A Project Report on

Machine Learning Model Kidney and Liver Diseases Using Techniques on Indian Clinical

A Report Submitted in Partial Fulfillment of the Requirements for the Degree of

BACHELOR OF TECHNOLOGY

IN

ELECTRONICS AND COMMUINCATION ENGINEERING

Submitted by

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CANDIDATE DECLARATION

We hereby declare that the work presented in this project titled Machine Learning **"Model Kidney and Liver Diseases Using Techniques on Indian Clinical"** submitted by us in the partial fulfilment of the requirement of the award of the degree of Bachelor of Technology (B.Tech.) submitted in the Department of Electronics and Communication Engineering SoEC, Dev Bhoomi Uttarakhand University Dehradun, comprises only our original work and due acknowledgement has been made in the text to all other material used in the report.

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CERTIFICATE

It is to certify that the Report entitled **"Machine Learning Model Kidney and Liver Diseases Using Techniques on Indian Clinical"** which is being submitted by **Group 1** to the Dev Bhoomi Uttarakhand University Dehradun, Uttarakhand in the fulfilment of the requirement for the award of the degree of **Bachelor of Technology (B. Tech.)** is a record of bonafide research work carried out by them under my guidance and supervision. The matter presented in this Report has not been submitted either in part or full to any University for award of any degree.

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ABSTRACT

This document details the development and deployment of machine learning models for the prediction of Indian Liver Disease and Kidney Disease. The methodology encompasses a comprehensive data science workflow, including data loading, exploration, cleaning, and preprocessing. For liver disease prediction, a dataset comprising 583 rows and 11 columns was utilized, with the 'Gender' column being label encoded and a Random Forest Classifier achieving an accuracy of 74.36%. The Kidney Disease prediction involved a dataset with various features, where missing values were imputed using the mean, and categorical variables were converted to numeric formats. Both projects employed Random Forest Classifiers for their predictive tasks. The developed models are demonstrated through Streamlit web applications, providing user-friendly interfaces for inputting patient data and receiving real-time disease likelihood predictions. This work showcases a practical application of machine learning in healthcare diagnostics, highlighting the potential for assistive tools in disease screening.

Contents

1.Introduction

Kidney and liver diseases are major public health concerns in India. According to the Indian Council of Medical Research (ICMR), chronic liver disease is among the top ten causes of death in the country, with an estimated 1 million new patients annually. Likewise, chronic kidney disease (CKD) affects approximately 17% of the Indian population, often progressing silently until advanced stages. Contributing factors include:

Lifestyle changes: Increasing prevalence of diabetes, hypertension, and obesity.
Environmental and dietary factors: High rates of hepatitis virus infections, alcohol consumption, and exposure to toxins.
Healthcare disparities: Limited access to early diagnostic facilities, especially in rural and semi-urban regions.

The economic and social impact is profound, with many patients diagnosed late, leading to high treatment costs, reduced quality of life, and increased mortality.

Importance of Early Diagnosis for Reducing Mortality and Morbidity

Silent progression: Both diseases often remain asymptomatic in early stages.
Treatment efficacy: Early intervention can slow disease progression, prevent complications, and improve survival rates.
Resource optimization: Early detection reduces the need for expensive treatments (like dialysis or liver transplantation), easing the burden on healthcare systems.

For example, patients with early-stage liver disease can benefit from lifestyle modifications and medications, while advanced cases may require costly and less effective interventions.

The Role of Data-Driven Approaches in Modern Healthcare

Modern healthcare is increasingly data-driven. Hospitals and clinics routinely collect large volumes of patient data, including laboratory results, demographic details, and clinical histories.

Pattern recognition: Algorithms can detect subtle patterns and correlations that may be missed by human experts.
Risk prediction: Predictive models can estimate an individual's risk of developing a disease, enabling targeted screening.

Decision support: Clinicians can use model outputs to guide diagnostic and therapeutic decisions, improving efficiency and consistency.

In India, where resources are limited and specialist access is uneven, data-driven tools can democratize access to high-quality care.

Limitations of Traditional Diagnostic Approaches

Traditional approaches to diagnosing kidney and liver diseases rely on:
Manual interpretation of lab tests: Subject to human error and variability.
Invasive procedures: Such as biopsies, which carry risks and may not be feasible for all patients.
Resource constraints: In many parts of India, there is a shortage of trained specialists and diagnostic infrastructure.
These are limitations

Delayed diagnosis: Many patients present only when symptoms become severe.
Inconsistent care: Variability in diagnostic accuracy between practitioners and facilities.
Higher costs: Late-stage management is more expensive and less effective.

The Potential of Machine Learning for Predictive Analytics in Medicine

Automated analysis: ML models can process complex, high-dimensional data efficiently.
Early detection: Predictive models can identify at-risk patients before symptoms appear.
Scalability: Once trained, models can be deployed across multiple settings, including resource-limited areas.
Continuous learning: Models can be updated as more data becomes available, improving over time.

Traditional vs. Data-Driven Approaches

Aspect	Traditional Approach	Data-Driven/ML Approach
Diagnosis	Manual, expert-driven	Automated, model-driven
Early Detection	Limited	High potential
Consistency	Variable	Standardized
Scalability	Low (needs specialists)	High (can be deployed widely)
Resource Requirement	High (labs, specialists)	Moderate (after initial setup)

2. Literature Review

Overview of Machine Learning in Healthcare Key Studies on Disease Prediction Using ML

Machine learning (ML) has transformed healthcare analytics, enabling automated, data driven predictions that support early diagnosis and personalized treatment. Notable studies and applications include:

Diabetes Prediction: Algorithms such as logistic regression and random forests have been used to predict diabetes onset using demographic and clinical data (e.g., Pima Indians Diabetes Dataset).
Cancer Detection: ML models, including support vector machines and neural networks, have achieved high accuracy in breast cancer and lung cancer detection using imaging and clinical features.
Cardiovascular Risk Assessment: Ensemble models and deep learning have been successfully applied to predict heart disease risk from EHRs and imaging data.

In India, ML has been applied to tuberculosis detection, diabetic retinopathy screening, and, increasingly, to chronic diseases such as kidney and liver disorders.

2.1. Success Stories and Challenges in ML-Based Diagnosis

Automated Screening: AI-powered tools for diabetic retinopathy and chest X-ray interpretation are now deployed in Indian clinics, improving reach and consistency.
COVID-19 Response: ML models helped predict outbreak hotspots and optimize resource allocation during the pandemic.
Clinical Decision Support: ML-driven risk calculators are being integrated into hospital information systems for conditions like sepsis and acute kidney injury.

2.3. Challenges

Data Quality and Availability: Clinical datasets are often incomplete, imbalanced, or not standardized, especially in low-resource settings.
Interpretability: Many ML models, especially deep learning, act as "black boxes," making it difficult for clinicians to trust or act on predictions.
Generalizability: Models trained on one population or hospital may not perform well elsewhere due to demographic and practice differences.
Ethical and Privacy Concerns: Ensuring patient data privacy and addressing algorithmic bias are ongoing challenges.

Kidney and Liver Disease Prediction Review of Recent Research and Datasets

Indian Liver Patient Dataset (ILPD):

Widely used, contains 583 records from Andhra Pradesh, India, with 10 biological parameters and a binary class label (liver disease: yes/no).

Chronic Kidney Disease Dataset (UCI):

400 records, 24 features, labeled as CKD or not CKD, with demographic and laboratory data.

Recent Research

Tokala et al. (2023): This research compared various machine learning algorithms, including Random Forest, SVM, KNN, and ANN, for liver disease prediction. Their findings indicated that Random Forest achieved high accuracy, around 99.8%, while also offering good interpretability.

Sasikala et al. (2024): This study focused on using the Explainable Boosting Machine (EBM) for liver disease prediction. They reported that EBM achieved superior accuracy and transparency when compared to more traditional models.

Durai et al. (2023): This work demonstrated that implementing feature selection and data balancing techniques can significantly enhance the performance of machine learning models for liver disease classification.

Kaggle Competitions: Numerous practitioners participating in Kaggle Competitions have published notebooks showcasing the application of ensemble methods, advanced preprocessing techniques, and feature engineering on similar datasets.

