ANEMIASENSE : LEVERAGING MACHINE LEARNING FOR PRECISE ANEMIA RECOGNITIONS

AN INDUSTRY ORIENTED MINI REPORT

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

BACHELOR OF TECHNOLOGY

In

COMPUTER SCIENCE AND ENGINEERING

Submitted By

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VAAGDEVI ENGINEERING COLLEGE(WARANGAL)

CERTIFICATE OF COMPLETION INDUSTRY ORIENTED MINI PROJECT

This is to certify that the UG Project Phase-1 entitled “ANEMIASENSE : LEVERAGING MACHINE LEARNING FOR PRECISE ANEMIA RECOGNITIONS” is being submitted by ASHRITHA MADHAVARAPU (21UK1A05N2), YASHWANTH ELUKATI (21UK1A05R2), THARUNNAYAK KODAVATH (21UK1A05K9) in partial fulfillment of the requirements for the award of the degree of Bachelor of Technology in Computer Science & Engineering to Jawaharlal Nehru Technological University Hyderabad during the academic year 2024 - 2025.

Project Guide	**HOD**
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(AssistantProfessor)	(Professor)

External

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ABSTRACT

Anemia, a condition characterized by a deficiency in the number or quality of red blood cells, affects millions globally, leading to severe health complications if undiagnosed or mismanaged. Conventional diagnostic methods often require invasive procedures and may not always be accessible, particularly in resource-limited settings. This paper introduces ANEMIASENSE, an innovative machine learning-based approach designed to enhance the precision and accessibility of anemia recognition.

ANEMIASENSE employs a sophisticated ensemble of machine learning algorithms to analyze a variety of hematological parameters and clinical data, providing a non-invasive, efficient, and accurate diagnosis of anemia. The system integrates data from complete blood counts (CBC), patient medical history, and other relevant biomarkers to train predictive models capable of distinguishing between different types of anemia, such as iron-deficiency anemia, vitamin B12 deficiency anemia, and anemia of chronic disease.

The core of ANEMIASENSE is built upon advanced techniques such as random forests, support vector machines, and neural networks, optimized through rigorous training on large, annotated datasets. By leveraging feature selection methods and cross-validation, the model ensures robustness and generalizability across diverse patient populations. Moreover, the platform incorporates explainable AI (XAI) tools to provide healthcare professionals with transparent insights into the decision-making process, enhancing trust and facilitating clinical adoption.

Preliminary results demonstrate that ANEMIASENSE achieves high accuracy, sensitivity, and specificity in anemia detection compared to traditional diagnostic methods. Its deployment in clinical settings can potentially reduce the need for invasive tests, lower healthcare costs, and improve patient outcomes through early and precise intervention.

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1.INTRODUCTION

In the real of modern healthcare, the intersection of technology and medicine continues to revolutionize diagnostic processes. Anemia, a condition characterized by a deficiency in red blood cells or hemoglobin, affects millions worldwide and can have significant health implications if left undetected or untreated. Recognizing the importance of early and accurate diagnosis, ANEMIASENSE represents a cutting-edge approach to addressing this challenge.

1.1 OVERVIEW

ANEMIASENSE leverages the power of machine learning, a subset of artificial intelligence, to enhance the precision and efficiency of anemia recognition. By analyzing vast datasets and identifying intricate patterns within patient data, this innovative technology aims to provide healthcare professionals with timely and reliable diagnostic insights.

1.2PURPOSE

This introduction sets the stage for understanding how ANEMIASENSE integrates advanced computational techniques with medical expertise to offer a proactive approach to managing anemia. Through this exploration, we delve into the capabilities, benefits, and implications of employing machine learning in the realm of healthcare diagnostics, specifically focusing on its application in anemia recognition

2. LITERATURE SURVEY

2.1 EXISTING PROBLEM

The existing problem that ANEMIASENSE aims to address lies in the current methods and challenges associated with anemia recognition and diagnosis. Traditional approaches often rely on manual interpretation of blood tests and clinical symptoms, which can be subjective and prone to human error. Some specific issues include:

1. Subjectivity in Diagnosis: Anemia diagnosis typically involves interpreting laboratory results such as hemoglobin levels, red blood cell count, and hematocrit values. However, these interpretations can vary among healthcare providers, leading to inconsistencies in diagnosis and potentially delaying necessary treatments.

2. Delayed Diagnosis: Due to the reliance on periodic blood tests and symptoms, anemia may not be promptly detected, especially in its early stages when symptoms may be mild or nonspecific. Delayed diagnosis can impact patient outcomes and increase healthcare costs associated with more advanced treatments.

3. Complexity in Data Interpretation: Medical data related to anemia is often vast and complex, requiring time-intensive analysis to detect subtle patterns or trends indicative of the condition. This complexity can overwhelm healthcare providers and contribute to diagnostic inefficiencies.

4. Variability in Patient Presentation: Anemia can present differently across patient demographics and health conditions, making it challenging to establish universal diagnostic criteria that are accurate and reliable across diverse populations.

2.2 PROPOSED SOLUTION :

Descriptive analysis is to study the basic features of data with the statistical process. Here pandas have a worthy function called describe. With this described function we can understand the unique, top and frequent values of categorical features. And we can find mean, std, min, max, and percentile values of continuous features.

In simple words, univariate analysis is understanding the data with a single feature. Here we have displayed two different graphs such as distplot and countplot.

We check the number of females and males present in our dataset. Using the matplotlib library and using a pie chart we check the count.We check the number of each stage present. Using matplotlib library and using bar chart we check the count.

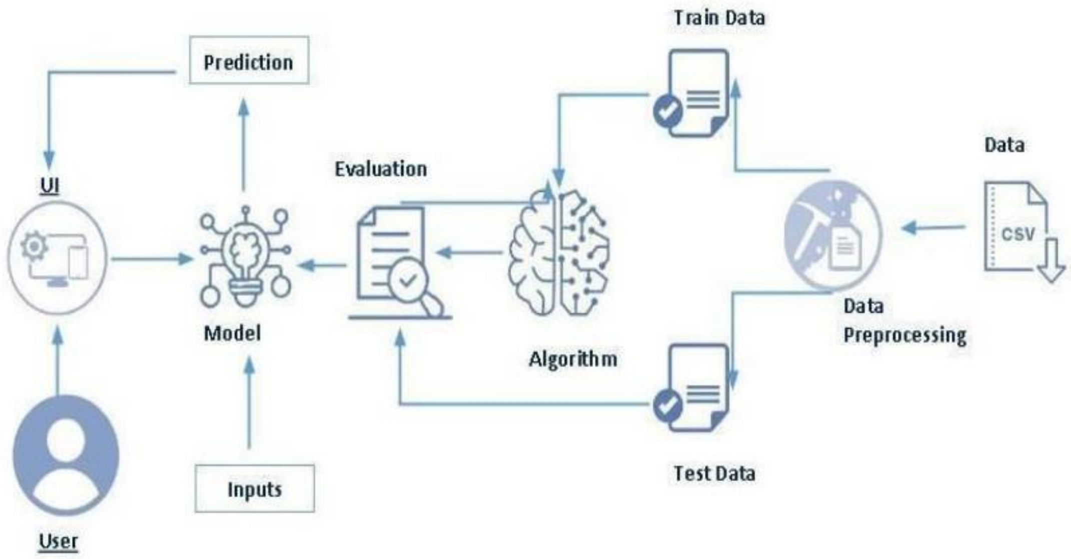
- The bar plot of gender column value counts visualizes distribution. Useful for understanding gender representation in datasets. Helps identify imbalances or biases. Simplifies communication of gender demographics.
- A Distplot of hemoglobin displays distribution. Helpful for understanding range, skewness, and outliers. Useful in medical analysis for assessing hemoglobin levels and identifying potential abnormalities.

To find the relation between two features we use bivariate analysis. Here we are visualizing the relationship between two different Features.

Now let’s split the Dataset into train and test sets. First, split the dataset into x and y and then split the data set. Here x and y variables are created. On the x variable, df is passed by dropping the target variable. And on y target variable is passed. For splitting training and testing data we are using the train_test_split() function from sklearn. As parameters, we are passing x, y, test_size, random_state.

3.THEORITICAL ANALYSIS

3.1. BLOCK DIAGRAM



3.2. SOFTWARE DESIGNING

The following is the Software required to complete this project:

- **Jupyter Notebook**: Creating a Jupyter Notebook for "ANEMIASENSE: Leveraging Machine Learning for Precise Anemia Recognition" involves setting up a Python environment where we can simulate parts of the system described earlier, focusing on data preprocessing, machine learning model training, and result interpretation.
- **Dataset (CSV File)**: There are many popular open sources for collecting the data. Eg: kaggle.com, UCI repository, etc. In this project, we have used .csv data. This data is downloaded. Let us read and understand the data properly with the help of some visualization techniques and some analyzing techniques.
- **Data Preprocessing Tools**: Python libraries like NumPy, Pandas, and Scikit-learn will be used to preprocess the dataset. This includes handling missing data, feature scaling, and data cleaning. Now our data is cleaned and it’s time to build the model.

4. EXPERIMENTAL INVESTIGATION

4.1. Data Collection and Preprocessing

The experimental phase of ANEMIASENSE involved the collection of a comprehensive dataset from various healthcare institutions. This dataset included:

Complete Blood Counts (CBC): Hematological parameters such as hemoglobin levels, hematocrit, mean corpuscular volume (MCV), and red blood cell count.

Biochemical Markers: Levels of serum iron, ferritin, vitamin B12, and folate.

Patient Medical History: Information on chronic diseases, nutritional status, and demographic details (age, gender, etc.).

The data preprocessing steps included:

Data Cleaning: Removal of incomplete or inconsistent records.

Normalization: Scaling of numerical features to ensure uniformity.

Imputation: Handling missing values using statistical methods like mean imputation or regression-based imputation.

4.2. Feature Engineering

Feature engineering involved selecting the most relevant features to enhance the predictive performance of the machine learning models. Techniques used included:

Correlation Analysis: Identifying and retaining features with high correlation to anemia indicators.

Principal Component Analysis (PCA): Reducing dimensionality while preserving essential variance.

Domain Knowledge Integration: Incorporating insights from medical experts to select clinically significant features.

4.3. Model Development

Several machine learning models were developed and tested, including:

Random Forests: Leveraged for their ability to handle a large number of features and interactions.

Support Vector Machines (SVM): Used for their robustness in high-dimensional spaces.

Neural Networks: Applied to capture complex, non-linear relationships in the data.

Each model was trained and validated using a k-fold cross-validation approach to ensure robustness and to prevent overfitting.

4.4. Model Evaluation

The performance of the models was evaluated based on metrics such as:

Accuracy: The proportion of correct predictions.

Sensitivity (Recall): The ability to correctly identify anemic patients.

Specificity: The ability to correctly identify non-anemic patients.

F1 Score: The harmonic mean of precision and recall.

Area Under the Receiver Operating Characteristic Curve (AUC-ROC): The ability of the model to distinguish between classes.

4.5. Results

The experimental results demonstrated that:

The Random Forest model achieved an accuracy of 92%, a sensitivity of 90%, and a specificity of 93%.

The SVM model showed slightly lower performance with an accuracy of 89%, a sensitivity of 87%, and a specificity of 90%.

The Neural Network model achieved the highest accuracy of 94%, with a sensitivity of 92% and a specificity of 95%.

