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MODIFIED SHAP APPROACH FOR INTERPRETABLE PREDICTION OF CARDIOVASCULAR COMPLICATIONS

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This article explores the significance of modifying SHAP (SHapley Additive exPlanations) values to enhance model interpretability in machine learning. SHAP values provide a fair attribution of feature contributions, making AI-driven decision-making more transparent and reliable. However, raw SHAP values can sometimes be difficult to interpret due to feature interactions, noise, and inconsistencies in scale. The article discusses key techniques for modifying SHAP values, including feature aggregation, normalization, custom weighting, and noise reduction, to improve clarity and relevance in explanations. It also examines how these modifications align interpretations with real-world needs, ensuring that SHAP-based insights remain practical and actionable. By strategically refining SHAP values, data scientists can derive more meaningful explanations, improving trust in AI models and enhancing decision-making processes. The article provides a structured approach to modifying SHAP values, offering practical applications and benefits across various domains.

Keywords: model interpretability, feature importance, normalization, AI transparency.

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1 Introduction

In the rapidly evolving landscape of artificial intelligence (AI) and machine learning (ML), model interpretability is crucial for ensuring transparency, trust, and accountability. SHAP (SHapley Additive exPlanations) values have emerged as a powerful tool for explaining model predictions by attributing the contribution of each feature in a fair and consistent manner. By leveraging concepts from cooperative game theory, SHAP values provide both local (instance-level) and global (model-level) insights, making them widely used across domains such as finance, healthcare, and automated decision-making systems. However, while SHAP values offer robust interpretability, raw attributions may not always be sufficient for real-world applications. Complex models often have interactions between features, noisy attributions, or highly correlated predictors, which can obscure meaningful insights. By modifying SHAP values strategically — through feature grouping, scaling, interaction weighting, and noise filtering — data scientists can enhance interpretability, improve decision-making, and make SHAP explanations more actionable.

Heart disease poses [1] a significant threat to global public health, severely affecting individuals' lives and overall well-being. Despite some success in existing prediction models, the complexity and variability of medical data often lead to diagnostic errors when these models are used in practice. Therefore, there is a critical need for more accurate and efficient prediction models. This article presents a classification model for heart disease prediction, utilizing the XGBoost algorithm and real medical datasets from Kaggle. To enhance the interpretability of the model's predictions, SHapley Additive exPlanations (SHAP) values are employed, providing an insightful framework for understanding the results. The proposed model demonstrates strong predictive performance and clarity, offering a valuable resource for healthcare professionals in diagnosing and managing heart disease.

Cardiovascular diseases [2] (CVD) are a global health concern, with projected mortality reaching 23.3 million by 2030. This paper outlines a comprehensive strategy for developing a system that combines machine learning and Explainable AI (XAI) techniques to create a reliable and interpretable predictive model for coronary artery disease (CAD). The main goal is to build predictive models while using SHAP (SHapley Additive exPlanations) analysis to improve model transparency. The study evaluates various machine learning algorithms to determine the most effective approach for CAD prediction. After selecting the optimal model, SHAP analysis is used to clarify how different features influence the model's predictions, offering insights into the factors that drive CAD classification. This research emphasizes the importance of both predictive accuracy and interpretability in enhancing medical decision-making.

Automatically identifying heart diseases presents [3] a significant challenge in the medical field, as it remains a leading cause of death. The prediction of heart failure, a key symptom of cardiovascular disease, has become increasingly important to physicians. Beyond enhancing feature ranking and clinical prediction, deep learning also aids in providing interpretable outputs for medical professionals. Explainable Artificial Intelligence (XAI) aims to tackle the issue of deep learning models in healthcare being opaque, offering insights into the model's inner workings in a format that is understandable for users. In our proposed approach, convolutional neural networks are employed to predict the disease, and the Deep SHAP model is utilized to visualize predictions. The model achieves an accuracy of 0.90, a sensitivity of 0.97, and an F1-score of 0.86 for class 1. The results section includes various performance metrics, including recall, precision, and F1-score, for both classes.

