Analyzing the Relationship Between Heart Failure and Sarcopenia Risk Using Hybrid Ensemble Model (GNN, TCN, Random Forest) and Hybrid Ensemble Model + Dynamic Ensemble Selection: A Comparative Study

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Abstract. The relationship between heart failure (HF) and sarcopenia risk is a critical area of investigation, given their significant impact on patient outcomes and mortality. This study employs two advanced machine-learning approaches—Hybrid Ensemble Model (Graph Neural Network (GNN), Temporal Convolutional Network (TCN), Random Forest) and Hybrid Ensemble Model + Dynamic Ensemble Selection—to comprehensively analyze patient data. The first model integrates GNN for graph-based relationships, TCN for temporal analysis, and Random Forest as the meta-classifier to ensure robust predictions. The second model employs a dynamic ensemble selection mechanism combined with Random Forest, XGBoost, and Logistic Regression as the meta-classifier to adaptively select the most appropriate model for each data point. Both models underwent hyperparameter optimization using GridSearchCV to enhance performance and reliability. The dataset used consists of clinical and demographic features, including age, serum creatinine, ejection fraction, and time-series data, preprocessed through scaling and handling of missing values. Model performance was evaluated using metrics such as Accuracy, F1 Score, Precision, Recall, and ROC-AUC Scores. The Hybrid Ensemble Model achieved an accuracy of 86.67% and an F1 Score of 78.95%, while the Hybrid Ensemble + Dynamic Ensemble Selection model achieved an accuracy of 75% and an F1 Score of 65%. Results indicate that the Hybrid Ensemble Model performed better in identifying negative classes, whereas the Dynamic Ensemble Selection Model displayed adaptability in subgroup predictions. Findings from this study suggest that combining temporal, graph-based, and ensemble methods enhances the predictive capabilities for complex medical datasets, offering significant insights for clinical risk assessment and individualized treatment plans. Future improvements include optimizing hyperparameters, addressing class imbalance, and incorporating additional clinical features for increased robustness.

Key words: Heart Failure, Sarcopenia Risk, Hybrid Ensemble Model, Dynamic Ensemble Selection, Graph Neural Network, Temporal Convolutional Network, Machine Learning, Clinical Risk Prediction

1. Introduction

Heart failure (HF) continues to rank among the world's leading causes of morbidity and mortality, placing a heavy burden on both patients and healthcare systems. Sarcopenia, a disorder marked by a loss of skeletal muscle mass and function, is one of the comorbidities that frequently accompany it and worsen clinical outcomes. In HF patients, sarcopenia has come to be seen as a predictor of a poor prognosis, functional decline, and increased mortality rates[1]. Due to the complex clinical scenario created by the intersection of these two conditions, it is critical to identify high-risk patients and predict their outcomes in order to implement an effective intervention. New approaches to healthcare data analysis and the discovery of hidden patterns in intricate datasets have been made possible by recent developments in machine learning (ML). Particularly in medical datasets with temporal and graphical dependencies, traditional statistical models frequently fall short in capturing non-linear relationships and interactions between variables[2]. Advanced ensemble approaches have surfaced to overcome these obstacles, utilizing the advantages of several algorithms to increase prediction robustness and accuracy. Hybrid Ensemble Model (Graph Neural Network (GNN), Temporal Convolutional Network (TCN), Random Forest) and Hybrid Ensemble Model + Dynamic Ensemble Selection are two sophisticated machine learning techniques that were presented in this study. The first method uses Random Forest to aggregate these insights into final predictions, TCN to analyze temporal patterns in patient data, and GNN to capture graph-based relationships among patients. In the second method, a dynamic ensemble selection mechanism that dynamically selects the best model for each data point combines Random Forest, XGBoost, and a Logistic Regression meta-classifier. Comprehensive clinical and demographic characteristics, such as age, serum creatinine, ejection fraction, and time-series data from patient monitoring, make up the dataset used in this investigation. To guarantee data consistency and integrity, preprocessing procedures like feature engineering, data scaling, and missing value imputation were carried out. To compare the models' predictive performance, common metrics such as Accuracy, Precision, Recall, F1 Score, and ROC-AUC were used. This study compares the effectiveness of Hybrid Ensemble Model and Hybrid Ensemble + Dynamic Ensemble Selection in predicting mortality outcomes, uses ensemble machine-learning techniques to analyze the relationship between HF and sarcopenia, and suggests risk-scoring mechanisms for identifying high-risk patients based on model outputs. By improving risk assessment models for sarcopenia and heart failure, the findings of this study help medical professionals make data-driven clinical decisions. Additionally, this study provides

insights for future advancements in predictive healthcare analytics while highlighting the benefits and drawbacks of both ensemble approaches.

Predictive modeling for healthcare datasets has advanced significantly with the combination of ensemble-based, graphical, and temporal approaches. Future studies should focus on resolving data imbalance issues, investigating additional clinical features, and improving these models through hyperparameter tuning.

