



Application of Shapley Additive Explanation Towards Determining Personalized Triage from Health Checkup Data

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Abstract. Machine learning has become a powerful tool to assist humans making decisions. In most cases, machine learning models act like a black box, a user can only view the outcome without knowing the decision-making process or the deciding factors. Explainable AI has shown good performance in interpreting prediction models and identifying the influential parameters behind the prediction/decision. Our previous works have been analyzing health checkup data collected by a digital healthcare system, called Portable Health Clinic (PHC), developed by us. The system uses a standard logic set based on WHO recommendations to triage the health status of a patient. The triage used in PHC is almost a static standard logic set that works for any patient at any age. We argue that the triage logic should vary from person to person. This paper attempts to use explainable AI to check whether triage could be personalized. An experiment has been carried out over a health check-up data set ($N = 44,460$), by applying XGBoost, a popular machine learning algorithm to predict a patient's health status (risky or not risky). An eXplainable AI (XAI) technique called SHAP is used to explain the prediction results. The SHAP value clearly indicates that each health parameter (BMI, Blood Pressure, hemoglobin, etc.) has different cut-off points for different age groups, which suggests that the threshold to determine one's health status is different and can be obtained. The results will be useful to improve the existing triage static logic. This paper demonstrates cut-off points for BMI and Blood Pressure (Systolic) for two age groups which is an indication of group triage. Our future work will search for the individual cut-off point for developing personalized triage. The obtained cut-off points need to be verified by health professionals.

Keywords: Explainable AI · Health Checkup · Personalized Triage

1 Introduction

Artificial intelligence (AI) and machine learning (as subset of AI) have shown an extremely high performance for many applications in various fields of science and

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technology. It allows a system to make predictions from existing data which can enable learning, reasoning, and decision-making. Machine learning algorithms can handle millions of data sets in a few seconds while the understanding of what happens in the models is not advancing at the same pace. The issue is more serious in sophisticated models such as deep neural networks [1,4]. Explainable AI (xAI) emerged to make it possible to build a model which can be interpreted and understood by the users or developers.

Explainable AI is a generic term to describe artificial intelligence. The results of the solution can be understood by humans. By applying the xAI techniques to the model which handles the data, the explanation for the results can be obtained. One way to achieve explainable AI is to develop powerful and fully explainable models, such as deep k-nearest neighbors and teaching explanations for decisions [1]. Another way is to explain the output of well-established machine learning models, instead of replacing models. An example is the Local Interpretable Model-agnostic Explanations (LIME) developed by Ribeiro et al. [2]. LIME is a novel explanation technique that explains the predictions of any classifier in an interpretable and faithful manner by learning an interpretable model locally around the prediction.

The most common explanations for classification models are feature importance [3]. Feature importance refers to the usefulness of the features to make certain decisions. More specifically, it describes the individual contribution of the corresponding feature to predict a target variable. Generally, feature importance can be divided into modular global and local importance. Global importance measures the importance of the whole model while a local importance measures the importance of one observation. One example of global feature importance is the calculations of Gini impurity in decision tree. Decision tree is a tree-like model which can cope with classification problems by starting at the root of a tree and taking the branch appropriate to the outcome until encountering a leaf node. Gini impurity will be calculated in each node which can measure the feature importance of the entire data set. Based on the B-Logic and the values of each checkup item, health status/risk level as a new variable for every patient can be determined.

The effectiveness of the Explainable AI technique has been examined in many research activities. Authors in [1] assessed the LIME, an xAI framework on a tabular dataset to predict rain, and it has been shown that LIME helps to increase model interpretability. Furthermore, Nohara et al. [4] adopted Shapley additive explanation (SHAP) to interpret a gradient-boosting decision tree model using real hospital data. In their experiments, the authors found that the interpretation by SHAP was mostly consistent with that of the existing methods. Another approach based on the XGBoost algorithm and SHAP method was proposed in [5]. It showed the ability to provide meaningful explanations of the prediction model by identifying the influential risk factors. These works are useful for interpreting machine learning models and can uncover the underlying relationships between features and outcomes.

1.1 Portable Health Clinic System

Portable Health Clinic (PHC) is a digital primary health screening system that aims to control non-communicable diseases (NCDs) and to provide affordable primary healthcare services to general people [6–12]. A PHC box contains basic diagnostic tools which can be easily carried by a female health worker, shown in Fig. 1.