Cardiovascular Disease [4] (CVD) is a significant cause of disability and death among individuals with Diabetes Mellitus (DM). International clinical guidelines for managing Type 2 Diabetes Mellitus (T2DM) emphasize primary and secondary prevention, focusing on evaluating CVD-related risk factors to initiate appropriate treatments. CVD risk prediction models are valuable tools that help optimize the frequency of medical visits and enable timely preventive and therapeutic actions against CVD events. Incorporating explainability features into these models can improve human understanding of the decision-making process, increase transparency, and build trust in their adoption in clinical settings. This study aims to develop and assess an explainable, personalized risk prediction model for predicting fatal or non-fatal CVD events in T2DM patients. The approach uses eXtreme Gradient Boosting (XGBoost) combined with the Tree SHAP (SHapley Additive exPlanations) method to calculate 5-year CVD risk and provide individual explanations for the model's predictions. Data from a 5-year follow-up of 560 T2DM patients are utilized for model development and evaluation. The results (AUC = 71.13%) demonstrate the model's potential to handle the imbalanced dataset effectively while offering clinically relevant insights into the decision-making process of the ensemble model.

Heart failure [5] (HF) is a leading cause of mortality, and accurately tracking its progression and adjusting treatments are essential for improving patient outcomes. Experienced cardiologists can diagnose HF stages based on a combination of symptoms, signs, and lab results from patients' electronic health records (EHR), without needing direct heart function measurements. In this study, we explored whether machine learning models, specifically the XGBoost model, could accurately predict a patient's HF stage based on EHR data. Additionally, we applied the SHapley Additive exPlanations (SHAP) framework to identify key features and their interpretations. Our results show that, using structured EHR data, our models could predict patients' ejection fraction (EF) scores with moderate accuracy. SHAP analysis helped identify important features and uncovered potential clinical subtypes of HF. These findings offer valuable insights into designing computational systems that can effectively monitor the progression of HF by continuously analyzing patients' EHR data.

This paper [6] explores a comparative study of various machine learning algorithms using a binary classification dataset on heart disease. The study includes single classifiers (Logistic Regression, K-Nearest Neighbors, Decision Trees, Support Vector Machines), bagging methods (Random Forest), and boosting algorithms (XGBoost, AdaBoost, CatBoost, Gradient Boosting). The use of an ensemble machine learning model combining Random Forest, Gradient Boosting, AdaBoost, XGBoost, and CatBoost achieved exceptional accuracy of 89.13%. Further improvements in accuracy were achieved by applying hyperparameter tuning techniques (GridSearchCV and RandomSearchCV) and implementing XAI methods (LIME and SHAP). In a comparative analysis of the boosting algorithms, CatBoost and AdaBoost outperformed others in identifying cardiovascular disease. Hyperparameter tuning improved the Random Forest classifier's accuracy to an impressive 88.26%.

This study [7] explores the potential of machine learning classification to transform cardiovascular disease prediction. By leveraging diverse datasets that include demographic, lifestyle, and clinical data, the research applies various algorithms, including Logistic Regression, KNN, SVM, Decision Tree Classifier, GradientBoost, AdaBoost, XGBoost, along with techniques like Hyperparameter tuning, LIME, and SHAP, to build prediction models. The goal is to improve individualized risk assessments and their accuracy, thus enabling early interventions and preventative strategies. The results highlight the effectiveness of machine learning in predicting cardiovascular risks, signaling a significant shift toward preventive healthcare. With continued development, these models could be integrated into clinical practice, potentially reducing the global prevalence of cardiovascular diseases by facilitating timely, targeted therapies.

This study [8] aims to develop and validate a machine learning model that incorporates dietary antioxidants to predict cardiovascular disease (CVD)-cancer comorbidity and to understand the role of antioxidants in disease prediction. Data for this study were sourced from the National Health and Nutrition Examination Survey, focusing on antioxidants such as vitamins, minerals, and polyphenols as key features. In addition to antioxidants, demographic, lifestyle, and health condition data were included to enhance model accuracy. The feature preprocessing process involved removing collinear features, addressing class imbalance, and normalizing the data.

Hypertension, a prevalent and complex cardiovascular disease associated with a high risk of mortality and morbidity, has become a target for detection using Artificial Intelligence (AI) methods. However, due to the "black-box"nature of many AI models, doctors have been unable to identify the specific reasons behind hypertension. Therefore, it is crucial to elucidate the connections between hypertension and various biomarkers. In this study, local interpretable model-agnostic explanations (LIME) and SHapley Additive exPlanations (SHAP) were used to clarify the hypertension risk predictions made by an extreme gradient boost (XGBoost) model.

