Predicting Patient Deterioration in ICUs [ML4ICU]

A PROJECT REPORT

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in partial fulfillment of the requirementsfor the degree of

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BONAFIDE CERTIFICATE

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ABSTRACT

Predicting Patient Deterioration in Intensive Care Units (ICUs), aims to develop a machine learning model that anticipates patient decline by analyzing real-time physiological data. In ICUs, critical signs like heart rate, respiratory rate, body temperature, oxygen saturation, systolic blood pressure, and diastolic blood pressure are continuously monitored, providing vital insights into a patient's condition. By leveraging this data, the model detects early warning signs of deterioration, allowing healthcare providers to take timely action before minor issues become severe. This predictive capability enhances clinical decision-making, supports better resource allocation, and helps prioritize patients who need urgent care, ultimately improving patient outcomes and reducing the risk of adverse events. By empowering proactive interventions and offering real-time alerts, this system optimizes ICU efficiency, potentially saves lives, and promotes a higher standard of care in critical environments.

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ABBREVIATIONS

ICU - Intensive Care Unit

HR - Heart Rate

RR - Respiratory Rate

BT - Body Temperature

SpO_2 - Oxygen Saturation

SBP - Systolic Blood Pressure

DBP - Diastolic Blood Pressure

MAP - Mean Arterial Pressure

HRV - Heart Rate Variability

BMI - Body Mass Index

ML - Machine Learning

EDA - Exploratory Data Analysis

SVC - Support Vector Classifier

AUC-ROC - Area Under the Receiver Operating Characteristic Curve

GRU - Gated Recurrent Unit

RNN - Recurrent Neural Network

LSTM - Long Short-Term Memory

MSIPA - Multi-Stage Interventional Patient Algorithm (hypothetical abbreviation; please replace if this isn't applicable)

TP - True Positive

FP - False Positive

TN - True Negative

FN - False Negative

F1-Score - F1 Score (a measure of model accuracy)

CPU - Central Processing Unit

API - Application Programming Interface

AI - Artificial Intelligence

CNN - Convolutional Neural Network

PCA - Principal Component Analysis

ICD - International Classification of Diseases

EHR - Electronic Health Record

CV - Cross-Validation

PPV - Positive Predictive Value

NPV - Negative Predictive Value

HMM - Hidden Markov Model

EMR - Electronic Medical Record

ANOVA - Analysis of Variance

SVM - Support Vector Machine

ROC - Receiver Operating Characteristic

TPR - True Positive Rate

FPR - False Positive Rate

SD - Standard Deviation

R2 - R-Squared (Coefficient of Determination)

NLP - Natural Language Processing

CT - Computed Tomogra

CHAPTER 1

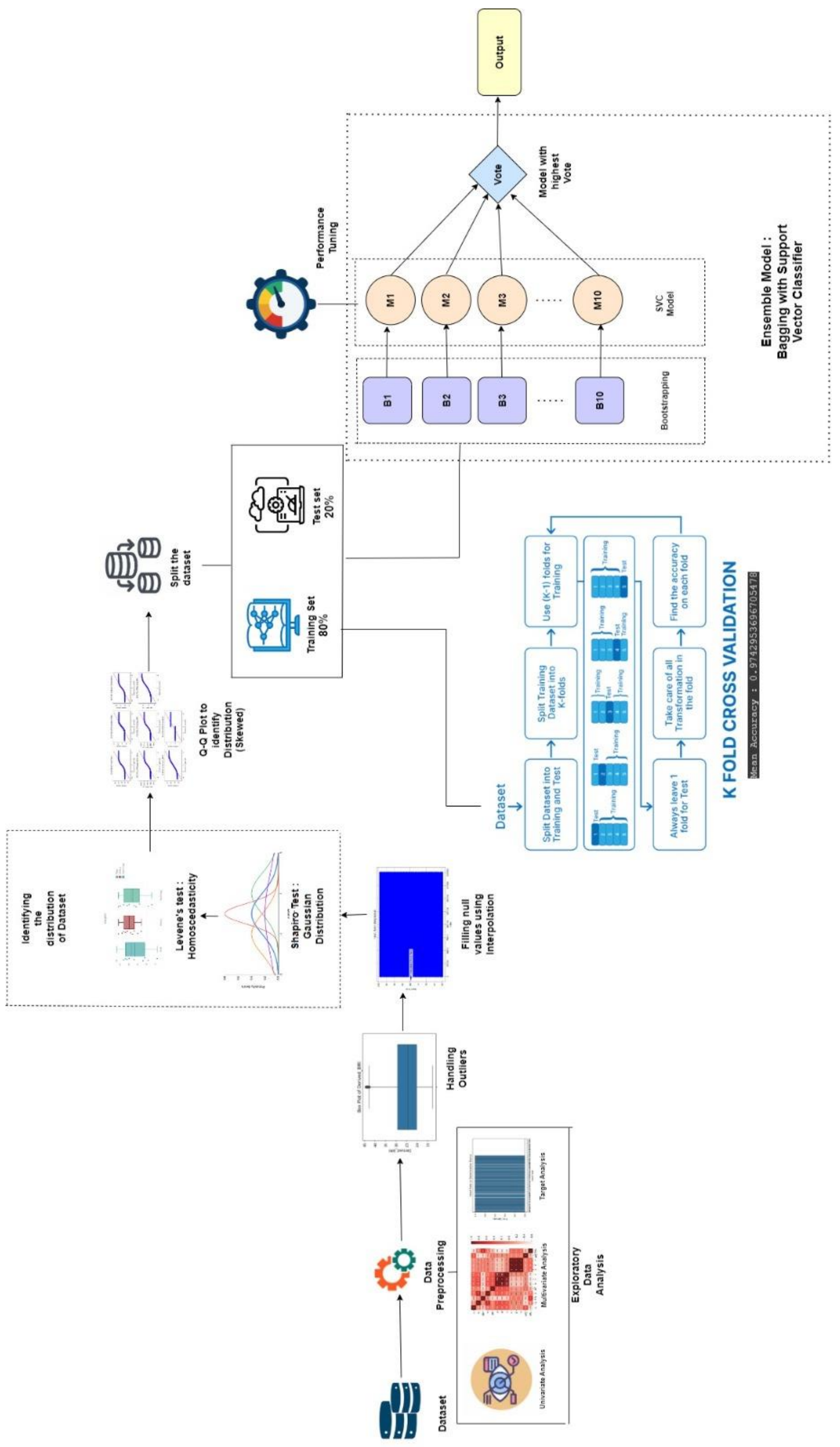
INTRODUCTION

In the high-stakes environment of an Intensive Care Unit (ICU), the difference between life and death can hinge on how quickly medical staff recognize and respond to a patient's declining condition. This project sets out to harness the power of machine learning to create a predictive tool that could help healthcare professionals spot early signs of patient deterioration, potentially saving lives and streamlining care. Using a rich dataset of vital signs—like heart rate, respiratory rate, blood pressure, oxygen levels, and body temperature—alongside derived metrics such as Heart Rate Variability (HRV), Pulse Pressure, and Mean Arterial Pressure (MAP), this project explores how data can be transformed into actionable insights. By analyzing and modeling patterns in these variables, our goal is to design a system that quickly and accurately signals when a patient's health may be about to take a turn for the worse. Through thoughtful data exploration, careful feature selection, and rigorous model training, we're building a tool that doesn't just predict risk but empowers ICU staff with valuable foresight. This project also includes a user-friendly web interface, allowing medical teams to input real-time patient data and receive instant risk predictions. By advancing ICU care with machine learning, we hope to give doctors and nurses a critical edge in the fight for their patients' lives.

1.1. Software Requirements Specifications

- **Python 3.8+**: Core programming language for the project.
- **Jupyter Notebook**: For data analysis and experimentation.
- **Pandas & NumPy**: Data handling and numerical operations.
- **Scikit-Learn & XGBoost**: Machine learning libraries for model building.
- **Matplotlib & Seaborn**: Data visualization tools for insights.
- **Flask/Django**: Framework for developing the web application interface.

1.2. Architecture



Dataset
Data Preprocessing
Univariate Analysis
Multivariate Analysis
Target Analysis
Exploratory Data Analysis
Handling Outliers
Filling null values using Interpolation
Shapiro Test : Gaussian Distribution
Levene's test : Homoscedasticity
Identifying the distribution of Dataset
Q-Q Plot to identify Distribution (Skewed)
Split the dataset
Training Set 80%
Test set 20%
Dataset
Split Dataset into Training and Test
Split Training Dataset into K-folds
Use (K-1) folds for Training
Always leave 1 fold for Test
Take care of all Transformation in the fold
Find the accuracy on each fold
K FOLD CROSS VALIDATION
Mean Accuracy : 0.9742953696705478
B1
B2
B3
B10
Bootstrapping
M1
M2
M3
M10
SVC Model
Performance Tuning
Vote
Model with highest Vote
Output
Ensemble Model : Bagging with Support Vector Classifier

Fig 1.1 : Architecture of the project

This architecture diagram presents a comprehensive workflow for building a machine learning model aimed at predicting patient deterioration in an ICU setting. Starting with the dataset, the process begins with Exploratory Data Analysis (EDA), where Univariate, Multivariate, and Target analyses are conducted to understand each variable’s distribution, relationships between variables, and the target outcome. This initial EDA phase provides insights into data patterns, allowing for informed decisions in subsequent steps. Following EDA, Data Preprocessing ensures the dataset is clean and prepared for modeling. Here, steps like identifying and handling outliers are crucial; extreme values in the data are visualized and managed to reduce noise. Missing values, often inevitable in medical data, are filled using interpolation techniques to maintain continuity without distorting underlying trends.

The architecture then moves into Distribution Analysis, where the data’s distribution characteristics are examined to ensure it meets assumptions required by the model. Tests like the Shapiro Test for normality and Levene’s Test for homoscedasticity are applied, along with Q-Q Plots to assess skewness in the data. These tests validate whether the data is approximately Gaussian or if transformations may be necessary. Once the data distribution is confirmed or adjusted, the dataset is split into Training and Testing sets with an 80-20 split, setting up the model for training while keeping a portion for unbiased evaluation.

K-Fold Cross Validation is then employed to further improve the model's reliability. By splitting the training set into multiple folds, this approach allows the model to train on different portions of data and test across various folds, producing a more robust model by averaging results across all folds. Each fold is processed with transformations and evaluated to ensure consistency across different subsets of the data, resulting in a mean accuracy score as shown in the diagram.

