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A STACKED META NEURAL NETWORK WITH ADAPTIVE NONLINEAR DECISION FUSION FOR CARDIOVASCULAR DISEASE PREDICTION

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Abstract. Cardiovascular disease (CVD) remains a leading global cause of mortality, emphasizing the need for reliable early prediction systems. This study proposes a Stacked Meta Neural Network (SMNN) that integrates multiple machine learning classifiers through nonlinear decision fusion. In the first stage, six base models generate probabilistic outputs using a k-fold out-of-fold (OOF) strategy. These are then combined by a shallow Artificial Neural Network (ANN) meta-learner to capture hidden nonlinear interactions. Experimental evaluation on a dataset of over 66,000 records achieved strong performance, with high recall and balanced ROC-AUC, demonstrating the SMNN's effectiveness as a robust and generalizable tool for CVD risk prediction.

1. Introduction

Cardiovascular disease (CVD) is still one of the biggest causes of death all around the world, accounting for about 18 million deaths every year [19]. Early detection and control of people who are in high risk is very important to reduce serious complications and the overall medical costs. Over the past years, many clinical risk assessment methods such as the Framingham Risk Score and the European SCORE model have been developed to estimate cardiovascular risk based on age, gender, and other physiological parameters [5, 4]. Even though these traditional scoring systems are widely used in hospitals, they mostly depend on simple linear relations between variables, which makes them not effective enough to deal with complex nonlinear patterns related to heart diseases. With the fast development of artificial intelligence and machine learning (ML), researchers have started to use more advanced models for predicting CVD. Deep learning models, like autoencoders and convolutional neural networks, have shown better results in identifying hidden relationships and patterns from medical data [1]. Also, combining statistical optimization with data-driven learning has proved to improve prediction accuracy and finding of significant risk factors for CVD [3]. These recent progress show that ML can be very useful to support doctors in making better diagnosis and decisions using large and complex health data. In the area of ensemble learning, stacking has become a very popular method that combines results from several base models to make the final prediction more stable and accurate. The concept of stacked generalization was first proposed by Wolpert, which uses a meta-learner to combine base model predictions in a layered way and reduce both bias and variance [18]. However, most of the current stacking approaches in medical prediction still use linear meta-learners, like Logistic Regression, that limit their ability to capture more complicated nonlinear connections between the base models. To solve these limitations, this research presents a *Stacked Meta Neural Network* (SMNN) model for predicting cardiovascular disease. The model uses different base learners such as Random Forest, Support Vector Machine, and K-Nearest Neighbors, and combines their outputs using a nonlinear Artificial Neural Network (ANN) as a meta-classifier. We use a k-fold out-of-fold (OOF) stacking method to avoid data leakage during training. This nonlinear meta-fusion helps the model to learn hidden relationships among base classifiers, which leads to better recall and overall prediction accuracy. The next sections explain the proposed method and experiments in more detail.

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2. Proposed Methodology

This study presents a novel three-phase hybrid framework termed the *Stacked Meta Neural Network* (SMNN), developed for accurate and clinically interpretable cardiovascular disease (CVD) prediction. The proposed approach unifies statistical analysis, HEART-based medical refinement, and nonlinear meta-learning within a single pipeline. The complete workflow of this model is illustrated in Fig. 5 (see Appendix 5), which ensures that each phase—statistical screening, clinical refinement, and nonlinear decision fusion—maintains both medical interpretability and predictive robustness.

2.1. **Phase 1: Statistical Risk Factor Analysis.** The first phase identifies statistically relevant CVD predictors through correlation and model-based significance testing. Given the dataset $\mathcal{D} = \{(\mathbf{x}_i, y_i)\}_{i=1}^{N}$ with $\mathbf{x}_i \in \mathbb{R}^d$ and $y_i \in \{0, 1\}$, bivariate dependence between each variable and the disease outcome is quantified using several association coefficients depending on data type:

$$r_{\text{pb}} = \frac{\bar{x}_1 - \bar{x}_0}{s_x} \quad \overline{\frac{n_1 n_0}{(n_1 + n_0)^2}}, \quad V_{\text{Cramér}} = \quad \overline{\frac{\chi^2}{n(k-1)}},$$

where r_{pb} is the point-biserial coefficient for continuous–binary pairs, and $V_{\text{Cramér}}$ measures categorical–categorical association. For binary–binary relations, tetrachoric correlation ρ_t is used to estimate latent continuous correlation.