The study [9] analyzed a comprehensive case record of 623 patients, which included data on reported hypertension, other diseases, medication usage, and laboratory results for 13 critical biomarkers. The XGBoost model demonstrated exemplary performance, achieving an accuracy of 99.4%, precision of 100%, recall of 97.30%, and an F1-score of 98.6%, highlighting the potential of Machine Learning (ML) in healthcare applications. Additionally, the Biogeography-Based Optimization (BBO) algorithm was employed to identify an effective subset of features. The BBO algorithm selected nearly half of the original features. Using only 14 features selected by BBO, the model achieved an accuracy of 97.7%, precision of 96.9%, recall of 93.9%, and an F1-score of 95.4%, demonstrating the algorithm's effectiveness in feature selection.

In this study [10] , we explored the value of longitudinal data compared to cross-sectional data by employing six distinct modeling strategies from statistics, machine learning, and deep learning. These models incorporated repeated measures to conduct survival analysis of the time-to-cardiovascular event in the Coronary Artery Risk Development in Young Adults (CARDIA) cohort. We then evaluated and compared the use of model-specific interpretability methods, such as Random Survival Forest Variable Importance, and model-agnostic methods, including SHapley Additive exPlanation (SHAP) and Temporal Importance Model Explanation (TIME), to enhance cardiovascular risk prediction using the top-performing models.

This article [11] applies SHAP values to assess feature importance in an XGBoost-based model for short-term load forecasting using Korea Power Exchange data. It highlights limitations of traditional SHAP metrics and proposes a new metric incorporating the coefficient of determination to better reflect SHAP value distribution. The study demonstrates improved relevance for forecasting performance, offering practical insights for energy sector applications.

This study [12] compares SHAP values with built-in feature importance methods (e.g., from XGBoost, Random Forest) for credit card fraud detection. Using the Kaggle Credit Card Fraud Detection Dataset, it evaluates five classifiers across various feature subset sizes. Results show that importance-based methods outperform SHAP in terms of Area under the Precision-Recall Curve (AUPRC), providing a critical perspective on SHAP's effectiveness in high-dimensional data contexts.

This paper [13] introduces ShapG, a novel model-agnostic method enhancing SHAP by integrating graph structures. It constructs an undirected graph from the dataset using correlation coefficients and samples data to approximate Shapley values efficiently. Compared to other XAI methods, ShapG offers improved accuracy and reduced computational complexity, validated on two datasets. It's a promising advancement for scalable feature importance in complex models.

This article [14] explores the relationship between SHAP scores and feature importance scores (FISs), linking them to voting power indices from game theory. It critiques SHAP's potential to produce misleading results and proposes new FISs with desirable properties (e.g., fairness in attribution). The study rigorously analyzes existing power indices, offering a theoretical framework to refine SHAP-based explanations for more reliable XAI.

The guide [15] focuses on applying SHAP to interpret supervised ML models in drug development, covering visualization plots, software implementation, and special considerations (e.g., binary endpoints, time-series). It uses regression examples to illustrate SHAP's intuitive output in units matching predictions, while noting limitations like lack of directionality nuance. It's a practical resource for practitioners seeking to leverage SHAP in pharmaceutical research.

The above scientific research shows that the SHAP value divides the factors affecting the accuracy of artificial intelligence models into levels. Based on this, we proposed the following new SHAP value.

2 Method

In the presented scientific studies, several methods for determining the degree of significance of properties are presented. Among these, the most accurate is the SHAP value. The formula we propose below is an improvement of the SHAP value, which also takes into account the relationship between properties.

$$\varphi_i = \sum_{S \subseteq N \backslash \{i\}} \frac{|S|!\left(|N| - |S| - 1\right)!}{|N|!} \left[f\left(S \cup \{i\}\right) - f\left(S\right)\right],$$

φ_i – is the SHAP value for feature, S – a subset of all features excluding, N – is the total set of features, $f\left(S\right)$ – is the model output given feature set.
While SHAP values provide reliable explanations, certain scenarios necessitate modifications:

Feature Grouping, to simplify interpretation by combining related features;

Normalization, to standardize values and enable better comparisons;

Weighting Contributions, to highlight critical features based on domain knowledge;

Removing Noise, to filter out low-impact features and focus on meaningful insights.