Following validation, the model building phase focuses on an Ensemble Model using Bagging with a Support Vector Classifier (SVC). In this approach, multiple bootstrapped subsets (B1, B2, etc.) are created from the training set, and each subset trains its own SVC model (M1, M2, etc.). This bootstrapping method helps in reducing variance and increasing stability in the predictions.

A final Voting Mechanism is then applied, where predictions from each SVC model are aggregated, and the prediction with the highest vote is selected as the output. This ensemble approach leverages the collective strengths of multiple models to enhance accuracy and mitigate individual model biases.

The final model undergoes Performance Tuning to optimize parameters and improve predictive capability. This iterative process refines model hyperparameters to ensure the highest possible performance on unseen data. The architecture’s design concludes with an Output section, where the model’s prediction is provided. Overall, this well-structured pipeline ensures that each aspect of data processing, model training, and evaluation is rigorously addressed, resulting in a reliable, high-performing predictive model for patient deterioration in ICUs.

CHAPTER 2

LITERATURE SURVEY

Predicting patient outcomes in the Intensive Care Unit (ICU) is critical for optimizing resources, improving patient care, and enabling clinicians to make timely, informed decisions. Multiple studies have applied machine learning (ML) and artificial intelligence (AI) methods to predict mortality and patient deterioration in ICUs, each contributing insights into model effectiveness and areas for enhancement. In [1], researchers explored mortality prediction using a Support Vector Machine (SVM) model that incorporated variables like fluid inputs, blood, urine outputs, Length of Stay (LOS), and patient weight, achieving an accuracy of 82% and suggesting the need for a richer dataset to improve accuracy. Meanwhile, [2] presented a detailed ICU monitoring system leveraging an Artificial Neural Network (ANN) with an accuracy of 86%, though high computational demands restricted its accessibility in resource-limited settings; the authors recommended future models with similar accuracy but reduced resource needs. Focusing on pediatric patients, [3] used a Random Forest Classifier (RFC) to predict patient states, achieving moderate precision and recall values (0.84 and 0.86, respectively) and proposing the development of a specialized risk scoring system that could surpass current assessment models in pediatric ICUs. In [4], an approach for predicting patient deterioration within 24 hours of ICU transfer was proposed, utilizing the EarlySense (ES) system with a Gradient Booster Classifier, which yielded an AUC-ROC of 0.81 and highlighted the importance of timely intervention, especially for extreme heart rate (HR) and respiratory rate (RR) values. Another study, [5], compared the performance of multiple algorithms, including Random Forest, SVM, Logistic Regression, and Decision Tree, for predicting circulatory failure, with Random Forest achieving the highest accuracy at 71%; this study noted that further sophistication could improve prediction accuracy across larger datasets.

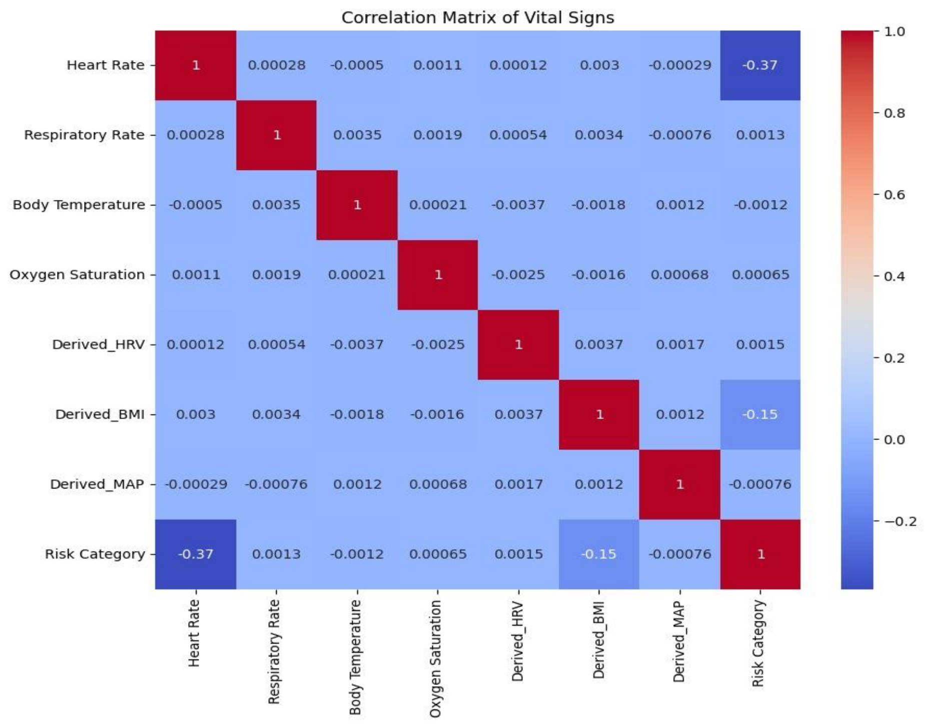
An investigation in [6] applied a cloud-based intelligent remote patient monitoring (IRPM) framework to ICU risk stratification, achieving a maximum readmission model accuracy of 67.53% with an AUROC of 0.7376, underscoring the utility of recent vital sign measurements in minimizing prediction error. The use of a Markov Decision Process (MDP) model in [7] was focused on optimizing ICU admission policies, though it was limited by the inability to differentiate between first-time ICU admissions and readmissions; the authors suggested a data-driven approach to classify more patient types. In [8], a mortality prediction model using Generative Adversarial Networks (GAN) and ensemble techniques demonstrated promise, though the simplistic selection of variables limited its performance, encouraging future models to consider variable correlations for enhanced accuracy. Another study, [9], introduced an ICU decision support system using association rule mining (ARM) to help clinicians predict outcomes and manage high-risk patients more effectively. Finally, [10] presented a patient-specific stacking ensemble model combining algorithms such as linear discriminant analysis, decision tree, and logistic regression to predict ICU mortality, designed under medical guidance for enhanced stability in multitask prediction. Collectively, these studies underscore the potential of AI-driven models in ICU settings but also highlight the ongoing need for improvements in accuracy, computational efficiency, and applicability across diverse patient groups.

CHAPTER 3

METHODOLOGY OF PREDICTING PATIENT DETERIORATION IN ICUs

3.1. Exploratory Data Analysis (EDA)

- Load the Dataset
- Handling Missing Values
- Univariate Analysis: Examine individual vital signs like heart rate, temperature, blood pressure, etc. Look for patterns, outliers, and trends in these features.
- Multivariate Analysis: Check for correlations between different vital signs and patient outcomes. This can help identify which features are more important.
- We’ve done using heatmap to check for correlation between the columns in the dataset, from this we can identify independent individual features for our project



	Heart Rate	Respiratory Rate	Body Temperature	Oxygen Saturation	Derived_HRV	Derived_BMI	Derived_MAP	Risk Category
Heart Rate	1	0.00028	-0.0005	0.0011	0.00012	0.003	-0.00029	-0.37
Respiratory Rate	0.00028	1	0.0035	0.0019	0.00054	0.0034	-0.00076	0.0013
Body Temperature	-0.0005	0.0035	1	0.00021	-0.0037	-0.0018	0.0012	-0.0012
Oxygen Saturation	0.0011	0.0019	0.00021	1	-0.0025	-0.0016	0.00068	0.00065
Derived_HRV	0.00012	0.00054	-0.0037	-0.0025	1	0.0037	0.0017	0.0015
Derived_BMI	0.003	0.0034	-0.0018	-0.0016	0.0037	1	0.0012	-0.15
Derived_MAP	-0.00029	-0.00076	0.0012	0.00068	0.0017	0.0012	1	-0.00076
Risk Category	-0.37	0.0013	-0.0012	0.00065	0.0015	-0.15	-0.00076	1

Fig 3.1 : Collinearity in dataset

Most of the other variables have very low correlation values (close to 0), meaning they don't show strong linear relationships with each other or the target variable (Risk Category).

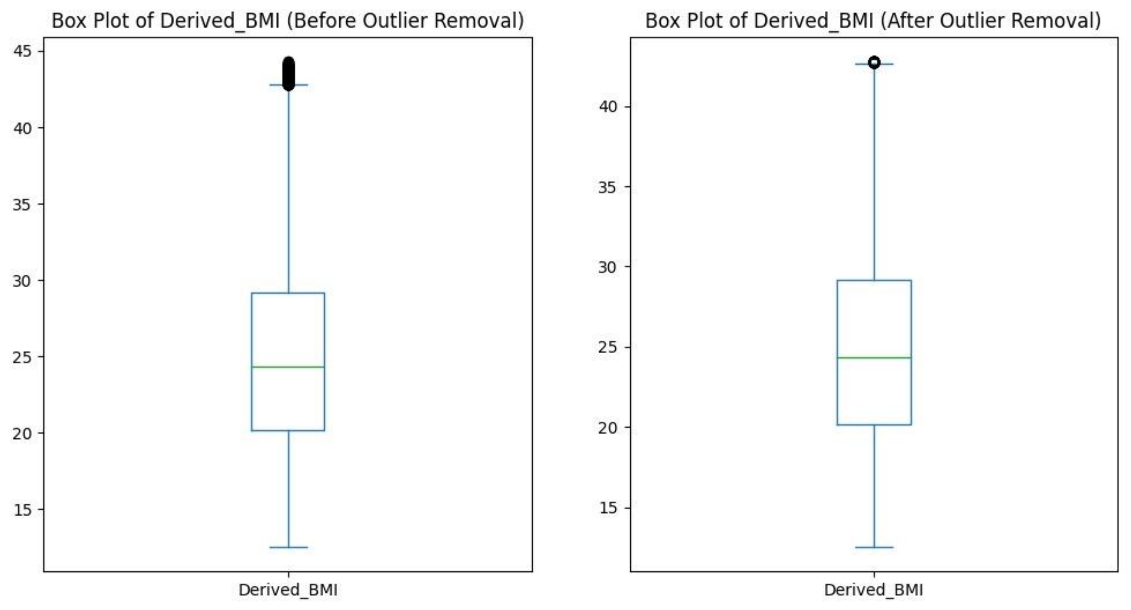


Fig 3.2 : The black circles above the whisker represent outliers.