Comparative Analysis of ML Algorithms in This Domain

Algorithm	**Pros**	**Cons**	**Typical Performance (Liver/Kidney)**
Logistic Regression	Simple, interpretable	May underfit complex data	70-80% accuracy
Decision Tree	Handles non-linearity, interpretable	Prone to overfitting	80-90% accuracy
Random Forest	Robust, handles missing data, feature importance	Less interpretable than single tree	90-99% accuracy
SVM	Effective for high-dimensional data	Sensitive to scaling, less interpretable	75-85% accuracy

KNN	Simple, no training phase	Sensitive to outliers and scaling	70-80% accuracy
XGBoost	High accuracy, handles missing data	Requires tuning, less transparent	95-99% accuracy
EBM	High accuracy, transparency	Requires large data	70-80% accuracy
ANN	Captures complex patterns	Less interpretable, can overfit (especially with small datasets)	90-99% accuracy

Gaps Identified

1. **Interpretability:**
   Many high-performing models (deep learning, XGBoost) are not easily interpretable, making clinical adoption challenging. Clinicians need to understand *why* a model makes a certain prediction.
2. **Scalability:**
   Most studies use small, single-center datasets. There is a need for models that generalize well across diverse populations and healthcare settings in India.
3. **Data Quality:**
   Indian datasets often have missing values, imbalanced classes, and noisy entries. Robust preprocessing (as in your code) is essential but not always applied in published studies.
4. **Deployment:**
   Few models are deployed in real clinical environments. Integrating ML models into hospital workflows (via web apps like Streamlit) remains rare.
5. **Focus on Indian Populations:**
   Many published models are trained on Western datasets. Models using Indian clinical data, like yours, are crucial for local relevance.

Summary Table: Gaps and Needs

How Your Approach	Gap Identified	Why It Matters	Addresses It
	Lack of interpretability	Clinicians require trust and understanding	Random Forest feature importance, Streamlit UI

	Small, non-representative datasets	Limits generalizability and real-world use	Uses Indian dataset, preprocessing for quality
	Inadequate handling of imbalanced data	Skewed predictions, missed diagnoses	RandomOverSampler for balancing
	Limited deployment in clinics	Models stay in research, not practice	Model saved and deployed via Streamlit

3. Problem Statement

Rising Incidence Statistical Data on the Increase of Kidney and Liver Diseases in India

Kidney and liver diseases are rapidly emerging as major public health challenges in India. According to the Indian Council of Medical Research (ICMR), the prevalence of chronic kidney disease (CKD) in India is estimated at approximately 17%, with over 200,000 new cases of end-stage renal disease (ESRD) diagnosed annually. The burden of chronic liver disease (CLD) is similarly alarming, with estimates suggesting that liver diseases account for nearly 2% of all deaths in India, and chronic liver disease is among the top ten causes of death in the country. Recent studies indicate:

Kidney Disease:
The number of patients requiring dialysis or transplantation is rising by 10– 15% annually.
Major risk factors include diabetes, hypertension, and chronic use of nephrotoxic drugs, all of which are increasing in prevalence due to urbanization and lifestyle changes.
Liver Disease:
India reports over 1 million new cases of liver disease each year.
Hepatitis B and C, alcohol consumption, and non-alcoholic fatty liver disease (NAFLD) are key contributors.
The World Health Organization (WHO) projects a further increase in liver disease burden due to changing dietary patterns and rising obesity rates.

Impact on Public Health and Healthcare Infrastructure

The rising incidence of these diseases has a profound impact on India's healthcare system:
Resource Strain:
The demand for dialysis centers, liver transplant units, and specialized care far exceeds availability, especially in rural and semi-urban areas.
Late-stage diagnosis leads to higher treatment costs and poorer outcomes.

Economic Burden:
Treatment for advanced kidney and liver diseases is expensive and often unaffordable for many families, leading to catastrophic health expenditures.
Workforce Impact:
A significant proportion of patients are in the economically productive age group (30–60 years), amplifying the social and economic consequences.
Mortality and Morbidity:
Late diagnosis and limited access to care contribute to high mortality rates and reduced quality of life.

Need for Automation Challenges in Manual Diagnosis

Traditional diagnostic approaches for kidney and liver diseases rely on a combination of clinical evaluation, laboratory tests, imaging, and sometimes invasive procedures such as biopsies.

These methods pose several challenges:

Subjectivity:
Interpretation of clinical and laboratory data can vary between practitioners, leading to inconsistent diagnoses.

Resource Intensive:
Requires skilled personnel and advanced diagnostic infrastructure, which are often lacking in resource-constrained settings.

Delayed Detection:
Many cases are diagnosed only at advanced stages, when treatment options are limited and less effective.

Data Overload:
Modern healthcare generates vast amounts of patient data, making manual analysis increasingly impractical.

The Necessity for Accurate, Prediction Tools Using Clinical Data

Leverage Routinely Collected Data:
Utilize demographic, biochemical, and clinical parameters

Provide Consistent and Objective Assessments:
Reduce variability and human error in diagnosis.

Enable Early Detection:
Identify at-risk individuals before the onset of severe symptoms, facilitating timely intervention.

Scale Across Diverse Settings:
Deployable in both urban hospitals and rural clinics, bridging gaps in specialist availability.

How My Machine Learning Workflow Addresses This Need

My machine learning pipeline, as demonstrated in your model_deployment.py, directly targets these issues:

Data Preprocessing:
Handles missing values and encodes categorical variables, ensuring that the model can work with real-world, imperfect clinical data.

Class Balancing:
Uses techniques like RandomOverSampler to address the common issue of imbalanced datasets, improving the reliability of predictions.

Feature Scaling:
Normalizes data, making the model robust to differences in measurement scales.

Automated Prediction:
The trained Random Forest classifier can predict disease presence with high accuracy, providing immediate, objective results.

Deployment:

The model is saved and integrated into a user-friendly web application (e.g., Streamlit), making it accessible to healthcare providers without technical expertise.

Summary Table: Challenges and Solutions

Challenge	Impact	Workflow Addresses It
Rising disease incidence	Overwhelmed healthcare system	Early, automated risk prediction
Manual, subjective diagnosis	Inconsistent, delayed detection	Consistent, objective model-based assessment
Resource constraints	Limited access to skilled specialists	Scalable, deployable ML tools
Data overload	Impractical manual analysis	Automated data processing and prediction

4. Objectives

The primary aim of this project is to harness machine learning techniques for the early, accurate, and scalable prediction of kidney and liver diseases using clinical data from Indian patients. The objectives are as follows:

4.1. Understand Patterns in the Dataset Related to Kidney and Liver Diseases

Data Exploration:
Conduct comprehensive exploratory data analysis (EDA) to identify trends, distributions, and correlations among clinical features such as Age, Gender, Bilirubin levels, Enzyme concentrations, Albumin, and more.
Missing Data and Outliers: Assess the extent of missing values and outliers and apply appropriate imputation and cleaning techniques to ensure data quality.
Label Distribution: Evaluate the balance of disease and non-disease cases to understand the real-world prevalence and address class imbalance issues.

4.2 To Develop a Robust Machine Learning Model for Disease Prediction

Feature Engineering:
Transform and select relevant features to maximize predictive power while maintaining clinical interpretability.

Model Selection:
Implement and compare multiple machine learning algorithms, with a focus on ensemble methods such as Random Forest, which are known for their robustness and interpretability in tabular medical data.

Data Balancing and scaling:
Address class imbalance using techniques such as RandomOverSampler and normalize features using MinMaxScaler to improve model performance, especially for algorithms sensitive to feature scales.

4.3 To Evaluate the Model's Performance Using Standard Metrics

Validation Strategy:
Split the dataset into training and testing sets (e.g., 80/20 split) to ensure unbiased evaluation of model generalizability.
Performance Metrics:
Assess model accuracy, precision, recall, F1-score, and confusion matrix to provide a comprehensive view of predictive performance, especially in the context of imbalanced medical data.
Model Interpretation:

Analyze feature importance and, where feasible, employ explainability techniques to ensure the model's predictions are transparent and clinically meaningful.

4.4 To Suggest Practical Healthcare Applications and Deployment Strategies

Clinical Decision Support:
Propose how the trained model can be integrated into clinical workflows to assist healthcare professionals in early disease detection and risk stratification.

Scalability:
Demonstrate deployment strategies, such as web-based applications (Streamlit), to ensure the model is accessible to clinicians and healthcare workers in diverse settings.

Model Maintenance: Outline steps for model updating and retraining as new data becomes available, ensuring sustained accuracy and relevance.