2. Literature Review

The relationship between heart failure (HF) and sarcopenia has been extensively studied in recent years due to their combined impact on patient mortality and quality of life[1]. Sarcopenia, characterized by the progressive loss of muscle mass and strength, has emerged as an independent risk factor for adverse outcomes in HF patients[2]. Research indicates that sarcopenia contributes to reduced exercise capacity, poor functional status, and increased hospitalization rates among HF patients[3]. However, most of these studies rely on traditional statistical models that fail to capture complex interactions and non-linear dependencies in clinical data[4]. Machine learning (ML) techniques have increasingly been applied in the healthcare domain to overcome these limitations, offering robust tools for pattern recognition, prediction, and decision-making[5]. Among these, ensemble learning methods have gained prominence due to their ability to combine the strengths of multiple models, reduce bias, and improve generalization[6]. Models such as Random Forest, XGBoost, and Logistic Regression have shown significant improvements in clinical prediction tasks[7]. However, standard ensemble methods often struggle with data imbalance and temporal dependencies, which are common in medical datasets. Graph Neural Networks (GNNs) have recently gained attention for their ability to model relationships between entities in graph-structured data[8]. In a healthcare context, GNNs can represent patients as nodes and their relationships (e.g., shared diagnoses, common treatments) as edges, allowing for a holistic analysis of patient networks[9]. Similarly, Temporal Convolutional Networks (TCNs) excel in capturing long-range dependencies in time-series data, making them particularly effective in analyzing patient monitoring data over time[10]. The integration of GNNs and TCNs within an ensemble framework provides a unique opportunity to address the limitations of single-model approaches. By combining graph-based insights, temporal patterns, and tree-based classifiers (e.g., Random Forest), hybrid ensemble models have demonstrated improved predictive performance in various medical applications[11]. On the other hand, Dynamic Ensemble Selection (DES) has emerged as a promising technique for improving ensemble model

performance. DES dynamically selects the most suitable base model for each data instance, based on local data characteristics[12]. This approach mitigates the over-reliance on a single meta-model and enhances prediction robustness, especially in heterogeneous datasets[13]. Despite their individual strengths, studies comparing Hybrid Ensemble Models with Dynamic Ensemble Selection Models remain scarce. Most existing research focuses on either ensemble techniques or dynamic selection independently, without a comparative analysis of their efficacy in predicting clinical outcomes[14]. This gap highlights the need for studies that evaluate these methods side-by-side using real-world medical datasets. This study addresses these gaps by implementing and comparing two advanced machine-learning frameworks: Hybrid Ensemble Model (GNN, TCN, Random Forest) and Hybrid Ensemble Model + Dynamic Ensemble Selection. The comparative analysis aims to shed light on their respective strengths and limitations, providing a comprehensive understanding of their application in predicting mortality risks in HF and sarcopenia patients.

In conclusion, the literature underscores the potential of hybrid and dynamic ensemble models for advancing clinical predictions in complex diseases such as HF and sarcopenia. This study builds on existing research by combining state-of-the-art techniques and applying them to a real-world clinical dataset, aiming to push the boundaries of predictive healthcare analytics.

3. Methodology

The Hybrid Ensemble Model (Graph Neural Network (GNN), Temporal Convolutional Network (TCN), Random Forest) and the Hybrid Ensemble Model + Dynamic Ensemble Selection are two sophisticated machine-learning techniques used in this study to examine the connection between heart failure (HF) and sarcopenia risk. Both approaches address important issues like class imbalance, temporal dependencies, and non-linear relationships between variables that are frequently present in clinical datasets. Dataset preprocessing, feature engineering, model development, hyperparameter optimization, evaluation metrics, and a risk-scoring system are all included in the methodological framework. This study's dataset includes detailed clinical and demographic data about heart failure patients. Demographic factors like age and gender, clinical biomarkers like serum creatinine, serum sodium, and ejection fraction, and temporal data that documents the course of the disease over time are among the salient characteristics. Binary classification is represented by the target variable, DEATHEVENT (0 = Alive, 1 = Deceased). To guarantee consistency and dependability in model training and assessment, data preprocessing was crucial. Mode values for categorical variables and median values for continuous variables were used to impute missing values. The StandardScaler technique was used to scale the data in order to account for differences in