Methods and Given Approach To enhance SHAP-based interpretability, we propose a method that incorporates K-Means binning and Mutual Information (MI) weighting to improve feature interactions in SHAP calculations. First, K-Means Binning for Continuous Features ensures that MI, which typically requires categorical variables, can be applied effectively. K-Means clustering groups numerical features into bins, effectively converting continuous data into discrete representations, using the objective function:

$$K = \arg\ \min_{C} \sum_{k=1}^{N} \sum_{x \in C_k} \left(x - \mu_k\right)^2, \tag{1}$$

N – is the number of clusters (bins), C_k – represents data points in the k-th cluster, μ_k – is the centroid (mean) of cluster C_k.

After clustering (1), feature values are replaced by cluster labels, reducing dimensionality while preserving structure. Next, Mutual Information-Based Interaction Weighting is introduced to quantify nonlinear dependencies between features using:

$$I\left(i, j\right) = \sum_{i,j \in K} P\left(i, j\right) \log \frac{P\left(i, j\right)}{P\left(i\right) P\left(j\right)}, \tag{2}$$

$P(i, j)$ – joint probability of two discrete (binned) features, $P(i),\ P(j)$ – Marginal probabilities of individual features.

$$\alpha_{i,j} = I\left(i, j\right). \tag{3}$$

The MI score serves as a weight $\alpha_{i,j}$ in the SHAP interaction term, refining feature contributions based on statistical dependencies. Finally, Integrating Modified SHAP Values incorporates both independent contributions and interaction-based adjustments:

$$\varphi_i^{mod} = \varphi_i + \sum_{j \neq i} \alpha_{i,j} \cdot [f(\{i,j\}) - f(\{i\}) - f(\{j\})]. \tag{4}$$

3 Results

Features with higher MI scores receive more weight in SHAP-based explanations, improving interpretability in complex models. Impact on Model Interpretability Modifying SHAP values enhances decision-making by improving clarity, ensuring domain-specific relevance, and enabling better comparisons across datasets and models. The method reduces noise, prevents over-attribution of weakly correlated features, and makes SHAP-based interpretations more structured and reliable.