- The 1st quartile (Q1) is the 25th percentile, and the 3rd quartile (Q3) is the 75th percentile. These values define the middle 50% of the data in the 'Derived_BMI' column.
- The IQR is calculated as IQR = Q3 - Q1. This range shows the spread of the central 50% of the data. The IQR is used to determine the boundaries for identifying outliers.
- Any data points in the 'Derived_BMI' column that fall below the lower bound or above the upper bound are considered outliers.

Step 1: Data Preprocessing : Understanding Data Distribution

- Done using histograms.

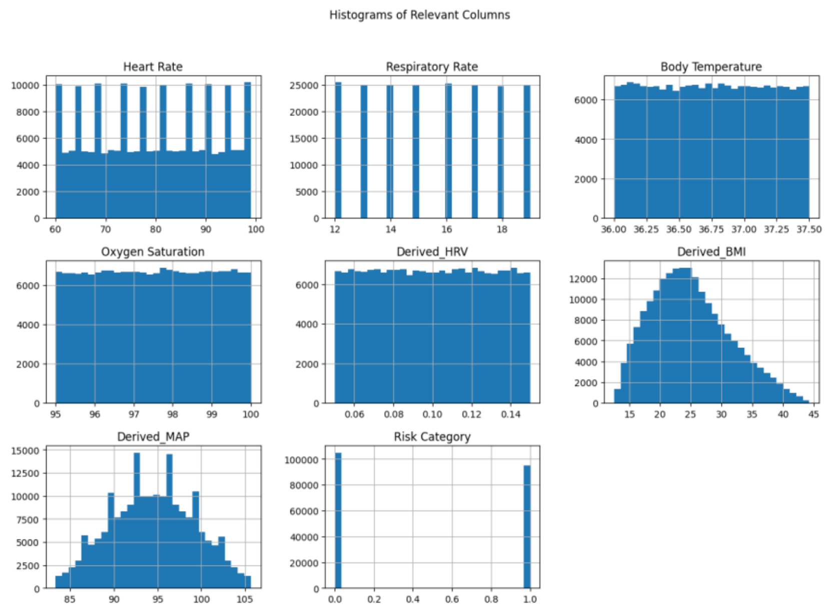


Fig 3.3 : Understanding the distribution of each variable in the dataset

- Heart Rate: The distribution appears roughly uniform, but there are gaps between bins, indicating a possible issue with data recording or binning. This could suggest discrete intervals in the data collection process.

- Derived_BMI: This feature shows a right-skewed distribution, with more values concentrated at lower BMI ranges and a long tail on the higher end.

- Derived_MAP and others: This feature shows a normal distribution, which is ideal for many machine learning models. No changes are necessary here.

Step 2: Data Preprocessing : Understanding Data Distribution In our dataset.

Done using Q-Q Plots.

The curves deviate significantly from the red line at both ends, suggesting that these features are not normally distributed. The "S" shape seen in most plots indicates that the distributions are likely skewed.

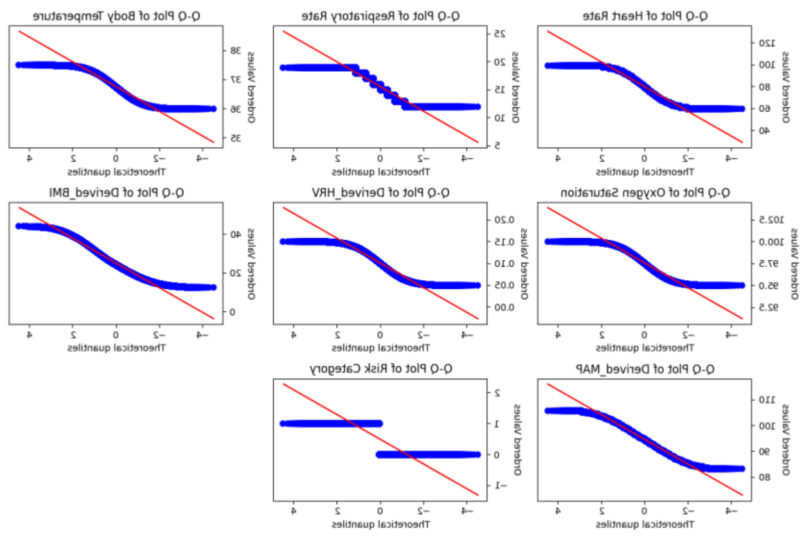


Fig 3.4 : Skew distribution in dataset

Step 3: Model Building

- Choose appropriate models: Selected models based on the nature of your data (in our case, classification) and we have used bagging with svc (an ensemble model).

Step 4: Model Training and Evaluation:

- Split data: Divide data into training (80%) and testing sets (20%) to evaluate model performance.
- Train models: Fit the selected models to the training data.
- Evaluate performance: Use appropriate metrics (e.g., accuracy, precision, recall, F1-score, RMSE) to assess model accuracy on the testing set.

3.2 Design of Modules

3.2.1. Bagging with SVC

Bagging (Bootstrap Aggregating) is a popular ensembling technique in machine learning that involves training multiple instances of a base model (e.g., decision trees, SVC) on different subsets of the training data and then combining their predictions. The step breakdown is:

- Bootstrap Sampling: The algorithm creates multiple bootstrap samples from the original training data. Each bootstrap sample is a random subset of the original data, with replacement. This means that some data points may appear multiple times in a bootstrap sample while others may not appear at all.

- Model Training: A base model (SVC) is trained on each bootstrap sample. This results in a collection of models, each with slightly different characteristics due to the different training data.

- Prediction and Combination: When making predictions on new data, each base model provides its own prediction. The final prediction is typically an aggregate of the individual predictions. Common aggregation methods include: Voting: The most common prediction among the base models is chosen as the final prediction

3.2.2. Benefits of Bagging with SVC:

- Reduced Overfitting: By training multiple SVCs on different subsets of the data, bagging can help to reduce overfitting, which is a common problem with SVCs, especially when using complex kernels.
- Improved Accuracy: Bagging can often improve the accuracy of SVC models, especially when the data is noisy or contains outliers.

- Increased Robustness: Bagging can make SVC models more robust to changes in the training data.
- Parallel Processing: Bagging can be easily parallelized, as each SVC model can be trained independently. This can significantly speed up the training process, especially for large datasets.

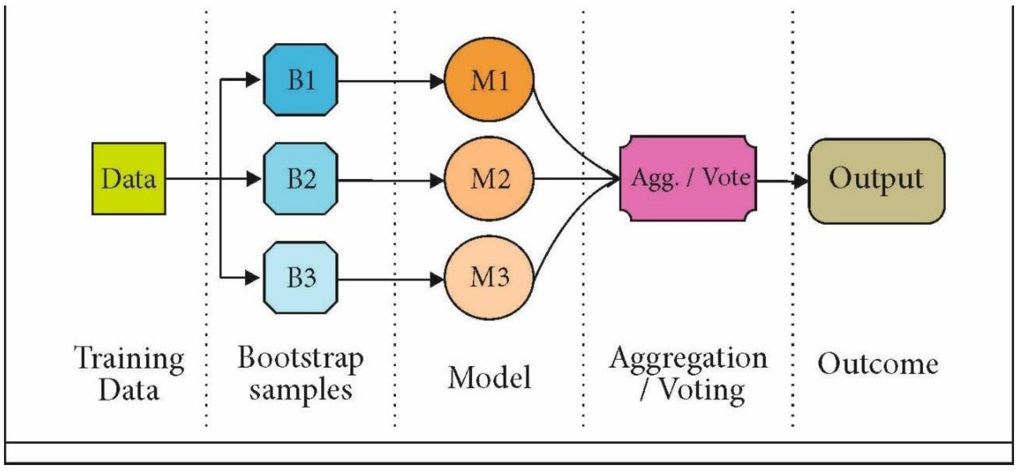
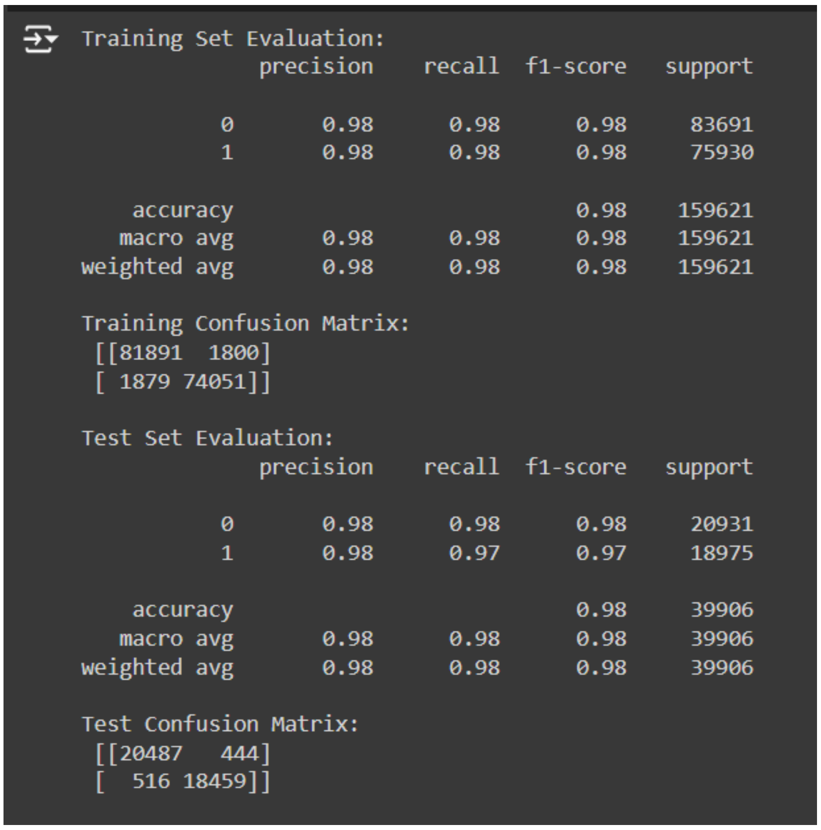


Fig 3.5 : Bagging algorithm Flowchart

CHAPTER 4

RESULTS AND DISCUSSIONS

4.1. Model Performance Analysis



```
Training Set Evaluation:
              precision    recall  f1-score   support

           0       0.98      0.98      0.98     83691
           1       0.98      0.98      0.98     75930

    accuracy                           0.98    159621
   macro avg       0.98      0.98      0.98    159621
weighted avg       0.98      0.98      0.98    159621

Training Confusion Matrix:
 [[81891  1800]
 [ 1879 74051]]

Test Set Evaluation:
              precision    recall  f1-score   support

           0       0.98      0.98      0.98     20931
           1       0.98      0.97      0.97     18975

    accuracy                           0.98     39906
   macro avg       0.98      0.98      0.98     39906
weighted avg       0.98      0.98      0.98     39906

Test Confusion Matrix:
 [[20487   444]
 [  516 18459]]
```

Fig 4.1 : Results

- Precision: The ratio of correctly predicted positive observations to the total predicted positives. For class 0, precision is 0.98, meaning 98% of predicted class 0 instances were correct. The same applies for class 1.
- Recall: The ratio of correctly predicted positive observations to all observations in the actual class. A recall of 0.98 for both classes means 98% of the actual class 0 and class 1 instances were correctly identified.
- F1-Score: The weighted average of precision and recall. A high F1-score of 0.98 indicates a strong balance between precision and recall.