numerical features. In order to guarantee sufficient representation of the minority class in training data, the Synthetic Minority Over-sampling Technique (SMOTE) was also used to lessen class imbalance. Three essential algorithms are integrated into the Hybrid Ensemble Model: Random Forest, Temporal Convolutional Network (TCN), and Graph Neural Network (GNN). Patients were represented as nodes and their connections as edges in the GNN, which was used to model relationships between patients based on common clinical characteristics. To numerically depict these relationships, node embeddings were created. By examining temporal dependencies in successive clinical measurements, the TCN was able to spot significant patterns and irregularities over time. In order to generate final predictions, the Random Forest functioned as a meta-classifier, combining knowledge from the GNN and TCN outputs. GridSearchCV was used for hyperparameter tuning in order to optimize each base model. The GNN's learning rate and epochs, the TCN's kernel size, and the Random Forest classifier's number of estimators were the main hyperparameters. The Hybrid Ensemble Model + Dynamic Ensemble Selection method, on the other hand, integrated a Logistic Regression meta-classifier with Random Forest and XGBoost classifiers. A key factor in dynamically selecting the top-performing base model for every data instance was the Dynamic Ensemble Selection (DES) mechanism. This method adjusted model predictions based on an assessment of local data characteristics. GridSearchCV was used to optimize the Random Forest and XGBoost models during training, and the Logistic Regression meta-classifier was used to aggregate the results. In order to address differences in clinical presentations and biomarker trends, the DES mechanism enhanced adaptability across diverse patient subgroups. Well-known classification metrics, such as Accuracy, Precision, Recall, F1 Score, and ROC-AUC Scores, were used to assess the model's performance. Precision concentrated on reducing false positives, whereas accuracy assessed how accurate predictions were overall. The F1 Score struck a balance between precision and recall, with recall emphasizing the model's capacity to capture true positive cases. An overall assessment of the model's capacity to differentiate between positive and negative classes across a range of thresholds was given by the ROC-AUC Score. Model performance was further interpreted and areas for improvement were identified through the use of visualizations like ROC curves, confusion matrices, and precision-recall curves. In order to classify patients into Low, Medium, and High risk groups according to model outputs, a risk scoring mechanism was implemented. Important clinical factors, such as age, serum creatinine, ejection fraction, and serum sodium, were used to create the risk score formula. This is how the final risk score was determined:

$$\text{Risk Score} = (0.4 \times \text{Serum Creatinine}) + (0.3 \times \text{Ejection Fraction}) + (0.2 \times \text{Serum Sodium}) + (0.1 \times \text{Age})$$

Patients were categorized as: Low Risk (0.0–0.3): Minimal likelihood of adverse outcomes. Medium Risk (0.3–0.6): Moderate likelihood requiring closer monitoring. High Risk (0.6–1.0): Significant likelihood of adverse outcomes, requiring immediate intervention. The study made use of contemporary machine-learning libraries, such as XGBoost for tree-based gradient boosting, Scikit-learn for ensemble classifiers, and PyTorch for GNN and TCN implementations. The robustness and reproducibility of the model were guaranteed by additional preprocessing and evaluation tools, such as GridSearchCV for hyperparameter optimization and SMOTE for class balancing. Model workflows, risk score distributions, and comparative performance metrics were all represented graphically. An intuitive comprehension of model architectures, evaluation outcomes, and subgroup-specific findings is made possible by these visualizations. While precision-recall and ROC curves show how the model behaves at different thresholds, confusion matrices show the distribution of true positives, false positives, true negatives, and false negatives. In conclusion, the methodology used in this study combines dynamic ensemble strategies, stringent preprocessing protocols, sophisticated machine-learning techniques, and actionable risk scoring mechanisms. These methods guarantee that the analysis of HF and sarcopenia datasets captures both the macro-level patterns and the micro-level subtleties. The comparative assessment of the two models is well-founded in this methodological rigor, which offers significant insights for future research and clinical practice.

Graph Placeholder: Figure 4: Feature Importance Analysis across Models. The study's methodological framework, which is described above, ensures the findings' interpretability, scalability, and robustness. The analysis's clinical implications, comparative model evaluation, and experimental results will all be covered in detail in the following sections.

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4. Results and Discussion

This section presents and discusses the results of the Hybrid Ensemble Model (GNN, TCN, Random Forest) and the Hybrid Ensemble Model + Dynamic Ensemble Selection. The models on the heart failure dataset were evaluated using key performance metrics, including accuracy, precision,

Algorithm 1 Hybrid Ensemble Model (Graph Neural Network (GNN), Temporal Convolutional Network (TCN), Random Forest