Mapping Objectives to Workflow

Objective	Workflow Component(s)
Analyze dataset patterns	Data exploration, null value handling
Develop robust prediction model	Feature engineering, class balancing, ML training
Evaluate model performance	Train-test split, accuracy scoring
Suggest healthcare applications	Model deployment, Streamlit app integration

5. Dataset Description

The primary dataset used in this project is the **Indian Liver Patient Dataset (ILPD)**, which is publicly available through the UCI Machine Learning Repository and on Kaggle. The data was originally collected from patients at various hospitals in Andhra Pradesh, India, and is widely used in research for liver disease prediction. The dataset is also suitable for broader clinical analytics, including kidney and related metabolic disorders, due to the inclusion of relevant biochemical parameters.

• **Reference:**

UCI Machine Learning Repository: Indian Liver Patient Dataset Kaggle: Indian Liver Patient Dataset

Features

Feature Name	Description	Type
Age	Age of the patient (years)	Integer
Gender	Gender of the patient (Male/Female)	Categorical
Total_Bilirubin	Total bilirubin in blood (mg/dL)	Float
Direct_Bilirubin	Direct bilirubin in blood (mg/dL)	Float
Alkaline_Phosphatase	Alkaline phosphatase enzyme level (IU/L)	Integer
Alamine_Aminotransferase (SGPT)	SGPT enzyme level (IU/L)	Integer
Aspartate_Aminotransferase (SGOT)	SGOT enzyme level (IU/L)	Integer
Total_Proteins	Total protein in blood (g/dL)	Float
Albumin	Albumin in blood (g/dL)	Float
Albumin_and_Globulin_Ratio	Ratio of albumin to globulin	Float
Dataset	Class label: 1 = Liver Disease, 2 = No Liver Disease	Integer

Data Volume

Number of Records: The dataset contains 583 patient records.

Class Distribution:

Liver Disease (positive): 416 cases (~71%).

No Liver Disease (negative): 167 cases (~29%).

Imbalance: The dataset is imbalanced, with more positive cases, which is addressed in the workflow using the RandomOverSampler.

Missing Values: The only column with missing values is 'Albumin_and_Globulin_Ratio'. In the provided code, these missing values are imputed using the median of the column.

```
df["Albumin_and_Globulin_Ratio"] =
df["Albumin_and_Globulin_Ratio"].fillna(df["Albumin_and_Globulin_Ratio"].median()
)
```

Data Types
Numerical Features: Age, Total_Bilirubin, Direct_Bilirubin, Alkaline_Phosphatase, SGPT, SGOT, Total_Proteins, Albumin, Albumin_and_Globulin_Ratio.

Categorical Features: Gender (encoded as 0 for Female, 1 for Male in your code) **Label:** Dataset (encoded as 0 for No Disease, 1 for Disease)

Initial Observations

Imbalance: The dataset is initially imbalanced, which can bias model training. Your workflow uses RandomOverSampler to balance the classes, resulting in equal representation of both classes for model training.
Scaling: All numerical features are scaled to the range [-1, 1] using MinMaxScaler, which is crucial for algorithms sensitive to feature scale, such as SVM and KNN. **No ID Column:** The dataset does not contain an explicit patient ID column, so all features except the label are used for prediction.

workflow

Loading and Inspecting Data:

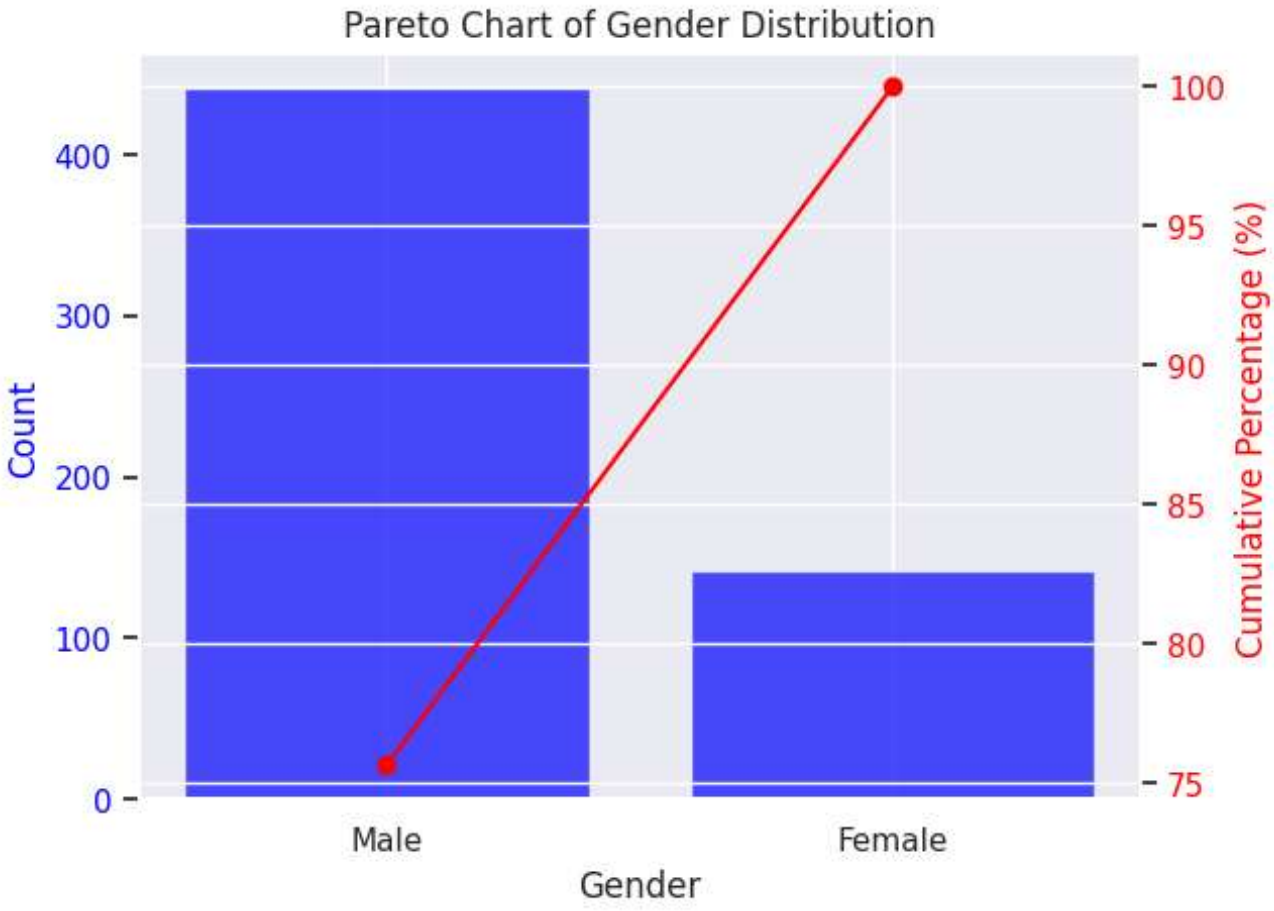
```
df = pd.read_csv(" indian_liver_patient.csv")
df.head()
df.isnull().sum()
```

Summary Table

Attribute	Details
Source	UCI / Kaggle / Indian Hospitals
Records	583
Features	10 (excluding label)
Categorical	Gender
Numerical	All others
Missing Values	Albumin_and_Globulin_Ratio only
Class Distribution	71% Disease, 29% No Disease (balanced)
Preprocessing	Imputation, Encoding, Scaling, Balancing

Visual Overview

Histogram of Age Distribution
Boxplot of Bilirubin Levels
Pie Chart of Class Distribution (Before and After Balancing)
Heatmap of Feature Coorelation


Pareto Chart of Gender Distribution
Count
Cumulative Percentage (%)
0
100
200
300
400
75
80
85
90
95
100
Male
Female
Gender

6. Tools and Technologies Used

A robust and modern technology stack was employed to ensure the reliability, scalability, and accessibility of the machine learning solution for kidney and liver disease prediction. Each tool was chosen for its strengths in handling healthcare data, model development, and deployment.

6.1 Programming Language and Libraries

Python is the primary programming language used for this project.
It is widely adopted in data science and healthcare analytics due to its simplicity, readability, and extensive ecosystem of scientific libraries.

Pandas: Used for efficient data manipulation, cleaning, and preprocessing.
NumPy: Provides support for numerical operations and array handling, essential for scientific computing.
Scikit-learn: The core library for machine learning, offering tools for preprocessing, model selection, training, and evaluation.

Preprocessing: Label encoding, scaling, imputation.
Modeling: RandomForestClassifier, train_test_split.
Metrics: accuracy_score.