- Support: The number of actual occurrences of each class. There are 83,691 instances of class 0 and 75,930 instances of class 1 in the training data.

  We almost get the same results for Testing set as well

  The confusion matrix shows that only a few instances are misclassified, confirming the model's strong performance.

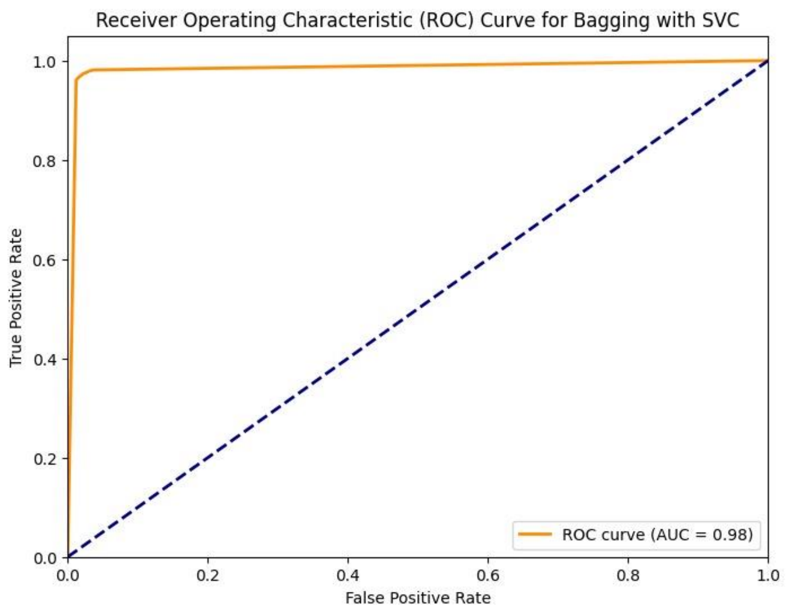


Fig 4.2 : Receiver Operating Characteristic curve for the model

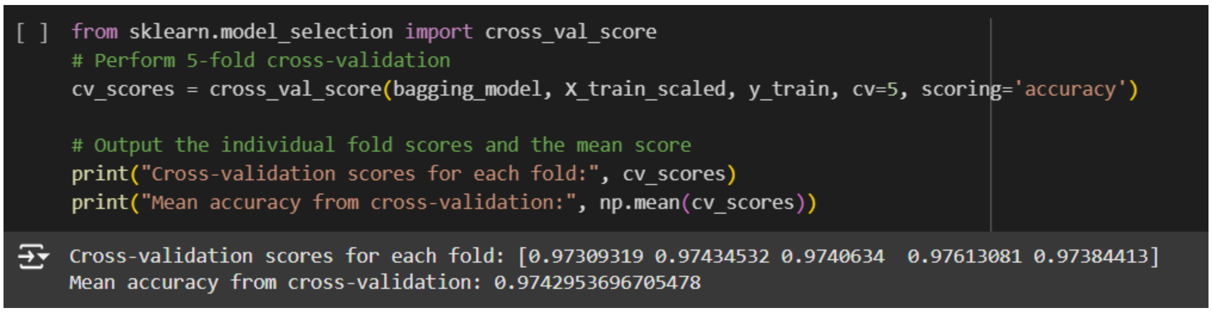
High AUC Value: The area under the curve (AUC) is 0.98, which indicates that the model has excellent discriminatory power between the positive and negative classes.

True Positive Rate (TPR) vs. False Positive Rate (FPR):

The curve stays close to the top-left corner, showing that the model has a high true positive rate while maintaining a low false positive rate. This means the model is very good at correctly identifying positive cases (e.g., patient deterioration) without generating many false positives (incorrectly predicting deterioration).

4.2. Checking for Model Overfit

Both the training and test performance were close (around 98% accuracy), which suggests the model generalizes well and is not overfitting. The confusion matrix showed very few false positives and false negatives in both the training and test sets, which aligns with good generalization. We'll check for the cross validation score to check, the performance remains consistently high across multiple folds.



```
[ ]  from sklearn.model_selection import cross_val_score
     # Perform 5-fold cross-validation
     cv_scores = cross_val_score(bagging_model, X_train_scaled, y_train, cv=5, scoring='accuracy')

     # Output the individual fold scores and the mean score
     print("Cross-validation scores for each fold:", cv_scores)
     print("Mean accuracy from cross-validation:", np.mean(cv_scores))
```

```
Cross-validation scores for each fold: [0.97309319 0.97434532 0.9740634  0.97613081 0.97384413]
Mean accuracy from cross-validation: 0.9742953696705478
```

Fig 4.3 : Results for K-Fold Cross Validation

The individual fold scores range from approximately 0.9731 to 0.9761, indicating that the model consistently achieves around 97.3% to 97.6% accuracy on different subsets of the data. This suggests that the model is likely well-fitted to the data. The mean accuracy across all folds is about 0.9743, or 97.43%. This is a strong indication that your model generalizes well to unseen data, as it maintains high accuracy even when evaluated on different subsets. The closeness of the fold scores suggests low variance, meaning that the model's performance is stable across different data splits. This is a positive sign, as it implies that the model is not overly sensitive to the specific training data used in any particular fold.

CHAPTER 5

COMPARATIVE ANALYSIS OF ALGORITHMS

Table 5.1 Comparative Analysis

Algorithm	Accuracy	Recall	Precision	F1-Score	AUC-ROC
Bagging with SVC	**98%**	**97%**	**98%**	**98%**	**0.980**
MSIPA	93.7%	91.4%	92.6%	92%	0.967
LSTM	89.2%	87.3%	88.5%	87.9%	0.941
GRU	88.5%	86.5%	87.7%	87.1%	0.935
RNN	85.4%	83.6%	84.8%	84.2%	0.913

- This comparison table showcases the strengths of various algorithms in predicting patient deterioration, revealing some clear front-runners.

- Bagging with Support Vector Classifier (SVC) takes the lead, boasting an impressive 98% accuracy and nearly perfect precision and F1-Score, making it a powerhouse for reliable predictions.

- Close behind is MSIPA, with a solid 93.7% accuracy and an AUC-ROC of 0.967, demonstrating it can also handle the task with strong recall and precision, though it falls just short of SVC's prowess. LSTM and GRU, both popular deep learning models, deliver decent performance with accuracies around 89% and 88.5%, respectively, reflecting their strength in capturing temporal patterns but still lagging behind the top contenders.

- Finally, RNN rounds out the list with 85.4% accuracy, proving capable yet clearly overshadowed by more advanced algorithms. This comparison highlights how bagging techniques paired with SVC can provide a winning edge in critical predictions for ICU patients

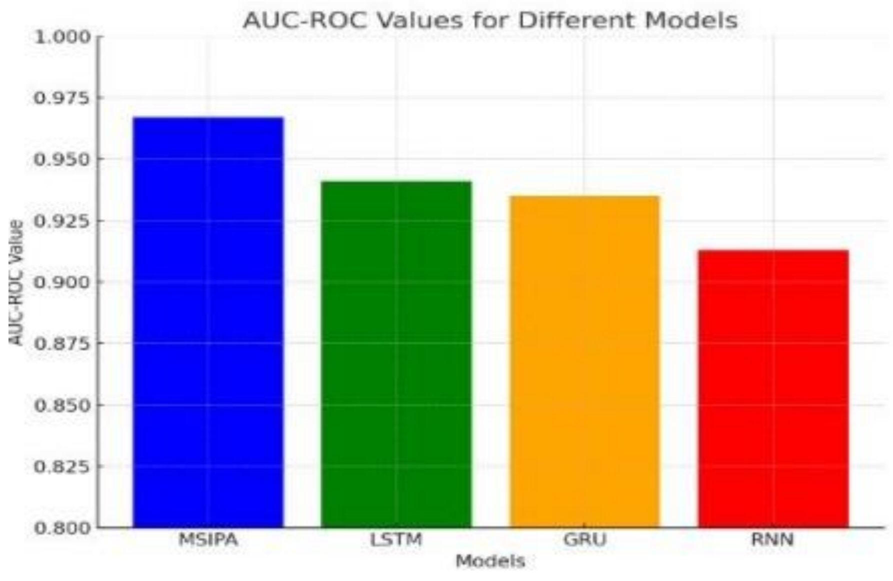


Fig 5.1. AUC-ROC of other algorithms

- MSIPA has the highest AUC-ROC value, around 0.975,
- LSTM and GRU have slightly lower AUC-ROC values, around 0.94 and 0.92, respectively.
- RNN has the lowest AUC-ROC value, around 0.89, suggesting it is the least effective among the models tested.