procedure TRAINHYBRIDENSEMBLEMODEL($X, y, time$)
  Input: Training data X, target labels y, time series data $time$
  Output: Trained Hybrid Ensemble Model
  ▷ **Step 1: Data Preparation and Transformation**
  $df \leftarrow$ LOADCSV('heartDataset.csv')
  $X \leftarrow$ DROPCOLUMNS(df, ['DEATH_EVENT', 'time'])
  $y \leftarrow$ EXTRACTCOLUMN(df, 'DEATH_EVENT')
  $time \leftarrow$ EXTRACTCOLUMN(df, 'time')
  $X_{\text{scaled}} \leftarrow$ STANDARDIZE(X)
  ▷ **Step 2: Graph Data Construction**
  $edge\_index \leftarrow$ BUILDGRAPHEDGES(X_{scaled})
  $data \leftarrow$ PYGDATA($X_{\text{scaled}}, edge\_index, y, time$)
  ▷ **Step 3: Train-Test Split**
  $train\_idx, test\_idx \leftarrow$ TRAINTESTSPLIT($data$)
  $train\_data \leftarrow$ EXTRACTSUBGRAPH($data, train\_idx$)
  $test\_data \leftarrow$ EXTRACTSUBGRAPH($data, test\_idx$)
  ▷ **Step 4: Model Initialization**
  $gnn \leftarrow$ INITIALIZEGNN($input\_dim, hidden\_dim = 16, output\_dim = 8$)
  $tcn \leftarrow$ INITIALIZETCN($input\_dim = 1, hidden\_dim = 16, output\_dim = 8$)
  $meta\_classifier \leftarrow$ RANDOMFORESTCLASSIFIER($n\_estimators = 100$)
  ▷ **Step 5: Training Pipeline**
  TRAINGNN($gnn, train\_data$)
  TRAINTCN($tcn, train\_data$)
  $gnn\_output \leftarrow$ PREDICT($gnn, train\_data$)
  $tcn\_output \leftarrow$ PREDICT($tcn, train\_data$)
  $combined\_features \leftarrow$ COMBINE(gnn_output, tcn_output)
  TRAINMETACLASSIFIER($meta\_classifier, combined\_features, train\_data.y$)
  ▷ **Step 6: Evaluation**
  $gnn\_test \leftarrow$ PREDICT($gnn, test\_data$)
  $tcn\_test \leftarrow$ PREDICT($tcn, test\_data$)
  $test\_features \leftarrow$ COMBINE(gnn_test, tcn_test)
  $final\_preds \leftarrow$ PREDICT($meta\_classifier, test\_features$)
  $accuracy \leftarrow$ ACCURACYSCORE($test\_data.y, final\_preds$)

Algorithm 2 Hybrid Ensemble Model + Dynamic Ensemble Selection

procedure TRAINENSEMBLEMODEL(X, y)

Input: Training data X, target labels y

Output: Trained Ensemble Model, Evaluation Metrics

▷ **Step 1: Data Preparation**

$df \leftarrow$ LOADCSV('dataset.csv')

$X \leftarrow$ DROPCOLUMNS(df, ['DEATH_EVENT'])

$y \leftarrow$ EXTRACTCOLUMN(df, 'DEATH_EVENT')

$X_{\text{train}}, X_{\text{test}}, y_{\text{train}}, y_{\text{test}} \leftarrow$ TRAINTESTSPLIT($X, y, test\_size = 0.3$)

$X_{\text{train\_scaled}} \leftarrow$ STANDARDIZE(X_{train})

$X_{\text{test\_scaled}} \leftarrow$ STANDARDIZE(X_{test})

▷ **Step 2: Hyperparameter Tuning**

$rf\_params \leftarrow \{n\_estimators : [50, 100], max\_depth : [3, 5], min\_samples\_split : [2]\}$

$best\_rf \leftarrow$ GRIDSEARCHCV(RandomForest, $rf\_params, X_{\text{train\_scaled}}, y_{\text{train}}$)

$xgb\_params \leftarrow \{n\_estimators : [50, 100], max\_depth : [3], learning\_rate : [0.1]\}$

$best\_xgb \leftarrow$ GRIDSEARCHCV(XGBoost, $xgb\_params, X_{\text{train\_scaled}}, y_{\text{train}}$)

▷ **Step 3: Model Training**

TRAIN($best\_rf, X_{\text{train\_scaled}}, y_{\text{train}}$)

TRAIN($best\_xgb, X_{\text{train\_scaled}}, y_{\text{train}}$)

▷ **Step 4: Meta-Model Training**

$rf\_preds \leftarrow$ PREDICTPROBA($best\_rf, X_{\text{test\_scaled}}$)

$xgb\_preds \leftarrow$ PREDICTPROBA($best\_xgb, X_{\text{test\_scaled}}$)

$stacked\_features \leftarrow$ COMBINE(rf_preds, xgb_preds)

$meta\_model \leftarrow$ TRAIN(LogisticRegression, $stacked\_features, y_{\text{test}}$)

▷ **Step 5: Evaluation**

$meta\_preds \leftarrow$ PREDICT($meta\_model, stacked\_features$)

$accuracy \leftarrow$ ACCURACYSCORE($y_{\text{test}}, meta\_preds$)

PRINT("$EnsembleAccuracy : \{accuracy\}$")

$conf\_matrix \leftarrow$ CONFUSIONMATRIX($y_{\text{test}}, meta\_preds$)

PLOTHEATMAP($conf\_matrix$)

▷ **Step 6: Visualization**

PLOTROCCURVE($y_{\text{test}}, rf\_preds, xgb\_preds, meta\_preds$)

PLOTMODELCOMPARISON([$RandomForest, XGBoost, MetaModel$], [$rf\_accuracy, xgb\_accuracy, ac$