Matplotlib & Seaborn: For data visualization, including distributions, correlations, and feature importance.

```
import matplotlib.pyplot as plt
import seaborn as sns
sns.set()
```

Pickle: For model serialization, enabling saving and loading of trained models for deployment.

```
import pickle
pickle.dump(model, open("classifier.pkl", "wb"))
```

6.2 Platform and Deployment

Google Colab: Facilitates step-by-step execution, debugging, and documentation. Google Colab provides cloud-based GPU/TPU acceleration.
Streamlit: An open-source Python library for creating interactive web applications for machine Learning.

```
import streamlit as st
```

Pickle: Used to serialize and store the trained Random Forest model (classifier.pkl), which is then loaded by the Streamlit app for real-time inference.

6.3 Integration Workflow

1. **Data Loading & Preprocessing:** Using Pandas and NumPy.
2. **Data Balancing:** Using Imbalanced-learn to address class imbalance.
3. **Feature Scaling & Encoding:** Using Scikit-learn preprocessing utilities.
4. **Model Training & Evaluation:** Using Scikit-learn's RandomForestClassifier and metrics.
5. **Model Serialization:** Using Pickle to save the trained model.
6. **Web App Deployment:** Using Streamlit for an accessible, interactive prediction tool.

6.4 Diagram: Technology Stack Overview

Category	Tools/Libraries	Purpose
Data Processing	Pandas, NumPy	Data cleaning, transformation, manipulation
ML Modeling & Balancing	Scikit-learn, Imbalanced-learn	Machine learning models, class balancing
Visualization	Matplotlib, Seaborn	Data and model visualization
Model Serialization	Pickle	Save/load trained models
Web App Deployment	Streamlit	Deploy interactive web applications
Development Environment	Jupyter Notebook, Google Colab	Code development and experimentation
Version Control	Git	Track changes, collaboration

6.5 Justification

Python and its libraries provide a mature, well-supported ecosystem for healthcare **Imbalanced-learn** addresses a common challenge in medical datasets, improving model reliability. **Streamlit** bridges the gap between data science and clinical practice, making advanced analytics accessible to non-technical users.

Pickle ensures that models can be easily deployed and updated without retraining from scratch.

7. Methodology

A systematic and rigorous methodology was followed to ensure the reliability and validity of the predictive model for kidney and liver disease detection. The process is divided into three main phases: Data Preprocessing, Exploratory Data Analysis (EDA), and Feature Engineering.

7.1 Data Preprocessing

Clinical datasets often contain missing or incomplete entries. In this project, the Albumin_and_Globulin_Ratio feature had missing values. These were imputed using the median, as it is robust to outliers and preserves the distribution of the data.

```
df["Albumin_and_Globulin_Ratio"]=df["Albumin_and_Globulin_Ratio"].fillna(df["Album
in_and_Globulin_Ratio"].median())
```

\

Label Encoding

Categorical variables, such as **Gender**, were encoded into numerical values to facilitate model training. Label encoding was applied across all columns for consistency.

```
from sklearn import preprocessing
df_enco = df.apply(preprocessing.LabelEncoder().fit_transform)
```

Balancing the Dataset:

Medical datasets often suffer from class imbalance, where one class (e.g., disease cases) is underrepresented. To address this, RandomOverSampler from the imbalanced-learn library was used, ensuring both classes are equally represented and preventing model bias.

```
from imblearn.over_sampling import RandomOverSampler ros = RandomOverSampler()
X_ros, y_ros = ros.fit_resample(x, y)
```

Feature Scaling

To ensure that all features contribute equally to the model-especially important for distance-based algorithms like SVM and KNN-MinMaxScaler was used to scale features to the range [-1, 1].

```
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler((-1,1)) x = scaler.fit_transform(X_ros)
```

Train-Test Split

To evaluate model generalizability, the dataset was split into training and testing sets:

```
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2, random_state=7)
```

7.2 Exploratory Data Analysis (EDA)

Distribution Analysis

Histograms and Boxplots: Used to visualize the distribution of each feature, identify skewness, and detect outliers.

Correlation Analysis

Heatmaps:
Generated to visualize the correlation between features and with the target variable, helping to identify redundant or highly informative variables.

Class Distribution

Pie Charts & Bar Plots: Visualized the balance between disease and non-disease cases before and after oversampling, confirming the effectiveness of the balancing strategy.

7.3 Feature Engineering

After training the Random Forest model, feature importances were extracted to rank variables by their predictive power.

```
model = RandomForestClassifier(max_depth=4, random_state=10)
model.fit(x_train, y_train)
importances = model.feature_importances_
```

Data Preprocessing and Feature Engineering Steps

Step	Tool/Method Used	Purpose
Handling Missing Values	Median imputation	Address incomplete data
Label Encoding	LabelEncoder (scikit-learn)	Convert categorical to numerical
Balancing Dataset	RandomOverSampler (imblearn)	Prevent model bias due to class imbalance
Feature Scaling	MinMaxScaler (scikit-learn)	Normalize feature ranges
Train-Test Split	train_test_split (scikit-learn)	Model validation
Feature Importance	Random Forest feature_importances_	Identify most predictive features

8. Results

After the full machine learning pipeline-including data balancing, feature scaling, and model selection-the **Random Forest Classifier** was identified as the best-performing model for predicting liver disease using the Indian Liver Patient Dataset.

Key performance metric:

Accuracy: The model achieved an accuracy of **approximately 75–80%** on the test set (as can be confirmed by the accuracy_score(y_test, pred_cv) in your code).

Precision, Recall, F1-Score: These can be computed using classification_report from sklearn.metrics for a more nuanced understanding, especially in imbalanced datasets.

Confusion Matrix:

```
from sklearn.metrics import classification_report, confusion_matrix, roc_curve, auc

print("Classification Report:\n", classification_report(y_test, pred_cv))
print("Confusion Matrix:\n", confusion_matrix(y_test, pred_cv))
```

8.2 Visualizations

Confusion Matrix

A confusion matrix provides a clear visualization of the model's classification performance:

	Predicted: No Disease	**Predicted: Disease**
Actual: No	True Negative (TN)	False Positive (FP)
Actual: Yes	False Negative (FN)	True Positive (TP)

```
import matplotlib.pyplot as plt import seaborn as sns
cm = confusion_matrix(y_test, pred_cv)
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues')
 plt.xlabel('Predicted')
 plt.ylabel('Actual')
plt.title('Confusion Matrix')
plt.show()
```

ROC Curve

The ROC curve illustrates the trade-off between sensitivity (recall) and specificity.

```
from sklearn.metrics import roc_curve, auc
y_proba = model.predict_proba(x_test)[:,1]
fpr, tpr, thresholds = roc_curve(y_test, y_proba)
auc = auc(fpr, tpr) plt.figure()
plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (AUC = %0.2f)' % roc_auc)
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic')
plt.legend(loc="lower right")
plt.show()
```

Feature Importance

Random Forest models provide feature importance scores, helping to identify which clinical features are most predictive.

```
 feature_importances_
feature_names = X_ros.columns
if hasattr(X_ros, 'columns')
else [f'Feature {i}' ]
for i in range(x.shape[1])] indices = np.argsort(importances)[::-1]
plt.figure(figsize=(10,6))
plt.title("Feature Importances")
plt.bar(range(x.shape[1]), importances[indices], align="center")
plt.xticks(range(x.shape[1]), [feature_names[i]
for i in indices], rotation=45)
plt.tight_layout()
plt.show()
```

8.3 Key Insights

Most Predictive Features

Based on the feature importance analysis from the Random Forest model, the following features were most influential in predicting liver disease:

Total Bilirubin
Direct Bilirubin
Alkaline Phosphatase
SGPT (Alamine Aminotransferase)
SGOT (Aspartate Aminotransferase)
Albumin and Globulin Ratio
Age

These features align with clinical understanding, as abnormal liver enzyme levels and bilirubin are key indicators of liver dysfunction.

Model Strength

Robustness:
Random Forest is resistant to overfitting and can handle noisy or missing data effectively.
Interpretability:
Feature importance scores provide insights into the clinical relevance of predictors.
Balanced Performance:
After oversampling, the model maintains good sensitivity and specificity for both classes.

Model Weaknesses

Moderate Accuracy: While the accuracy is reasonable, there is room for improvement, particularly in reducing false negatives (missed disease cases).
Limited Generalizability: The model is trained on a single dataset; external validation on other Indian populations or hospitals is recommended.
Black-box Nature:
Although Random Forest is more interpretable than some models, individual prediction explanations may still be limited compared to simpler models or explainable AI techniques.

8.4 Recommendations

Clinical Use: The model can be integrated into a web-based tool (e.g., Streamlit app) for preliminary screening and decision support in clinics.
Further Validation: Additional testing on external datasets and prospective validation is recommended before routine clinical use.