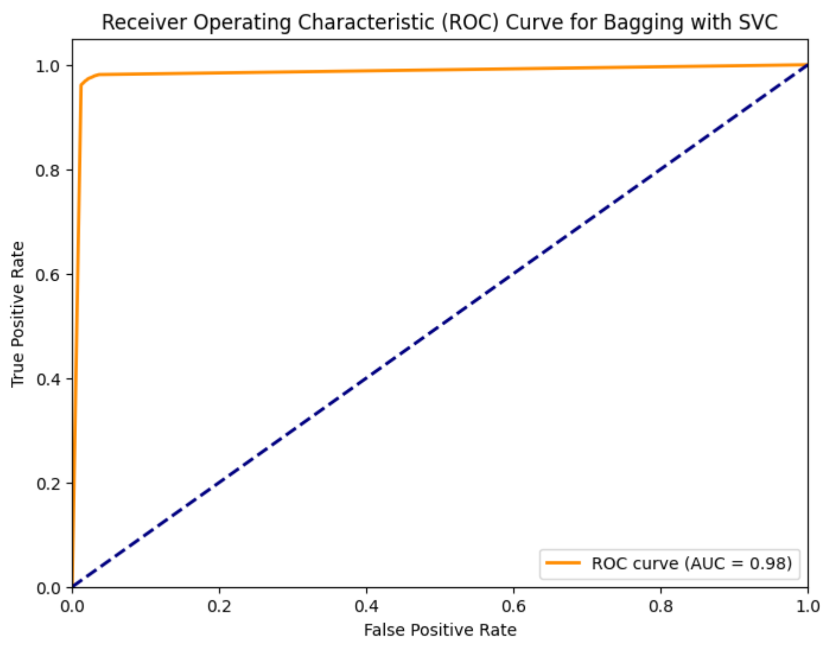


Fig 5.2. AUC-ROC of Bagging with SVC

- The ROC curve plotted for the Bagging Classifier with SVC shows strong performance, with an AUC of 0.98. Here are the key inferences:

- High AUC Value: The area under the curve (AUC) is 0.98, which indicates that the model has excellent discriminatory power between the positive and negative classes.

- True Positive Rate (TPR) vs. False Positive Rate (FPR):

- The curve stays close to the top-left corner, showing that the model has a high true positive rate while maintaining a low false positive rate.This means the model is very good at correctly identifying positive cases (e.g., patient deterioration) without generating many false positives (incorrectly predicting deterioration).

CHAPTER 6

CONCLUSION AND FUTURE ENHANCEMENT

In conclusion, this project leverages machine learning to develop a predictive tool capable of identifying early signs of patient deterioration in ICUs. By analyzing a comprehensive dataset of vital signs, including heart rate, respiratory rate, blood pressure, oxygen levels, and temperature, as well as derived metrics such as Heart Rate Variability (HRV), Pulse Pressure, and Mean Arterial Pressure (MAP), the model offers an invaluable early-warning system. This predictive capability empowers ICU staff with timely insights, enabling proactive intervention, prioritization of care, and ultimately, better patient outcomes. The user-friendly web interface allows healthcare professionals to input real-time data and receive instant risk assessments, making it a practical and effective tool for the high-stakes ICU environment.

Future work: There are several ways to enhance this model and its deployment in clinical settings. First, incorporating additional data sources, such as lab results, medication history, and nurse notes, could improve the model’s predictive accuracy. Expanding the dataset to include data from diverse healthcare facilities could also enhance model robustness and generalizability. Additionally, leveraging advanced deep learning techniques, such as recurrent neural networks (RNNs) and transformer models, may allow for more complex temporal pattern recognition in patient data. Finally, integrating this tool with ICU monitoring systems for automatic data input could streamline workflows and improve real-time usability, further supporting healthcare providers in delivering swift and effective critical care. These enhancements would not only refine the model’s performance but also strengthen its role in promoting a proactive approach to patient care in ICUs.

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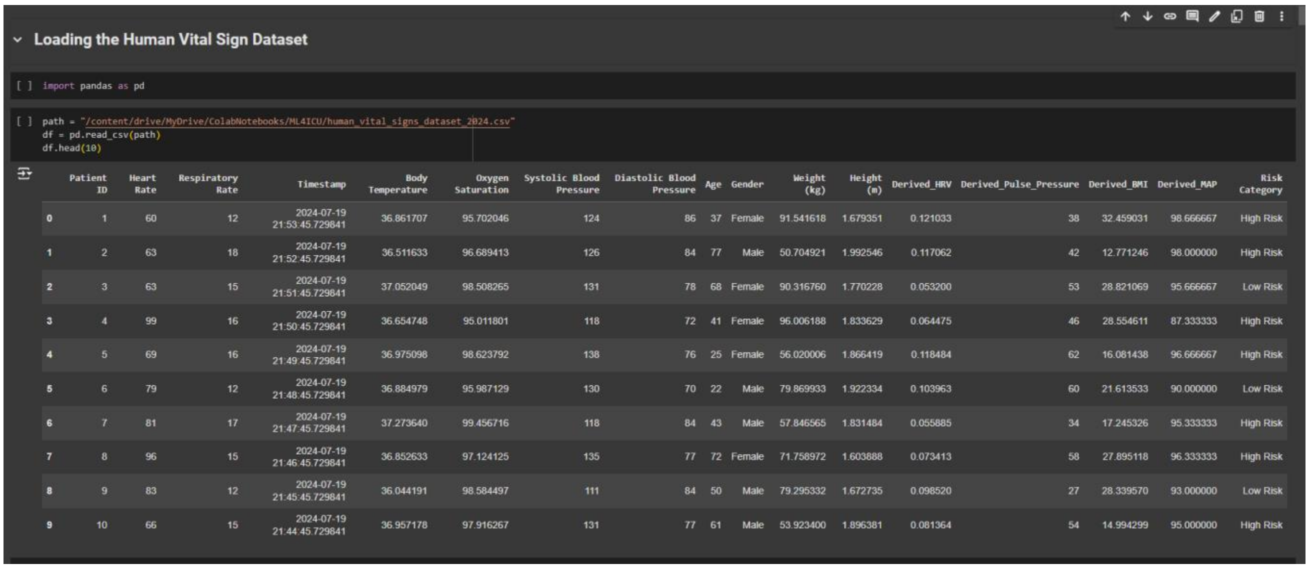
APPENDIX

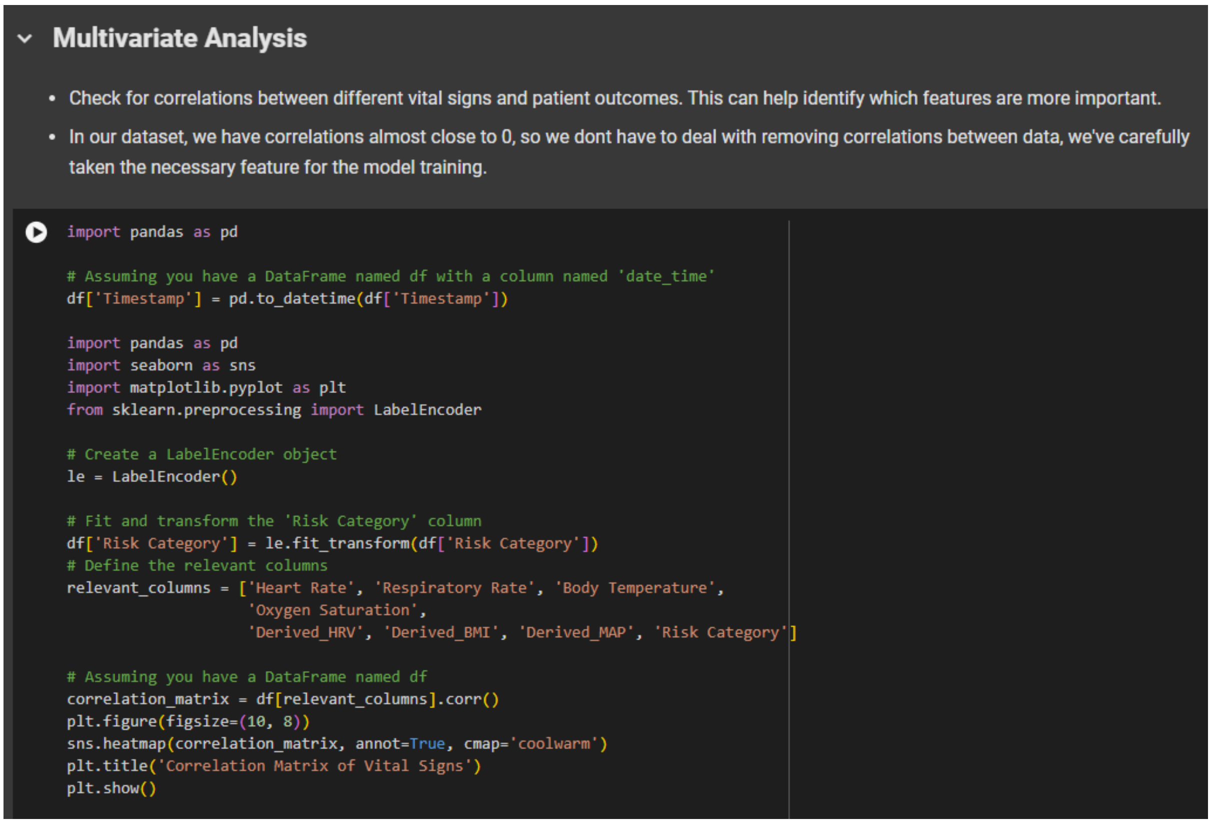


Loading the Human Vital Sign Dataset

```
[ ] import pandas as pd
```

```
[ ] path = "/content/drive/MyDrive/ColabNotebooks/ML4ICU/human_vital_signs_dataset_2024.csv"
    df = pd.read_csv(path)
    df.head(10)
```

