

```
Accuracy: 0.8347457627118644
[[ 91  23]
 [ 16 106]]
              precision    recall  f1-score   support

           1       0.85      0.80      0.82       114
           2       0.82      0.87      0.84       122

    accuracy                           0.83       236
   macro avg       0.84      0.83      0.83       236
weighted avg       0.84      0.83      0.83       236
```

4.5 Model Deployment: Testing and Validation

Testing and validation are crucial phases in the deployment of machine learning models for liver disease detection, ensuring that the algorithms perform reliably in real-world settings. The testing phase involves applying the trained model to a separate, unseen dataset to assess its predictive accuracy and generalizability. Key metrics such as accuracy, sensitivity, specificity, precision, and recall are calculated to evaluate the model’s performance. Validation ensures the model's robustness by verifying its ability to maintain high performance across diverse patient populations and conditions.

During testing, the model's predictions are compared against actual clinical outcomes to measure its effectiveness in identifying liver diseases such as hepatitis, cirrhosis, and liver cancer. The validation process includes techniques like cross-validation and external validation using datasets from different sources or institutions to confirm the model’s reliability.

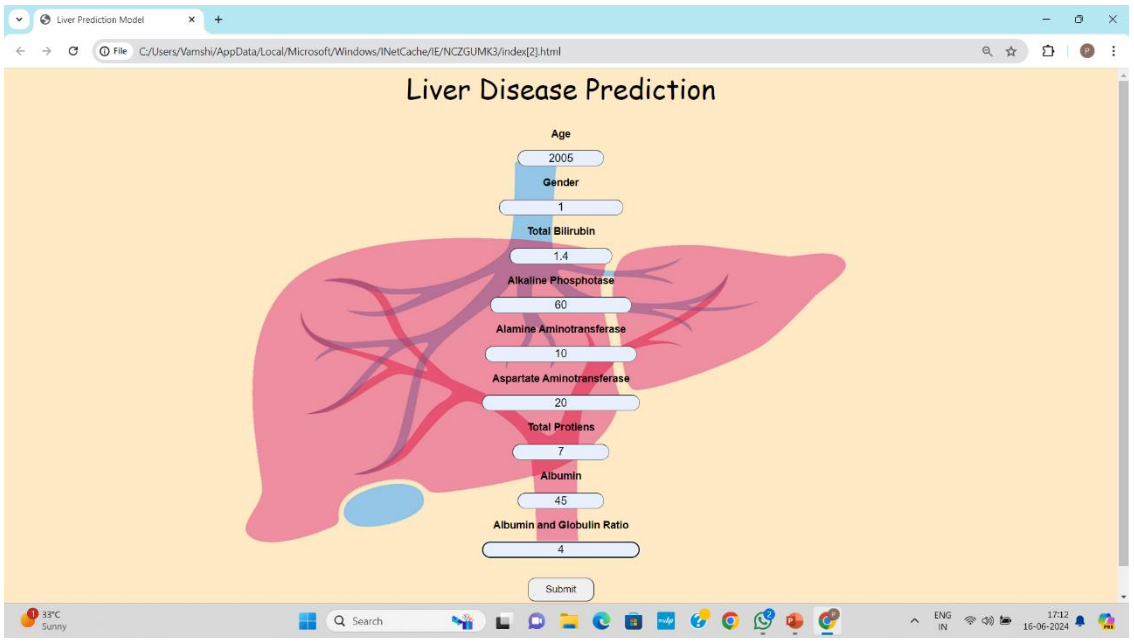
Furthermore, real-time testing in a clinical environment is conducted to observe the model's integration with existing healthcare workflows. This step helps identify any practical challenges or limitations, such as the model's response time, ease of use by healthcare professionals, and its ability to handle incomplete or noisy data. Continuous feedback from clinicians is essential to refine and improve the model's functionality and accuracy.

4.6 Application GUI’s Development

Developing an intuitive and user-friendly graphical user interface (GUI) is essential for the successful deployment of machine learning models for liver disease detection. The GUI bridges complex algorithms and healthcare professionals, enabling seamless interaction with the model’s functionalities. Initially, requirement analysis is conducted to understand end-user needs, focusing on essential features like data input, result visualization, and report generation. The design phase involves creating wireframes and mockups, emphasizing usability and accessibility, with elements such as forms, buttons, and visual graphs. Development follows, using frameworks like React, Angular, or Python-based tools to build responsive and interactive interfaces. Integration with machine learning models ensures functionalities for data upload, running predictions, and displaying results. Thorough testing, including usability testing with end-users, ensures smooth operation and accurate result representation. Deployment within healthcare systems involves compatibility checks, user training, and establishing maintenance plans for updates and enhancements. An effective GUI enhances user experience, improves accuracy, increases efficiency, and encourages adoption, ultimately leading to better diagnostic capabilities and patient outcomes.