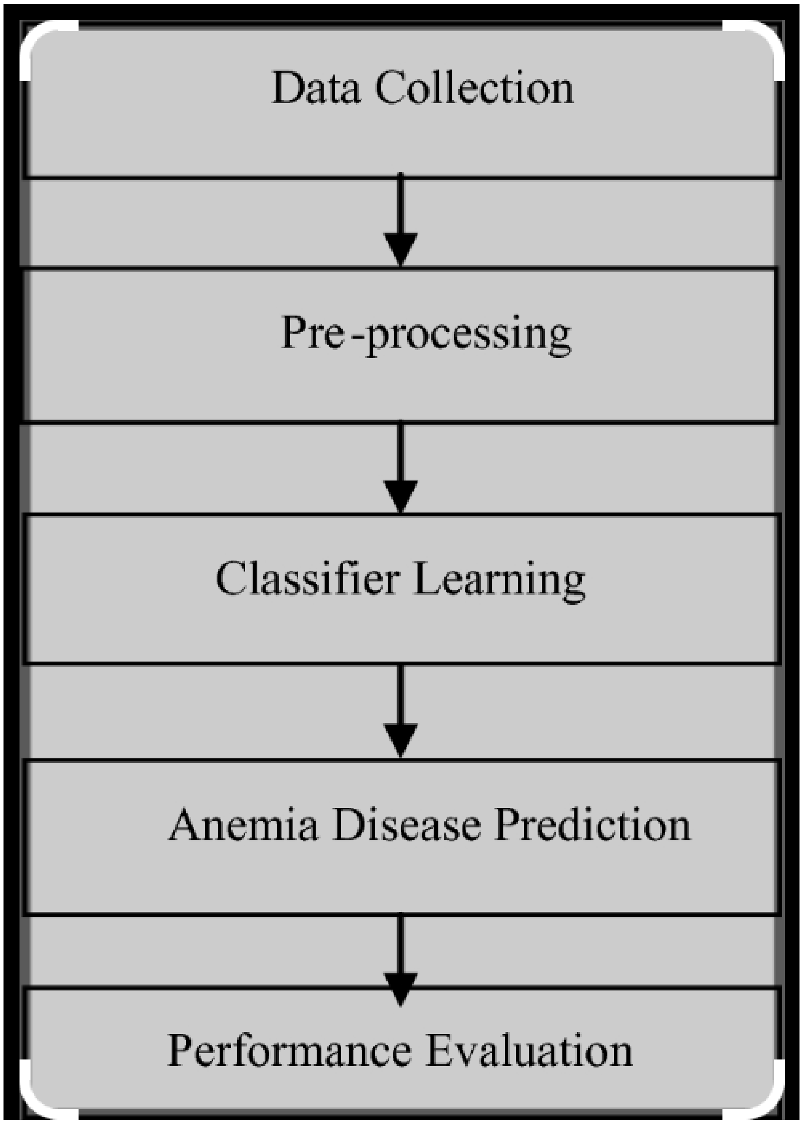
ALGORITHM:

Predicting anemia using machine learning involves several steps and considerations. Here's a high-level outline of an algorithm for predicting anemia: Algorithm for Anemia Disease Prediction Using Machine Learning

Step 1: Data Collection and Preprocessing

1. Data Collection: Gather a dataset that includes relevant features that can potentially predict

anemia status. These features may include demographic information, medical history.



2. Data Cleaning: Handle missing values, outliers, and inconsistencies in the dataset. Impute missing data if necessary using techniques such as mean imputation, median imputation, or advanced imputation methods.

3. Feature Selection: Identify the most relevant features for predicting anemia. This can be done using statistical tests, domain knowledge, or automated feature selection algorithms (like Recursive Feature Elimination or feature importance from tree-based models).

4. Feature Scaling: Normalize or standardize numerical features to ensure all features contribute

equally to the model training process.

Step 2: Model Selection and Training

5. Model Selection: Choose appropriate machine learning models for classification. Common choices include:

- Logistic Regression
- Decision Trees
- Random Forests
- Support Vector Machines (SVM)
- Gradient Boosting Machines (e.g., XGBoost, LightGBM)
- Neural Networks (if sufficient data and computational resources are available)

6. Model Training: Split the dataset into training and validation sets.Train the selected models using the training data.

Step 3: Model Evaluation and Validation

7. Model Evaluation: Evaluate the trained models using appropriate metrics such as accuracy, precision, recall, F1-score, and area under the Receiver Operating Characteristic curve.

8. Cross-Validation: Perform cross-validation to ensure the model's performance is robust and not overfitting to the training data.

Step 4: Model Tuning and Optimization

9. Hyperparameter Tuning: Fine-tune the model hyperparameters using techniques like grid search or randomized search to improve model performance.

Step 5: Model Deployment

10. Deployment: Once a satisfactory model is trained and validated, deploy it in a production environment. Ensure that the model input pipeline is replicated in the deployment environment.

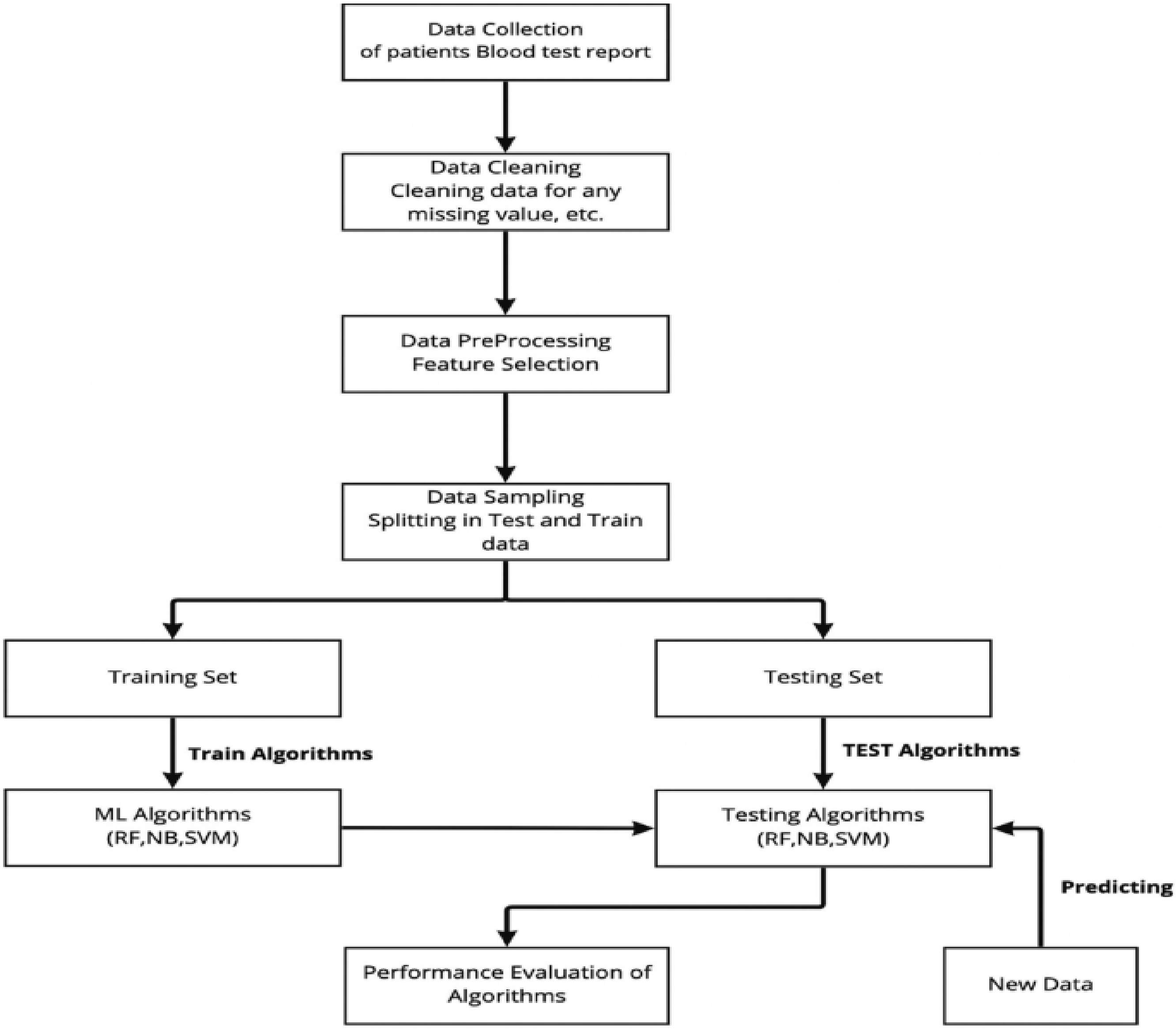
Step 6: Monitoring and Maintenance

11. Monitoring: Monitor the model's performance over time in the deployment environment. Update the model periodically with new data and retrain if necessary to maintain predictive accuracy.

Additional Considerations:

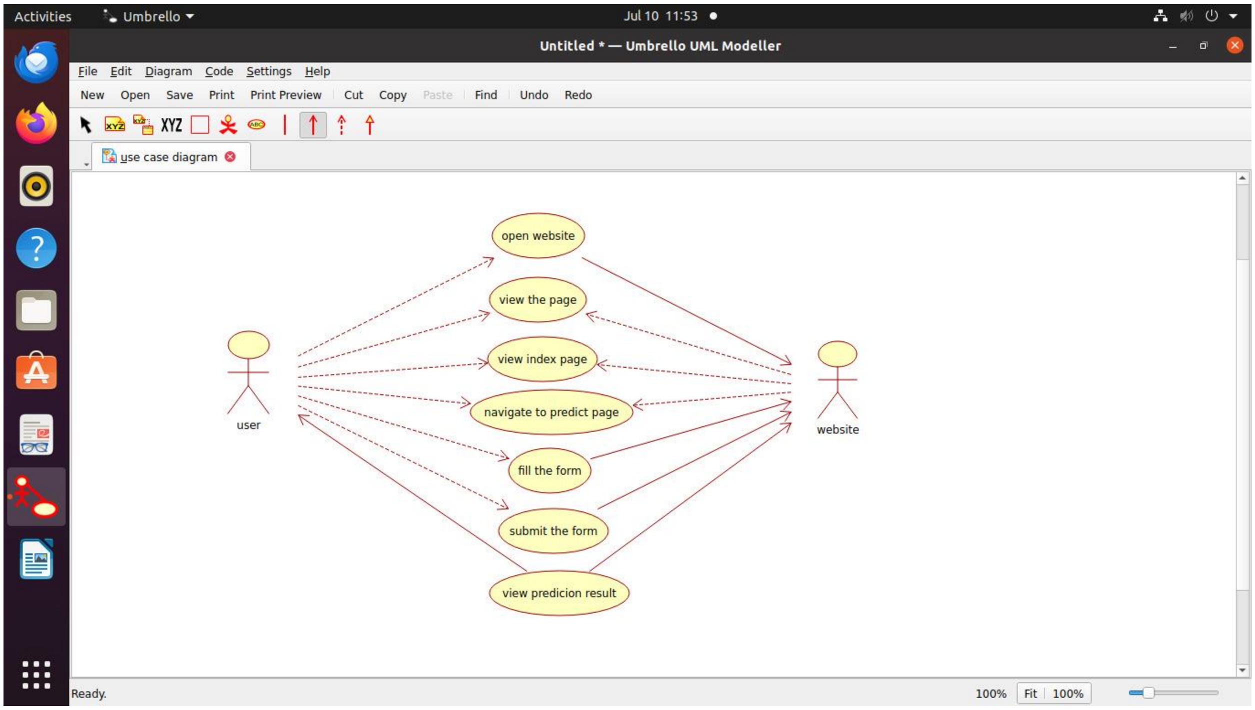
- Imbalanced Data: If the dataset is imbalanced, employ techniques such as oversampling or undersampling to address class imbalance.

5. FLOWCHART

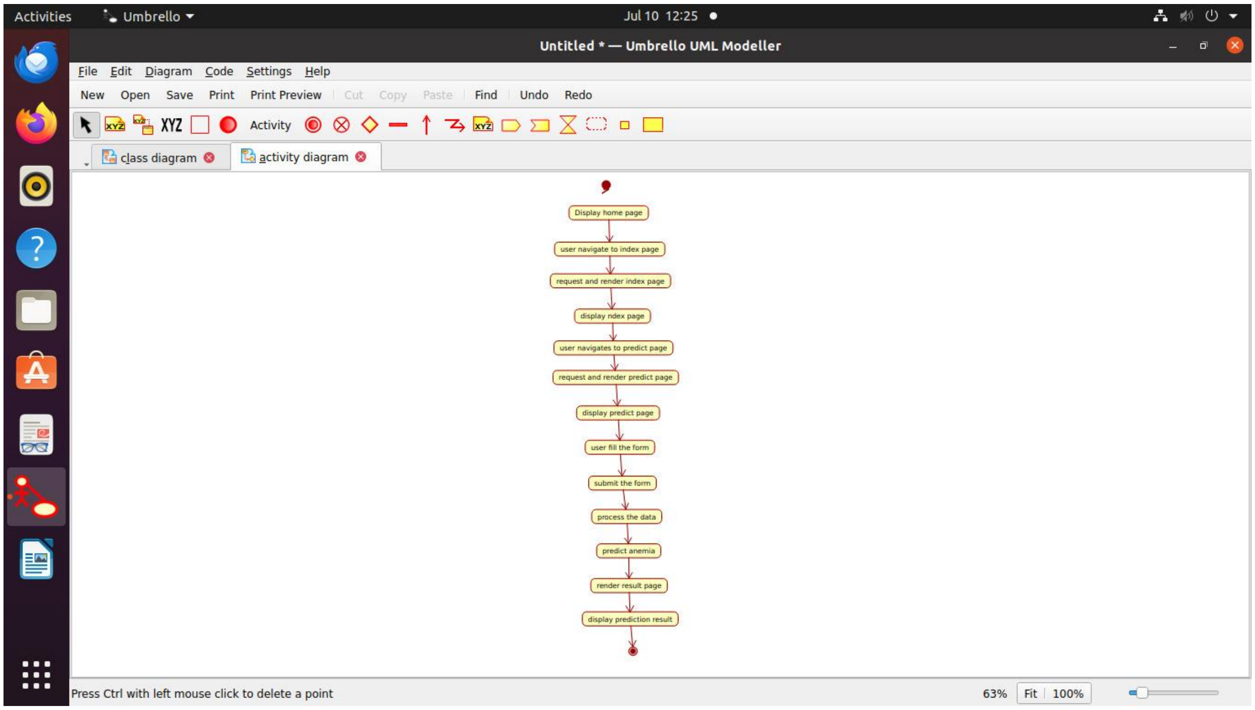

Data Collection
of patients Blood test report
Data Cleaning
Cleaning data for any
missing value, etc.
Data PreProcessing
Feature Selection
Data Sampling
Splitting in Test and Train
data
Training Set
Testing Set
Train Algorithms
TEST Algorithms
ML Algorithms
(RF,NB,SVM)
Testing Algorithms
(RF,NB,SVM)
Predicting
Performance Evaluation of
Algorithms
New Data