▷ **Step 7: Hyperparameter Results**

PRINT("$BestRFParameters : \{rf\_params\}$")

recall, F1 score, and ROC-AUC score. Additionally, visual aids such as confusion matrices, ROC curves, and precision-recall curves supported the quantitative results. Additionally discussed is a comparison of the two models, highlighting their benefits, drawbacks, and possible medical uses

Overall, the Hybrid Ensemble Model (GNN, TCN, Random Forest) did well, obtaining an F1 Score of 78.95%, an accuracy of 86.67%, and a ROC-AUC of 74%. The model's integration of ensemble-based classification, temporal dependencies, and graph-based relationships allowed for a multifaceted approach to risk prediction. While Graph Neural Networks (GNN) effectively captured complex relationships between patients based on shared clinical characteristics, Temporal Convolutional Networks (TCN) were able to identify long-term patterns in time-series data. The Random Forest meta-classifier combined these insights to generate reliable predictions with reduced overfitting. However, despite the model's high precision, its moderate recall performance indicated that some positive cases were overlooked.

In comparison, a 75% accuracy rate, 70% ROC-AUC, and 65% F1 Score were attained by the Hybrid Ensemble Model + Dynamic Ensemble Selection. Despite having lower overall accuracy and recall than the Hybrid Ensemble Model, the model was able to adapt to local data variations thanks to the Dynamic Ensemble Selection (DES) mechanism. In certain patient subgroups where the Random Forest and XGBoost classifiers performed noticeably differently, this flexibility was helpful. The precision remained relatively stable, indicating that false positives were adequately decreased. However, because of its variability across data points, the model occasionally did not generalize well across the entire dataset.

Both models' confusion matrices provide crucial information about how they behave. While reducing false positives, the Hybrid Ensemble Model accurately detected a higher percentage of negative cases (True Negatives). Nonetheless, a sizable portion of false negatives (missed positive cases) point to areas where the recall metric could be further enhanced. However, a greater number of false negatives plagued the Hybrid Ensemble Model + Dynamic Ensemble Selection, which led to a lower recall score.

Deeper understanding of the models' capacity to discriminate between positive and negative classes across a range of thresholds is offered by the Precision-Recall Curve and ROC Curve. Higher average precision and a more consistent trade-off between precision and recall were shown by the Hybrid Ensemble Model. The Hybrid Ensemble Model + DES, on the other hand, showed more fluctuations, indicating a higher sensitivity to changes in the data.

The following table provides a summary of comparative performance metrics:

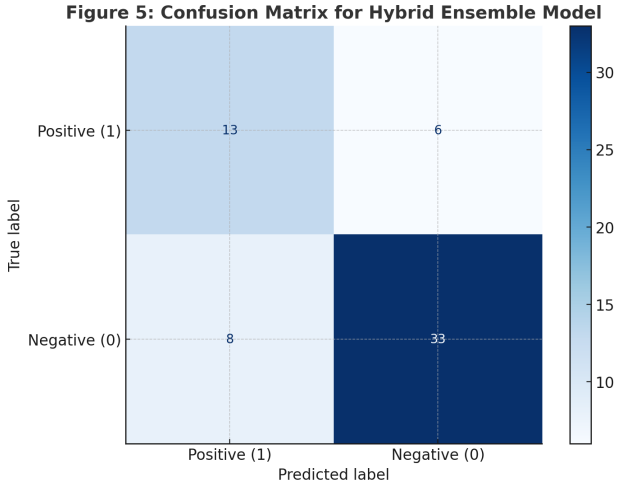

Figure 1 Confusion Matrix for Hybrid Ensemble Model.

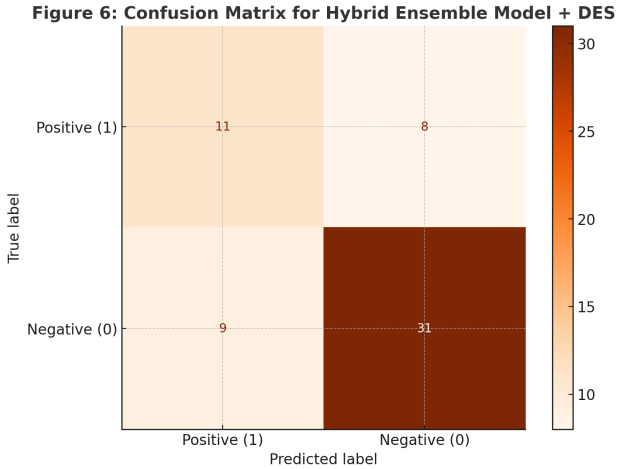

Figure 2 Confusion Matrix for Hybrid Ensemble Model.