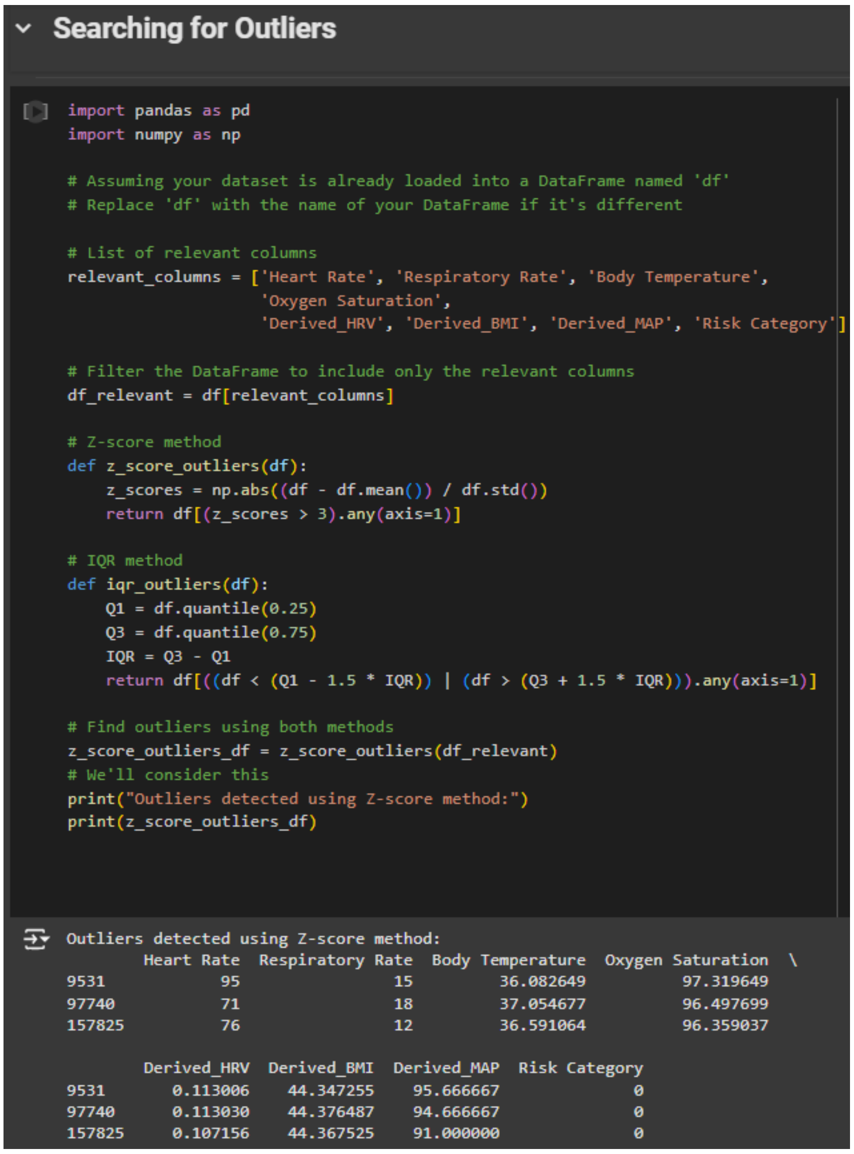
```
   Patient  Heart  Respiratory                  Timestamp       Body     Oxygen  Systolic Blood  Diastolic Blood  Age  Gender     Weight    Height  Derived_HRV  Derived_Pulse_Pressure  Derived_BMI  Derived_MAP       Risk
        ID   Rate         Rate                            Temperature Saturation        Pressure         Pressure                      (kg)       (m)                                                                Category
0        1     60           12  2024-07-19 21:53:45.729841  36.861707  95.702046             124               86   37  Female  91.541618  1.679351     0.121033                      38    32.459031    98.666667  High Risk
1        2     63           18  2024-07-19 21:52:45.729841  36.511633  96.689413             126               84   77    Male  50.704921  1.992546     0.117062                      42    12.771246    98.000000  High Risk
2        3     63           15  2024-07-19 21:51:45.729841  37.052049  98.508265             131               78   68  Female  90.316760  1.770228     0.053200                      53    28.821069    95.666667   Low Risk
3        4     99           16  2024-07-19 21:50:45.729841  36.654748  95.011801             118               72   41  Female  96.006188  1.833629     0.064475                      46    28.554611    87.333333  High Risk
4        5     69           16  2024-07-19 21:49:45.729841  36.975098  98.623792             138               76   25  Female  56.020006  1.866419     0.118484                      62    16.081438    96.666667  High Risk
5        6     79           12  2024-07-19 21:48:45.729841  36.884979  95.987129             130               70   22    Male  79.869933  1.922334     0.103963                      60    21.613533    90.000000   Low Risk
6        7     81           17  2024-07-19 21:47:45.729841  37.273640  99.456716             118               84   43    Male  57.846565  1.831484     0.055885                      34    17.245326    95.333333  High Risk
7        8     96           15  2024-07-19 21:46:45.729841  36.852633  97.124125             135               77   72  Female  71.758972  1.603888     0.073413                      58    27.895118    96.333333  High Risk
8        9     83           12  2024-07-19 21:45:45.729841  36.044191  98.584497             111               84   50    Male  79.295332  1.672735     0.098520                      27    28.339570    93.000000   Low Risk
9       10     66           15  2024-07-19 21:44:45.729841  36.957178  97.916267             131               77   61    Male  53.923400  1.896381     0.081364                      54    14.994299    95.000000  High Risk
```



Multivariate Analysis

- Check for correlations between different vital signs and patient outcomes. This can help identify which features are more important.
- In our dataset, we have correlations almost close to 0, so we dont have to deal with removing correlations between data, we've carefully taken the necessary feature for the model training.

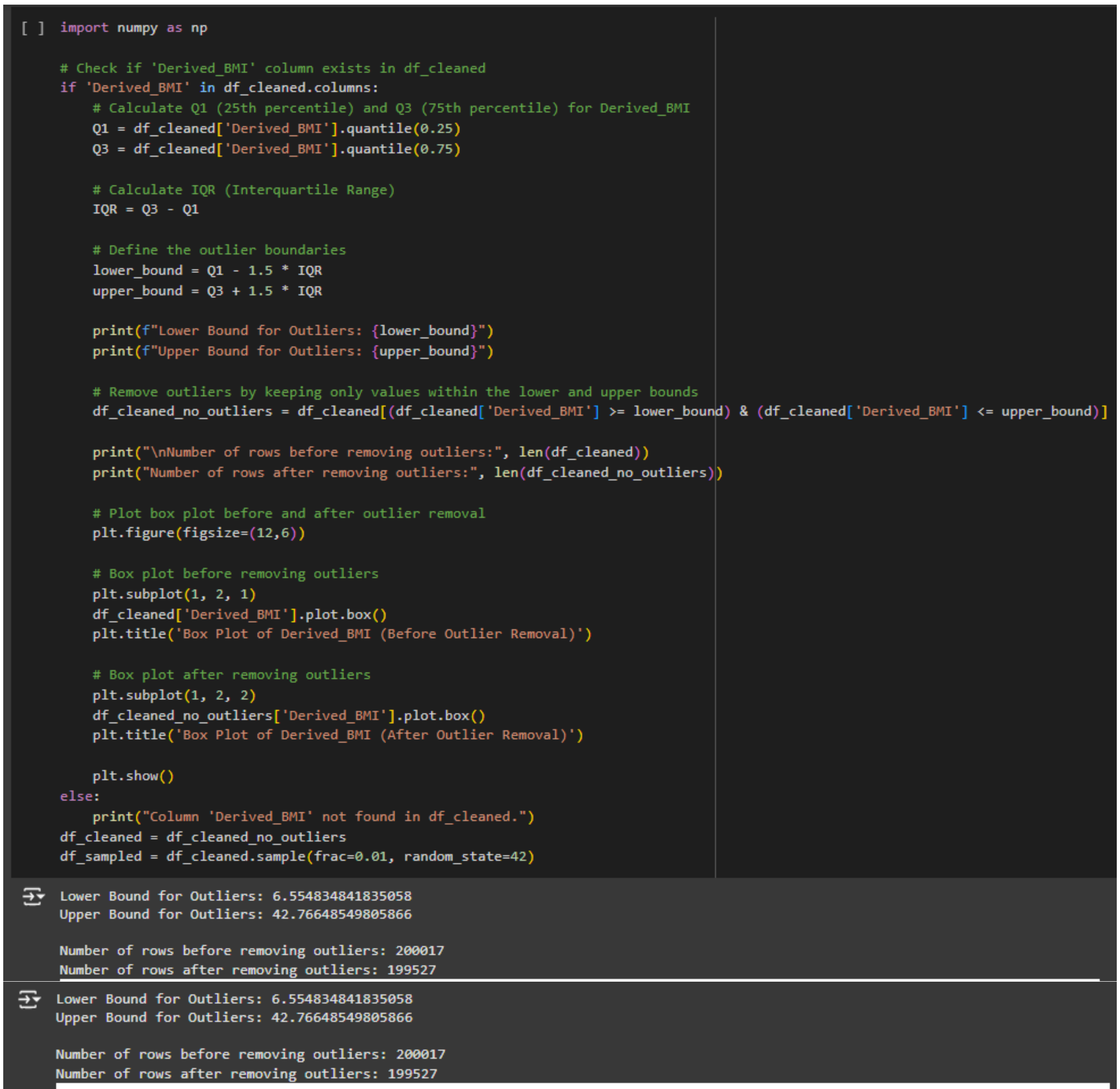
```python
import pandas as pd

# Assuming you have a DataFrame named df with a column named 'date_time'
df['Timestamp'] = pd.to_datetime(df['Timestamp'])

import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.preprocessing import LabelEncoder

# Create a LabelEncoder object
le = LabelEncoder()

# Fit and transform the 'Risk Category' column
df['Risk Category'] = le.fit_transform(df['Risk Category'])
# Define the relevant columns
relevant_columns = ['Heart Rate', 'Respiratory Rate', 'Body Temperature',
                    'Oxygen Saturation',
                    'Derived_HRV', 'Derived_BMI', 'Derived_MAP', 'Risk Category']

# Assuming you have a DataFrame named df
correlation_matrix = df[relevant_columns].corr()
plt.figure(figsize=(10, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm')
plt.title('Correlation Matrix of Vital Signs')
plt.show()
```



Searching for Outliers

```python
import pandas as pd
import numpy as np

# Assuming your dataset is already loaded into a DataFrame named 'df'
# Replace 'df' with the name of your DataFrame if it's different

# List of relevant columns
relevant_columns = ['Heart Rate', 'Respiratory Rate', 'Body Temperature',
                    'Oxygen Saturation',
                    'Derived_HRV', 'Derived_BMI', 'Derived_MAP', 'Risk Category']

# Filter the DataFrame to include only the relevant columns
df_relevant = df[relevant_columns]

# Z-score method
def z_score_outliers(df):
    z_scores = np.abs((df - df.mean()) / df.std())
    return df[(z_scores > 3).any(axis=1)]

# IQR method
def iqr_outliers(df):
    Q1 = df.quantile(0.25)
    Q3 = df.quantile(0.75)
    IQR = Q3 - Q1
    return df[((df < (Q1 - 1.5 * IQR)) | (df > (Q3 + 1.5 * IQR))).any(axis=1)]

# Find outliers using both methods
z_score_outliers_df = z_score_outliers(df_relevant)
# We'll consider this
print("Outliers detected using Z-score method:")
print(z_score_outliers_df)
```