A health worker visits a patient’s home with the PHC box, takes the clinical measurements, and uploads the health-related information to the online PHC database server. This data can be accessed by remote doctors or researchers as shown in Fig. 2 [13]. In order to improve the quality of PHC service and make proper decisions, an understanding of the PHC big data is indispensable. xAI can be used to compute the explanations for any black-box model with high accuracy. By the interpretable understanding of the machine learning models which processed PHC big data, PHC should ideally provide actionable and helpful advice for patients’ prevention.

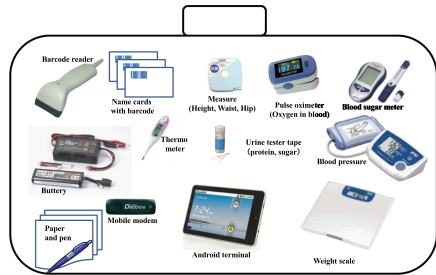


Fig. 1. A prototype of the PHC with 12 basic diagnostic tools which can measure more than 12 clinical parameters [7].

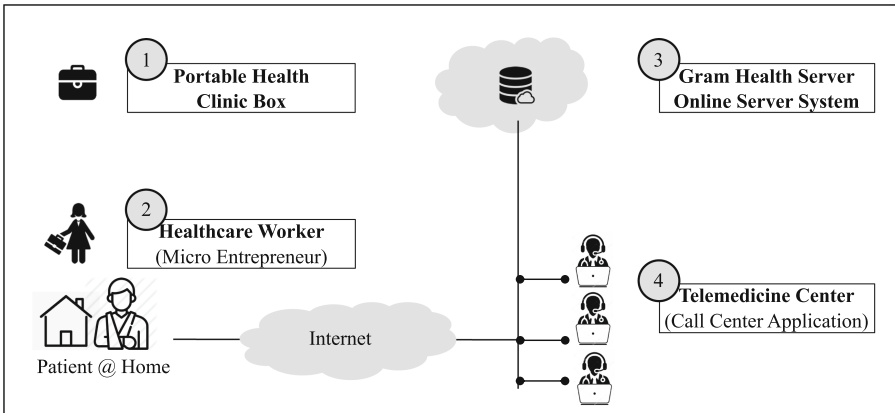


Fig. 2. PHC System Architecture. The system comprises four components: (1) PHC Device Box (2) Health Worker (3) Database System and (4) Telemedicine Center [14].

1.2 Research Motivation and Objective

In the PHC system, a standard triage logic (we call it B-Logic or Bangladesh Logic) is used to judge the health status of a patient. The results are graded in four risk categories: green (healthy), yellow (caution), orange (affected), and red (emergency) as shown in Fig. 3 [7,14]. Based on the values of each checkup item in B-Logic, the health status level for each patient can be added as a new variable.

By design, the B-Logic is almost static for all the patients. In B-logic (as in Fig. 3), the gender of a patient is the only dynamic variable for three parameters e.g. Waist, Waist-Hip Ratio, and Blood Uric Acid. These can be considered as a group behavior of the logic. However, health behavior should vary from person to person. Therefore, a personalized triage needs to be designed. However, it is not an easy task for a human being manually design and follow such a personalized triage. Doctors do it from their own experience. A machine learning tool can learn from previous experience to determine a personalized triage to make a personalized clinical decision. Thus, it is important to develop a personalized logic that can determine the health status of an individual patient. The objective of this paper is to investigate whether personalized triage can be obtained by interpreting the explainable AI tools.

The rest of the paper is organized as follows. Section 2 introduces the techniques and analysis framework used in this research. Section 3 discusses the process of the experiment and the findings. Finally, the conclusions and future research directions are presented in Sect. 4.

2 Prediction and eXplainable AI

This section describes the technologies that are used for prediction and their explanations. A machine learning algorithm named XGBoost is used to predict the health status from health checkup data. A popular explainable AI framework, SHAP (SHapley Additive exPlanations) is used to explain the predicted health status.

2.1 XGBoost

Among many machine learning algorithms for prediction, XGBoost (eXtreme Gradient Boosting), has gained significant attention in the last few years for its high performance in solving data science problems. XGBoost is an implementation of gradient boosted decision tree algorithm proposed by Chen et al. [17]. It can construct boosted trees efficiently, and operate in a parallel way, to solve classification, regression, and ranking problems [18]. This work selected XGBoost to predict the health status of the PHC patients. The model training and data analysis were performed with Python 3.7, using the XGBoost package and scikit-learn library.