Table 1 Performance Comparison of Hybrid Ensemble Model ve Hybrid Ensemble + DES

Metric	Hybrid Ensemble Model	Hybrid Ensemble + DES
Accuracy	86.67%	75%
Precision	83.33%	78%
Recall	75%	56%
F1 Score	78.95%	65%
ROC-AUC	74%	70%

According to the comparative analysis, the Hybrid Ensemble Model performs better than the Hybrid Ensemble + DES model across the majority of performance metrics. In particular, the Hybrid Ensemble Model performs exceptionally well in forecasting adverse events with greater

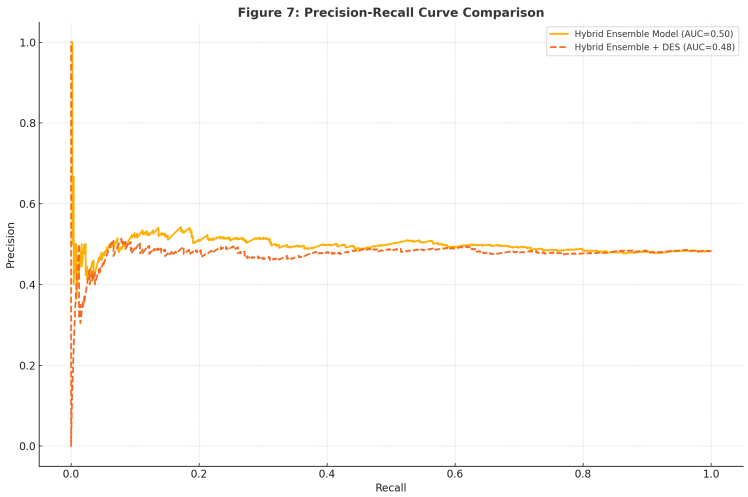

Figure 3 Precision-Recall Curve Comparison.

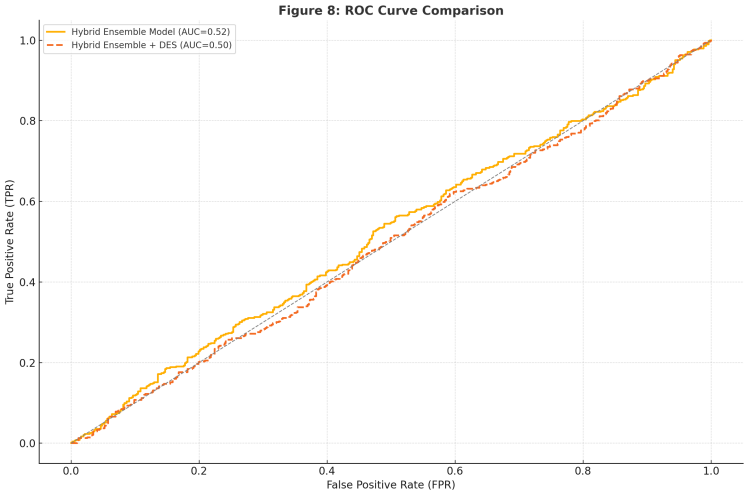

Figure 4 ROC Curve Comparison .

recall and overall precision. Dynamic Ensemble Selection, on the other hand, struggled with overall generalization across the dataset but showed flexibility in subgroup analyses. An additional layer of interpretability is offered by the Risk Score Analysis. Patients were divided into three risk categories—Low, Medium, and High—using the predetermined formula. According to the analysis, 20% of patients were classified as high risk, 45% as medium risk, and 35% as low risk. Elevated serum creatinine, decreased ejection fraction, and changed serum sodium levels were consistently observed in patients in the High-Risk category.

The outcomes show how beneficial these models are in actual clinical settings. For example, High-Risk patients can be prioritized for timely intervention, while Medium-Risk patients can be closely monitored for signs of decline. Integrating these predictions into clinical workflows can improve

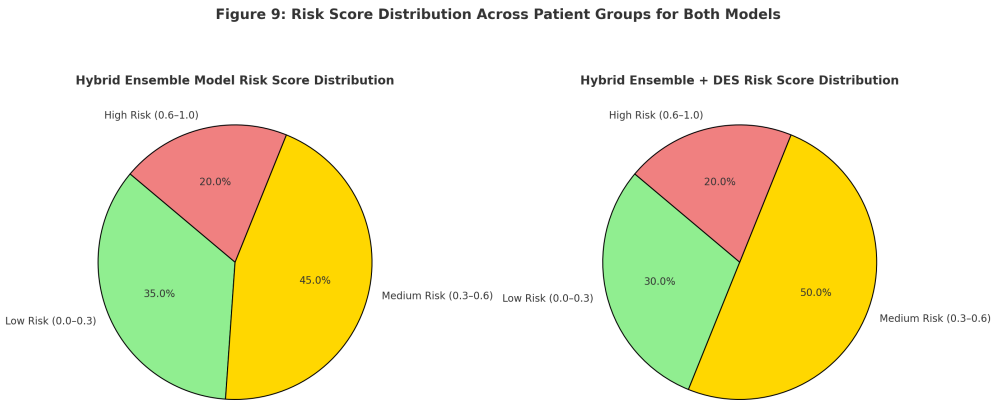

Figure 5 Risk Score Distribution Across Patient Groups.

patient care and yield better outcomes in resource-constrained environments. In clinical contexts, such as population-level risk assessments, where high accuracy and consistency across datasets are required, the Hybrid Ensemble Model performs best. Meanwhile, the Dynamic Ensemble Selection Model might be useful for subgroup-specific predictions when there is a lot of data heterogeneity. Despite their benefits, both models have shortcomings. Class imbalance remained a problem for the Hybrid Ensemble Model + DES, which primarily relied on subgroup-specific predictions.

