

# Hepatitis Disease Detection by Hybrid Algorithm Machine Learning Model

CSCI 3430 Machine Learning Assignment 2





## **Group Members**

- **Mohamed Moubarak  
Mohamed Misbahou  
Mkouboi 1820705**
- **Karim Fazlul 1822049**
- **Mohammad Afif Muhajir  
1816203**



# Introduction

## Hepatitis Disease

Hepatitis is usually the result of a viral infection or liver damage caused by alcohol, and symptoms include yellowing of the eyes and skin (jaundice), loss of appetite, a high temperature, dark urine, and feeling unusually tired all the time

## Machine Learning in Medical Field

Machine Learning in medical field provides methods, tools, and technique that can help solving diagnostic and prognostic problems in a variety of medical domains.

## Hybrid Algorithm/Model

Hybrid Algorithm/Model refers to a technique under Machine Learning and Deep Learning that is to combine more than 1 base algorithm to solve the same problem.



# Technical Report Sections

Computation Methods

## Use of Hybrid Algorithm

In this project we are tasked to implement hybrid model for our program. The chosen technique is called “Blending”.

Dataset

## Hepatitis Dataset

This project will be conducted using an Hepatitis dataset prepared by a third-party.

Algorithm Explanation

## Blending Algorithm

Blending is a colloquial term for ensemble learning with a stacking-type architecture model



# Technical Report Sections

Data Preprocessing

## Dataset Preparation for ML Model

The explanation of steps we are taking to preprocess our dataset will be explained here

Analysis of Result

## Result Comparison

The result of our hybrid algorithm model will be compared with another model for accuracy value comparison to determine how good is our model.

Flowchart

## Flowchart Explanation

This section will show our project executions stages in a flowchart



# Technical Report



# Computation Method and Dataset

- For this project, we are tasked to experiment with a branch of Machine Learning model which is the “Hybrid Model/Algorithm”.
- Our Dataset is an Hepatitis electronic health record that has been prepared by a third-party on an online repository. The dataset consists of 20 attributes and 142 instances of Data.



# Dataset Attributes Table

Attribute	Description
Class	Integer (1= Die, 0=Live)
AGE	Integer value
STEROID	Integer (1= Yes, 0=No)
ANTIVIRALS	Integer (1= Yes, 0=No)
FATIGUE	Integer (1= Yes, 0=No)
MALAISE	Integer (1= Yes, 0=No)
ANOREXIA	Integer (1= Yes, 0=No)
LIVER BIG	Integer (1= Yes, 0=No)
LIVER FIRM	Integer (1= Yes, 0=No)
SPLEEN PALPABLE	Integer (1= Yes, 0=No)

SPIDERS	Integer (1= Yes, 0=No)
ASCITES	Integer (1= Yes, 0=No)
VARICES	Integer (1= Yes, 0=No)
BILIRUBIN	Float, continuous value
ALK PHOSPHATE	Integer, real number
SGOT	Integer, real number
ALBUMIN	Float, continuous value
PROTIME	Integer, real number
HISTOLOGY	Integer (1= Yes, 2=No)



