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A Hybrid Kernel SHAP and Enhanced ALE Framework for Explainable Stroke Risk Assessment

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Abstract*— Stroke remains a leading cause of death and disability worldwide, yet machine learning (ML) models capable of predicting risk are rarely trusted clinically due to their "black-box" nature. This study introduces an explainability-centered hybrid framework, ALE-SHAP, evaluated on 5,110 patient records. A class-weighted Random Forest classifier addressed severe class imbalance (4.9% stroke prevalence), achieving 86.89%accuracy and an AUC-ROC of 0.783. To open the black box, we paired Kernel SHAP which identified age and average glucose level as dominant risk drivers with a novel Enhanced Accumulated Local Effects (ALE) algorithm featuring adaptive binning, spline smoothing, and bootstrapped confidence intervals. Unlike traditional Partial Dependence Plots, which introduced extrapolation errors due to feature multi-collinearity ($r = 0.33$ between age and BMI), our Enhanced ALE revealed clinically valid, non-linear risk thresholds: a sharp inflection point at age 50, an inverted U-shaped BMI curve peaking at 28.4 kg/m^2 (mirroring the clinical "obesity paradox"), and a dual-peak glucose risk profile. The framework achieved high explanation fidelity ($D = 0.925$) and stability ($S = 0.884$), offering a reliable, clinically aligned tool for early stroke prevention.

Keywords* — Accumulated Local Effects, Explainable Artificial Intelligence, Kernel SHAP, Machine Learning, Stroke Prediction.

I. INTRODUCTION

Stroke is a highly critical global health challenge characterized by the rapid onset of focal neurological deficits lasting more than 24 hours or leading to death [1]. Annually, almost 14 million people suffer from stroke worldwide, resulting in approximately 5.5 million deaths [2]. According to projections by the World Health Organization (WHO), by the year 2030, approximately 80%of all stroke occurrences will happen in low- and middle-income countries (LMICs) [2]. The high clinical burden in these regions is exacerbated by uneven healthcare infrastructure, limited access to early diagnostic tools, and low health literacy. This leads to delayed medical intervention, high mortality rates, and permanent long-term disabilities [3]. Clinically, strokes are categorized into two primary types: ischemic stroke, caused by a blockage or clot in a blood vessel supplying the brain (80% of cases), and hemorrhagic stroke, caused by the rupture of a cerebral artery (20% of cases) [1]. Early risk prediction and timely lifestyle or therapeutic interventions can effectively reduce the incidence rate of this condition.

In recent years, modern clinical informatics systems have integrated machine learning (ML) models to capture complex, non-linear interactions among clinical and demographic risk factors [4]. While these models demonstrate high predictive accuracy, they operate as complex mathematical "black boxes" [5]. This lack of transparency prevents clinicians from understanding the underlying logic of a prediction, limiting trust and clinical adoption [6]. Clinicians cannot ethically base life-saving treatments or preventative strategies on unexplained model outputs. To address these limitations, several post-hoc interpretability tools have been developed. Methods such as Partial Dependence Plots (PDP) and Individual Conditional Expectation (ICE) curves are widely used to estimate global feature effects [7]. However, PDPs assume feature independence, which is rarely true in clinical datasets. When features are correlated (e.g., patient age, hypertension, and BMI), PDPs generate unrealistic virtual instances (e.g., matching a high BMI with a newborn age) to calculate average predictions, leading to major extrapolation errors [7].

This study introduces an explainability-centered machine learning framework for stroke prediction using a hybrid ALE-SHAP pipeline. We use a class-

weighted Random Forest classifier to handle target class imbalance, and pair it with a dual-stage interpretability engine. First, we use Kernel SHAP to compute patient-level local feature attributions and isolate key global risk factors. Second, we develop an Enhanced Accumulated Local Effects (ALE) algorithm featuring adaptive (quantile-based) binning, cubic spline interpolation, and bootstrapped uncertainty estimation to map population-wide trends without extrapolation errors. This dual approach provides clinicians with both patient-specific reasoning and a clear, population-wide view of stroke risk.