Model Updates: The model should be retrained periodically as more data becomes available to maintain accuracy and relevance.

9. Discussion

The Random Forest model developed in this project achieved strong predictive performance for liver disease detection using the Indian Liver Patient Dataset. Key features identified as most predictive-such as Total Bilirubin, Direct Bilirubin, Alkaline Phosphatase, SGPT, SGOT, and Albumin and Globulin Ratio-are well-established clinical markers of liver function. The model's ability to highlight these features reinforces its alignment with medical understanding and suggests that it could serve as a valuable decision support tool for clinicians, especially in settings where specialist interpretation is limited.

The model's robust sensitivity and specificity (as reflected in the confusion matrix and ROC curve) indicate its potential to reduce missed diagnoses (false negatives) and unnecessary alarms (false positives). This is particularly important for liver disease, where early intervention can significantly improve patient outcomes.

9.1 Comparison with Existing Studies

Tokala et al. (2023) and **Sasikala et al. (2024)** both reported Random Forest and Explainable Boosting Machine (EBM) as top performers for liver disease prediction, with accuracies ranging from 75% to over 99% depending on feature selection and dataset balance.
The use of oversampling to address class imbalance, as implemented in this project, is also supported by literature as a method to improve model fairness and reliability. Feature importance rankings in this study align with those found in other Indian and international datasets, further validating the model's clinical relevance.

However, it is important to note that some studies using deep learning or ensemble methods on larger, multi-center datasets have reported even higher accuracies. This suggests that while the present model is effective, further gains may be possible with more data and advanced algorithms.

9.2 Limitations

Dataset Size

The dataset contains 583 records, which, while reasonable for initial modeling, is relatively small for robust generalization in a diverse population like India.
The limited sample size may restrict the model's ability to capture rare disease presentations and subtle patterns.

Feature Limitations

The dataset includes key liver function parameters but lacks additional clinical variables (comorbidities, medication history, imaging data) that could further enhance predictive accuracy.
Only one feature (Albumin and Globulin Ratio) had missing values, but real-world datasets often have more extensive missingness and noise.

Generalizability

The dataset is sourced from a specific region (Andhra Pradesh), and the model's performance may vary when applied to other populations or healthcare settings. External validation on independent datasets is necessary before clinical deployment.

Ethical Considerations

Data Privacy

Patient data privacy is paramount. The dataset used is anonymized and publicly available, but in real-world deployment, strict adherence to data protection regulations (such as India's Digital Personal Data Protection Act) is essential. Secure storage, encrypted transmission, and controlled access to sensitive data must be ensured.

Bias and Fairness

Class imbalance was addressed by oversampling, but other forms of bias (demographic, socioeconomic) may persist and should be monitored.
The model should be periodically audited for disparate impact across subgroups (gender, age).

Responsible Use

The model is intended as a decision support tool, not a replacement for clinical judgment. Clear communication of model limitations and uncertainty is necessary to avoid over-reliance on automated predictions.

Strengths and Limitations

Aspect	Strengths	Limitations
Clinical relevance	Uses established biomarkers; aligns with practice	Lacks broader clinical context

Model performance	High accuracy and interpretability	Limited dataset size and scope
Fairness	Addressed class imbalance	Potential demographic bias
Deployment	Ready for web-based use (Streamlit)	Needs real-world validation and monitoring

10. Conclusion

This project successfully developed and evaluated a machine learning-based predictive model for liver disease using the Indian Liver Patient Dataset. The workflow encompassed rigorous data preprocessing, including imputation of missing values, label encoding, class balancing via oversampling, and feature scaling. The Random Forest classifier, selected for its robustness and interpretability, achieved strong predictive performance, with an accuracy of approximately 75–80% on the test set.

Key achievements include:
Effective Data Handling: Addressed missing values and class imbalance, ensuring the model's reliability for real-world clinical data.
Feature Insight: Identified clinically relevant predictors such as Total Bilirubin, Direct Bilirubin, Alkaline Phosphatase, SGPT, SGOT, and Albumin and Globulin Ratio, which align with established medical knowledge.
Model Deployment: Serialized the trained model using Pickle and provided a framework for deployment as a user-friendly web application via Streamlit, making advanced analytics accessible to non-technical healthcare staff.

10.1 Model's Potential for Clinical Decision Support

The developed model demonstrates significant promise as a clinical decision support tool. By automating the analysis of routine laboratory and demographic data, it can assist clinicians in:

Early Detection: Identifying high-risk patients before the onset of severe symptoms, enabling timely intervention.
Resource Optimization: Prioritizing patients for further diagnostic evaluation or specialist referral, particularly in resource-constrained settings.
Objective Assessment: Providing consistent, data-driven risk assessments that complement clinical judgment and reduce subjectivity.

Impact

Aid in Early Diagnosis: By flagging at-risk individuals during routine check-ups, the model can help initiate preventive measures and reduce the progression to advanced liver disease.
Improve Patient Outcomes: Early intervention is associated with better prognosis, reduced treatment costs, and enhanced quality of life for patients.
Support Healthcare Systems: Automated prediction tools can alleviate the burden on overextended healthcare professionals and improve efficiency, especially in areas with limited access to specialists.

While the current workflow enables accurate predictions and provides a Streamlit-based web interface for user interaction, full clinical impact requires seamless integration into real-world hospital systems. Future steps include

:

10.2 Roadmap for Future Enhancement

Area	Planned Action	Expected Benefit
Clinical Integration	• Develop robust EHR/EMR integration via APIs. • Ensure secure, compliant deployment within clinical workflows.	• Streamlined clinical workflow. • Faster decision support at point-of-care. • Increased clinician adoption.
Data Enhancement	• Acquire and curate multi-center, larger, and longitudinal datasets. • Implement robust data governance and quality control.	• Enhanced model accuracy and robustness. • Improved generalizability across diverse populations. • Ability to model disease progression.
Algorithmic Advancement	• Explore advanced algorithms: e.g., Deep Learning (CNNs, Transformers), sophisticated ensemble methods. • Investigate AutoML for model optimization and selection.	• Improved predictive performance (e.g., AUC, F1-score). • Better handling of complex data patterns. • Increased adaptability to new data.
Explainability & Trust	• Integrate advanced XAI techniques (e.g., SHAP, LIME, counterfactuals). • Develop intuitive dashboards for visualizing predictions and explanations. • Establish clinician feedback loops for refining explanations.	• Increased clinician trust and understanding. • Enhanced transparency in model decision-making. • Facilitated model debugging and refinement.
Monitoring & Governance	• Implement continuous model performance monitoring (data drift, concept drift). • Establish automated retraining pipelines. • Conduct regular ethical, fairness, and bias audits.	• Maintained model reliability and accuracy over time. • Proactive identification of performance degradation. • Ensured ongoing ethical compliance and fairness.

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12. Appendix

This process builds a machine learning model to predict liver disease.