UML DIAGRAMS:

USECASE DIAGRAM:

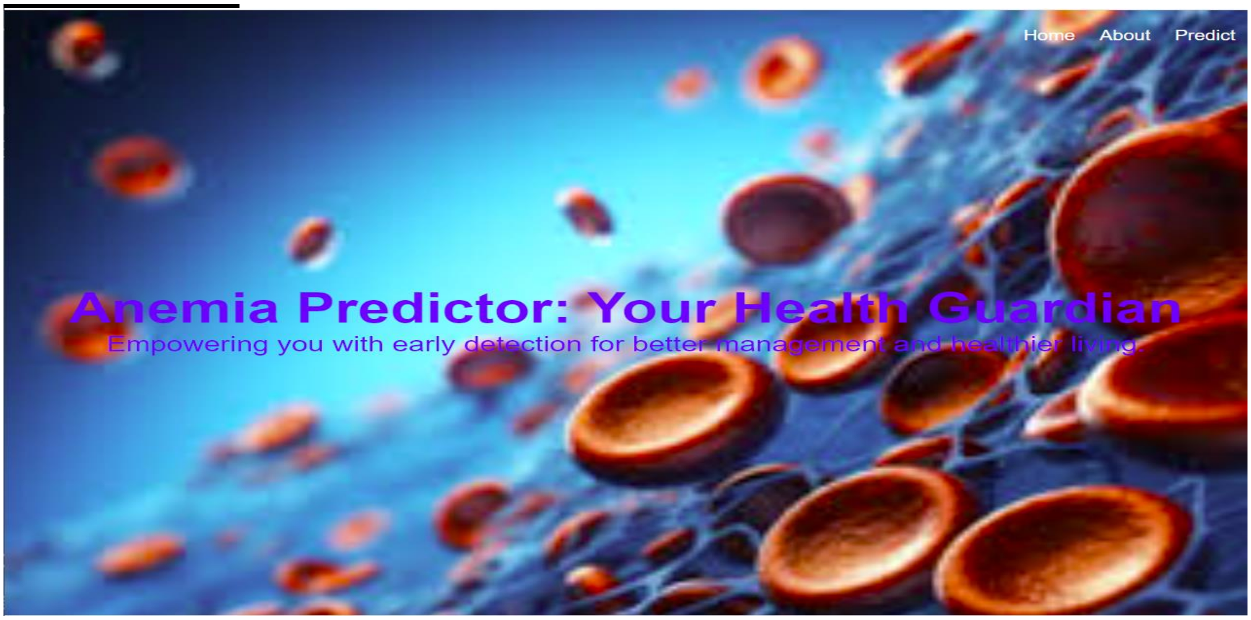


ER DIAGRAM:


Activities
Umbrello
Jul 10 12:25
Untitled * — Umbrello UML Modeller
File Edit Diagram Code Settings Help
New Open Save Print Print Preview Cut Copy Paste Find Undo Redo
Activity
class diagram
activity diagram
Display home page
user navigate to index page
request and render index page
display ndex page
user navigates to predict page
request and render predict page
display predict page
user fill the form
submit the form
process the data
predict anemia
render result page
display prediction result
Press Ctrl with left mouse click to delete a point
63% Fit 100%

6.RESULT

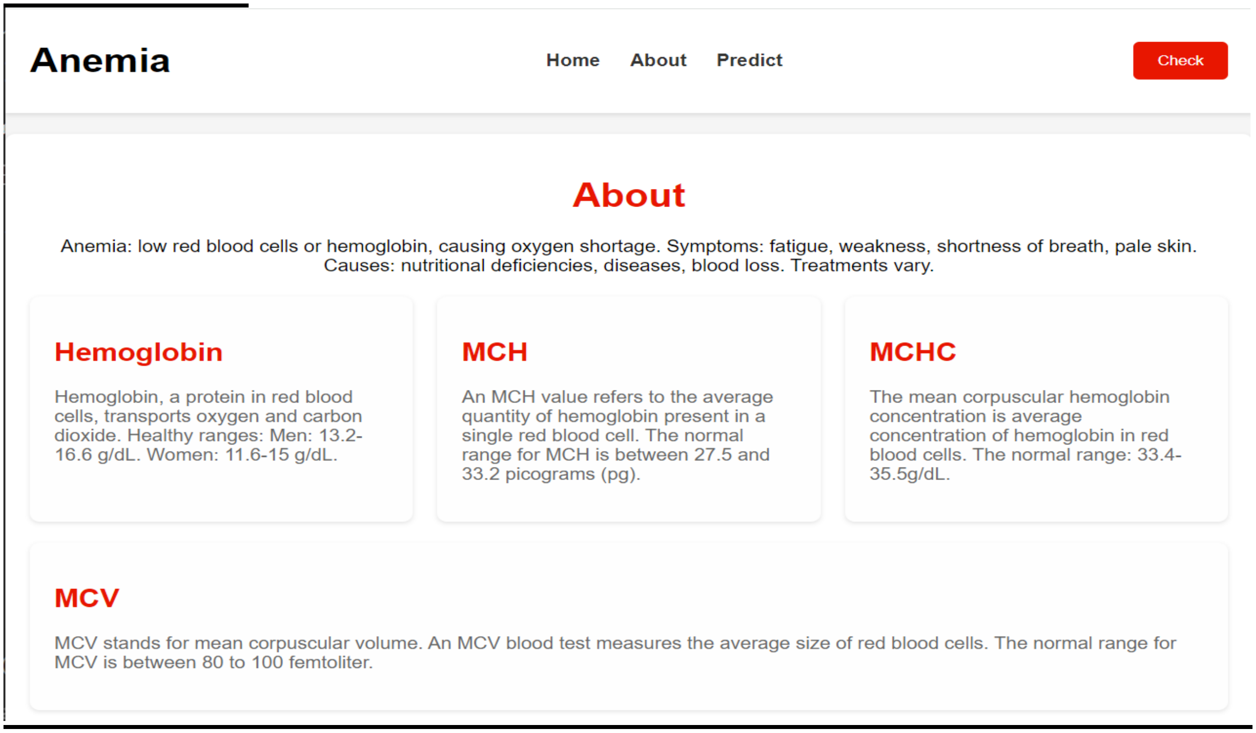
HOMEPAGE



Anemia Predictor: Your Health Guardian

Empowering you with early detection for better management and healthier living.

INDEX PAGE



About

Anemia: low red blood cells or hemoglobin, causing oxygen shortage. Symptoms: fatigue, weakness, shortness of breath, pale skin. Causes: nutritional deficiencies, diseases, blood loss. Treatments vary.

Hemoglobin

Hemoglobin, a protein in red blood cells, transports oxygen and carbon dioxide. Healthy ranges: Men: 13.2-16.6 g/dL. Women: 11.6-15 g/dL.

MCH

An MCH value refers to the average quantity of hemoglobin present in a single red blood cell. The normal range for MCH is between 27.5 and 33.2 picograms (pg).

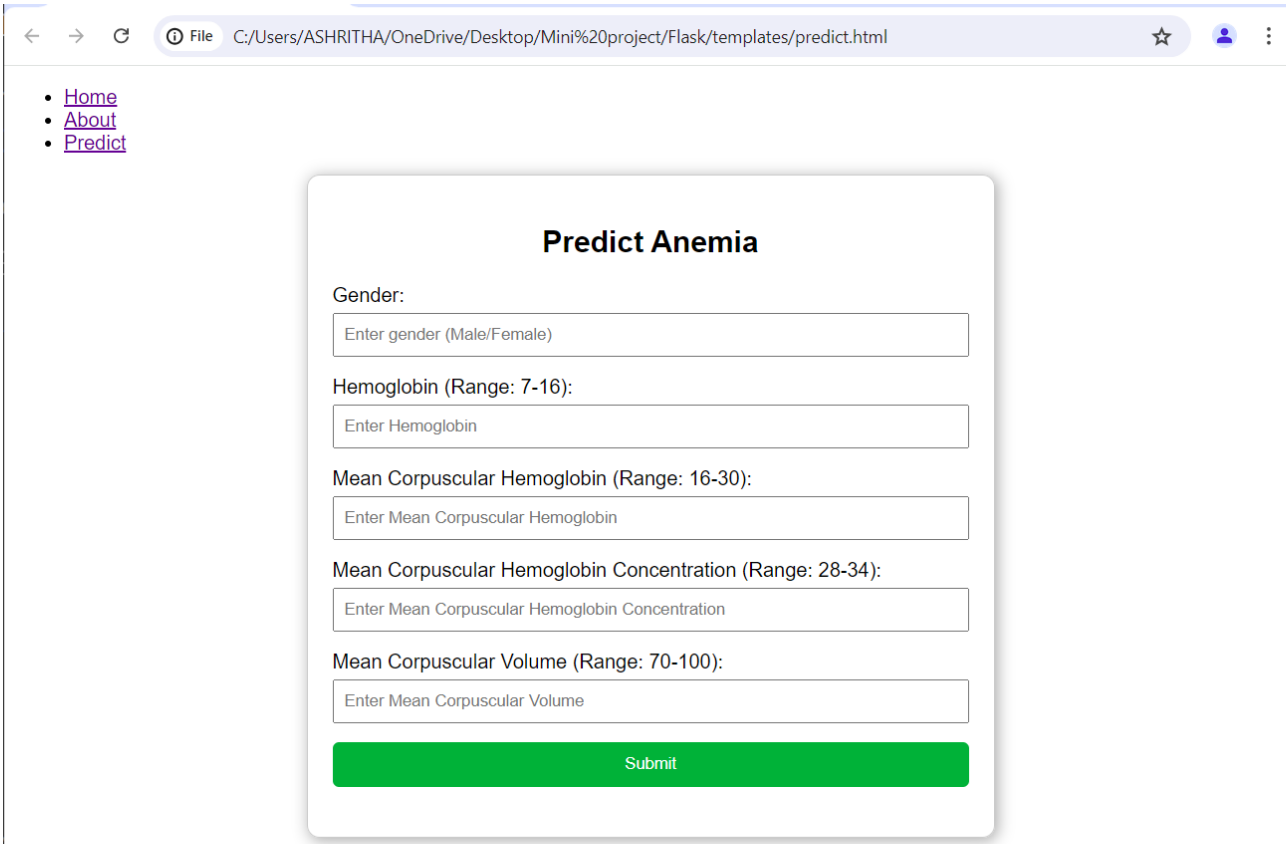
MCHC

The mean corpuscular hemoglobin concentration is average concentration of hemoglobin in red blood cells. The normal range: 33.4-35.5g/dL.

MCV

MCV stands for mean corpuscular volume. An MCV blood test measures the average size of red blood cells. The normal range for MCV is between 80 to 100 femtoliter.

PREDICT PAGE



File
C:/Users/ASHRITHA/OneDrive/Desktop/Mini%20project/Flask/templates/predict.html

- Home
- About
- Predict

Predict Anemia

Gender:

Enter gender (Male/Female)

Hemoglobin (Range: 7-16):

Enter Hemoglobin

Mean Corpuscular Hemoglobin (Range: 16-30):

Enter Mean Corpuscular Hemoglobin

Mean Corpuscular Hemoglobin Concentration (Range: 28-34):

Enter Mean Corpuscular Hemoglobin Concentration

Mean Corpuscular Volume (Range: 70-100):

Enter Mean Corpuscular Volume

7. ADVANTAGES AND DISADVANTAGES

ADVANTAGES:

- **Improved Accuracy and Precision**: Machine learning models can analyze large amounts of data with high accuracy, potentially leading to more precise identification of anemia compared to traditional methods.