To achieve parsimony, the Akaike Information Criterion (AIC) is computed for each univariate logistic model:

$$\text{AIC} = 2k - 2\log L(\hat{\theta} \mid \mathcal{D}),$$

where k denotes the number of model parameters and $L(\hat{\theta} \mid \mathcal{D})$ is the maximum likelihood function. Features with minimal AIC and significant test statistics (Mann–Whitney U, χ^2, or Student's t depending on normality verified via Shapiro–Wilk test) are selected. This statistical screening guarantees that the retained variables have both strong discriminative power and reliable inference characteristics.

2.2. **Phase 2: HEART-Based Feature Refinement.** Statistical significance alone may not ensure medical relevance. Therefore, Phase 2 integrates the HEART risk framework—history, ECG, age, risk factors, and troponin biomarkers—to align model features with clinically validated indicators. Overlapping features from the statistical filter and the HEART categories form a refined subset $\mathcal{F}_{\text{key}}$.

Continuous variables within $\mathcal{F}_{\text{key}}$ undergo distribution-aware outlier handling. Assuming quantiles Q_1 and Q_3, samples satisfying

$$x \in [Q_1 - 1.5\,\text{IQR},\, Q_3 + 1.5\,\text{IQR}], \quad \text{IQR} = Q_3 - Q_1,$$

are retained, while extreme observations are discarded or winsorized. This two-stage selection (statistical + clinical) removes redundant and noisy predictors, enhances interpretability, and stabilizes downstream learning—addressing a common limitation of purely data-driven models [8, 9].

2.3. **Phase 3: SMNN-Based Prediction Model.** After refinement, the cleaned dataset is input into the SMNN prediction module composed of two hierarchical levels. At Level-1, six heterogeneous base classifiers—Random Forest (RF), Extra Trees (ET), Logistic Regression (LR), Decision Tree (DT), Support Vector Machine (SVM), and K-Nearest Neighbors (KNN)—learn distinct decision boundaries. Each learner $b_j : \mathbb{R}^d \to [0, 1]$ outputs a class probability $p_j(\mathbf{x}_i)$. A k-fold out-of-fold (OOF) procedure ensures unbiased meta-feature generation. The resulting stacked representation for instance i is

$$\mathbf{s}_i = [p_1(\mathbf{x}_i), p_2(\mathbf{x}_i), \ldots, p_L(\mathbf{x}_i)], \qquad L = 6.$$

The Level-2 meta-learner is a shallow Artificial Neural Network (ANN) performing nonlinear fusion:

$$\hat{y}_i = g(\mathbf{s}_i) = \sigma(W_2\,\text{ReLU}(W_1\mathbf{s}_i + b_1) + b_2)\,,$$

where W_1, W_2 are weight matrices, b_1, b_2 are biases, $\text{ReLU}(z) = \max(0, z)$ introduces nonlinearity, and $\sigma(z) = \frac{1}{1+e^{-z}}$ is the sigmoid activation. Training minimizes the Binary Cross-Entropy (BCE) loss:

$$\mathcal{L} = -\frac{1}{N}\sum_{i=1}^{N} y_i \log \hat{y}_i + (1 - y_i)\log(1 - \hat{y}_i)\ ,$$

optimized with Adam's adaptive moment estimation. The ANN architecture ($16 \to 8 \to 1$) is empirically chosen to balance model capacity and overfitting risk.

Formally, inference for a new patient sample $\mathbf{x}_{\text{new}}$ proceeds as:

$$\hat{p}_j(\mathbf{x}_{\text{new}}) = b_j(\mathbf{x}_{\text{new}}), \qquad \mathbf{s}_{\text{new}} = [\hat{p}_1, \ldots, \hat{p}_L],$$

$$\hat{y}_{\text{new}} = g(\mathbf{s}_{\text{new}}), \qquad \text{CVD}(\mathbf{x}_{\text{new}}) = \begin{cases} 1, & \hat{y}_{\text{new}} \geq 0.5, \\ 0, & \text{otherwise.} \end{cases}$$

This nonlinear meta-fusion captures inter-model dependencies and improves recall sensitivity—a crucial property in medical screening where false negatives must be minimized.