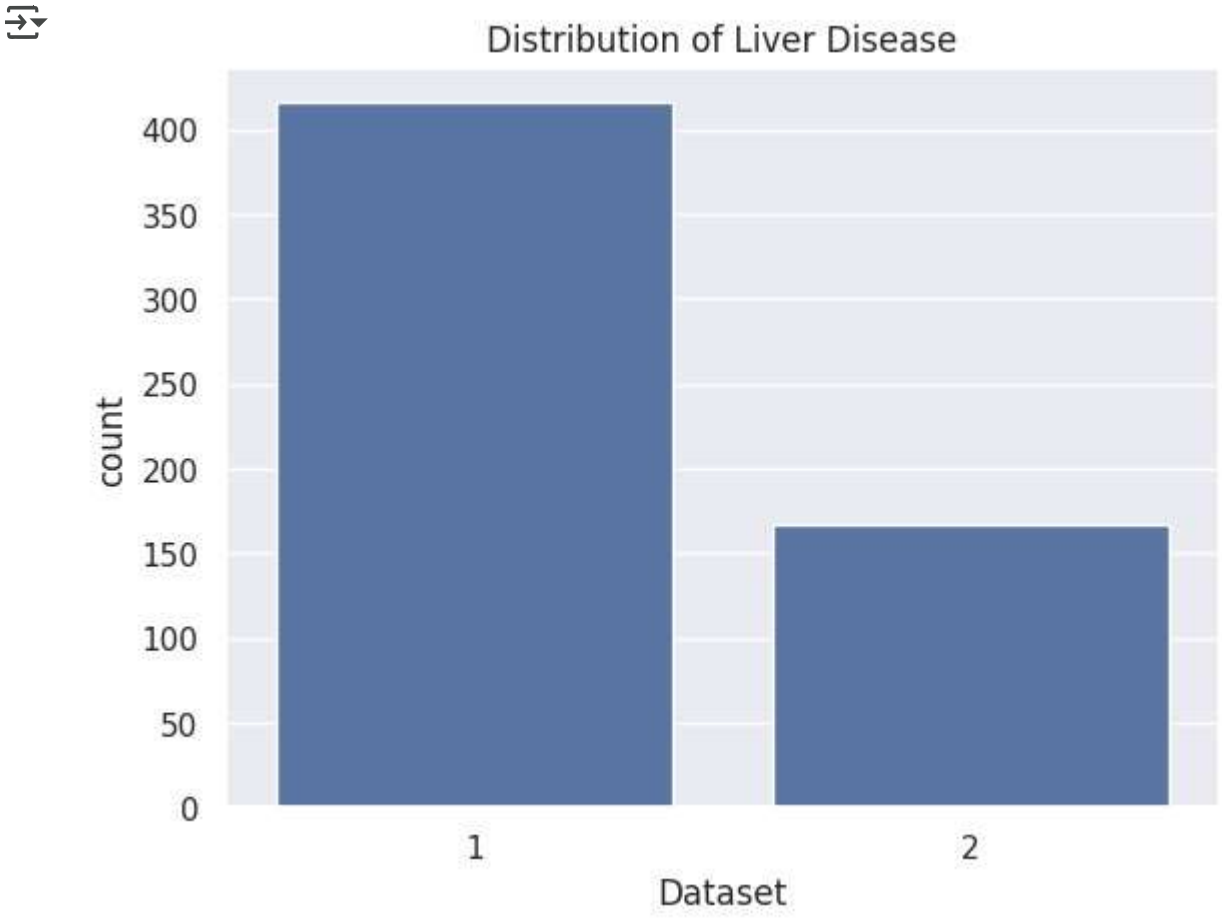
- **Libraries Used:** Essential Python libraries like pandas (for data handling), numpy (for calculations), scikit-learn (for machine learning), and seaborn/matplotlib (for visualization) are imported. Warnings are also filtered.
- **Data Loading & Overview:** The "indian_liver_patient.csv" dataset is loaded. It contains 583 patient records and 11 columns (features).
- **Data Cleaning:** No missing values were found in this specific dataset (in the given output).
- **Data Preprocessing:** The 'Gender' column, which is categorical, is converted to numerical (Male: 1, Female: 0).
- **Data Splitting:** The data is divided into features (X) and the target variable ('Dataset' - 1 for liver disease, 2 for no liver disease) (y). This is then split into training (80%) and testing (20%) sets.
- **Model Training:** A Random Forest Classifier model is trained using the training data.
- **Model Evaluation:**
  - **Accuracy:** The model achieved an accuracy of approximately 74.36% on the test set.
  - **Confusion Matrix:** Shows how many predictions were correct or incorrect for each class.
  - **Classification Report:** Provides detailed metrics like precision, recall, and f1-score for each class. For liver disease (class 1), precision was 0.81 and recall was 0.86. For no liver disease (class 2), precision was 0.50 and recall was 0.40.
- **Visualization:** A count plot shows the distribution of liver disease cases in the dataset. A correlation heatmap visualizes relationships between features.

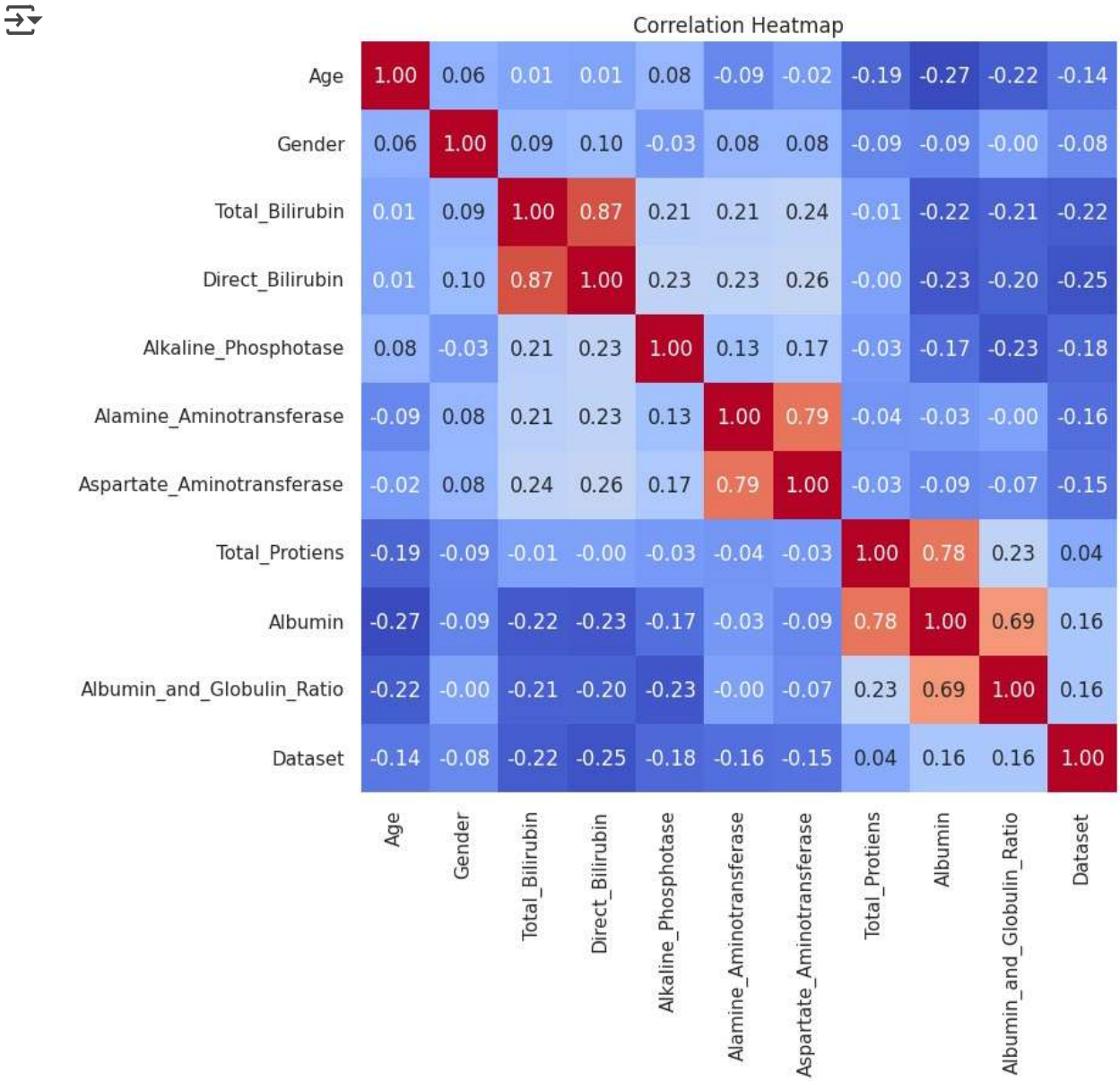
Code Snippets

Python

```
# Imports
import warnings [cite: 2]
warnings.filterwarnings("ignore") [cite: 3]
import numpy as np [cite: 4]
import pandas as pd [cite: 5]
from sklearn.preprocessing import MinMaxScaler [cite: 6]
import seaborn as sns [cite: 7]
sns.set() [cite: 8]

# Load the Dataset
df = pd.read_csv("indian_liver_patient.csv") [cite: 7]
print(df.head()) [cite: 8]

# Check the shape of the dataset
print("Shape of the dataset:", df.shape) [cite: 9]

# Check data types and missing values
print(df.info()) [cite: 13, 14, 15]

# Convert categorical variables to numeric
```

```
df['Gender'] = df['Gender'].map({'Male': 1, 'Female': 0}) [cite: 16]

# Prepare Data for Modeling
X = df.drop('Dataset', axis=1) # Features [cite: 16]
y = df['Dataset'] # Target variable [cite: 16]

from sklearn.model_selection import train_test_split [cite: 16]
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42) [cite: 16]

# Model Training
from sklearn.ensemble import RandomForestClassifier [cite: 16]
model = RandomForestClassifier(n_estimators=100, random_state=42) [cite: 16]
model.fit(X_train, y_train) [cite: 16]

# Model Evaluation
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report [cite: 17]
y_pred = model.predict(X_test) [cite: 17]
accuracy = accuracy_score(y_test, y_pred) [cite: 17]
print("Accuracy:", accuracy) [cite: 20]
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred)) [cite: 20]
print("Classification Report: \n", classification_report(y_test, y_pred)) [cite: 20, 21]

# Visualizations
import matplotlib.pyplot as plt [cite: 22]
import seaborn as sns [cite: 22]
sns.countplot(x='Dataset', data=df) [cite: 22]
plt.title('Distribution of Liver Disease') [cite: 22]
plt.show() [cite: 22]
#Correlation heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(df.corr(), annot=True, fmt=".2f", cmap='coolwarm')
plt.title('Correlation Heatmap')
plt.show()
```


Distribution of Liver Disease
count
400
350
300
250
200
150
100
50
0
1
2
Dataset



Making AI Apps for Liver and Kidney Disease

We used computer programs to build tools that can predict if someone has liver or kidney disease.