PHC B-Logic and Human Acceptable Range									
No.	Parameter	Spec.	Data Type	Lower Warning	Green	Yellow	Orange	Red	Upper Warning
1	Height		dec	<100.0					>200.0
2	Weight (kg)		dec	<25					>100.0
3	BMI		dec		<25	>=25 & <30	>=30 & <35	>=35	
4	Waist (cm)	Male	dec	<40.0	<90.0	>= 90.0	NA	NA	>120.0
		Female	dec	<40.0	<80.0	>= 80.0	NA	NA	>110.0
5	Hip (cm)		dec	<40.0					>120.0
6	Waist Hip Ratio	Male	dec		<0.90	>= 0.90	NA	NA	
		Female	dec		<0.85	>= 0.85	NA	NA	
7	Temperature (C)		dec	<33.0	<37.0	>=37.0 & <37.5	>=37.5	NA	>39.0
8	HBSAg				negative			positive	
9	Smoking								
10	Urine Sugar				-	++	Others		
11	Urine Protein				-	+-	Others		
12	Urinary Urobilinogen				+-		Others		
13	Oxygenation of Blood (%)		int	>100	>=96	>=93 & <96	>=90 & <93	<90	<92
14	Blood Pressure (mmHg)	Systolic	int	<70	<130	>=130 & < 140	>=140 & <180	>=180	>220
15		Diastolic	int	<50	<85	>=85 & <90	>=90 & <110	>=110	>140
16	Blood Sugar (mmol/dl)	RBS	dec	<3.0	<7.78	>=7.78 & <11.11	=11.11 & <16.6	>=16.67	>30.0
17		FBS	dec	<3.0	<5.56	>=5.56 & <7.0	>=7.0 & <11.11	>=11.11	>20.0
18	Blood Hemoglobin (g/dl)		dec	>18.0	>=12.0	>=10.0 & <12.0	>=8.0 & <10.0	<8.0	<6.0
19	Blood Grouping								
20	Pulse Rate (bit/min)		int	<50	>=60 & <100	>= 50 & <60	<50 OR >=120	NA	>130
21	Arrhythmia				Normal		Others		
22	Blood Cholesterol (mg/dl)		dec	<120.0	<=200.0	>200.0 & <=225.0	>225.0 & <240.0	>=240.0	>300.0
23	Blood Uric Acid (mg/dl)	Male	dec	<2.5	>3.5 & <=7.0		>7.0 & <8.0	>=8.0	>12.0
		Female	dec	<2.5	>2.4 & <=6.0		>6.0 & <7.0	>=7.0	>12.0

Fig. 3. Concept of B-Logic and Human Acceptance Range for each clinical parameter. Each health checkup item is compared against a risk stratification matrix based on International diagnosis standards (WHO) [6].

2.2 Shapley Additive Explanation

There are various xAI techniques such as LIME (Local Interpretable Model-Agnostic Explanations) [2], SHAP (SHapley Additive exPlanations) [16], GRAD-CAM (GRADient Class Activation Mapping) [19], DeepLIFT(Deep Learning Important FeaTures) and so on [20]. Among them, SHAP has been proven to show a powerful and insightful measure of the importance of a feature in machine learning model [15]. Therefore, we applied it in this work to explain the prediction results by XGBoost.

As mentioned in Sect. 1.1, tree-based machine learning algorithms like decision tree or XGBoost can provide interpretation by calculating the gini impurity or gain, which quantified the contribution to the outcome by each feature. However, Lundberg et al. found that gain is inconsistent and proposed a unified framework for interpreting predictions, SHAP [4, 16]. It is a game theoretic approach that can explain the output of any machine learning model by applying SHAP values to represent the feature importance. SHAP values have proved to be consistent and SHAP summary plots are very useful for overiewing the results.