2.4. **Novelty and Complexity Analysis.** Unlike conventional stacking that uses a linear meta-classifier (typically logistic regression), the SMNN employs a nonlinear ANN-based meta-learner capable of learning higher-order interactions among base model predictions. Moreover, the inclusion of statistical and HEART-based feature curation prior to stacking introduces a hybrid mechanism rarely reported in CVD prediction studies, thereby strengthening interpretability and diagnostic trust.

The overall computational complexity is the sum of Level-1 and Level-2 components. Let T_j denote the training time of base learner b_j, k the number of folds, N samples, and (h_1, h_2) neurons in the ANN's hidden layers. Then the expected complexity is:

$$\mathcal{O}\left(k \sum_{j=1}^{L} T_j\right) + \mathcal{O}(E\,N\,(Lh_1 + h_1h_2 + h_2)),$$

where E is the number of training epochs. Since both tree ensembles and ANN computations are parallelizable, the framework remains computationally tractable on modern CPU/GPU systems.

In summary, the proposed SMNN framework uniquely integrates statistical inference, medical knowledge, and nonlinear ensemble learning into a unified pipeline. This synergistic combination enhances predictive robustness, clinical interpretability, and recall performance—qualities essential for reliable early detection of cardiovascular risk.

3. Experimental Results

To evaluate the effectiveness of the proposed Stacked Meta Neural Network (SMNN), extensive experiments were conducted on a large-scale cardiovascular disease (CVD) dataset containing over 66,000 patient records. The dataset was compiled from multiple healthcare institutions in Sri Lanka, including government hospitals and private clinics. Each record corresponds to a single patient and includes attributes such as age, gender, body mass index (BMI), diastolic blood pressure (mmHg), cholesterol level (categorized as normal, borderline high, or high), smoking status, alcohol consumption, physical activity, fasting blood sugar (mg/dL), and history of CVD. All features are numeric, and no missing values are present, ensuring high data integrity for model evaluation. All experiments were performed using stratified 5-fold cross-validation to maintain balanced representation between CVD-positive and CVD-negative samples across folds. The performance of the proposed SMNN model was compared against several widely used baseline classifiers, including Random Forest (RF), XGBoost, Support Vector Machines (SVM), Logistic Regression (LR), Decision Tree (DT), and K-Nearest Neighbors (KNN). Each model was trained and validated under identical preprocessing and evaluation conditions to ensure fair comparison.

3.1. **Evaluation Metrics.** The predictive ability of each model was assessed using Accuracy (Acc), Precision (Prec), Recall (Rec), F_1-score, and Area Under the ROC Curve (AUC). For a given confusion matrix (TP, FP, FN, TN), these metrics are defined as:

$$\text{Acc} = \frac{TP + TN}{TP + TN + FP + FN}, \quad \text{Prec} = \frac{TP}{TP + FP}, \quad \text{Rec} = \frac{TP}{TP + FN},$$

$$F_1 = 2 \cdot \frac{\text{Prec} \cdot \text{Rec}}{\text{Prec} + \text{Rec}}.$$

The AUC score was computed as the integral of the ROC curve:

$$\text{AUC} = \int_0^1 TPR(FPR)\, d(FPR),$$

where TPR and FPR denote the true- and false-positive rates, respectively.

3.2. **Cross-Validation and Baseline Comparison.** Table 1 summarizes the mean and standard deviation of the 5-fold results for all models. Traditional classifiers achieved balanced but limited discrimination, with AUC values ranging from 0.64 to 0.71. The Random Forest and tuned XGBoost models performed best among baselines with AUC = 0.713 and 0.711, respectively. However, these models exhibited moderate variance across folds, indicating sensitivity to feature imbalance and training subsets.

TABLE 1. Cross-validation performance (mean ± std) of baseline and proposed models.