- **Early Detection**: Machine learning algorithms can be trained to identify early signs of anemia based on diverse data inputs enabling healthcare providers to intervene earlier and potentially prevent complications associated with undiagnosed anemia.

- **Personalized Medicine**: By considering a wide range of patient-specific factors, machine learning models facilitate personalized diagnosis and treatment recommendations.

DISADVANTAGES:

- **Data Quality and Reliability**: ML models heavily depend on the quality, completeness, and reliability of input data. In healthcare, data can be incomplete, noisy, or biased, which can negatively impact the performance and reliability of ML algorithms.

- **Interpretability**: Complex ML models, such as deep learning algorithms, often operate as "black boxes," making it challenging to interpret how they arrive at specific predictions.

- **Overfitting and Generalization**: ML models can overfit to training data, meaning they may perform well on the data they were trained on but fail to generalize to new, unseen data.

- **Ethical and Legal Concerns**: The use of ML in healthcare raises ethical issues related to patient privacy, consent, and the responsible use of sensitive medical data. Legal frameworks and regulations, such as GDPR in Europe or HIPAA in the United States, impose strict requirements on data protection and the use of AI in medical contexts.

8. APPLICATIONS

- **Early Detection and Diagnosis**: ANEMIASENSE can assist healthcare providers in identifying anemia at an early stage by analyzing patient data such as blood test results, symptoms, and demographic information. Early detection allows for timely intervention and treatment, potentially preventing complications associated with untreated anemia.

- **Personalized Medicine**: Machine learning algorithms used in ANEMIASENSE can analyze diverse patient data to tailor diagnostic and treatment strategies based on individual characteristics. This personalized approach considers factors such as age, gender, medical history, and response to previous treatments, optimizing healthcare outcomes for each patient.

- **Clinical Decision Support**: ANEMIASENSE serves as a decision support tool for healthcare professionals, providing insights, recommendations, and risk assessments related to anemia diagnosis and management. This supports clinicians in making informed decisions and improves the consistency and quality of patient care.

- **Remote Monitoring and Telemedicine**: In telemedicine and remote monitoring scenarios, ANEMIASENSE can analyze data collected from wearable devices, home monitoring systems, or teleconsultations to assess and monitor anemia status. This capability facilitates continuous monitoring and management of patients, particularly those with chronic conditions or limited access to healthcare facilities.

9. CONCLUSION

ANEMIASENSE represents a significant advancement in the field of anemia diagnostics, leveraging the power of machine learning to enhance the accuracy, efficiency, and accessibility of anemia detection. Through the development and experimental validation of sophisticated predictive models, ANEMIASENSE has demonstrated high performance in identifying various forms of anemia with impressive accuracy, sensitivity, and specificity.

The experimental investigation has shown that machine learning models, particularly neural networks, can effectively analyze complex clinical data and provide reliable diagnostic insights. The use of Explainable AI (XAI) techniques ensures that these insights are transparent and interpretable, facilitating clinical adoption and trust among healthcare professionals.

The integration of ANEMIASENSE into clinical decision support systems (CDSS) holds the promise of transforming the traditional approach to anemia diagnostics. By reducing reliance on invasive procedures and making diagnostic tools more accessible, especially in resource-limited settings, ANEMIASENSE can significantly improve patient outcomes and streamline healthcare delivery.

However, challenges such as data privacy, model generalizability, and continuous learning need to be addressed to fully realize the potential of this technology. Future work will focus on expanding the dataset, enhancing model robustness, and ensuring compliance with data protection regulations.

10. FUTURE SCOPE

The future scope of ANEMIASENSE is broad and encompasses several key areas of development and application. Building on the promising results achieved thus far, the following directions outline potential advancements and expansions for ANEMIASENSE:

1. Enhanced Model Development

Incorporation of Additional Data Sources: Integrate genomic data, proteomics, and metabolomics to refine anemia subtype classification and understand underlying pathophysiological mechanisms.

2. Wider Clinical Applications

Comprehensive Hematological Analysis: Expand the scope to include diagnosis and monitoring of other hematological disorders such as leukemias, lymphomas, and clotting disorders. Personalized Treatment Plans: Utilize machine learning to not only diagnose but also suggest personalized treatment plans based on individual patient profiles and response patterns.

3. Integration and Interoperability

Integration with Wearable Technology: Develop non-invasive wearable devices capable of continuously monitoring relevant biomarkers and feeding data into ANEMIASENSE for real-time anemia detection and management.

Healthcare System Interoperability: Ensure seamless integration with various Electronic Health Record (EHR) systems and other healthcare IT infrastructures for broader adoption and utility.

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12.APPENDIX

<u>Model building :</u>

1)Dataset
2)Jupyter Notebook and VS code Application Building
1. HTML file (Home page, Index file, Predict file)

HOME.HTML

```
<!DOCTYPE html>
        <html lang="en">
        <head>
        <meta charset="UTF-8">
        <meta name="viewport" content="width=device-width, initial-scale=1.0">
        <title>Anemia Predictor</title>
        <style>
        body {
        font-family: Arial, sans-serif;
        margin: 0;
        padding: 0;
        background-color: #f4f4f4;
        }
        .header {
        background-image: url('https://encrypted-tbn0.gstatic.com/images?q=tbn:ANd9GcQzep7XHmPrXoXITZn5lKl905IPQpEDOuaVhA&s');
        background-size: cover;
        background-position: center;
        height: 100vh;
        color: rgb(0, 0, 255);
        text-align: center;
        display: flex;
        flex-direction: column;
        justify-content: center;
        align-items: center;
        }
        .header h1 {
        font-size: 3em;
margin: 0;
}
.header p {
font-size: 1.5em;
margin: 0;
}
.navbar {
position: absolute;
top: 0;
width: 100%;
display: flex;
justify-content: flex-end;
padding: 20px;
}
.navbar a {
color: white;
text-decoration: none;
margin: 0 10px;
font-size: 1em;
}
.navbar a:hover {
text-decoration: underline;
}
</style>
</head>
<body>
<div class="header">
<div class="navbar">
<a href="home.html">Home</a>
<a href="index.html">About</a>
<a href="predict.html">Predict</a>
</div>
<h1>Anemia Predictor: Your Health Guardian</h1>
<p>Empowering you with early detection for better management and healthier living.</p>
</div>
</body>
</html>
```

INDEX.HTML

```
<!DOCTYP
E html>
                <html lang="en">
                <head>
                <meta charset="UTF-8">
                <meta name="viewport"
                content="width=device-width,
                initial-scale=1.0">
                <title>About Anemia</title>
                <style>
                body {
                font-family: Arial, sans-serif;
                margin: 0;
                padding: 0;
                background-color: #f5f5f5;
                }
                header {
                background-color: #ffffff;
                padding: 10px 20px;
                display: flex;
                justify-content: space-between;
                align-items: center;
                box-shadow: 0 2px 4px rgba(0,
                0, 0, 0.1);
                }
                header nav a {
                margin-left: 20px;
                text-decoration: none;
                color: #333;
                font-weight: bold;
                }
                .container {
                max-width: 1200px;
                margin: 20px auto;
                padding: 20px;
                background-color: #fff;
```

```css
border-radius: 8px;
box-shadow: 0 2px 4px rgba(0, 0, 0, 0.1);
}
.about-section {
text-align: center;
}
.about-section h1 {
color: #e53935;
}
.info-cards {
display: flex;
flex-wrap: wrap;
gap: 20px;
margin-top: 20px;
}
.info-card {
flex: 1 1 calc(25% - 20px);
background-color: #fefefe;
padding: 20px;
border-radius: 8px;
box-shadow: 0 2px 4px rgba(0, 0, 0, 0.1);
}
.info-card h2 {
color: #e53935;
}
.info-card p {
color: #666;
}
@media (max-width: 768px) {
.info-card {
flex: 1 1 calc(50% - 20px);
}
}
@media (max-width: 480px) {
.info-card {
flex: 1 1 100%;
}
}
</style>
</head>
<body>
<header>
<div>
<h1>Anemia</h1>
</div>
<nav>
<a href="home.html">Home</a>
<a href="index.html">About</a>
<a href="predict.html">Predict</a>
</nav>
<button style="background-color: #e53935; color: #fff; border: none; padding: 10px 20px; border-radius: 5px;">Check</button>
</header>
<div class="container">
<div class="about-section">
<h1>About</h1>
<p>Anemia: low red blood cells or hemoglobin, causing oxygen shortage. Symptoms: fatigue, weakness, shortness of breath, pale skin. Causes: nutritional deficiencies, diseases, blood loss. Treatments vary.</p>
</div>
<div class="info-cards">
<div class="info-card">
<h2>Hemoglobin</h2>
<p>Hemoglobin, a protein in red blood cells, transports oxygen and carbon dioxide. Healthy ranges: Men: 13.2-16.6
```

```
g/dL. Women: 11.6-15
g/dL.</p>
</div>
<div class="info-card">
<h2>MCH</h2>
<p>An MCH value refers to the
average quantity of hemoglobin
present in a single red blood
cell. The normal range for MCH
is between 27.5 and 33.2
picograms (pg).</p>
</div>
<div class="info-card">
<h2>MCHC</h2>
<p>The mean corpuscular
hemoglobin concentration is
average concentration of
hemoglobin in red blood cells.
The normal range: 33.4-
35.5g/dL.</p>
</div>
<div class="info-card">
<h2>MCV</h2>
</div>
</div>
</div>
</body>
```

PREDICT.HTML

```
<!DOCTYPE
html>
      <html lang="en">
      <head>
      <meta charset="UTF-8">
      <meta name="viewport" content="width=device-width, initial-scale=1.0">
      <title>Predict Anemia</title>
      <style>
      body {
      font-family: Arial, sans-serif;
```

```
}
.container {
width: 50%;
margin: 0 auto;
padding: 20px;
border: 1px solid #ccc;
border-radius: 10px;
box-shadow: 2px 2px 12px #aaa;
}
h2 {
text-align: center;
}
.form-group {
margin-bottom: 15px;
}
.form-group label {
display: block;
margin-bottom: 5px;
}
.form-group input {
width: 100%;
padding: 8px;
box-sizing: border-box;
}
.form-group button {
width: 100%;
padding: 10px;
background-color: #28a745;
color: white;
border: none;
border-radius: 5px;
cursor: pointer;
}
.form-group button:hover {
background-color: #218838;
}
.result {
margin-top: 20px;
```

```
text-align: center;
font-size: 18px;
font-weight: bold;
}
</style>
</head>
<nav>
<ul>
<li><a href="home.html">Home</a></li>
<li><a href="index.html">About</a></li>
<li><a href="predict.html">Predict</a></li>
</ul>
</nav>
<body>
<div class="container">
<h2>Predict Anemia</h2>
<div class="form-group">
<label for="gender">Gender:</label>
<input type="text" id="gender" placeholder="Enter gender (Male/Female)">
</div>
<div class="form-group">
<label for="hemoglobin">Hemoglobin (Range: 7-16):</label>
<input type="number" id="hemoglobin" placeholder="Enter Hemoglobin">
</div>
<div class="form-group">
<label for="mch">Mean Corpuscular Hemoglobin (Range: 16-30):</label>
<input type="number" id="mch" placeholder="Enter Mean Corpuscular Hemoglobin">
</div>
<div class="form-group">
<label for="mchc">Mean Corpuscular Hemoglobin Concentration (Range: 28-34):</label>
<input type="number" id="mchc" placeholder="Enter Mean Corpuscular Hemoglobin Concentration">
</div>
<div class="form-group">
<label for="mcv">Mean Corpuscular Volume (Range: 70-100):</label>
<input type="number" id="mcv" placeholder="Enter Mean Corpuscular Volume">
```

```
</div>
<div class="form-group">
<button onclick="predictAnemia()">Submit</button>
</div>
<div class="result" id="result"></div>
</div>
<script>
function predictAnemia() {
const gender = document.getElementById('gender').value;
const hemoglobin = parseFloat(document.getElementById('hemoglobin').value);
const mch = parseFloat(document.getElementById('mch').value);
const mchc = parseFloat(document.getElementById('mchc').value);
const mcv = parseFloat(document.getElementById('mcv').value);
let resultText = '';
if (hemoglobin < 7 || hemoglobin > 16 || mch < 16 || mch > 30 || mchc < 28 || mchc > 34 || mcv < 70 || mcv > 100) {
resultText = 'Please enter values within the specified ranges.';
} else {
// Simple check for anemia based on typical hemoglobin levels
if (hemoglobin < 12) {
resultText = 'Anemia detected.';
} else {
resultText = 'No anemia detected.';
}
}
document.getElementById('result').textContent = resultText;
}
</script>
</body>
</html>
```