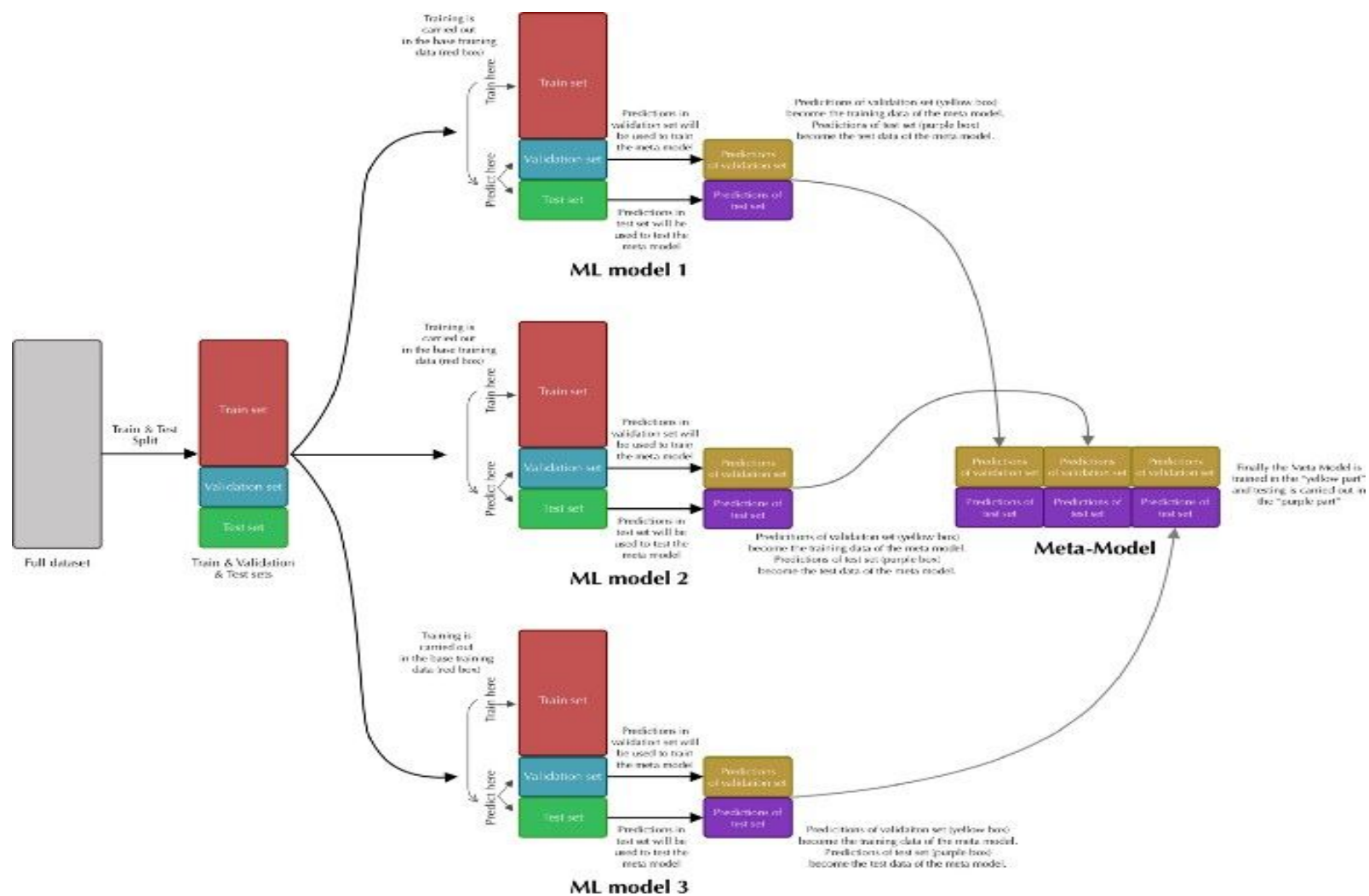


# Algorithm Explanation

Our project uses a form of hybrid model named “Blending”. The way that the algorithm works is similar to another technique called “stacked generalization”.

It can be understood that these two models works by involving two or more base models, often referred to as level-0 models, and a meta-model that combines the predictions of the base models referred to as a level-1 model. The meta-model is trained on the predictions made by base models on out-of-sample data.

The only difference is blending doesn't accommodate a validation technique that is essential in stacked generalization.