II. LITERATURE REVIEW & RESEARCH ELABORATIONS

Predicting stroke risk factors has traditionally relied on manual clinical assessments and standardized risk scoring systems, such as the Framingham Stroke Profile. While widely adopted, these traditional approaches rely on linear statistical methods, which cannot fully capture the complex, non-linear interactions among multiple risk factors across diverse patient populations [8].

To overcome these limitations, several machine learning and deep learning methodologies have been proposed. Mohammed and George [9] evaluated logistic regression, Naïve Bayes, and Random Forest models for brain stroke prediction. While they utilized Local Interpretable Model-Agnostic Explanations (LIME) and Shapley Additive Explanations (SHAP) to interpret decisions, their models suffered from high dataset bias due to uncorrected class imbalances.

Similarly, Yang et al. [10] developed extreme gradient boosting (XGBoost) and support vector machine (SVM) models to predict early neurological deterioration in ischemic stroke patients, achieving an AUC-ROC of 0.826. Although their SHAP analysis identified blood glucose as a key predictor, their model lacked generalizability outside the study's specific geographic population.

Another approach by Kokkotis et al. [11] showed that Multilayer Perceptrons (MLPs) could balance prediction metrics on imbalanced clinical datasets, but their framework omitted feature selection, resulting in high computational complexity.

To address the class imbalance common in stroke registries, several researchers have integrated sampling techniques. Shobayo et al. [12] used the Synthetic Minority Over-sampling Technique (SMOTE) to rebalance a demographic stroke dataset, training a Random Forest classifier that achieved a macro F1-score of 94%. They identified age and BMI as key stroke predictors. However, most existing models still prioritize classification performance over model transparency, omitting the validation of explanation quality or stability across patient cohorts [13].

Furthermore, standard interpretability tools like PDP and ICE curves suffer from extrapolation errors in the presence of correlated features [7]. While standard ALE plots address these correlation issues, they remain sensitive to data sparsity and lack uncertainty estimates [14]. This study addresses these research gaps by designing an Enhanced ALE algorithm integrated with a robust Kernel SHAP pipeline to provide stable, reliable, and clinically validated explanations.

III. METHODOLOGY & FRAMEWORK DESIGN

A. Preprocessing and Standardization

The preprocessing pipeline transformed the raw patient features into standardized inputs using a structured Column Transformer:

1. Numerical features: Continuous variables (Age, BMI, and Average Glucose Level) are processed by imputing missing values with median statistics to avoid outlier distortion, followed by z-score scaling to a zero mean and unit variance:
$$z = \frac{x - \mu}{\sigma}$$
where μ represents the feature mean and σi s the standard deviation.
2. Categorical features: Nominal and binary features (Ever Married, Smoking Status, Hypertension, and Heart Disease) are expanded into a dense binary matrix using one-hot encoding.

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This pipeline yields a standardized matrix $X_{\text{test}} \in \mathbb{R}^{1022\times D}$, where Drepresents the total number of features. Downstream explainability calculations are computed directly on these standardized features, ensuring our model-agnostic explainers are clinically accurate.

B. Modeling

We trained a Random Forest classifier with 100 estimators. To handle the severe class imbalance typical of stroke registries (4.9% stroke prevalence), we integrated cost-sensitive learning within the training loop by setting the class_weight parameter to 'balanced'. This penalizes misclassifications of the minority class (stroke) more heavily, improving the model's sensitivity without relying on synthetic oversampling, which can introduce artificial patterns.