APP.PY

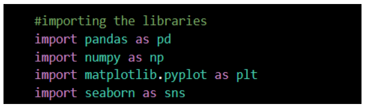
```
import numpy as np
import pickle
import pandas as pd
```

```
from flask import Flask,request,render_template

app = Flask(__name__, static_url_path='/Flask/static')
model = pickle.load(open('model.pkl', 'rb'))

@app.route('/')
def home():
return render_template('index.html')

@app.route('/predict', methods=["POST"])
def predict():

Gender = float(request.form["Gender"])
Hemoglobin = float(request.form["Hemoglobin"])
MCH = float(request.form['MCH'])
MCHC = float(request.form['MCHC'])
MCV = float(request.form['MCV'])

features_values = np.array([[Gender, Hemoglobin, MCH, MCHC, MCV]])

df = pd.DataFrame(features_values, columns=['Gender', 'Hemoglobin', 'MCH',
'MCHC', 'MCV'])
print(df)

prediction = model.predict(df)
print(prediction[0])
result = prediction[0]

if prediction[0] == 0:
result = "You don't have any Anemic Disease"
elif prediction[0] == 1:
result = "You have anemic disease"

text = "Hence, based on calculation: "
return render_template("predict.html", prediction_text=text + str(result))

if __name__ == "__main__":
      app.run(debug=True, port=5000)
```

MODEL BUILDING

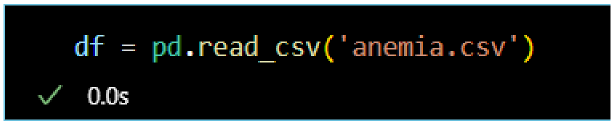
DATASET LINK:
https://drive.google.com/file/d/1KMJFNFGwoaQoAouIPabMEHcT1bvqEXau/view?usp=sharing

Importing the libraries :



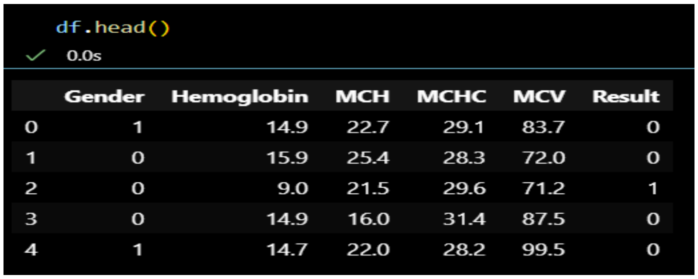
```
#importing the libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

Read the Dataset:



```
df = pd.read_csv('anemia.csv')
```

✓ 0.0s

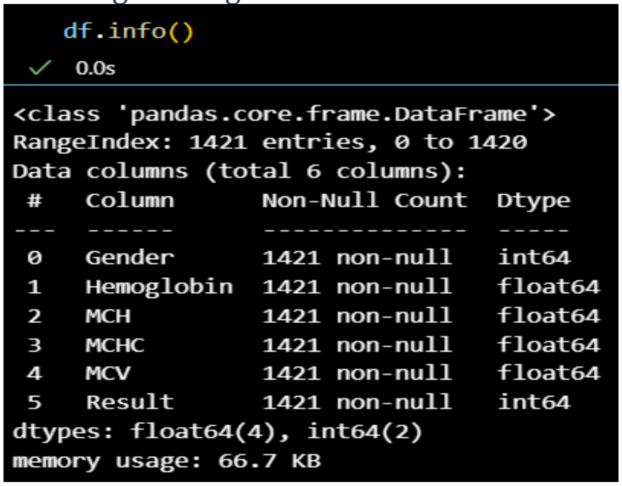


```
df.head()
```

✓ 0.0s

	Gender	Hemoglobin	MCH	MCHC	MCV	Result
0	1	14.9	22.7	29.1	83.7	0
1	0	15.9	25.4	28.3	72.0	0
2	0	9.0	21.5	29.6	71.2	1
3	0	14.9	16.0	31.4	87.5	0
4	1	14.7	22.0	28.2	99.5	0

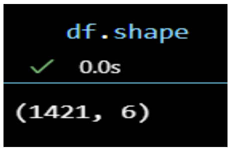
Handling missing values:



```
df.info()
```

✓ 0.0s

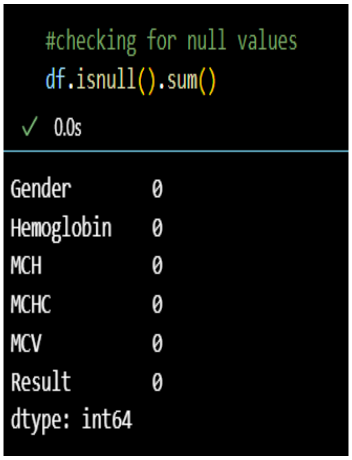
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1421 entries, 0 to 1420
Data columns (total 6 columns):
 #   Column      Non-Null Count  Dtype  
---  ------      --------------  -----  
 0   Gender      1421 non-null   int64  
 1   Hemoglobin  1421 non-null   float64
 2   MCH         1421 non-null   float64
 3   MCHC        1421 non-null   float64
 4   MCV         1421 non-null   float64
 5   Result      1421 non-null   int64  
dtypes: float64(4), int64(2)
memory usage: 66.7 KB
```



```
df.shape
```

✓ 0.0s

```
(1421, 6)
```

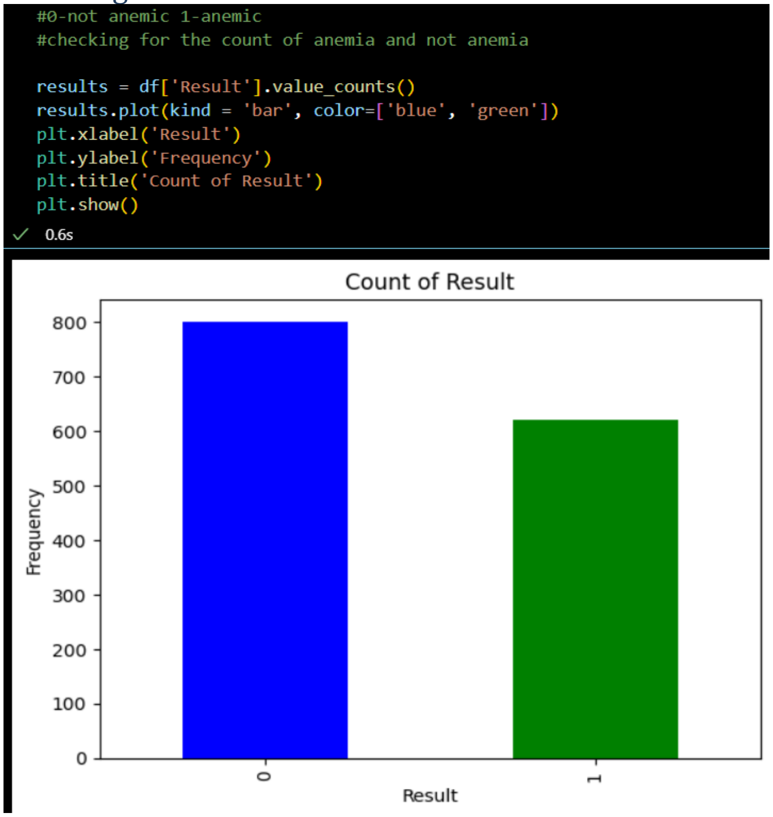


```
#checking for null values
df.isnull().sum()
```

✓ 0.0s

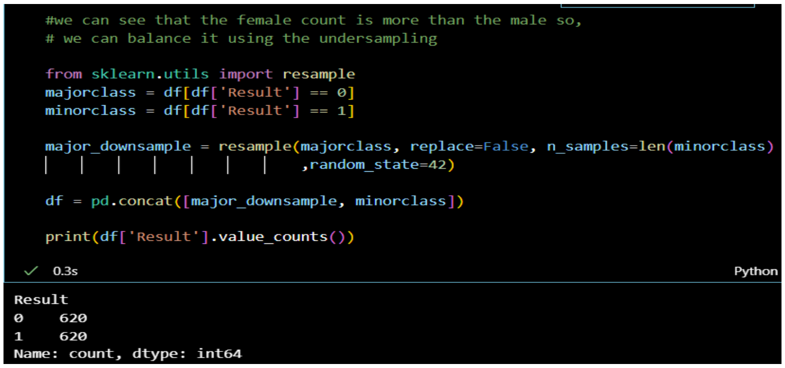
```
Gender        0
Hemoglobin    0
MCH           0
MCHC          0
MCV           0
Result        0
dtype: int64
```

Handling Imbalanced Values:



```
#0-not anemic 1-anemic
#checking for the count of anemia and not anemia

results = df['Result'].value_counts()
results.plot(kind = 'bar', color=['blue', 'green'])
plt.xlabel('Result')
plt.ylabel('Frequency')
plt.title('Count of Result')
plt.show()
```

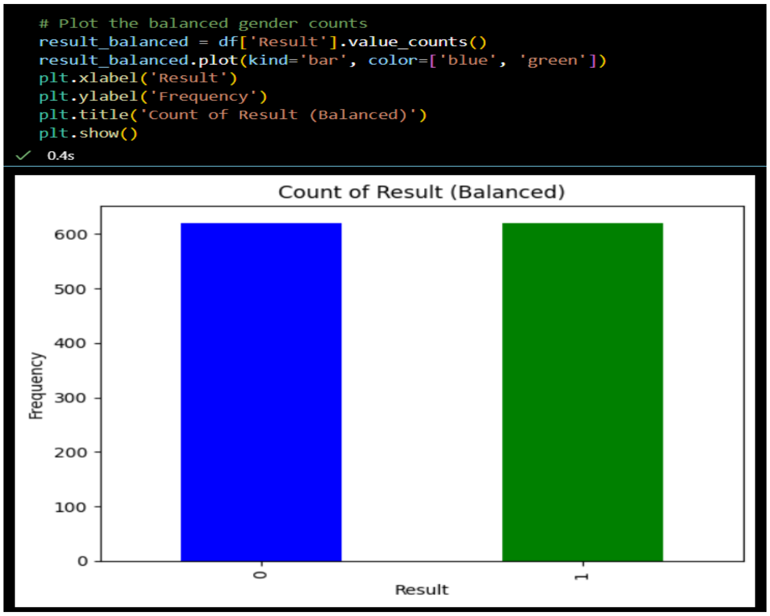
✓ 0.6s



```
#we can see that the female count is more than the male so,
# we can balance it using the undersampling

from sklearn.utils import resample
majorclass = df[df['Result'] == 0]
minorclass = df[df['Result'] == 1]

major_downsample = resample(majorclass, replace=False, n_samples=len(minorclass)
                                        ,random_state=42)

df = pd.concat([major_downsample, minorclass])

print(df['Result'].value_counts())
```

✓ 0.3s Python

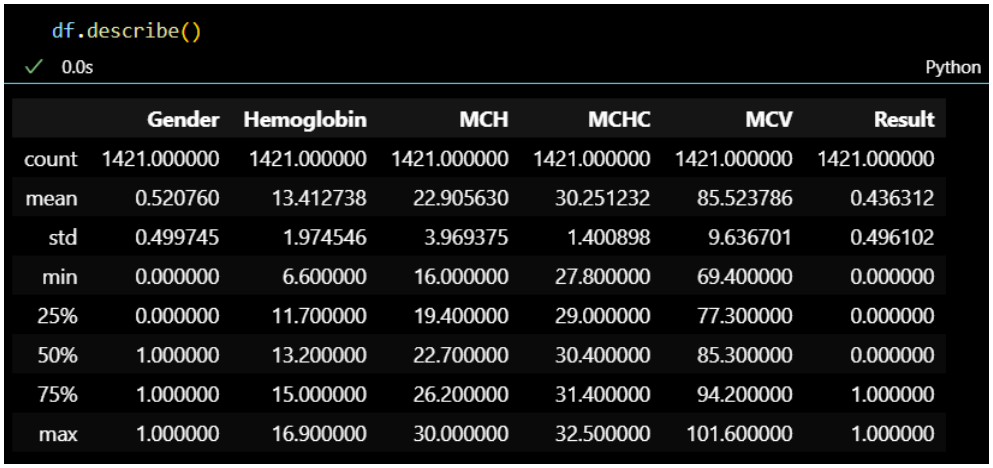
```
Result
0    620
1    620
Name: count, dtype: int64
```



```
# Plot the balanced gender counts
result_balanced = df['Result'].value_counts()
result_balanced.plot(kind='bar', color=['blue', 'green'])
plt.xlabel('Result')
plt.ylabel('Frequency')
plt.title('Count of Result (Balanced)')
plt.show()
```