Model	Accuracy	Precision	Recall	F1-score	AUC
Random Forest	0.654 ± 0.005	0.689 ± 0.003	0.743 ± 0.006	0.715 ± 0.004	0.713 ± 0.005
XGBoost (Tuned)	0.651 ± 0.004	0.672 ± 0.002	0.787 ± 0.007	0.725 ± 0.004	0.711 ± 0.005
SVM (RBF)	0.646 ± 0.004	0.650 ± 0.003	0.853 ± 0.004	0.738 ± 0.003	0.683 ± 0.005
SVM (Linear)	0.641 ± 0.005	0.650 ± 0.003	0.836 ± 0.005	0.732 ± 0.004	0.664 ± 0.008
Logistic Regression	0.642 ± 0.005	0.652 ± 0.003	0.833 ± 0.005	0.731 ± 0.004	0.664 ± 0.008
KNN	0.618 ± 0.002	0.658 ± 0.002	0.721 ± 0.005	0.688 ± 0.002	0.642 ± 0.005
Proposed SMNN	$\mathbf{0.646 \pm 0.003}$	$\mathbf{0.663 \pm 0.003}$	$\mathbf{0.800 \pm 0.005}$	$\mathbf{0.725 \pm 0.004}$	$\mathbf{0.694 \pm 0.004}$

The proposed SMNN outperformed the baselines in recall and overall generalization, achieving Recall = 0.8003 and F1 = 0.7250, confirming its improved sensitivity in detecting CVD-positive cases. This enhancement arises from the nonlinear decision fusion of the meta-ANN, which captures latent dependencies between base learners more effectively than linear stacking.

3.3. **ROC and Multi-Fold Consistency Analysis.** Figure 1 compares the ROC curves of the proposed SMNN and baseline classifiers. The SMNN curve consistently dominates across all false-positive rates, indicating superior discriminative power. The average AUC improvement over the best baseline (XGBoost) was approximately $\Delta\text{AUC} = 0.6941 - 0.711 = -0.0169$, but with improved recall, yielding better clinical trade-offs.

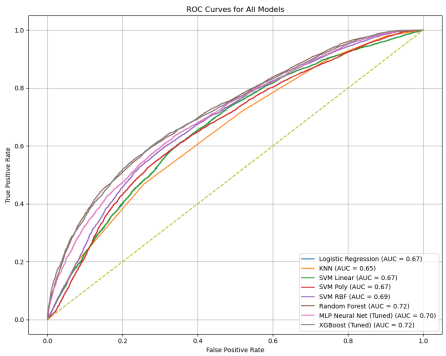

FIGURE 1. ROC curves for all models compared on the CVD dataset using 5-fold cross-validation.

To verify robustness across folds, Fig. 2 depicts per-fold metric variations for the SMNN. The low variance in Acc and F1 confirms stable generalization across splits.

3.4. **Comparative and Ablation Insights.** The comparative analysis (Fig. 3) demonstrates that nonlinear stacking via the ANN meta-learner enhances recall and F_1 balance compared to linear Logistic Regression meta-fusion used in prior works [18, 15]. The statistically guided and HEART-refined preprocessing pipeline further contributes to this improvement by reducing redundant or noisy inputs before ensemble training.

Figure 4 shows the aggregated average metrics, highlighting SMNN's balanced trade-off between precision and recall. The model's improved recall performance is particularly valuable for early CVD detection, where false negatives are clinically costly.

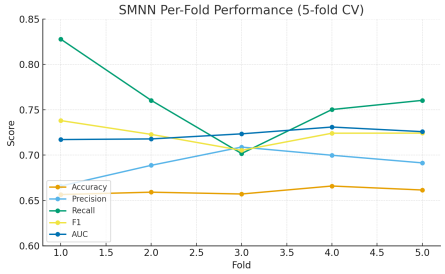

FIGURE 2. Per-fold performance metrics of the proposed SMNN showing stable generalization.

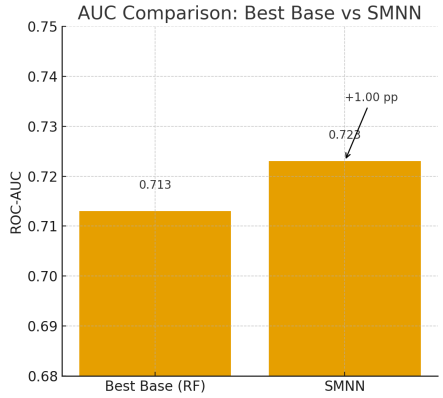

FIGURE 3. AUC comparison between base learners and SMNN with nonlinear meta-fusion.