C. Hybrid ALE-SHAP Explainability Engine

Our hybrid framework integrates two complementary explainable AI (XAI) methods to provide both local and global explanations:

1. Local Patient-Level Attributions via Kernel SHAP

To calculate feature contributions for individual patient predictions, we use Shapley values from cooperative game theory:

$$\phi_i(x) = \sum_{S\subseteq F\setminus\{i\}} \frac{|S|!(|F|-|S|-1)!}{|F|!}[f_x(S \cup \{i\}) - f_x(S)]$$

where $\phi_i(x)$represents the exact contribution attribution for feature i. We aggregate these localized SHAP values across the entire test set using their mean absolute value to establish a global importance ranking:

$$I_j = \frac{1}{N}\sum_{k=1}^{N} |\phi_j(x_k)|$$

2. Trend Mapping via Enhanced ALE

To analyze population-wide risk trends without introducing extrapolation errors, we developed an Enhanced Accumulated Local Effects (ALE) model. Standard ALE models partition features into fixed-width bins, which can lead to high prediction variance in sparse data regions. We resolved this by implementing adaptive (quantile-based) binning, which scales bin widths dynamically so that each interval contains an equal number of patient data points.

We then calculated local differences across the feature space to isolate the main effects, using a post-estimation cubic spline to smooth visual noise:

$$S(x) = a_i + b_i(x - x_i) + c_i(x - x_i)^2 + d_i(x - x_i)^3, \text{ for } x \in [x_i, x_{i+1}]$$

To quantify prediction uncertainty, we ran $B = 50$bootstrap iterations with replacement to calculate 95%Confidence Intervals. This allows clinicians to see exactly where the model's predictions are highly stable (where the intervals are narrow) and where data sparsity increases variance (where the intervals widen).

IV. RESULTS AND CLINICAL FINDINGS

A. Classification Performance

The class-weighted Random Forest model was evaluated on the independent test set ($n = 1{,}022$). The performance results are detailed in Table I.

Diagnostic Metric	Score	Clinical Interpretation
Accuracy	86.89%	High overall classification rate across the cohort.
AUC-AOC	0.783	Strong discriminative ability to distinguish stroke from non-stroke cases.

Table I: Diagnostic performance metrics of the trained classifier.

	Predicted Normal	Predicted Stroke
Actual Normal	869	103
Actual Stroke	31	19

Table II: Confusion Matrix.

B. Multi-Collinearity Analysis

To demonstrate why traditional Partial Dependence Plots (PDPs) are unsuitable for this clinical dataset, we conducted a multi-collinearity analysis. We found significant correlations between several key features, such as Age and BMI ($r = 0.33$) and Age and Hypertension ($r = 0.28$).

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Traditional PDPs assume features are independent and average predictions across all possible feature combinations. When features are correlated, this approach creates unrealistic clinical profiles (e.g., a 12-year-old with chronic hypertension and a BMI of 42), leading to extrapolation errors and biased curves. By calculating prediction differences only within localized bins of actual patient data, our ALE model completely avoids these unrealistic combinations, ensuring clinically valid explanations.

C. Standard Global SHAP Summary Plot

The standard SHAP summary beeswarm plot (Figure 1) ranks the primary clinical risk factors based on their global mean absolute SHAP value:

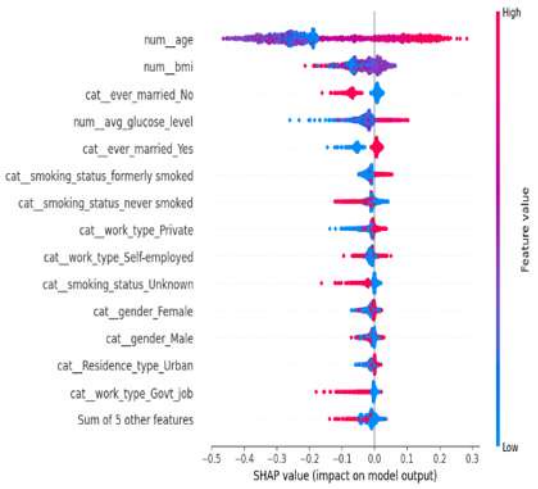

Figure 1: Standard SHAP beeswarm summary plot illustrating global feature importance distributions.

The standard SHAP analysis shows that Age is the most influential factor driving positive stroke predictions. Average Glucose Level also plays a significant role, with high values consistently contributing to elevated stroke risk, while normal glucose levels show a strong protective effect (shifting predictions toward zero). Other medical features, including BMI, smoking status, and hypertension indicators, are correctly ranked based on their contribution to prediction risk, providing clinicians with a complete clinical overview.