2.3 Towards Developing a Personalized Logic/Triage

The final goal of this research is to investigate the possibility of identifying personalized triage by analyzing past health records by using an eXplainable AI tool. A personalized logic/triage is a cut-off point to categorize the person to be healthy or not healthy. The current NCD triage developed by WHO for Bangladesh and applied by the PHC system is a generalized one for all the population. This paper argues that it can be made more appropriate by developing a personalized one. As for the first step towards that goal, this paper attempts to develop a logic for a group. By understanding how the clinical parameters contribute to the patient's prediction, it will be possible to discover the threshold to determine a patient's health status, which will lead to the development of a personalized triage logic. This section explains the process to design a personal logic and a group logic.

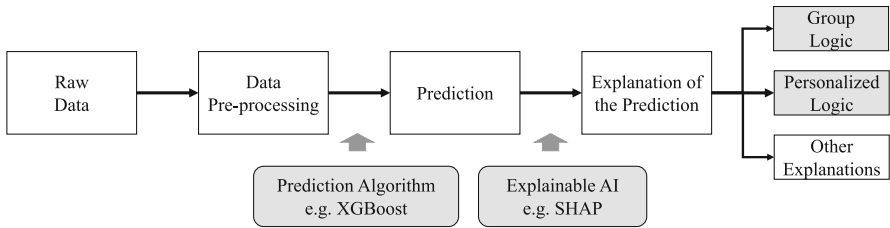


Fig. 4. A schematic view to show the development of personalized & group logic process.

A. Personalized Triage/Logic. Figure 4 shows the process to find out personalized and group logic from raw data sets. Firstly, the collected PHC data set is processed based on the criteria described in Sect. 3.1. Then the processed data is fed to the XGBoost model to predict the health status of all the patients. SHAP, an Explainable AI technique is applied to the prediction results to obtain the explanation. The SHAP value explains how the health parameters contribute to a patient's health status. The SHAP value also indicates a cut-off point between the healthy and unhealthy status. A personalized logic set can be determined from these cut-off points for each health parameter.

B. Group Logic. Figure 5 shows the process to obtain group logic based on the PHC data set. The general idea is to select the patients who have the same feature values. For example, in this work, we divided the patients into several groups based only on their age. Then the explainable AI algorithms were used to explain the models which handle different age groups. Through the explanation, we will be able to understand how the features influence the health status of the group with a certain age. The other age groups are treated in the same way. Finally, we can develop the logic to determine the health status of different age groups.

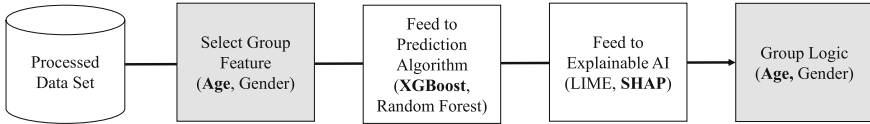


Fig. 5. Block diagram to present intuition for the way to achieve group logic.

3 Experiment, Results, and Discussions

The section describes the experiment environment and characteristics of the data set. The data preprocessing criteria, selection of prediction algorithm, and xAI tool are also explained.

3.1 Data Preprocessing

A list of 44,460 health checkup data have been collected since 2010 by using PHC as shown in Fig. 2. The data collection environment is explained in [10]. We have applied the data preprocessing steps (as in Fig. 6) on the raw data to solve the missing values and outlier problems [22, 23]. The number of features in the raw data (V0) is 34, since it contains personal information such as name, checkup ID, and mobile number which has no relationship with our study, 7 of them will be removed. Then we applied the human acceptable range as a standard to replace the outliers with null values. Finally, after removing the rows containing the null values, we will get a complete dataset (V3). Moreover, among the 22 columns in V3, 6 unnecessary features (e.g. Checkup date, Site id) besides the target feature were removed. The final dataset (V3) contains 3085 records and 16 features that had been used for our research.

The categorical data include urinary glucose, urinary protein, urinary Urobilinogen, arrhythmia, and health status. These are encoded by label according to the triage status. For convenience, patients under Green and Yellow are considered as a new group, “Healthy”. In the same way, those who are under Orange and Red are classified as “Unhealthy”.

3.2 Prediction of Health Status by XGBoost

After the data preprocessing steps, XGBoost was applied to predict the health status of the patient with a training to test ratio of 70:30. A 10-fold cross-validation process was used to evaluate the performance of the model. The accuracy (according to Eq. 1) was 99%, which indicated that XGBoost achieved a good prediction accuracy. Furthermore, the confusion matrix is given in Table 1. Balanced accuracy is 99% which can be calculated through Eq. 2, 3, 4, where TP is true positive, FP is false positive, FN is false negative and TN is true negative.