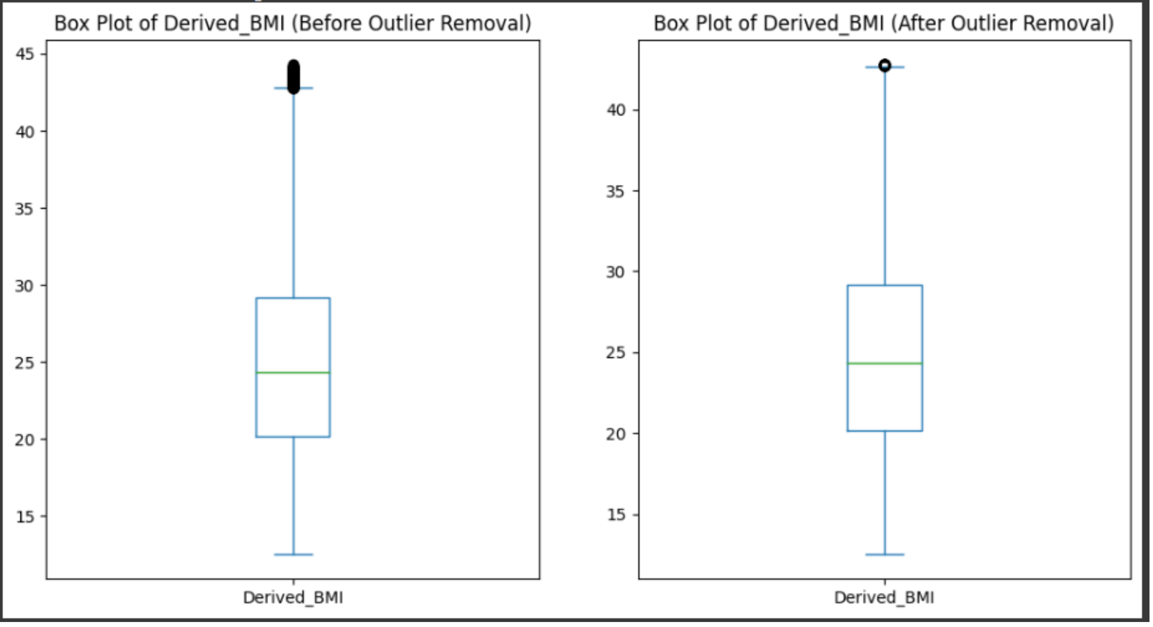
```
Outliers detected using Z-score method:
        Heart Rate  Respiratory Rate  Body Temperature  Oxygen Saturation  \
9531            95                15         36.082649          97.319649
97740           71                18         37.054677          96.497699
157825          76                12         36.591064          96.359037

        Derived_HRV  Derived_BMI  Derived_MAP  Risk Category
9531       0.113006    44.347255    95.666667              0
97740      0.113030    44.376487    94.666667              0
157825     0.107156    44.367525    91.000000              0
```

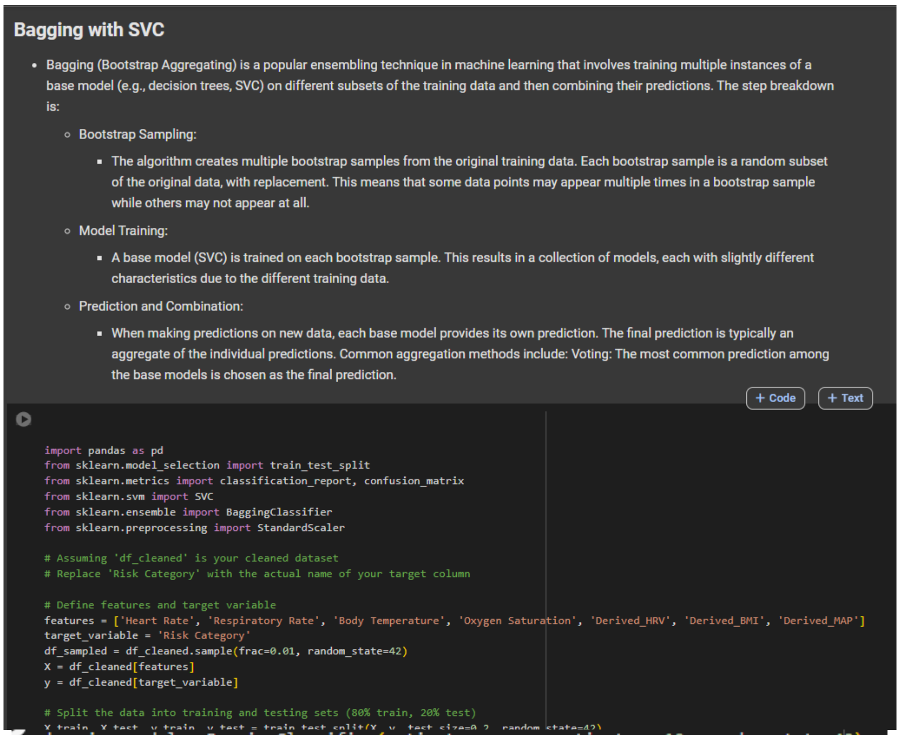


```
[ ] import numpy as np

    # Check if 'Derived_BMI' column exists in df_cleaned
    if 'Derived_BMI' in df_cleaned.columns:
        # Calculate Q1 (25th percentile) and Q3 (75th percentile) for Derived_BMI
        Q1 = df_cleaned['Derived_BMI'].quantile(0.25)
        Q3 = df_cleaned['Derived_BMI'].quantile(0.75)

        # Calculate IQR (Interquartile Range)
        IQR = Q3 - Q1

        # Define the outlier boundaries
        lower_bound = Q1 - 1.5 * IQR
        upper_bound = Q3 + 1.5 * IQR

        print(f"Lower Bound for Outliers: {lower_bound}")
        print(f"Upper Bound for Outliers: {upper_bound}")

        # Remove outliers by keeping only values within the lower and upper bounds
        df_cleaned_no_outliers = df_cleaned[(df_cleaned['Derived_BMI'] >= lower_bound) & (df_cleaned['Derived_BMI'] <= upper_bound)]

        print("\nNumber of rows before removing outliers:", len(df_cleaned))
        print("Number of rows after removing outliers:", len(df_cleaned_no_outliers))

        # Plot box plot before and after outlier removal
        plt.figure(figsize=(12,6))

        # Box plot before removing outliers
        plt.subplot(1, 2, 1)
        df_cleaned['Derived_BMI'].plot.box()
        plt.title('Box Plot of Derived_BMI (Before Outlier Removal)')

        # Box plot after removing outliers
        plt.subplot(1, 2, 2)
        df_cleaned_no_outliers['Derived_BMI'].plot.box()
        plt.title('Box Plot of Derived_BMI (After Outlier Removal)')

        plt.show()
    else:
        print("Column 'Derived_BMI' not found in df_cleaned.")
    df_cleaned = df_cleaned_no_outliers
    df_sampled = df_cleaned.sample(frac=0.01, random_state=42)
```

```
Lower Bound for Outliers: 6.554834841835058
Upper Bound for Outliers: 42.76648549805866

Number of rows before removing outliers: 200017
Number of rows after removing outliers: 199527
```

```
Lower Bound for Outliers: 6.554834841835058
Upper Bound for Outliers: 42.76648549805866

Number of rows before removing outliers: 200017
Number of rows after removing outliers: 199527
```