# Implementation and Process





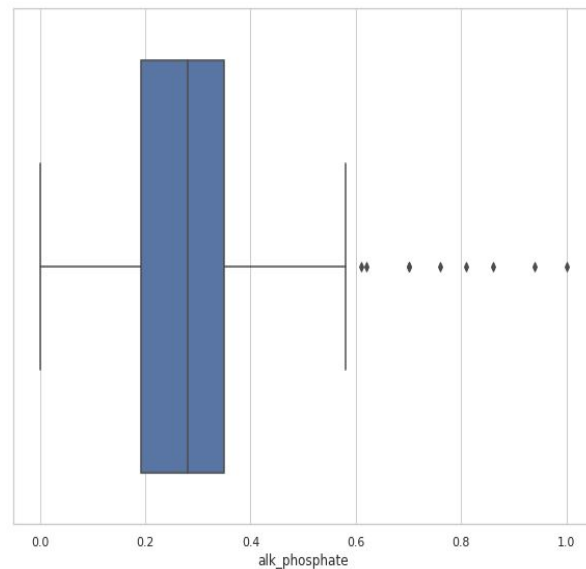
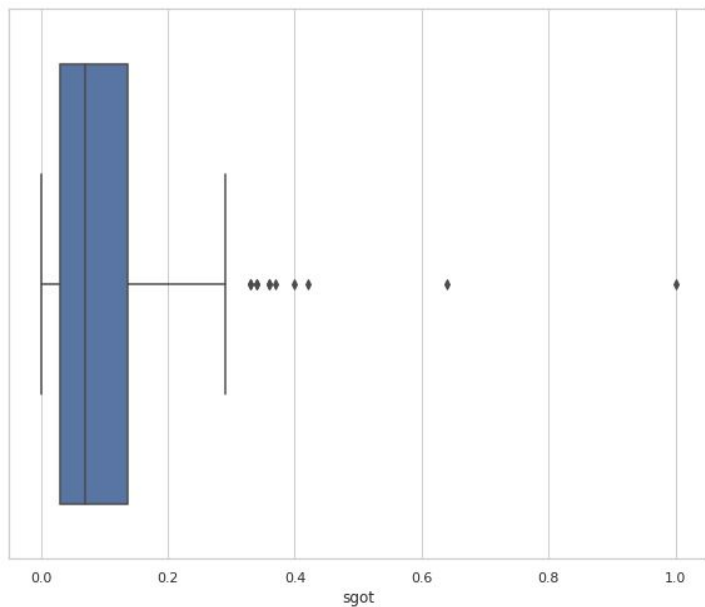
In this portion of the study, we will explain how our programme model manages data. This will comprise building the model, coding it, training it, and testing it before assessing the results.



# **Analysis of Results**



# Model Training and Testing Results





# Explanation of the process





# Data Acquired

## Data Normalization

- Distribution of data has a significant effect on the ML model as most of the machine learning model assumes that data are in a normal distribution, data without normal distribution can cause the model to learn the wrong feature because of the variance difference of such feature.
- We have used standard normalization to normalize our data and it is mathematically expressed as

$$Z = (x - \mu) / \sigma$$

## Outlier Removal

- Outliers are data points that are 3 standard deviations apart from the mean. These values can have a significant influence on our model performance. They are not common in natural events, and most of the time they are caused by mistakes while data is being prepared for analysis.
- We used a numpy built-in function to construct a mask of data points that are three standard deviations away from the mean, then filtered them out using the `thai` mask.