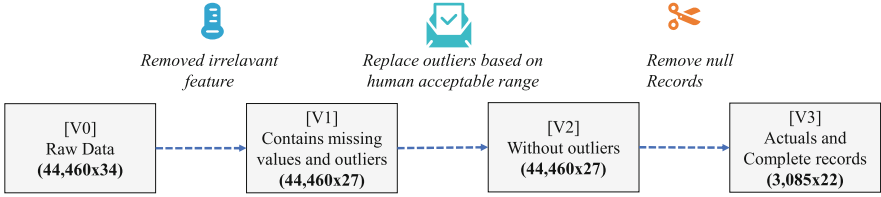


Fig. 6. PHC data preprocessing for prediction

Table 1. The confusion matrix for PHC data health status prediction model.

Actual	Predicted	
	Negative	Positive
Negative	596	3
Positive	0	327

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$Balanced\ Accuracy = \frac{TPR + TNR}{2} \tag{2}$$

$$TPR = \frac{TP}{TP + FN} \tag{3}$$

$$TNR = \frac{TN}{TN + FP} \tag{4}$$

Figure 7 shows the feature importance scores calculated through the gain method by XGBoost. We observe that among the 16 clinical parameters, urinary protein is detected as the most influential feature to determine health status. Arrhythmia, bp_dia, and blood_hemoglobin are also highly ranked features. Gender, waist, waist_hip_ratio, age_oncheckup, and oxygen_of_blood have the least effect on the prediction of health status. However, through this result, it’s difficult to understand how every feature influences the target i.e. how the value of a feature bring positive or negative contributions to the prediction. Therefore, Shapley Additive Explanation will be used to discover the potential relationship behind the features.

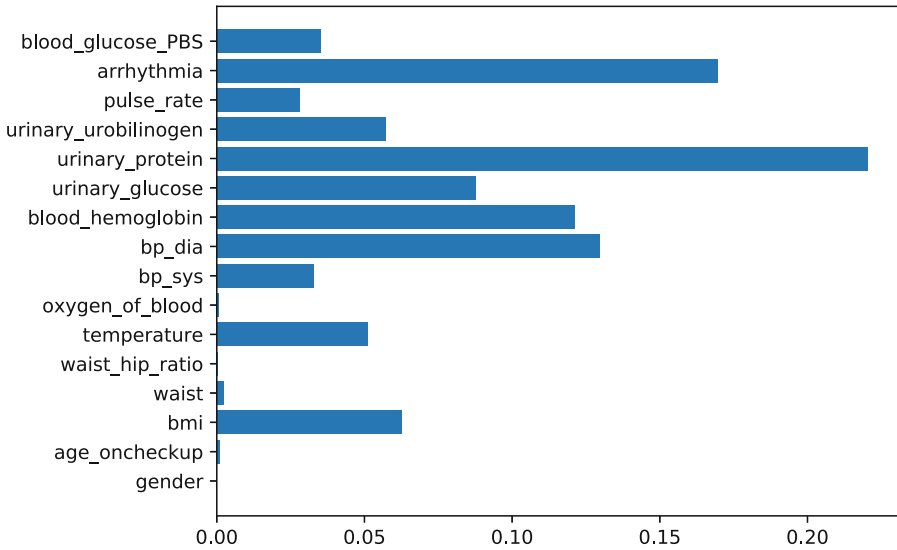


Fig. 7. The Prediction result of XGBoost. Y-axis shows different health parameters and X-axis shows the feature importance to determine health status. Global feature importance values showing urinary protein was selected as the most influential feature.

3.3 Use of SHAP to Explain the Prediction Results

The SHAP summary plot shows the positive and negative contribution of the features with the target variable. Each point on the summary plot is a Shapley value for a feature and an instance. Figure 8 shows the explanation for the XGBoost model which handled the data processed in Sect. 3.1 and it delivers the following information:

- **Feature importance:** In the y-axis direction, features are ranked in descending order according to their importance. In this study, blood hemoglobin was extracted as the most influential feature.
- **Impact:** The x-axis shows whether the feature has a positive or negative contribution to the target value. The points distributed on the positive x-axis have a positive impact on the status of unhealthy, and the negative points on the x-axis lead to a healthy status.
- **Original value:** Color indicates the value of the feature. Blue indicates low and red indicates high for that individual instance. For categorical features with only two possible values such as arrhythmia, it will take only two colors, but numerical data like bmi or blood pressure can contain the whole spectrum.
- **Correlation:** Through combining the impact and original value, we found that a low value of blood hemoglobin increases the risk, which indicates blood hemoglobin is negatively correlated with the target variable, that is, patients’ health status.