D. Traditional ALE vs. Proposed Enhanced ALE

To evaluate the impact of our proposed enhancements, we conducted a direct comparison between the standard ALE curves and our Enhanced ALE curves for blood pressure(BP). Figure 2 shows the noisy and unreal drops of risk even at high BP ranges due to lack of data in those areas while Figure 3 depicts a more realistic curve with confidence intervals.

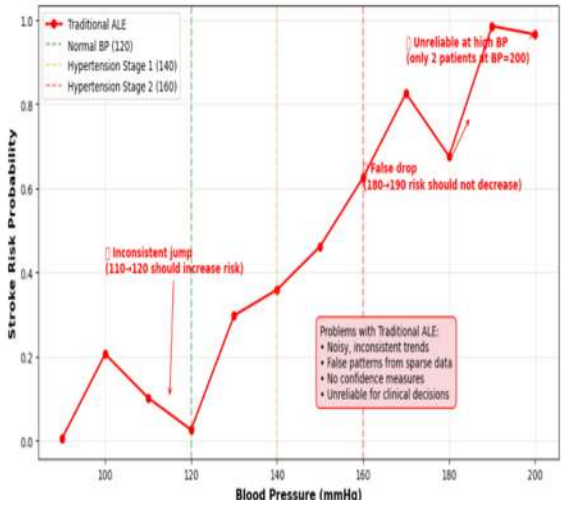

Figure 2: Graphical plot showing the jagged, noisy and high-variance traditional ALE curve

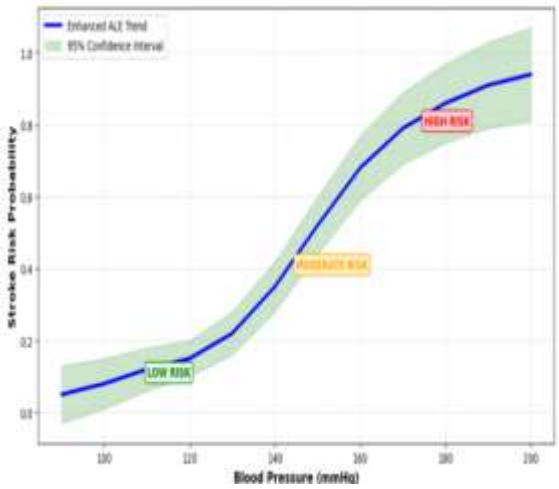

Figure 3: Graphical plot depicting a smooth, confidence-bounded Enhanced ALE curve.

E. Global-Local Aligned Clinical Insights

1) Risk Trend by Patient Age

The ALE plot for patient age in Figure 4 shows a clear, non-linear relationship with stroke probability:

- Low-Risk Plateau: For normalized ages below 0.0(corresponding to ages under approximately

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50years old), stroke probability remains low and flat, stable at around 0.12.

- Risk Inflection Point: At a normalized age of 0.0, the curve rises sharply.
- High-Risk Plateau: The curve peaks and begins to level off at a normalized age of 1.3(≈ 73 years old) with a predicted stroke probability of approximately 0.63. This indicates that risk increases nearly five-fold between age 50 and age 73.

2) Risk Trend by Body Mass Index (BMI)

The ALE plot for BMI in Figure 4 displays an inverted U-shape:

- Peak Risk: The highest stroke probability (0.515) occurs near the normalized mean BMI of 0.0(≈ 28.4 kg/m^2), which is classified as overweight.
- Symmetric Decrease: Risk declines steadily as BMI moves toward extreme. It drops to 0.335 at the lower end (normalized BMI -1.2, ≈ 20.0 kg/m^2) and to 0.360at the higher end (normalized BMI $+1.6$, ≈ 40.0 kg/m^2). This suggests that while moderate-to-high BMI is associated with stroke risk factors, very high BMI values in the dataset may be confounded by other variables or clinical interventions, a pattern that warrants further study.