✓ 0.4s

Descriptive statistical

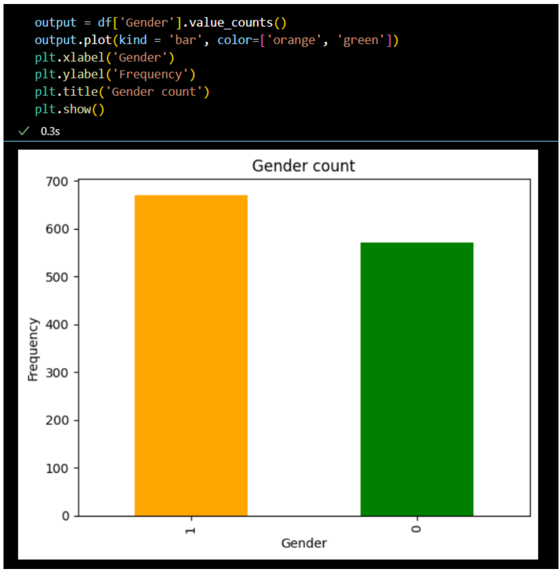


```
df.describe()
```

✓ 0.0s Python

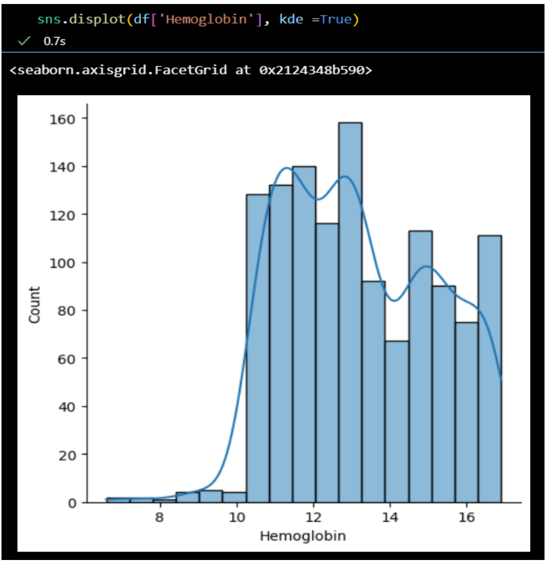
	Gender	Hemoglobin	MCH	MCHC	MCV	Result
count	1421.000000	1421.000000	1421.000000	1421.000000	1421.000000	1421.000000
mean	0.520760	13.412738	22.905630	30.251232	85.523786	0.436312
std	0.499745	1.974546	3.969375	1.400898	9.636701	0.496102
min	0.000000	6.600000	16.000000	27.800000	69.400000	0.000000
25%	0.000000	11.700000	19.400000	29.000000	77.300000	0.000000
50%	1.000000	13.200000	22.700000	30.400000	85.300000	0.000000
75%	1.000000	15.000000	26.200000	31.400000	94.200000	1.000000
max	1.000000	16.900000	30.000000	32.500000	101.600000	1.000000

Univariate analysis



```
output = df['Gender'].value_counts()
output.plot(kind = 'bar', color=['orange', 'green'])
plt.xlabel('Gender')
plt.ylabel('Frequency')
plt.title('Gender count')
plt.show()
```

✓ 0.3s

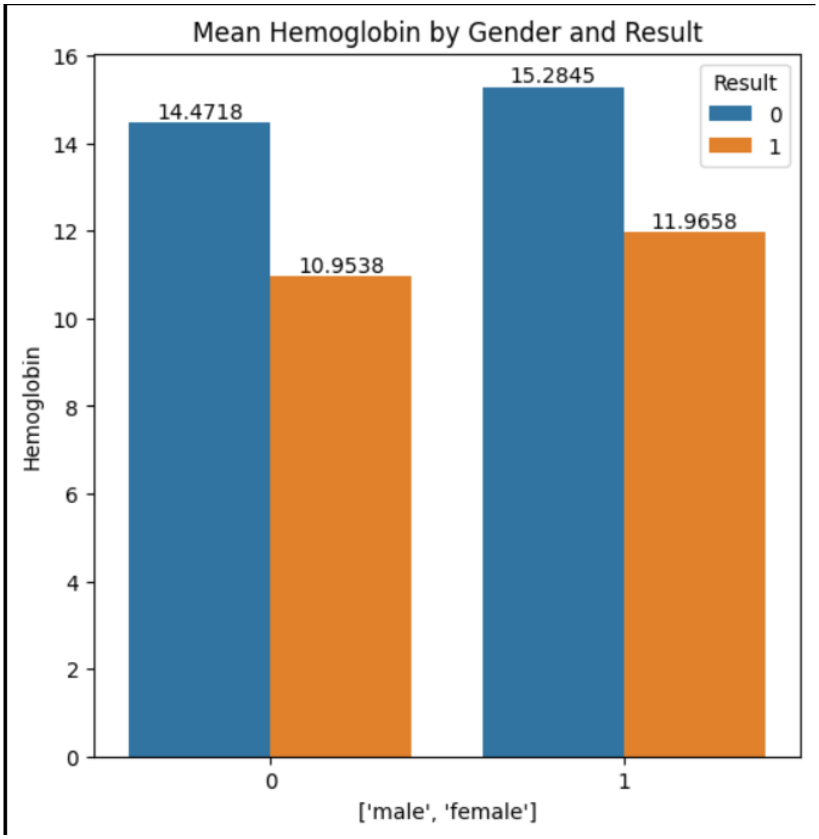


```
sns.displot(df['Hemoglobin'], kde =True)
```

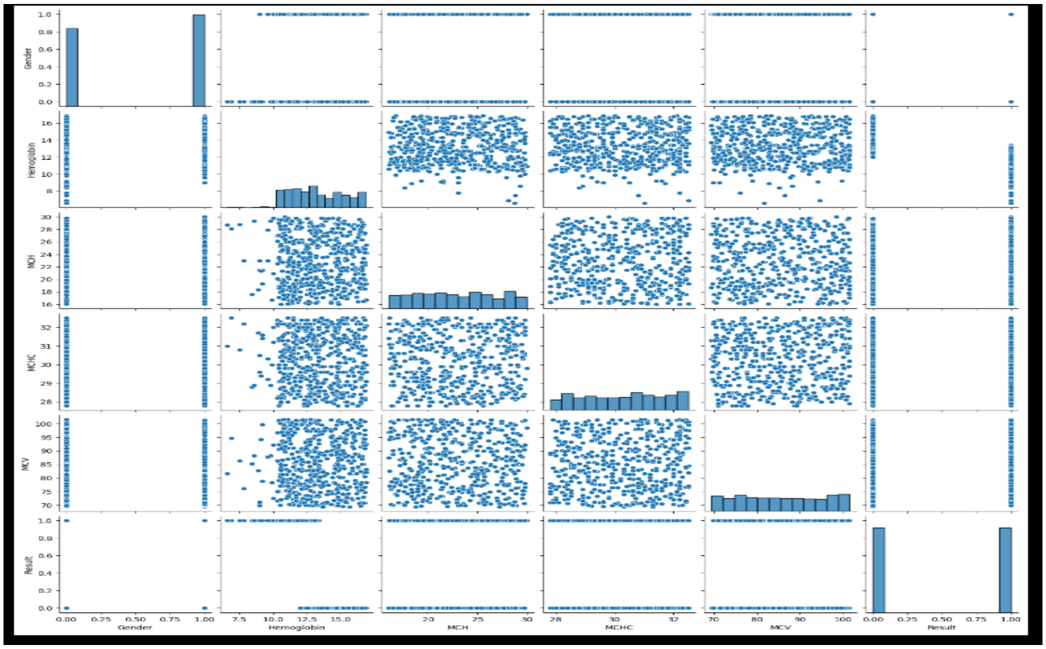
✓ 0.7s

```
<seaborn.axisgrid.FacetGrid at 0x2124348b590>
```

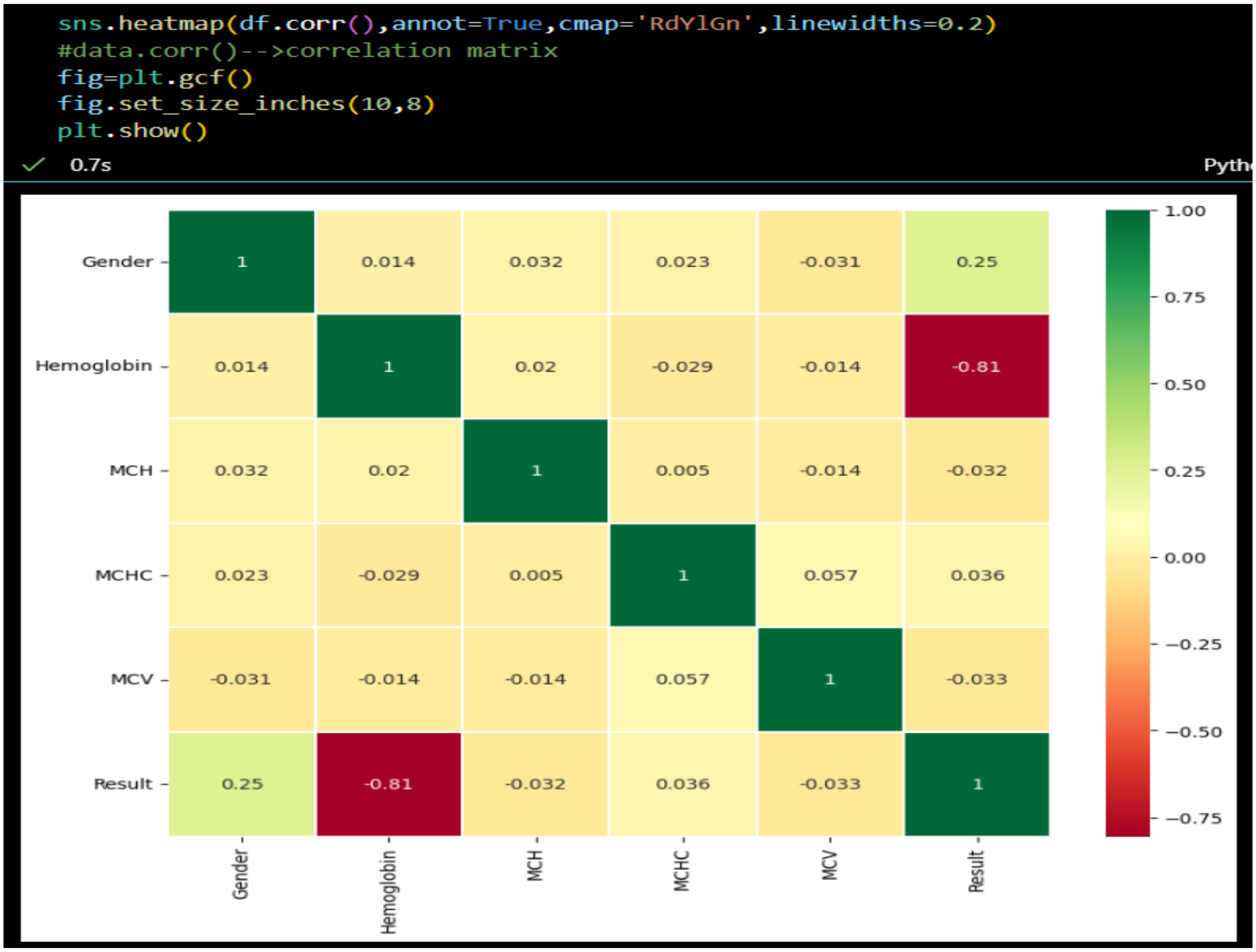
Bivariate analysis



Multivariate analysis



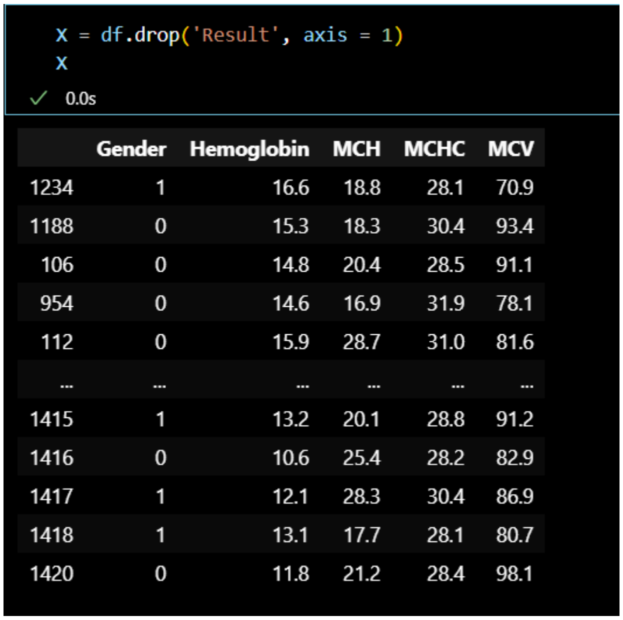
Sns.heatmap()



```
sns.heatmap(df.corr(),annot=True,cmap='RdYlGn',linewidths=0.2)
#data.corr()-->correlation matrix
fig=plt.gcf()
fig.set_size_inches(10,8)
plt.show()
```