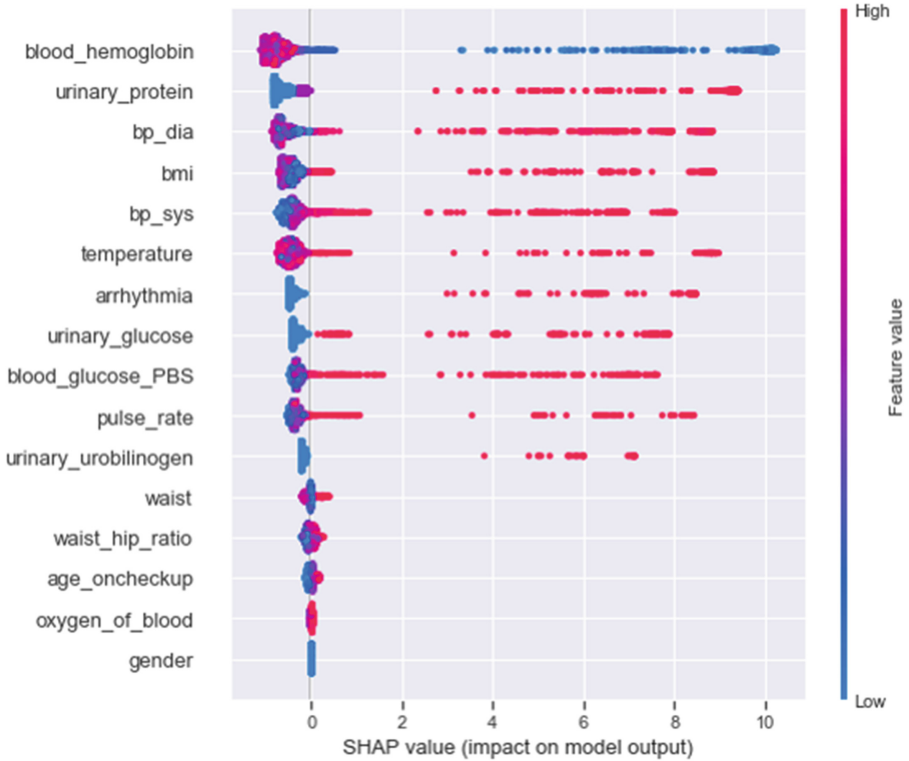


Fig. 8. SHAP Summary Plot output for explaining XGBoost. The figure shows the sorted feature importance and the relationship between each feature and target i.e. the health status. Among 16 of them, blood hemoglobin is detected as the most influential feature.

For detailed analysis, we plot the SHAP dependence plot of BMI for the different age groups in Fig. 9. It shows the relationship between BMI and its' effect on health status. Each dot is a single prediction from the dataset and the x-axis represents the value of BMI. The figure on the left shows the result by SHAP for patients whose age is 25. We observe that a higher BMI value causes a higher risk to be unhealthy. Moreover, SHAP values are above zero when BMI is higher than 26, in contrast, there are some negative dots for the 35-year-old group on the right side until a BMI value of 27.5. The results suggest that for different age groups, the standard to determine a patient's health status should be different.

Figure 10 shows the impact of blood pressure (systolic) on health status. The figure indicates that a value of approximately 130 is the threshold of a healthy status for patients whose age is 25 and the threshold for 35-year-old group patients should be about 135. Furthermore, the summary of several considered features' cut-off points is shown in Table 2. In this way, we are able to design a new standard for every feature in the PHC dataset based on patients' age.