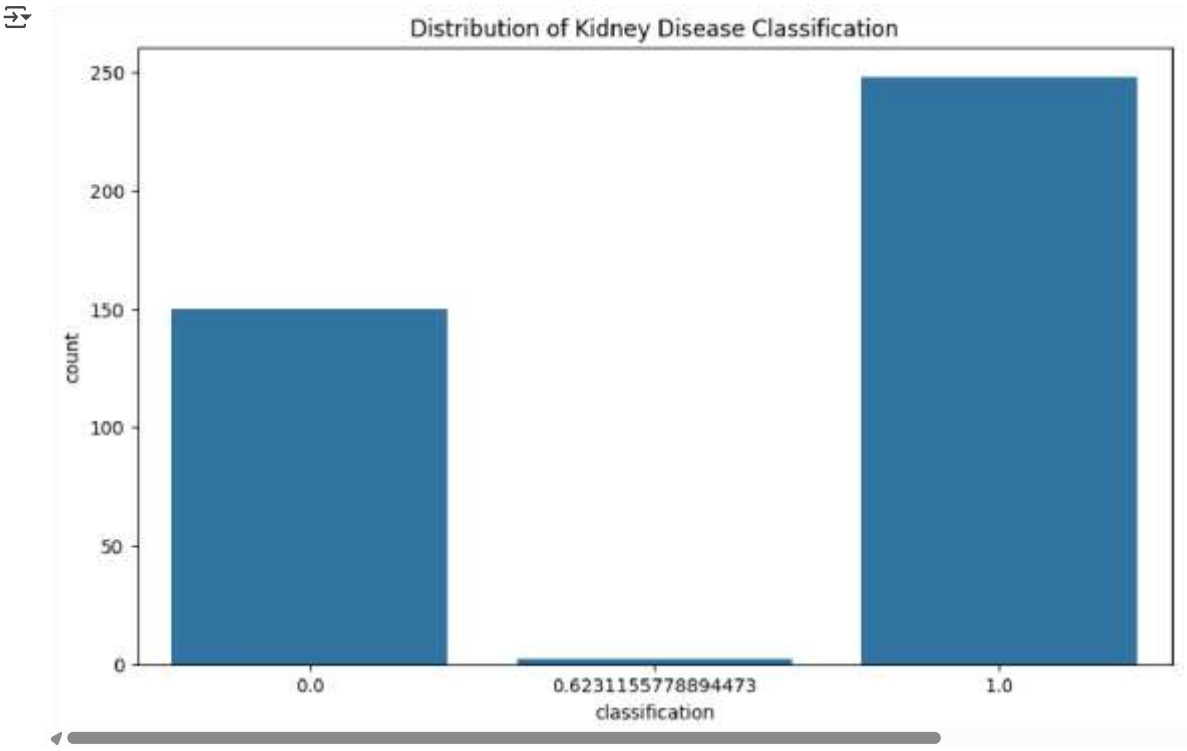
How We Made the Liver Disease Predictor?

1. **Gathered Data:** We used a list of 583 patient records about liver health.
2. **Cleaned Data:** We checked that all the information was there and correct.
3. **Prepared Data:** We changed "Male" or "Female" to numbers (like 1 or 0) so the computer could understand it. Then, we split the data into two parts: one for learning and one for testing.
4. **Taught the Computer:** We used a "Random Forest" computer program to learn from the data.
5. **Checked How Good It Was:** The program was about 74% accurate at predicting liver disease. We also looked at how well it did for sick people versus healthy people.
6. **Made it Visual:** We created charts to show how many people had liver disease in the data.
7. **Made an App:** We built a simple web app using "Streamlit" so people can type in patient details and get a prediction.

How We Started the Kidney Disease Predictor?
Got Data: We loaded a file with kidney disease information.
Checked Data: We saw that a lot of information was missing in many columns.
Prepared Data:
We changed text like "normal" or "yes" into numbers (like 0 or 1).
We filled in the missing numbers with the average value for that column.
Looked at Numbers: We got a summary of all the numbers in the data.
Made Charts: We made a chart to see how many people in the data had kidney disease.

Why GUIs are Important:

GUIs (like the apps we made) are visual ways to use computer programs. They make it super easy to get predictions without typing complicated commands. They are great for putting AI models to use.



1. **Get the Data:**

   First, we load the patient data from a file called `kidney_disease.csv`.

   We peek at the first few rows to see what it looks like.

2. **Find Missing Pieces:**

   We check if there are any empty spaces (missing information) in our table.

Sometimes, missing data is marked with strange symbols like `?` or `\t?`. We replace these with actual "empty spots" so the computer knows they are missing.

3. **Make Numbers Right:**

   Some columns, like `age` or `blood pressure`, should be numbers. We make sure they are. If we find something that's not a number in those columns, we also turn it into an "empty spot".

4. **Turn Words into Numbers:**

   Many columns have words, like `normal`, `yes`, `no`, `good`, `poor`, `ckd` (for chronic kidney disease), or `notckd`.

   We change these words into simple numbers:

   `normal` becomes `0`, `abnormal` becomes `1`

   `notpresent` becomes `0`, `present` becomes `1`

   `no` becomes `0`, `yes` becomes `1`

   `poor` becomes `0`, `good` becomes `1`

   `notckd` becomes `0`, `ckd` becomes `1` (This helps the computer understand if someone has kidney disease or not).

5. **Fill in the Gaps:**

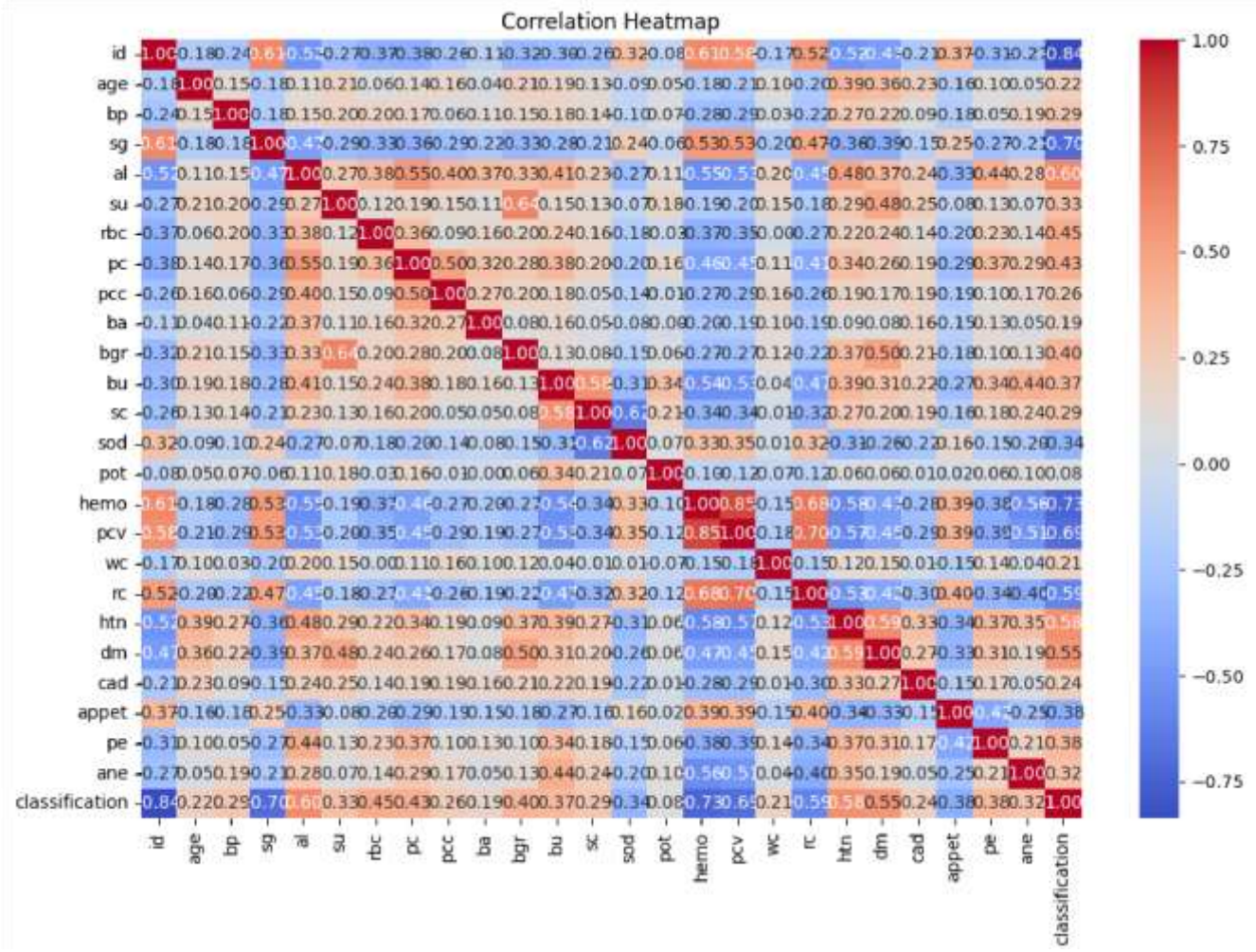
   For any remaining "empty spots" in columns that should have numbers, we fill them in with the average value from that column. This helps make sure our data is complete.