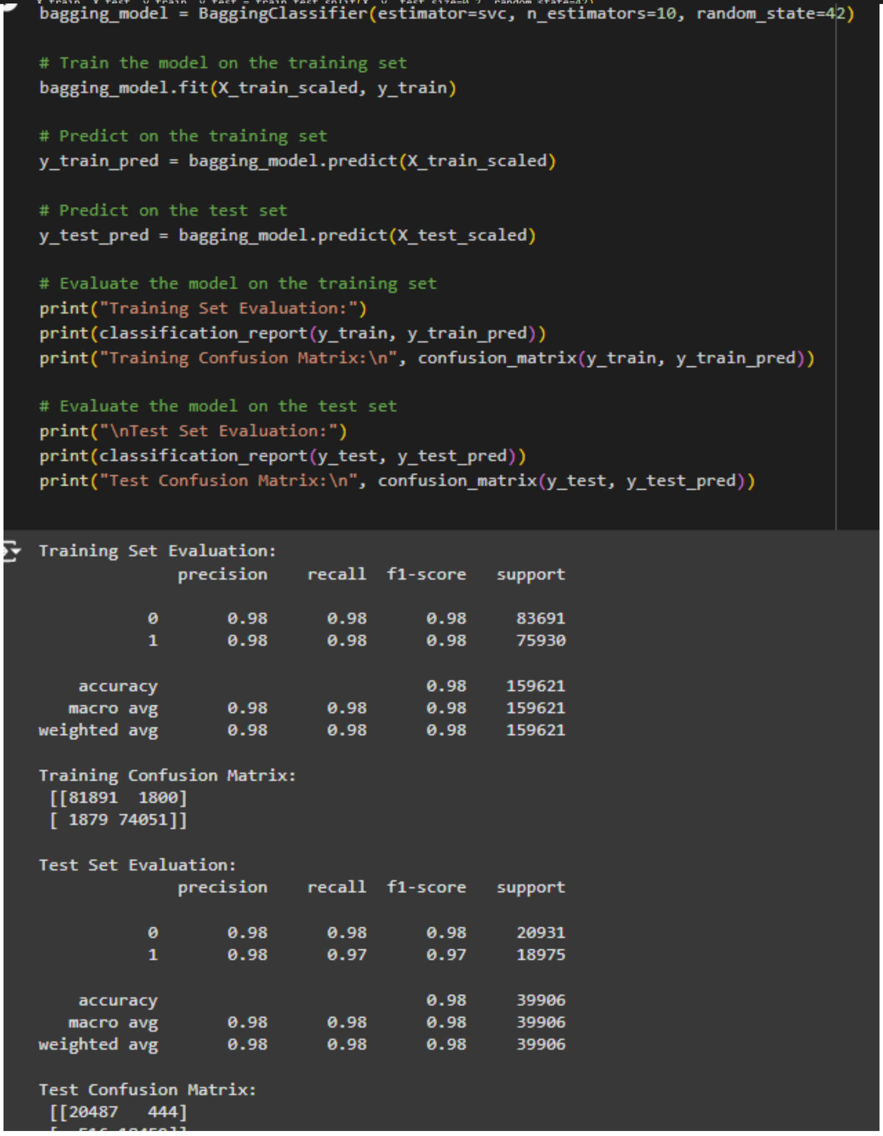




Bagging with SVC

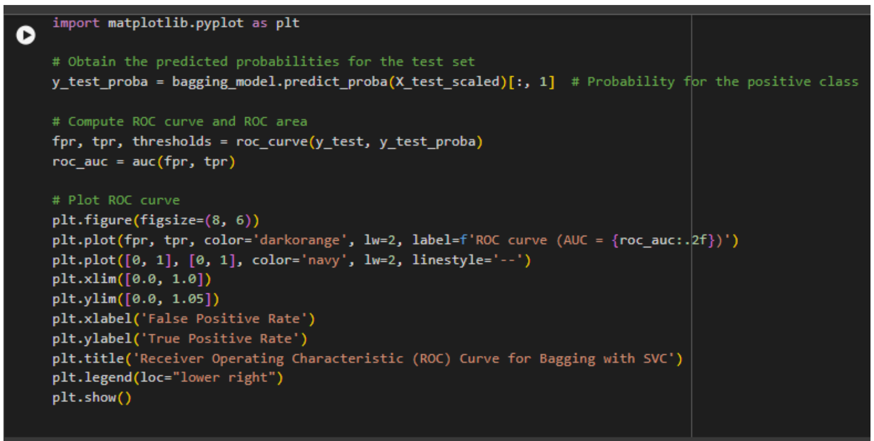
- Bagging (Bootstrap Aggregating) is a popular ensembling technique in machine learning that involves training multiple instances of a base model (e.g., decision trees, SVC) on different subsets of the training data and then combining their predictions. The step breakdown is:
  - Bootstrap Sampling:
    - The algorithm creates multiple bootstrap samples from the original training data. Each bootstrap sample is a random subset of the original data, with replacement. This means that some data points may appear multiple times in a bootstrap sample while others may not appear at all.
  - Model Training:
    - A base model (SVC) is trained on each bootstrap sample. This results in a collection of models, each with slightly different characteristics due to the different training data.
  - Prediction and Combination:
    - When making predictions on new data, each base model provides its own prediction. The final prediction is typically an aggregate of the individual predictions. Common aggregation methods include: Voting: The most common prediction among the base models is chosen as the final prediction.

```python
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.svm import SVC
from sklearn.ensemble import BaggingClassifier
from sklearn.preprocessing import StandardScaler

# Assuming 'df_cleaned' is your cleaned dataset
# Replace 'Risk Category' with the actual name of your target column

# Define features and target variable
features = ['Heart Rate', 'Respiratory Rate', 'Body Temperature', 'Oxygen Saturation', 'Derived_HRV', 'Derived_BMI', 'Derived_MAP']
target_variable = 'Risk Category'
df_sampled = df_cleaned.sample(frac=0.01, random_state=42)
X = df_cleaned[features]
y = df_cleaned[target_variable]

# Split the data into training and testing sets (80% train, 20% test)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

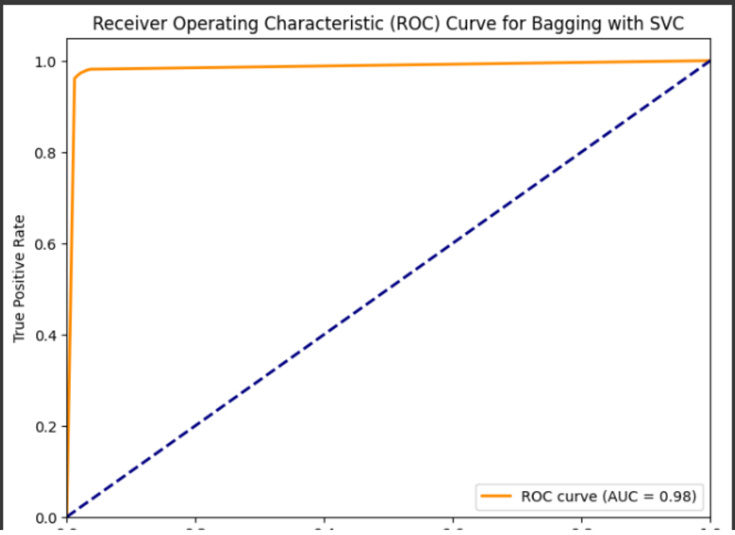


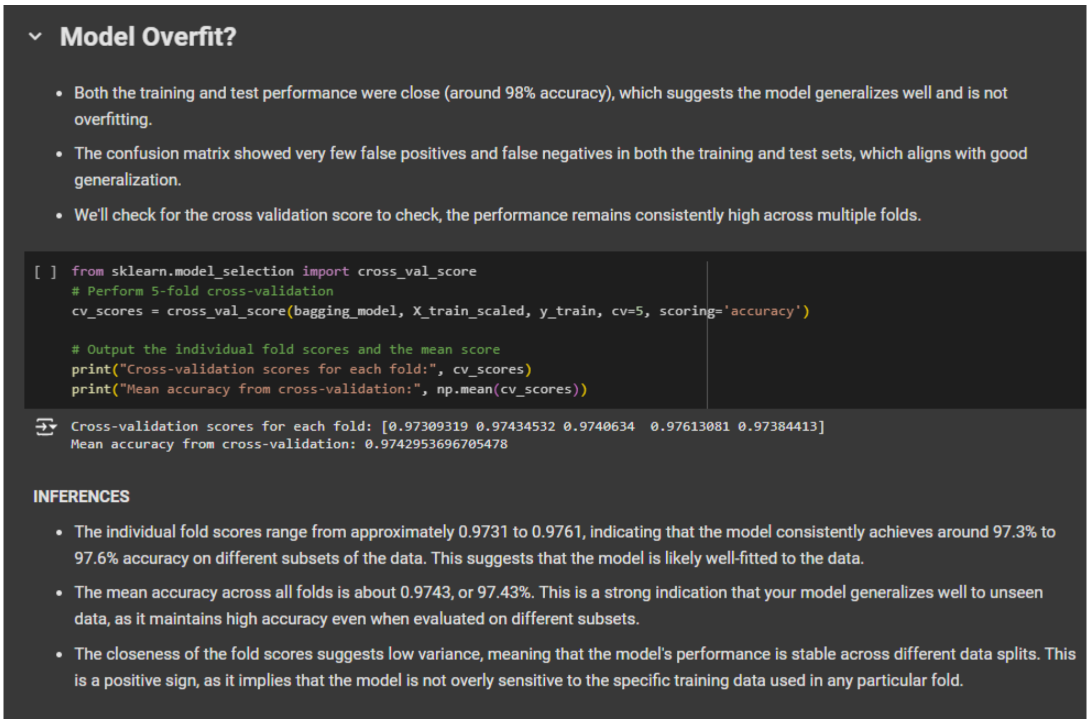
```python
bagging_model = BaggingClassifier(estimator=svc, n_estimators=10, random_state=42)

# Train the model on the training set
bagging_model.fit(X_train_scaled, y_train)

# Predict on the training set
y_train_pred = bagging_model.predict(X_train_scaled)

# Predict on the test set
y_test_pred = bagging_model.predict(X_test_scaled)

# Evaluate the model on the training set
print("Training Set Evaluation:")
print(classification_report(y_train, y_train_pred))
print("Training Confusion Matrix:\n", confusion_matrix(y_train, y_train_pred))

# Evaluate the model on the test set
print("\nTest Set Evaluation:")
print(classification_report(y_test, y_test_pred))
print("Test Confusion Matrix:\n", confusion_matrix(y_test, y_test_pred))
```

```
Training Set Evaluation:
              precision    recall  f1-score   support

           0       0.98      0.98      0.98     83691
           1       0.98      0.98      0.98     75930

    accuracy                           0.98    159621
   macro avg       0.98      0.98      0.98    159621
weighted avg       0.98      0.98      0.98    159621

Training Confusion Matrix:
 [[81891  1800]
 [ 1879 74051]]

Test Set Evaluation:
              precision    recall  f1-score   support

           0       0.98      0.98      0.98     20931
           1       0.98      0.97      0.97     18975

    accuracy                           0.98     39906
   macro avg       0.98      0.98      0.98     39906
weighted avg       0.98      0.98      0.98     39906

Test Confusion Matrix:
 [[20487   444]
 [  516 18459]]
```



```python
import matplotlib.pyplot as plt

# Obtain the predicted probabilities for the test set
y_test_proba = bagging_model.predict_proba(X_test_scaled)[:, 1]  # Probability for the positive class

# Compute ROC curve and ROC area
fpr, tpr, thresholds = roc_curve(y_test, y_test_proba)
roc_auc = auc(fpr, tpr)

# Plot ROC curve
plt.figure(figsize=(8, 6))
plt.plot(fpr, tpr, color='darkorange', lw=2, label=f'ROC curve (AUC = {roc_auc:.2f})')
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) Curve for Bagging with SVC')
plt.legend(loc="lower right")
plt.show()
```





Model Overfit?

- Both the training and test performance were close (around 98% accuracy), which suggests the model generalizes well and is not overfitting.
- The confusion matrix showed very few false positives and false negatives in both the training and test sets, which aligns with good generalization.
- We'll check for the cross validation score to check, the performance remains consistently high across multiple folds.

```python
from sklearn.model_selection import cross_val_score
# Perform 5-fold cross-validation
cv_scores = cross_val_score(bagging_model, X_train_scaled, y_train, cv=5, scoring='accuracy')

# Output the individual fold scores and the mean score
print("Cross-validation scores for each fold:", cv_scores)
print("Mean accuracy from cross-validation:", np.mean(cv_scores))
```

```
Cross-validation scores for each fold: [0.97309319 0.97434532 0.9740634  0.97613081 0.97384413]
Mean accuracy from cross-validation: 0.9742953696705478
```

INFERENCES

- The individual fold scores range from approximately 0.9731 to 0.9761, indicating that the model consistently achieves around 97.3% to 97.6% accuracy on different subsets of the data. This suggests that the model is likely well-fitted to the data.
- The mean accuracy across all folds is about 0.9743, or 97.43%. This is a strong indication that your model generalizes well to unseen data, as it maintains high accuracy even when evaluated on different subsets.
- The closeness of the fold scores suggests low variance, meaning that the model's performance is stable across different data splits. This is a positive sign, as it implies that the model is not overly sensitive to the specific training data used in any particular fold.