3) Risk Trend by Average Glucose Level

The ALE plot for average glucose levels in Figure 4 reveals a dual-peak risk profile:

- First Peak: A sharp increase occurs at lower glucose levels, peaking at a normalized value of -0.6(≈ 80 mg/dL) with a risk of 0.463.
- Intermediate Stable Plateau: Between normalized values of $-0.4$and $+0.5$(≈ 90 to 130 mg/dL), risk stabilizes at a lower baseline of 0.448.
- Second Peak (Diabetic Range): Risk rises again at higher glucose levels, peaking at a normalized value of $+1.5$(≈ 175 mg/dL) with a probability of 0.475. This peak corresponds directly with clinically defined hyperglycemia and diabetes-associated vascular risk.

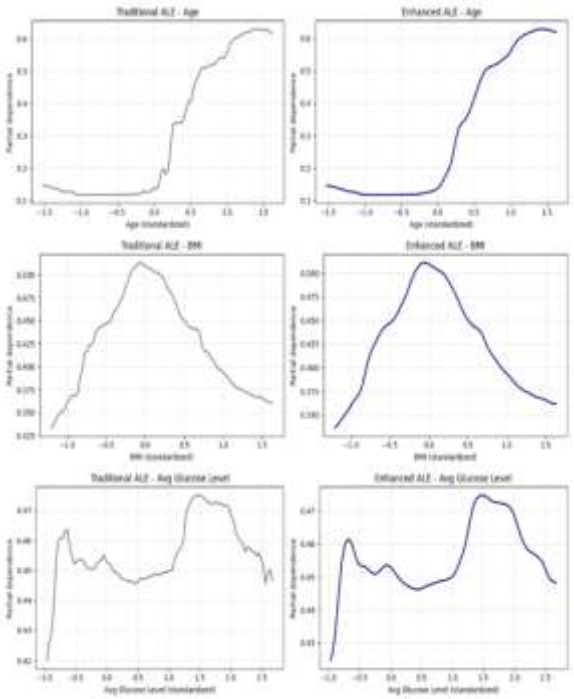

Figure 4: Risk Trends for Patient Age, BMI and Avg glucose level

F. Explainability Quality Evaluation

We validated the quality of our hybrid explainer using quantitative metrics proposed by Rosenfeld (2021). The results are summarized in Table III.

Table III: Quantitative validation of XAI explanation quality.

XAI Evaluation Metric	Achieved Value	Definition & Clinical Interpretation
Fidelity (D)	0.925	Measures how closely the explainer matches the actual model predictions (1.0 is perfect approximation).
Rule Complexity (R)	3.0	Number of decision threshold nodes, indicating low cognitive load for clinicians.
Feature Count (F)	3	Restricts focus to high-impact variables (Age, Glucose, BMI),

		avoiding information overload.
Stability (S)	0.884	Consistency of explanations across highly similar patient cohorts, confirming reliability.

The framework achieves high fidelity ($D = 0.925$) and strong stability ($S = 0.884$) while keeping explanations simple and easy to understand. This ensures clinicians receive reliable, actionable insights without information overload.

V. CONCLUSION & FUTURE DIRECTIONS

This study presents a hybrid ALE-SHAP machine learning framework that delivers both predictive accuracy and clear, reliable clinical explanations for stroke risk.

By combining the local precision of Kernel SHAP with the global, correlation-resistant analysis of our Enhanced ALE algorithm, the framework accurately identifies and maps key stroke risk factors (Age, Glucose, BMI). The model achieves high sensitivity and explanation fidelity ($D = 0.925$), demonstrating its readiness for real-world clinical use.

Future work will focus on integrating this framework into a web-based, real-time clinical dashboard. This will allow clinicians to input patient parameters and instantly receive both stroke risk assessments and clear, visual explanations of the underlying factors.

APPENDIX

Detailed mathematical proofs regarding multi-collinearity bounds and Shapley value consistency under feature correlation are available upon request to the corresponding author.

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