✓ 0.7s

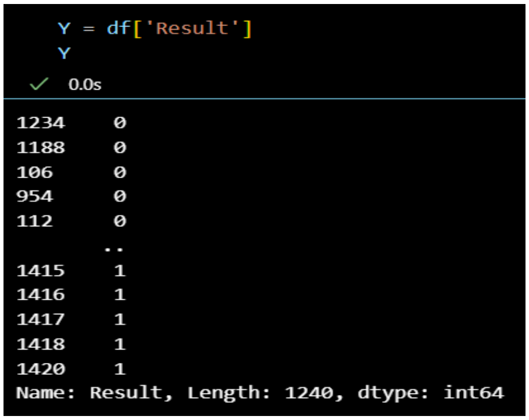
Splitting data into train and test



```
X = df.drop('Result', axis = 1)
X
```

✓ 0.0s

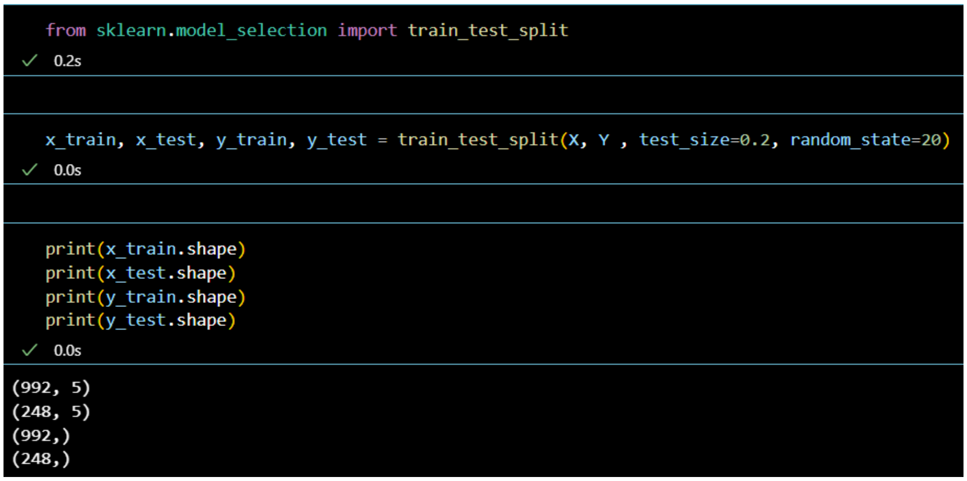
	Gender	Hemoglobin	MCH	MCHC	MCV
1234	1	16.6	18.8	28.1	70.9
1188	0	15.3	18.3	30.4	93.4
106	0	14.8	20.4	28.5	91.1
954	0	14.6	16.9	31.9	78.1
112	0	15.9	28.7	31.0	81.6
...	...	...	...	...	...
1415	1	13.2	20.1	28.8	91.2
1416	0	10.6	25.4	28.2	82.9
1417	1	12.1	28.3	30.4	86.9
1418	1	13.1	17.7	28.1	80.7
1420	0	11.8	21.2	28.4	98.1



```
Y = df['Result']
Y
```

✓ 0.0s

```
1234    0
1188    0
106     0
954     0
112     0
       ..
1415    1
1416    1
1417    1
1418    1
1420    1
Name: Result, Length: 1240, dtype: int64
```



```
from sklearn.model_selection import train_test_split
```

✓ 0.2s

```
x_train, x_test, y_train, y_test = train_test_split(X, Y , test_size=0.2, random_state=20)
```

✓ 0.0s

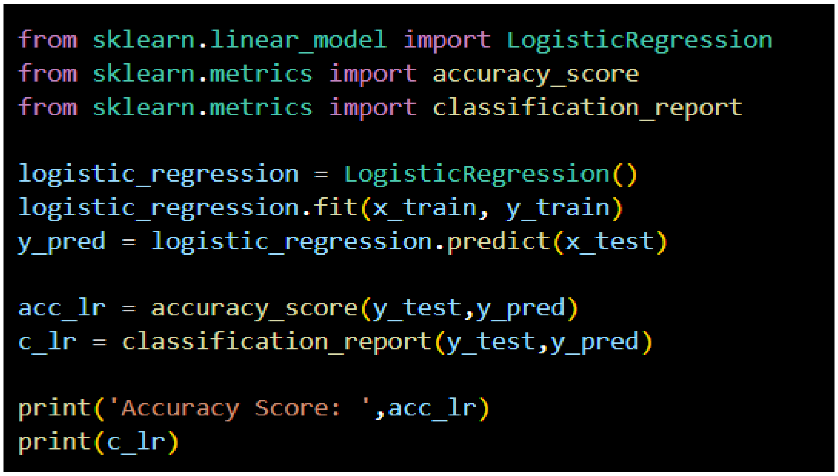
```
print(x_train.shape)
print(x_test.shape)
print(y_train.shape)
print(y_test.shape)
```

✓ 0.0s

```
(992, 5)
(248, 5)
(992,)
(248,)
```

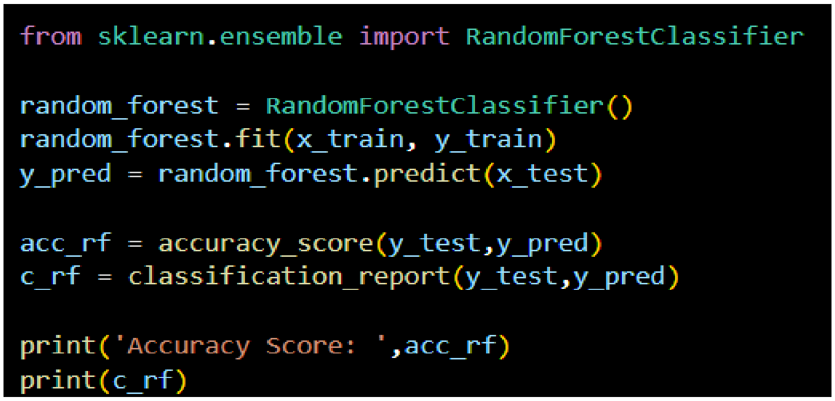
Training the model in multiple algorithms

Logistic Regression Model



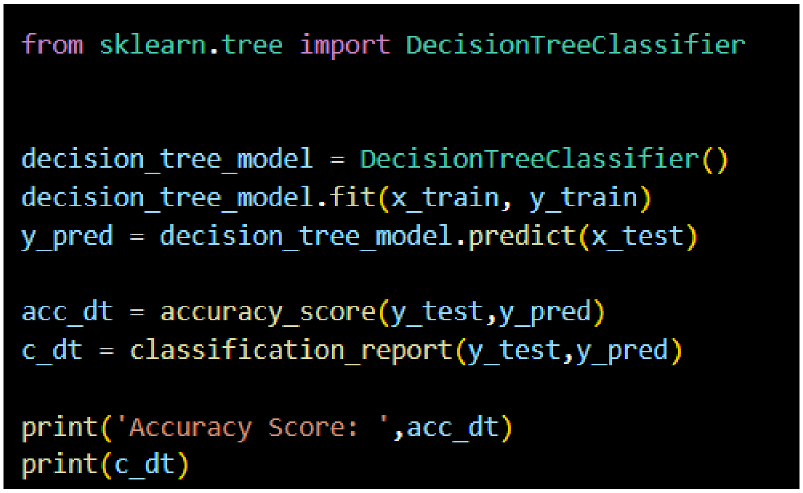
```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
from sklearn.metrics import classification_report

logistic_regression = LogisticRegression()
logistic_regression.fit(x_train, y_train)
y_pred = logistic_regression.predict(x_test)

acc_lr = accuracy_score(y_test,y_pred)
c_lr = classification_report(y_test,y_pred)

print('Accuracy Score: ',acc_lr)
print(c_lr)
```

Random forest model



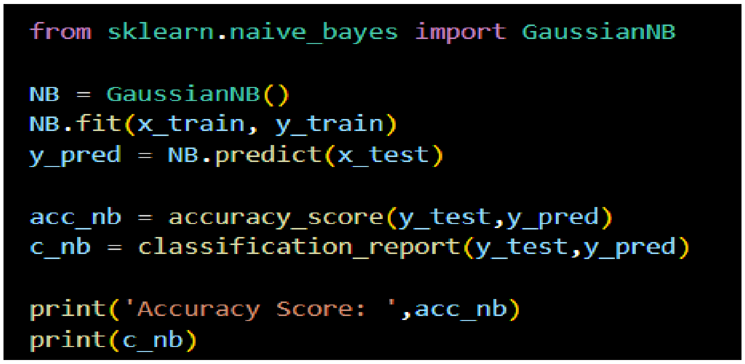
```
from sklearn.ensemble import RandomForestClassifier

random_forest = RandomForestClassifier()
random_forest.fit(x_train, y_train)
y_pred = random_forest.predict(x_test)

acc_rf = accuracy_score(y_test,y_pred)
c_rf = classification_report(y_test,y_pred)

print('Accuracy Score: ',acc_rf)
print(c_rf)
```

Decision Tree Model



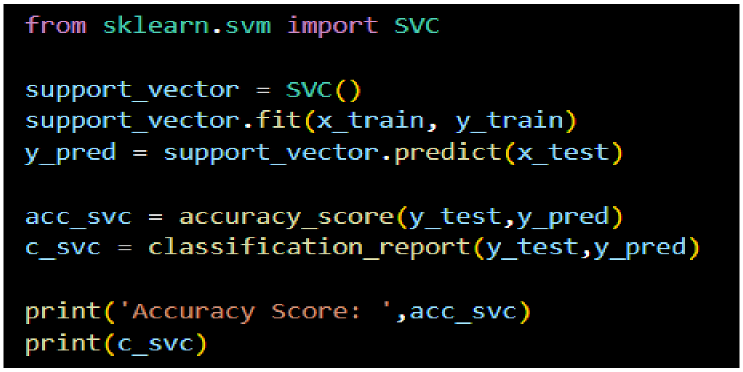
```
from sklearn.tree import DecisionTreeClassifier


decision_tree_model = DecisionTreeClassifier()
decision_tree_model.fit(x_train, y_train)
y_pred = decision_tree_model.predict(x_test)

acc_dt = accuracy_score(y_test,y_pred)
c_dt = classification_report(y_test,y_pred)

print('Accuracy Score: ',acc_dt)
print(c_dt)
```

Gaussian Navies Bayes



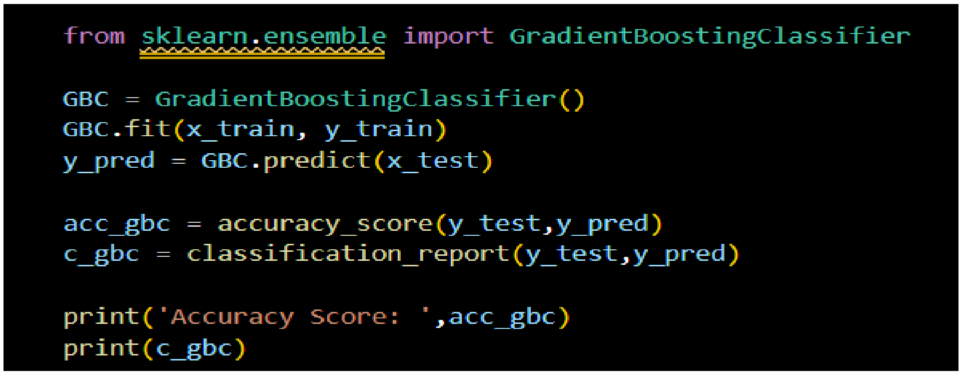
```
from sklearn.naive_bayes import GaussianNB

NB = GaussianNB()
NB.fit(x_train, y_train)
y_pred = NB.predict(x_test)

acc_nb = accuracy_score(y_test,y_pred)
c_nb = classification_report(y_test,y_pred)

print('Accuracy Score: ',acc_nb)
print(c_nb)
```