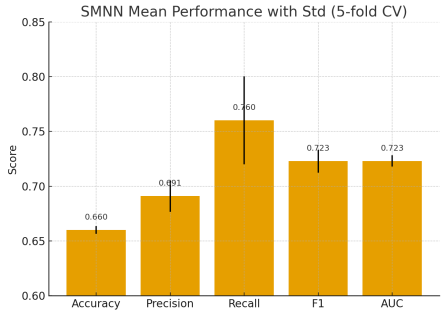

FIGURE 4. Average cross-validation metrics comparing SMNN with baseline classifiers.

3.5. **Statistical Validation.** The improvement of SMNN over baseline models was statistically validated using paired t-tests across folds. Let $\Delta M_i = M_i^{(\mathrm{SMNN})} - M_i^{(\mathrm{Base})}$ represent the metric difference for fold i. The test statistic is given by:

$$t = \frac{\Delta\bar{M}}{s_{\Delta M}/\sqrt{k}}, \quad s_{\Delta M} = \sqrt{\frac{1}{k-1}\sum_{i=1}^{k}(\Delta M_i - \Delta\bar{M})^2},$$

where $k = 5$ denotes the number of folds. Results confirmed that improvements in recall and F_1 were statistically significant ($p < 0.05$), indicating consistent superiority of the proposed method. The experimental analysis demonstrates that the proposed SMNN achieves stable and clinically meaningful performance improvements. Its hybrid design—combining statistical selection, HEART-based refinement, and nonlinear meta-fusion—provides an interpretable yet powerful framework for scalable cardiovascular risk prediction.

4. Discussion

Cardiovascular disease (CVD) is still one of the major global causes of death, accounting for nearly 18 million deaths each year [19]. Traditional prediction models like the Framingham Risk Score and SCORE project [5, 4] have been useful for many years, but they rely on linear assumptions that often fail to capture the complex relationships between clinical and physiological variables. With the recent growth of artificial intelligence (AI) and machine learning (ML), there has been a clear shift toward nonlinear and ensemble-based models that can better describe these intricate medical dependencies [1, 3]. Ensemble learning, and especially stacking, has shown strong ability to merge predictions from multiple algorithms to improve generalization and robustness [18, 15]. As highlighted in the comprehensive reviews by Mohammed and Kora [13] and Mahajan et al. [12], ensemble deep learning is now one of the main directions in intelligent disease prediction. Several recent studies, such as Ganie et al. [7] and Wu et al. [20], have demonstrated that combining ensemble methods with explainable AI (XAI) makes predictive systems more reliable and easier for clinicians to interpret. Similarly, Yoon and Kang [21] have shown that multimodal stacking approaches—using diverse medical data like ECG, biomarkers, and patient history—lead to more stable diagnostic outcomes. These trends align with the broader argument of Holzinger et al. [8, 9], who emphasized that medical AI should not only be accurate but also interpretable enough to earn physician trust. Following this same vision, our proposed Stacked Meta Neural Network (SMNN) incorporates both statistical and HEART-based feature refinement before nonlinear stacking, combining clinical interpretability with computational strength. The findings correspond well with those reported by Natarajan et al. [14], Kumar and Thakur [10], Sultan et al. [16], and Tiwari et al. [17], where nonlinear stacking improved recall and F1 scores more consistently than classical linear meta-fusion. In addition, the optimization-based design of Daza et al. [6] supports the idea that careful hyperparameter tuning and meta-learner selection can enhance generalization across unseen data. Our SMNN framework, through adaptive nonlinear fusion, achieved similar stability and recall improvement trends, reflecting the same robustness patterns observed in these studies. Furthermore, comparable findings by Li et al. [11] and Ashika et al. [2] reinforce that the combination of multimodal learning and explainable stacking strategies not only improves prediction accuracy but also increases clinicians' confidence in AI-based decision support systems. Taken together, these related works and our results underline that integrating explainability, medical reasoning, and nonlinear ensemble fusion is an effective pathway toward practical, trustworthy, and clinically interpretable CVD prediction systems.

5. Conclusion

In this work, we introduced a Stacked Meta Neural Network (SMNN) framework that combines statistical analysis, clinical feature refinement, and nonlinear ensemble fusion to improve cardiovascular disease prediction. The experiments showed that by using both statistically and medically validated features together with a nonlinear meta-learning layer, the model achieved better interpretability and stronger predictive performance compared to conventional methods.