4.7 Results

FIG 1:



Liver Prediction Model

C:/Users/Vamshi/AppData/Local/Microsoft/Windows/INetCache/IE/NCZGUMK3/index[2].html

Liver Disease Prediction

Age: 2005

Gender: 1

Total Bilirubin: 1.4

Alkaline Phosphotase: 60

Alamine Aminotransferase: 10

Aspartate Aminotransferase: 20

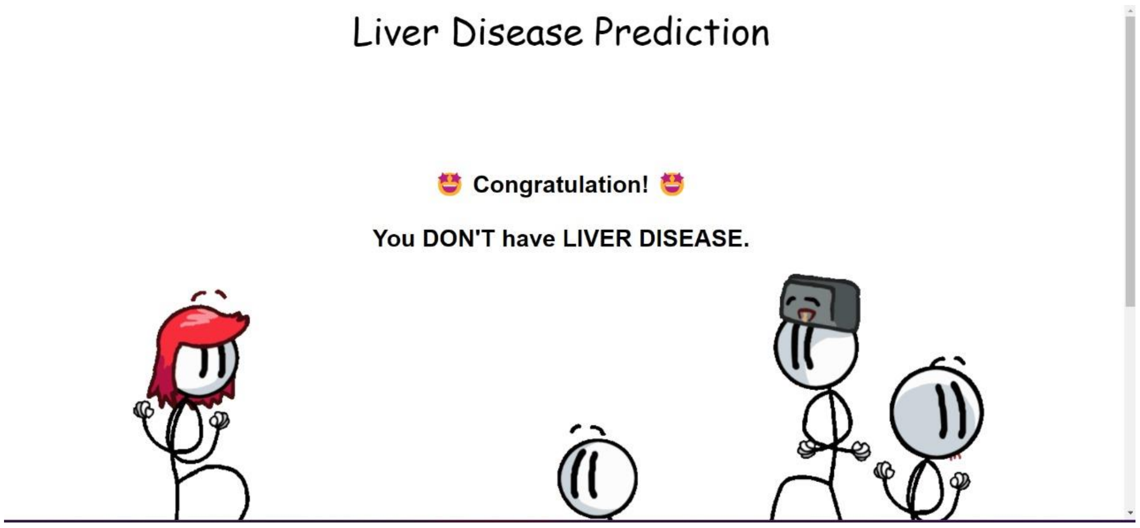
Total Protiens: 7

Albumin: 45

Albumin and Globulin Ratio: 4

Submit

FIG 2:



Liver Disease Prediction

🤩 Congratulation! 🤩

You DON'T have LIVER DISEASE.

5. CONCLUSION

5.1 Project Conclusion

In conclusion, the development and deployment of a user-friendly graphical user interface (GUI) for machine learning models in liver disease detection represent a pivotal advancement in healthcare technology. By bridging the gap between sophisticated algorithms and clinical practice, a well-designed GUI streamlines data input, enhances result visualization, and facilitates informed decision-making for healthcare professionals. Through rigorous testing and integration with machine learning models, the GUI ensures reliability and accuracy in predicting and diagnosing liver diseases such as hepatitis, cirrhosis, and hepatocellular carcinoma. Moreover, its intuitive design fosters user adoption and efficiency, ultimately improving diagnostic outcomes and patient care. As technology continues to evolve, ongoing maintenance and updates will be essential to uphold usability standards and incorporate advancements, ensuring the GUI remains a valuable tool in the medical field.

5.2 Future Scope

Looking ahead, the future scope for GUI development in conjunction with machine learning models for liver disease detection holds promising opportunities for advancing healthcare:

- **Enhanced Interactivity and Personalization:** Future GUIs can leverage advancements in natural language processing (NLP) and user interaction design to offer more intuitive and personalized experiences. This could involve voice commands for data input, adaptive interfaces based on user preferences, and real-time feedback mechanisms.

- **Integration of Multi-modal Data:** Incorporating diverse data sources such as genomic data, wearable device outputs, and patient-reported outcomes into GUIs can enrich diagnostic capabilities. This integration would enable comprehensive patient profiling and more accurate disease predictions.

- **Real-time Decision Support:** GUIs equipped with real-time analytics and decision support systems can assist healthcare providers in making timely and informed decisions. This could include predictive alerts for disease progression, treatment response monitoring, and risk assessment based on continuous patient data streams.

- **AI-driven Automation:** Advancements in artificial intelligence (AI) algorithms, including reinforcement learning and autonomous systems, can automate routine tasks within GUIs. This automation can streamline workflows, reduce human error, and optimize resource allocation in clinical settings.

- **Telemedicine and Remote Monitoring:** GUIs tailored for telemedicine applications can facilitate remote consultations, enabling healthcare providers to remotely access and interpret diagnostic results. This capability is especially beneficial for rural areas and underserved populations, improving access to specialized care.

- **Ethical Considerations and Data Privacy:** As GUIs handle sensitive patient data, future developments must prioritize robust data privacy measures and ethical guidelines. Implementing secure data storage, encryption protocols, and transparent data usage policies will be essential to maintain patient trust and regulatory compliance.

- **Collaborative Research and Global Health Initiatives**: GUIs that support collaborative research efforts and global health initiatives can accelerate knowledge sharing and innovation in liver disease detection. By fostering international collaborations and data sharing frameworks, GUIs can contribute to advancing healthcare equity and addressing global health challenges.