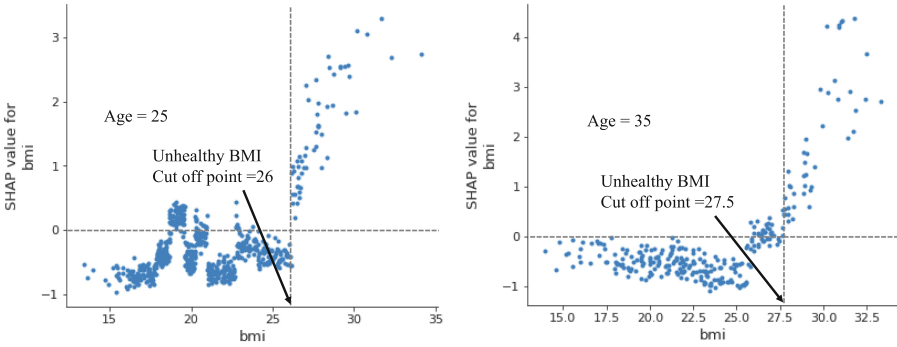


Fig. 9. SHAP Dependence Plot of BMI. The left figure shows the SHAP value for Age = 25 and the right figure shows the same for Age = 35. Two dotted lines are drawn in a way such that no negative SHAP value exist on the right side. This way, the cut-off points for both the ages are determined.

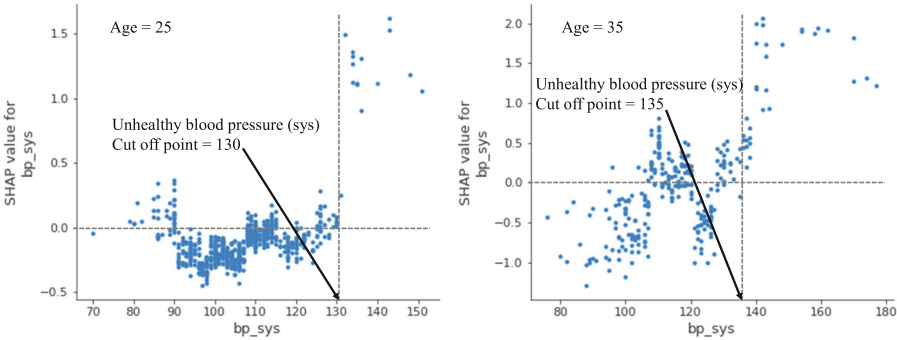


Fig. 10. SHAP Dependence Plot of blood pressure (systolic). The left side is the result of the 25-year-old group, the right side is for the 35-year-old group. The cut-off point for the age group 25 is indicated as 130, and for the age group 35, the cut-off point is 135.

Table 2. The cut-off points for different clinic parameters show the threshold of a healthy status for the two age group patients.

Feature	Cut-off Point(Age25)	Cut-off Point(Age35)
bmi	26	27.5
bp_sys	130	135
waist_hip_ratio	0.93	0.91
temperature	98.7	98.7
bp_dia	88	89
blood_hemoglobin	9.8	9.9
blood_glucose_PBS	133	141

4 Conclusions and Future Work

This paper used explainable AI to determine a cut-off point for a person's binary health status i.e. personalized triage. The research began with determining triage for an age group. A PHC data set (N = 44,460) and a popular machine learning algorithm, XGBoost were used to predict a patient's health status (risky or not risky). An eXplainable AI (XAI) technique called SHAP is used to explain the prediction results. The SHAP value clearly indicated the cut-off point for each health parameter (BMI, Blood Pressure, hemoglobin, urinary protein, etc.) for different age groups. The results suggest that the threshold to determine one's health status is different and can be obtained, which is useful for us to refine the existing triage static logic. Cut-off points for BMI were found for different age groups. For example, the cut-off point of BMI for the age group 25 was 26 whereas, for the age group 35, the value was 27.5 respectively. The obtained cut-off points need to be verified by health professionals. Moreover, the SHAP summary plot showed the ability to identify the risky feature for the PHC dataset by calculating the SHAP value as a global feature importance score. As a result, blood hemoglobin is detected as the most influential feature to determine a patient's health status and it shows that lower blood hemoglobin causes a higher risk of unhealthy.

In terms of future work, we will continue the research about Explainable AI and try to implement the novel explainable framework on PHC dataset. Through the understanding of how the clinical parameters contribute to an individual patient's prediction, we should ideally discover the threshold to determine a patient's health status, which leads to the development of a personalized triage logic. We aim to implement the SHAP dependence plot for each age group in the PHC database. The current size of the dataset for some age groups is not sufficient to build the model, imputation of the raw PHC dataset will increase the size of the data and will be considered.

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