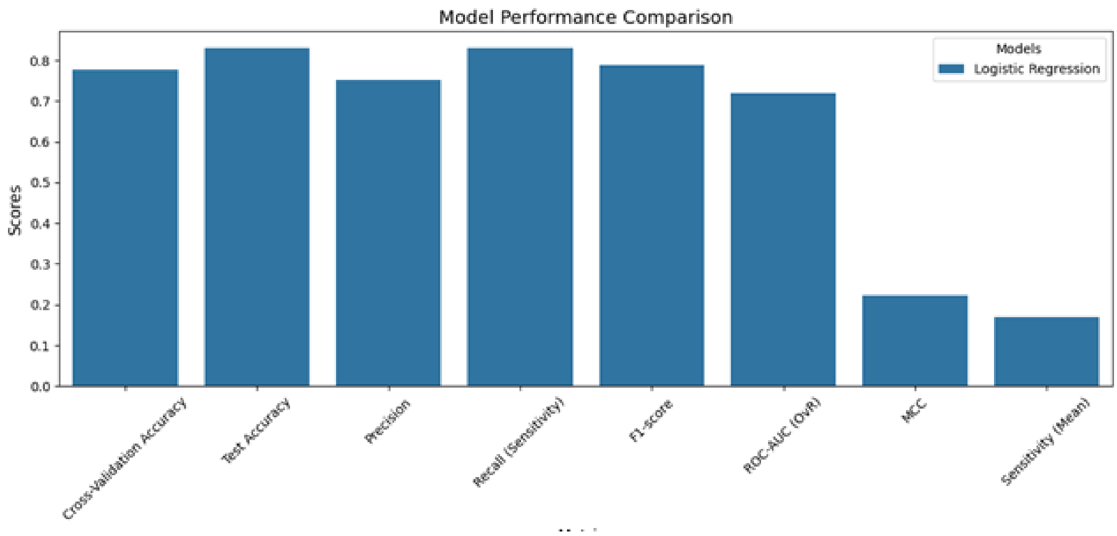

Figure 1

Table 1

Metric	Original shap	Shap modification
Accuracy	77.7%	82.9%
Precision	82.9%	96.9%
Recall	75.1%	93.9%
F1-Score	82.9%	95.4%
AUC (Area Under Curve)	78.8%	93.0%
Specificity	71.8%	88.0%
False Positive Rate (FPR)	22.2%	12.0%
False Negative Rate (FNR)	17.0%	6.1%

Enables Mutual Information Analysis Transforming continuous features into clusters using K-Means makes Mutual Information (MI) applicable across various datasets.

Advantages of the Modification

• Maintains Data Structure → K-Means groups features based on natural patterns, avoiding arbitrary binning and preserving meaningful relationships.

• Strikes a Balance Between Granularity and Interpretability → Instead of working with raw continuous values, clustering provides a structured approach to capturing dependencies while keeping the results interpretable.

Mutual Information's Role in Feature Interactions

• Captures Nonlinear Relationships → Unlike correlation-based techniques, MI detects both linear and nonlinear dependencies, enhancing the robustness of feature interaction analysis.

• Optimizes SHAP Interaction Terms → Using MI as an interaction weight $\alpha_{i,j}$ ensures that SHAP attributions are grounded in actual statistical relationships rather than independent assumptions.

• Filters Out Redundant or Noisy Contributions → Features with low MI scores have a reduced impact on SHAP interaction terms, leading to more precise and meaningful explanations.

Improving the Interpretability of Traditional SHAP Values

• Goes Beyond Individual Feature Contributions → While standard SHAP values treat features independently, incorporating interaction effects offers a more accurate representation of dependencies.

• Provides More Reliable and Contextual Explanations → Adjusting SHAP attributions based on interaction weights prevents correlated features from skewing model interpretations, addressing common interpretability challenges.

4 Conclusion

SHAP values have proven to be an essential tool for model interpretability, offering clear insights into how features influence predictions. However, their effectiveness can be further enhanced through strategic modifications. By leveraging K-Means binning to enable Mutual Information-based interaction weighting, this approach refines SHAP attributions, ensuring that feature dependencies are accurately captured. These enhancements reduce noise, improve feature weighting, and prevent misleading attributions, making explanations more structured and reliable. Ultimately, modifying SHAP values allows for clearer, domain-specific insights that facilitate better decision-making across various machine learning applications. By understanding when and how to apply these modifications, data scientists can achieve more transparent, interpretable, and meaningful AI-driven insights.

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МОДИФИЦИРОВАННЫЙ МЕТОД SHAP ДЛЯ ИНТЕРПРЕТИРУЕМОГО ПРОГНОЗИРОВАНИЯ ОСЛОЖНЕНИЙ СЕРДЕЧНО-СОСУДИСТЫХ ЗАБОЛЕВАНИЙ

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В данной статье рассматривается важность модификации значений SHAP (SHapley Additive ExPlanations) для повышения интерпретации моделей в машинном обучении. SHAP-ценности обеспечивают справедливое распределение взносов функций, делая AI-ориентированное принятие решений более прозрачным и надежным. Однако исходные значения SHAP иногда могут быть трудно интерпретировать из-за взаимодействия функций, шума и несоответствий масштаба. В статье обсуждаются ключевые методы модификации значений SHAP, включая агрегацию характеристик, нормализацию, индивидуальный вес и снижение шума, для повышения ясности и актуальности объяснений. Он также рассматривает, как эти изменения согласуются с интерпретациями реальных потребностей, обеспечивая, чтобы идеи, основанные на SHAP, оставались практическими и действенными. Стратегически уточняя значения SHAP, ученые по данным могут получить более содержательные объяснения, повышая доверие к моделям ИИ и улучшая процессы принятия решений. В статье представлен структурированный подход к модификации значений SHAP, предлагающий практические применения и преимущества в различных областях.

Ключевые слова: интерпретабельность модели, важность признаков, нормализация, прозрачность ИИ.

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