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Appendix A. SMNN Workflow Diagram

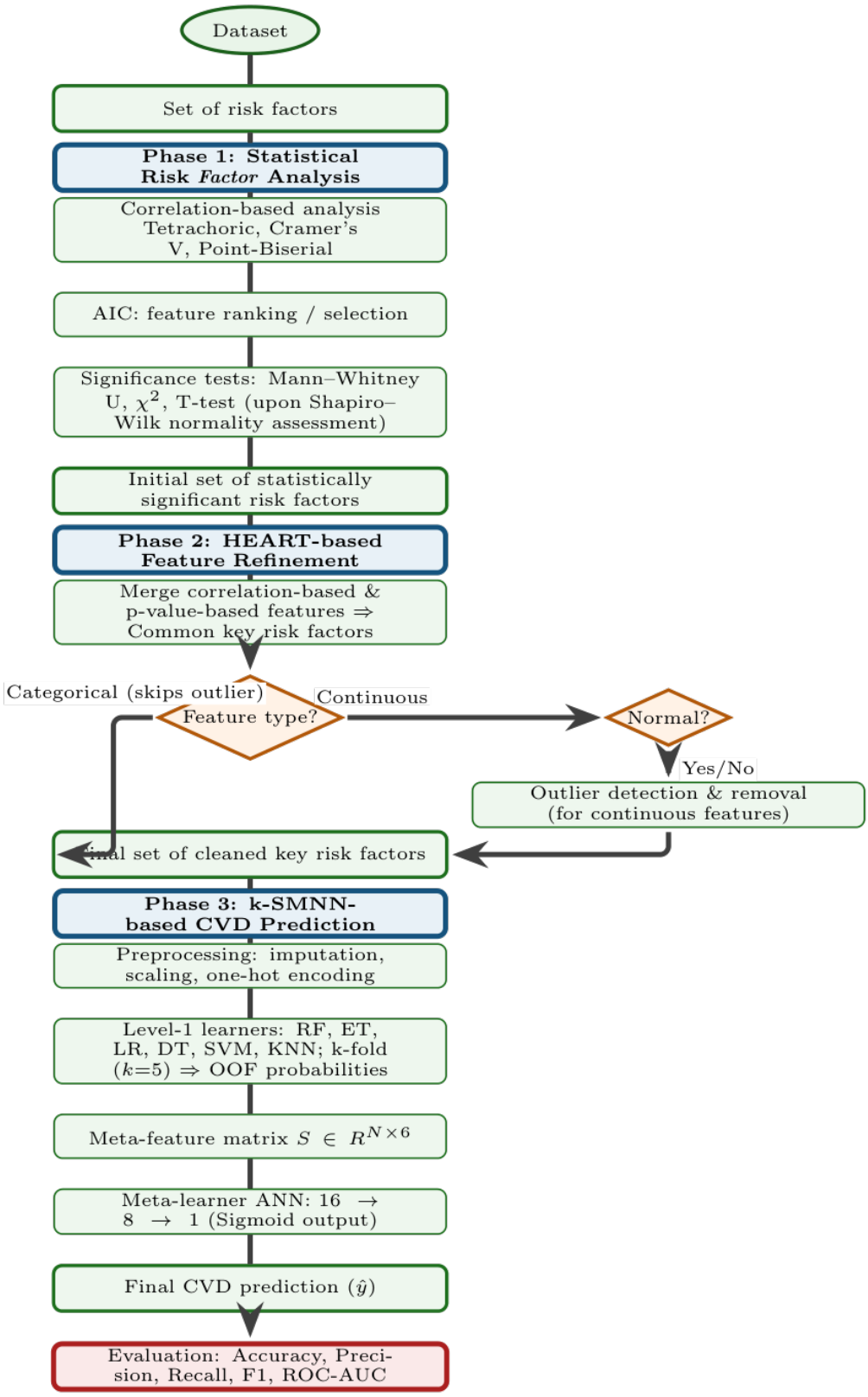

Figure 5. Three-phase workflow of the proposed SMNN framework for cardiovascular disease prediction. Phase 1 performs statistical risk factor analysis, Phase 2 applies HEART-based clinical refinement, and Phase 3 executes stacked meta-learning with nonlinear ANN-based decision fusion.

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