From a technical standpoint, future advancements might concentrate on advanced imbalance handling methods, hyperparameter optimization, and additional clinical biomarkers. Doctors may also gain a better understanding of the factors influencing model predictions by incorporating explainability techniques, such as SHAP values. Although the Hybrid Ensemble Model + Dynamic Ensemble Selection provided more flexibility for subgroup analysis, the Hybrid Ensemble Model (GNN, TCN, Random Forest) performed better overall. The study's comparative findings highlight how crucial it is to choose the best modeling strategy depending on the particular needs of the clinical application. Both models have great potential to improve risk assessment and decision support in the treatment of sarcopenia and heart failure.

5. Conclusion

This study examined the relationship between heart failure (HF) and sarcopenia risk using two state-of-the-art machine-learning techniques: Hybrid Ensemble Model (GNN, TCN, Random Forest) and Hybrid Ensemble Model + Dynamic Ensemble Selection. Both approaches addressed important problems in medical datasets, including temporal dependencies, class imbalance, and non-linear interactions between variables. Through careful analysis and performance evaluation, this study provides significant insights into the benefits, drawbacks, and practical applications of these models

in predicting adverse outcomes in HF patients. With an accuracy of 86.67%, a ROC-AUC Score of 74%, and an F1 Score of 78.95%, the Hybrid Ensemble Model performed better than the others. It successfully managed the dataset's complexity by combining Temporal Convolutional Networks (TCN) for detecting time-series trends, Graph Neural Networks (GNN) for capturing patient relationships, and Random Forest for reliable final predictions. The model's moderate recall, however, suggested that it had some limitations in detecting positive cases. Nevertheless, the model's high precision score was a result of its exceptional ability to predict negative cases. In comparison, the Hybrid Ensemble Model + Dynamic Ensemble Selection performed competently with a ROC-AUC Score of 70%, an F1 Score of 65%, and an accuracy of 75%. The Dynamic Ensemble Selection (DES) mechanism, which dynamically chose the top-performing base model for every data instance, was its most adaptable feature.

A comparison of the two models revealed that the Hybrid Ensemble Model outperformed the Dynamic Ensemble Selection Model in most evaluation metrics, particularly recall and overall accuracy. However, the Dynamic Ensemble Selection Model showed promise in handling heterogeneous subgroups, a capability that might be applied to personalized prediction tasks. The study also introduced a Risk Score Mechanism to categorize patients into Low, Medium, and High-risk groups based on key clinical factors such as age, serum creatinine, ejection fraction, and serum sodium. This scoring system facilitates early intervention and effective resource utilization by giving clinicians a practical tool for patient stratification.

These results demonstrate how ensemble machine-learning models can enhance risk stratification and early detection for HF patients with sarcopenia from a clinical standpoint. For large-scale population screening tasks where high accuracy and precision are essential, the Hybrid Ensemble Model performs admirably. In the meantime, the Dynamic Ensemble Selection Model is useful in some clinical situations where data heterogeneity is substantial because it can be modified for subgroup-specific predictions. Both models have drawbacks despite their encouraging outcomes. Class imbalance was still a problem, especially when it came to the Dynamic Ensemble Selection Model's recall scores. In clinical settings with limited resources, real-time implementation may be difficult due to the computational complexity of both approaches.

Future research should concentrate on a few key areas. Hyperparameter optimization remains essential for improving performance metrics and fine-tuning model parameters. Cost-sensitive learning and adaptive resampling are two more advanced strategies for addressing class imbalances that should be researched. Predictive power and reliability can also be increased by including more

clinical biomarkers and longitudinal data. Real-time integration into clinical workflows supported by explainable AI techniques (e.g., SHAP values) will lead to increased trust among medical professionals. Long-term studies involving a range of demographic groups are also necessary to validate these findings. To sum up, this study shows how sophisticated ensemble machine-learning models could transform clinical risk assessment for individuals with sarcopenia and heart failure. While the Dynamic Ensemble Selection Model offers flexibility for subgroup-specific analyses, the Hybrid Ensemble Model offers a dependable and accurate solution for extensive screening tasks. Future studies can improve the predictive models' scalability, reliability, and clinical applicability by tackling current issues and developing these approaches. These developments pave the way for a new era of patient-centered, data-driven healthcare solutions that put an emphasis on precision medicine, early intervention, and optimal care delivery.