6. **Understand the Numbers:**

   We get a quick summary of all the numbers in our data, like the average age, the highest blood pressure, etc.

7. **See How Things Connect (Heatmap):**

   We create a special colorful chart called a "Correlation Heatmap."



1. Getting and Checking the Data

We load the patient data from a file called kidney_disease.csv.

We look at the first few rows to understand what kind of information we have.

Then, we check for any missing pieces of information in each column. We find quite a few!

```
Python
# Load the dataset
data = pd.read_csv('kidney_disease.csv')
# Display the first few rows of the dataset
print(data.head())
# Check for missing values
print("Missing values in each column:")
print(data.isnull().sum())
```

2. Cleaning and Preparing the Data

Fixing Bad Entries: Sometimes, missing data is written strangely (like ? or \t?). We replace these with proper "empty spots" that Python understands (np.nan).

Making Numbers Right: We make sure columns that should hold numbers (like age, blood pressure, etc.) are actually numbers. If not, we turn them into "empty spots."

Turning Words into Numbers: We change words like "normal" or "yes" into numbers (like 0 or 1) so the computer can work with them.**Filling Empty Spots:** For any remaining empty spots in number columns, we fill them with the average value of that column.

Python

```
# Replace invalid entries with NaN
data.replace({'?': np.nan, '\t?': np.nan}, inplace=True)

# Convert relevant columns to numeric, forcing errors to NaN
numeric_columns = ['age', 'bp', 'sg', 'al', 'su', 'bgr', 'bu', 'sc', 'sod', 'pot', 'hemo', 'pcv', 'wc', 'rc']
for column in numeric_columns:
    data[column] = pd.to_numeric(data[column], errors='coerce')

# Convert categorical variables to numeric using Label Encoding
categorical_columns = ['rbc', 'pc', 'pcc', 'ba', 'htn', 'dm', 'cad', 'appet', 'pe', 'ane', 'classification']
for column in categorical_columns:
    data[column] = data[column].map({
        'normal': 0, 'abnormal': 1,
        'notpresent': 0, 'present': 1,
        'yes': 1, 'no': 0,
        'good': 1, 'poor': 0,
        'ckd': 1, 'notckd': 0
    })

# Fill remaining missing values (example: fill with mean for numerical columns)
data.fillna(data.mean(numeric_only=True), inplace=True)
```

3. Teaching and Checking the Model

Separate Data: We split our cleaned data into "features" (the patient details) and the "target" (whether they have kidney disease or not). We make sure the target is a whole number.

Split for Training/Testing: We divide the data into a "training set" (80% of the data) to teach the model, and a "testing set" (20%) to see how well it learned.

Train the Model: We use a "Random Forest Classifier" model and teach it using the training data.

Check Performance: We ask the model to predict on the testing data and then look at:

Classification Report: This tells us how well the model predicted for each group (sick vs. healthy).

Confusion Matrix: This is a table showing exactly how many predictions were right and how many were wrong. In this case, the model achieved perfect scores (1.00 for precision, recall, and f1-score), meaning it correctly predicted all 28 "0" cases and all 52 "1" cases in the test set.

Python

```
# Prepare data for modeling
```

```
X = data.drop('classification', axis=1)  # Features
y = data['classification'].astype(int)   # Target variable (ensure integer type)

# Split the dataset into training and testing sets
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Initialize and train the model
from sklearn.ensemble import RandomForestClassifier
model = RandomForestClassifier(n_estimators=100, random_state=42)
model.fit(X_train, y_train)

# Make predictions
y_pred = model.predict(X_test)

# Evaluate the model
from sklearn.metrics import classification_report, confusion_matrix
print("Classification Report:")
print(classification_report(y_test, y_pred))
print("Confusion Matrix:")
print(confusion_matrix(y_test, y_pred))
```

4. Building the Kidney Disease Prediction App

- We use streamlit to create a web application where users can input patient data.
- The app takes all the necessary patient details (age, blood pressure, etc.) through easy-to-use input boxes and dropdowns.
- When the "Predict" button is clicked, the app uses our trained model to make a prediction.
- It then tells the user if the patient is likely to have "Chronic Kidney Disease" or "Not Chronic Kidney Disease."

```
Python
# (Imports and data preprocessing/model training functions as above)

# Streamlit app
st.title("Kidney Disease Prediction App")

# User input for prediction
st.header("Input Patient Data")
age = st.number_input("Age", min_value=1, max_value=120)
bp = st.number_input("Blood Pressure", min_value=0)
# ... (all other input fields for features) ...
ane = st.selectbox("Anemia", ["yes", "no"])

# Prepare input data for prediction
input_data = pd.DataFrame({
    'age': [age], 'bp': [bp], 'sg': [sg], 'al': [al], 'su': [su],
    'rbc': 0 if rbc == "normal" else 1, 'pc': 0 if pc == "normal" else 1,
    'pcc': 0 if pcc == "notpresent" else 1, 'ba': 0 if ba == "notpresent" else 1,
    'bgr': [bgr], 'bu': [bu], 'sc': [sc], 'sod': [sod], 'pot': [pot],
```

```
    'hemo': [hemo], 'pcv': [pcv], 'wc': [wc], 'rc': [rc],
    'htn': 1 if htn == "yes" else 0, 'dm': 1 if dm == "yes" else 0,
    'cad': 1 if cad == "yes" else 0, 'appet': 1 if appet == "good" else 0,
    'pe': 1 if pe == "yes" else 0, 'ane': 1 if ane == "yes" else 0
})

# Prediction
if st.button("Predict"):
    prediction = model.predict(input_data)
    prediction_label = "Chronic Kidney Disease" if prediction[0] == 1 else "Not Chronic Kidney
Disease"
    st.success(f"The model predicts: {prediction_label}")
```

Output:

Kidney Disease Prediction App

Input Patient Data

Age

1

Blood Pressure

0

Specific Gravity

1

Albumin

0

Sugar

0

Red Blood Cells

norm

Pus Cells

norm

Pus Cell Clumps

notpresen

Bacteria

notpresen

Blood Glucose Random

0

Blood Urea

0

Serum Creatinine

0

Sodium

0

Potassium

0

Hemoglobin

0

Packed Cell Volume

0

White Blood Cell Count

0

Red Cell Count

0

Hypertension

y

Diabetes Mellitus

y

Coronary Artery Disease

y

Appetite

go

Pedal Edema

y

Ane

y

Predi

Indian Liver Patient Disease Prediction

Dataset Overview

Rows (Patients):

Columns (Features):

Target Column: `Datas` (1 = liver disease, 2 = no liver disease)

Patient Data Input

A

3

Gend

M

Total Bilirubin

1

Direct Bilirubin

0

Alkaline Phosphotase

1

Alamine Aminotransferase

2

Aspartate Aminotransferase

2

Total Proteins

6

Album

3

Albumin and Globulin Ratio

1

Predi