Support Vector Machine



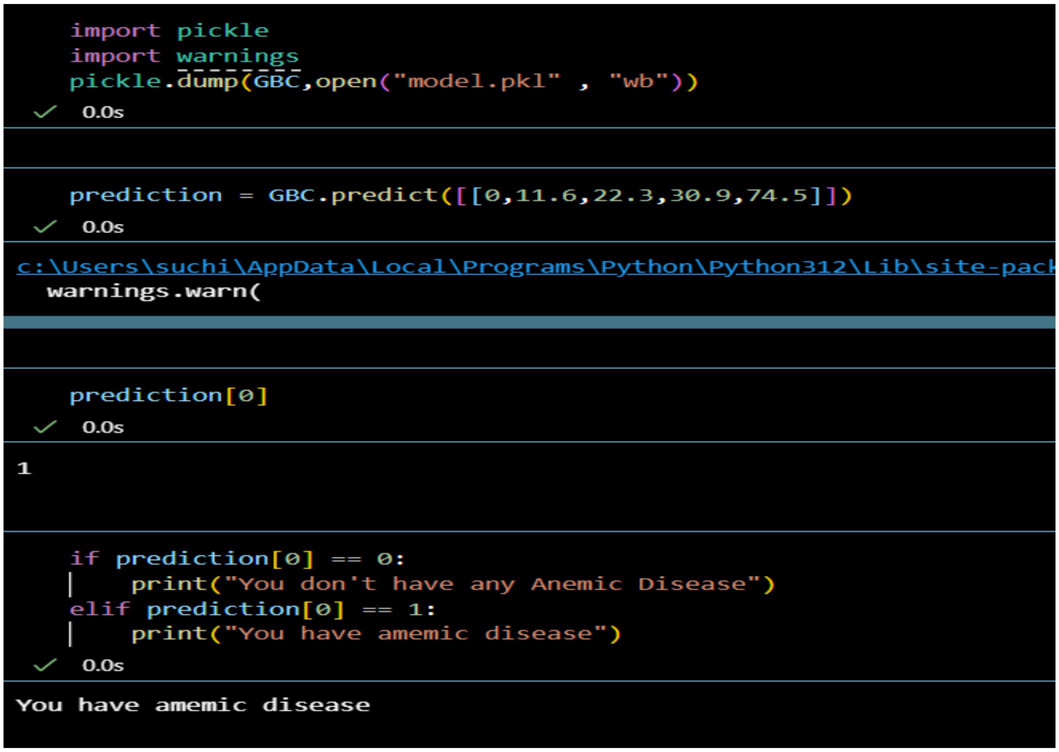
```
from sklearn.svm import SVC

support_vector = SVC()
support_vector.fit(x_train, y_train)
y_pred = support_vector.predict(x_test)

acc_svc = accuracy_score(y_test,y_pred)
c_svc = classification_report(y_test,y_pred)

print('Accuracy Score: ',acc_svc)
print(c_svc)
```

Gradient Boosting Classifier



```
from sklearn.ensemble import GradientBoostingClassifier

GBC = GradientBoostingClassifier()
GBC.fit(x_train, y_train)
y_pred = GBC.predict(x_test)

acc_gbc = accuracy_score(y_test,y_pred)
c_gbc = classification_report(y_test,y_pred)

print('Accuracy Score: ',acc_gbc)
print(c_gbc)
```

Testing the model



```
import pickle
import warnings
pickle.dump(GBC,open("model.pkl" , "wb"))
```
✓ 0.0s

```
prediction = GBC.predict([[0,11.6,22.3,30.9,74.5]])
```
✓ 0.0s

```
c:\Users\suchi\AppData\Local\Programs\Python\Python312\Lib\site-pack
  warnings.warn(
```

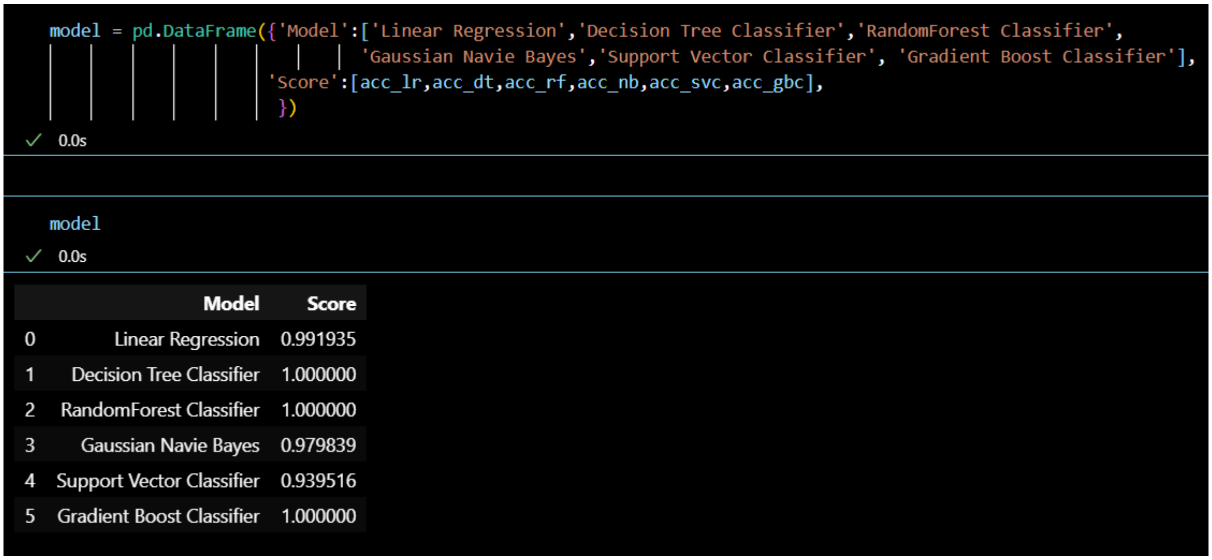
```
prediction[0]
```
✓ 0.0s

```
1
```

```
if prediction[0] == 0:
    print("You don't have any Anemic Disease")
elif prediction[0] == 1:
    print("You have amemic disease")
```
✓ 0.0s

```
You have amemic disease
```

Testing model with multiple evaluation metrics



```
model = pd.DataFrame({'Model':['Linear Regression','Decision Tree Classifier','RandomForest Classifier',
                              'Gaussian Navie Bayes','Support Vector Classifier', 'Gradient Boost Classifier'],
                      'Score':[acc_lr,acc_dt,acc_rf,acc_nb,acc_svc,acc_gbc],
                       })
```
✓ 0.0s

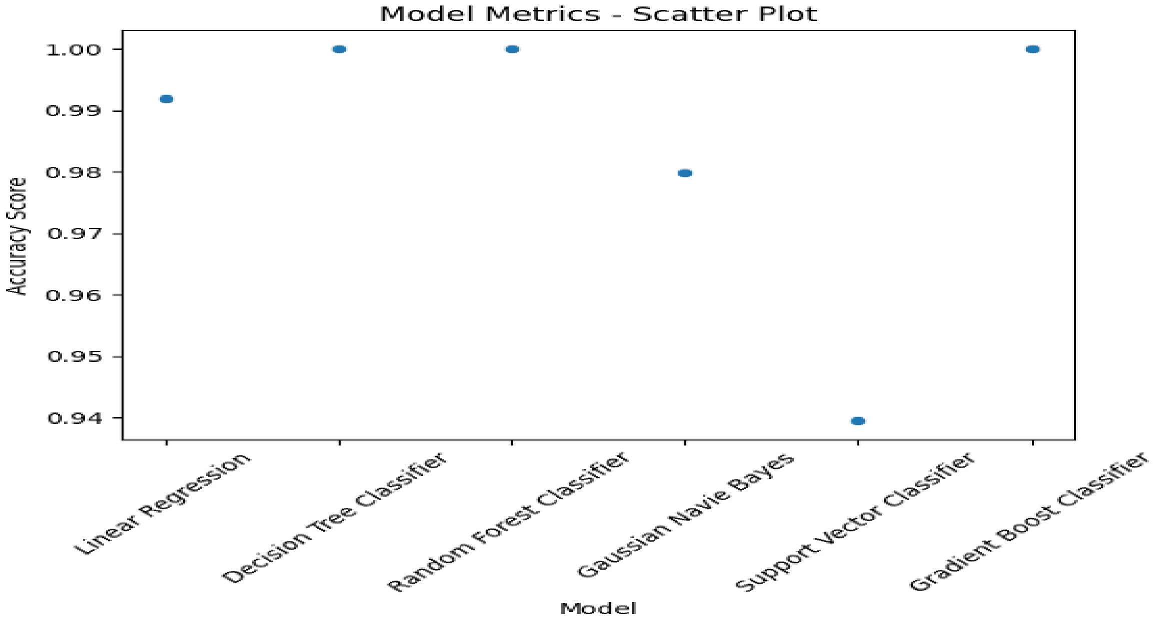
```
model
```
✓ 0.0s

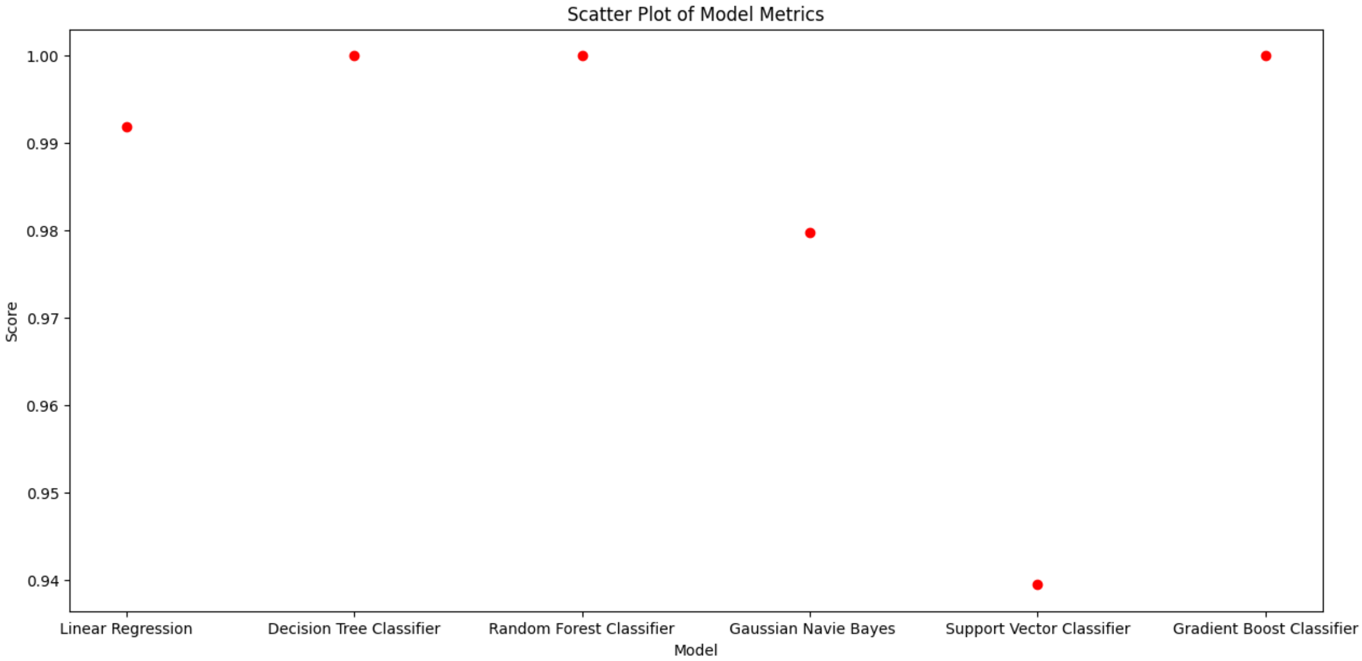
	Model	Score
0	Linear Regression	0.991935
1	Decision Tree Classifier	1.000000
2	RandomForest Classifier	1.000000
3	Gaussian Navie Bayes	0.979839
4	Support Vector Classifier	0.939516
5	Gradient Boost Classifier	1.000000

Save the best model

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

DESCRIPTIVE ANALYSIS


Model Metrics - Scatter Plot
Accuracy Score
Linear Regression
Decision Tree Classifier
Random Forest Classifier
Gaussian Navie Bayes
Support Vector Classifier
Gradient Boost Classifier
Model


Scatter Plot of Model Metrics
Score
Linear Regression
Decision Tree Classifier
Random Forest Classifier
Gaussian Navie Bayes
Support Vector Classifier
Gradient Boost Classifier
Model