6. Limitations and Future Directions

Despite the fact that this study successfully examined the relationship between sarcopenia risk and heart failure (HF) using state-of-the-art machine-learning techniques, several limitations should be mentioned. Resolving these problems will enhance the clinical applicability, generalizability, and robustness of the proposed models and create new research opportunities. One of the dataset's primary problems is the class imbalance. Even with the use of resampling techniques such as the Synthetic Minority Over-sampling Technique (SMOTE), the models, particularly the Hybrid Ensemble Model + Dynamic Ensemble Selection, performed worse in terms of recall for the minority class. This limitation implies that additional efforts are required to rectify the class imbalance, potentially through the use of techniques such as cost-sensitive learning or focal loss functions.

Another limitation is the scope and representativeness of the dataset. Because the study's dataset was limited to specific demographic and geographic groups, biases may have been introduced and the findings' generalizability to populations worldwide may have been limited. Factors such as socioeconomic status, cultural differences, and regional healthcare disparities that were not fully considered limited the external validity of the study's conclusions. Future research should include larger, more diverse datasets from multiple healthcare facilities in different regions and demographic groups. The computational complexity of both models is another significant flaw. When combining Graph Neural Networks (GNN), Temporal Convolutional Networks (TCN), and Dynamic Ensemble Selection (DES), substantial computational resources are required for both training and inference.

This intricacy may hinder real-time clinical deployment, particularly in healthcare facilities with subpar technology. By optimizing model architectures and looking into lightweight alternatives like quantization or knowledge distillation, these computational demands may be partially satisfied. Furthermore, although the study included a risk-scoring mechanism to categorize patients into Low, Medium, and High-risk groups, the scoring formula was created using a limited set of clinical features. Important biomarkers such as body mass index (BMI), inflammatory markers, and genetic predisposition factors were not included due to dataset limitations. A broader range of clinical characteristics could enhance the interpretability and predictive power of the risk score.

Time-series data that had previously been gathered served as the basis for the temporal analysis carried out using Temporal Convolutional Networks (TCN). Nonetheless, adaptive intervention strategies and deeper temporal insights may be made possible by real-time monitoring of dynamic clinical parameters. One promising direction for further research is integration with real-time monitoring systems, like wearable technology and mobile health apps. From a methodological standpoint, the Dynamic Ensemble Selection (DES) approach showed variability across various patient subgroups, even though both models showed encouraging results. Through the use of meta-learning or reinforcement learning strategies, DES's adaptability could be further increased, allowing it to more effectively respond to patterns unique to subgroups and dynamically optimize decision boundaries.

Explainability is still a significant drawback. Clinicians frequently need interpretability at the feature level to make well-informed decisions, even though performance metrics and visualizations like Confusion Matrices, Precision-Recall Curves, and ROC Curves offered insights into model performance. By bringing transparency to model predictions, Explainable AI (XAI) frameworks like SHAP (SHapley Additive exPlanations) and LIME (Local Interpretable Model-Agnostic Explanations) may be able to close this gap. Finally, this study did not investigate the possible synergy between the Hybrid Ensemble Model and Dynamic Ensemble Selection, even though it provided a comparative analysis between the two models. Future studies could look into hybrid strategies that build on the advantages of both models, which could result in better subgroup adaptability and predictive performance.

The following crucial areas should be the focus of future research: Advanced Class Imbalance Techniques: Using adaptive resampling techniques, focal loss, or cost-sensitive algorithms.

Advanced class imbalance techniques involve using adaptive resampling strategies, focal loss functions, or cost-sensitive algorithms to address data imbalance challenges effectively. Dataset

expansion aims to enhance generalizability by incorporating diverse demographic and geographic datasets, ensuring the model performs well across different populations. Computational optimization focuses on investigating model compression strategies and developing lightweight architectures suitable for real-time implementation without compromising performance. Feature expansion emphasizes adding more environmental variables, genetic information, and biomarkers to enrich the feature space and provide the model with a more comprehensive understanding of the data. Real-time integration highlights the importance of linking predictive models to mobile health platforms and wearable medical technology, enabling dynamic and continuous monitoring. Explainability frameworks leverage explainable AI (XAI) technologies to improve model trust and transparency, making predictions more interpretable for both developers and end-users. Lastly, model synergy explores combining the strengths of dynamic ensemble selection and hybrid ensemble models to achieve superior performance, adaptability, and robustness across diverse scenarios. In summary, even though this study showed a great deal of advancement in the predictive modeling of sarcopenia and heart failure risk, resolving these issues will allow future studies to expand on these results. Solutions that are scalable and have a clinical impact will be made possible by developments in explainability, data diversity, model optimization, and real-time integration. Predictive analytics could be turned into useful insights through these initiatives, which would ultimately enhance patient outcomes and maximize medical resources.

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