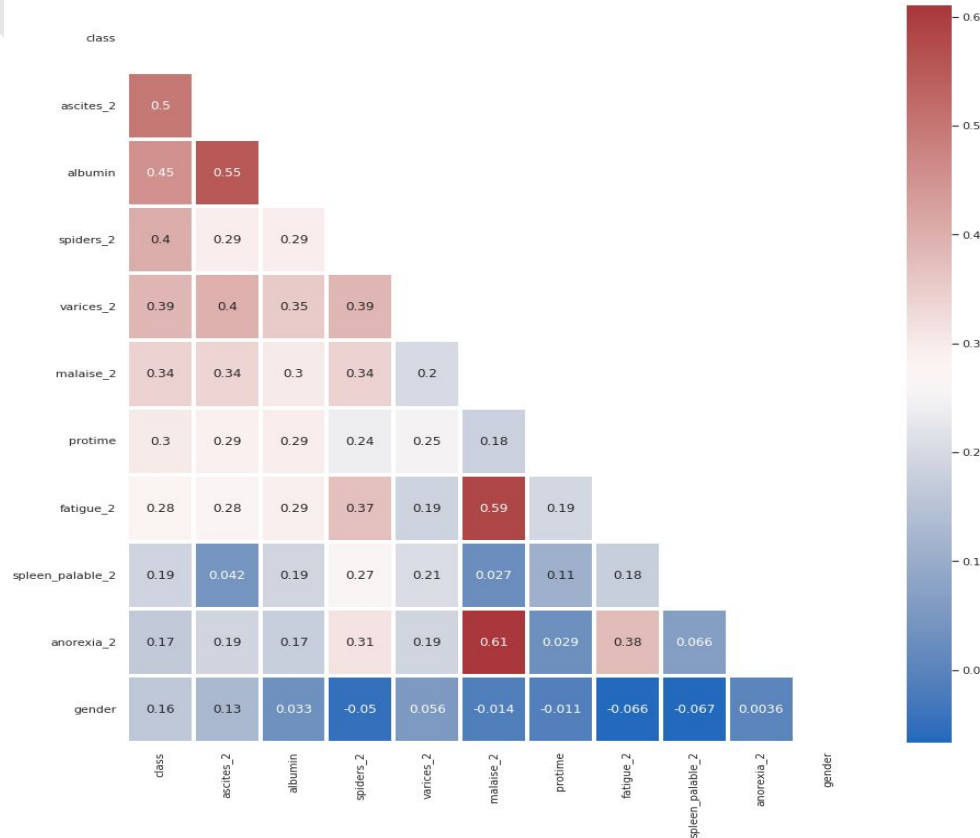




# Explanation of results

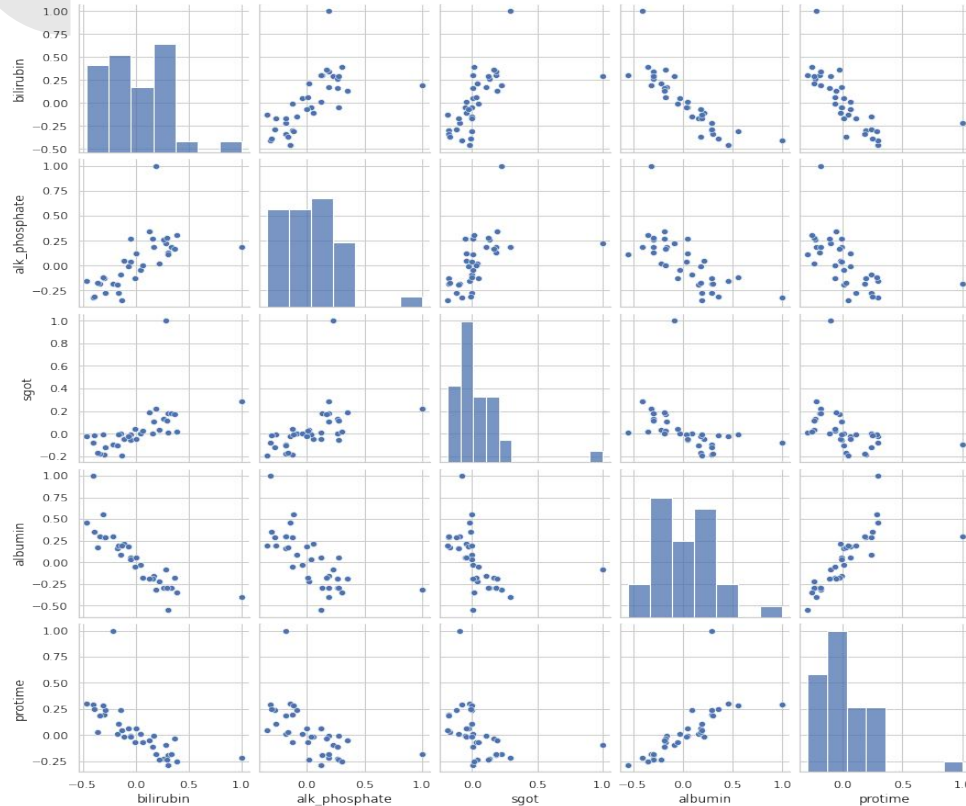


# Figure- Correlation Plot



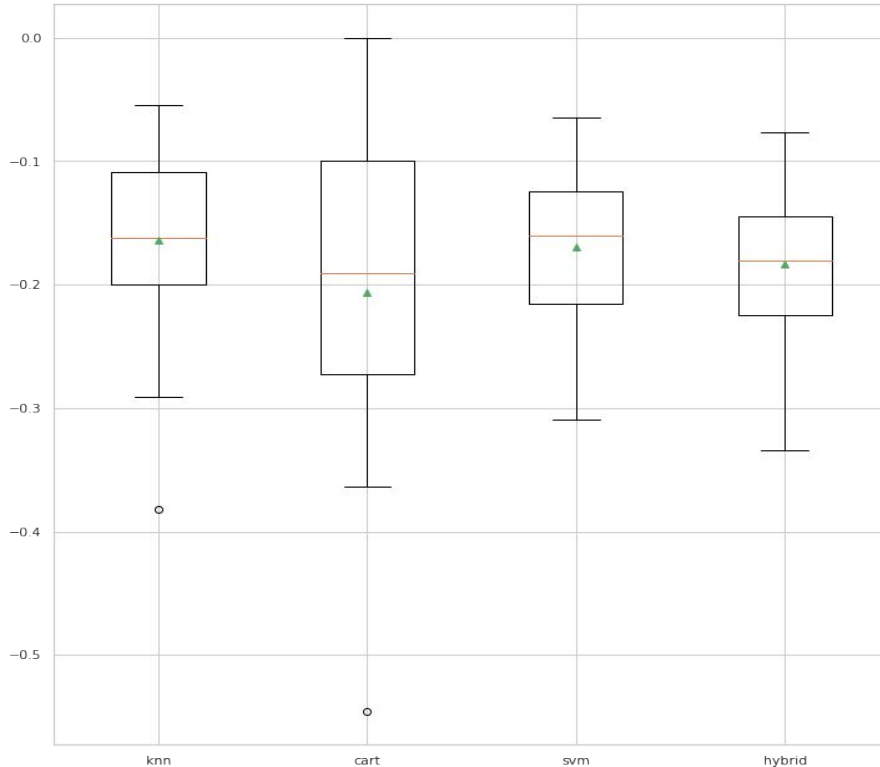
Ascites and albumin are highly correlated with each other so we can eliminate one of them for feature reduction. Ascites have the highest correlation while gender has the lowest correlation with the predicted label, as shown in the figure below. Figure shows the distribution of correlation of attributes with another attribute in a pair.

## Figure- Linear Relationship between top five features in the dataset



Graph represents the correlation of the top 5 features (based on statistical analysis) of the data set. The diagonal components of the figure represent the relation with the feature itself, that is why the shape of the graph appears to be in natural form. Protamine has a negative correlation with bilirubin while a strong correlation with albumin.

## Figure - Analysis of the result



Cross-validation is a popular approach for evaluating a machine learning model's generalization performance. In this graph, the average of the support vector machines(SVM) has been compared to our hybrid model. The last one has almost the same result as our hybrid and is underfitting.



# Flowchart

**FLOWCHART FOR Hepatitis Detection Deep Learning**

