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RESEARCH ARTICLE

Comparative Study of Machine Learning and Deep Learning Models for Early Prediction of Ovarian Cancer

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ABSTRACT Ovarian cancer remains one of the most difficult gynecological cancers to detect early, often resulting in poor survival rates. This study presents a comparative analysis of machine learning (ML) and deep learning (DL) models for the early prediction of ovarian cancer using clinical and biomarker data. The dataset undergoes comprehensive preprocessing, including handling missing values, outlier removal, normalization, and dimensionality reduction via PCA. Feature selection methods such as Feature Importance, Recursive Feature Elimination (RFE), and autoencoder-based techniques are employed to enhance model performance. Various classifiers, including KNN, SVM, Logistic Regression, Random Forest, and deep networks like ANN, FNN, CNN, and RNN, are evaluated. Ensemble models such as Bagging, AdaBoost, Stacking, and XGBoost are also implemented. Our results show that the Feedforward Neural Network (FNN), combined with autoencoder-based feature selection, achieved the highest accuracy (85.71%), indicating its potential as a reliable predictive model for ovarian cancer. This comparative study highlights the significance of integrating optimized preprocessing, feature engineering, and model selection for effective early diagnosis.

INDEX TERMS Autoencoders, data preprocessing, deep learning, ensemble learning, feature selection, machine learning, medical diagnosis, ovarian cancer.

I. INTRODUCTION

Ovarian cancer is among the most aggressive and fatal gynecological malignancies, primarily due to its asymptomatic progression in the early stages and the absence of reliable diagnostic methods for timely detection [1]. Traditional screening approaches, such as imaging techniques and biomarker-based blood tests, have limited sensitivity and specificity, often detecting the disease only in its advanced stages when treatment options are less effective [2]. Consequently, one of the main reasons behind cancer-related mortality among women is Ovarian Cancer. The critical challenge in combating this disease lies in developing early detection mechanisms that are accurate, non-invasive, and cost-effective, which could significantly improve survival rates and patient outcomes [3].

With the advent of data-driven methodologies, Machine Learning (ML) and Deep Learning (DL) have become influential tools in medical diagnostics [4]. These methods can analyze large volumes of complex data, uncovering hidden patterns and correlations that may elude traditional statistical methods. By leveraging ML and DL models, researchers aim to develop predictive models which are capable of distinguishing between benign and malignant cases with high accuracy [5]. The integration of these advanced computational techniques in ovarian cancer diagnosis presents an opportunity to enhance early detection, optimize clinical decision-making, and ultimately improve patient prognosis [3].

This study aims to develop accurate ML and DL-based models for ovarian cancer detection by optimizing feature selection, evaluating classification strategies, and identifying the most effective combination of preprocessing and modeling techniques. To achieve this, we systematically examined

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ML classifiers (KNN, SVM, LR, RF), DL models (ANN, FNN, RNN, CNN), ensemble methods (Stacking, Bagging, AdaBoost, XGBoost), and feature selection approaches including autoencoders. Our contribution lies in determining the optimal pipeline for robust prediction using clinical and biomarker data.

To accomplish these objectives, Ovarian dataset considered from the secondary source is preprocessed to ensure data quality, consistency, and reliability [6]. The preprocessing involves removing outliers, handling missing values, applying Principal Component Analysis (PCA) for dimensionality reduction, and normalizing the dataset to improve model generalization [7]. Establishing a baseline, four widely used ML classifiers—K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Logistic Regression (LR), and Random Forest (RF) are employed to assess their predictive performance [5]. Recognizing the importance of feature selection in enhancing model accuracy, four distinct techniques such as Feature Importance Graph, Recursive Feature Elimination (RFE), Univariate Selection, and Correlation Analysis are applied to select the most important features while removing redundant or irrelevant ones [8]. The baseline classifiers are then reassessed using the refined feature set to quantify improvements in predictive accuracy.

To further enhance performance, ensemble learning techniques, including Stacking, Bagging, XGBoost, and AdaBoost are incorporated [9]. These methods combine multiple models to improve generalization, mitigate overfitting, and boost classification accuracy are incorporated. Additionally, as deep learning has shown promising results in complex medical applications, the effectiveness of Artificial Neural Networks (ANN), Feedforward Neural Networks (FNN), Recurrent Neural Networks (RNN), and Convolutional Neural Networks (CNN) in detecting intricate data patterns are explored [10]. To complement traditional feature selection, an autoencoder-based feature selection, a deep learning approach that learns efficient representations of input data is also employed [6], allowing to assess its impact on classification performance.

This study systematically examines these techniques to determine the optimal combination of preprocessing, feature selection, and classification methods for ovarian cancer prediction. Successful outcomes could aid in developing more accurate, scalable, and accessible diagnostic tools, helping healthcare professionals detect ovarian cancer earlier and enhance patient survival rates.

In this paper, Section II provides detailed review of the literature, Section III provides the detailed research methodology, Section IV provides the results of algorithm implementations and analysis techniques followed by key observations and their implications for healthcare practice and Section V concludes the paper.

II. LITERATURE REVIEW

A detailed literature review is carried out to explore various techniques used in the prediction of ovarian cancer and other healthcare related dataset. Wang and Zhang compared various DL models, including ResNet, DenseNet, Vision Transformer, and Swin Transformer, against expert subjective assessments for evaluating ovarian tumor malignancy using transvaginal ultrasound. Their findings demonstrated that, except for the Vision Transformer, the models performed comparably to expert evaluations. Notably, the Swin Transformer achieved an AUC of 0.92, with a sensitivity of 87.2% and a specificity of 94.3% [11].Chen and Zhou investigated the effectiveness of ensemble learning algorithms in predicting ovarian cancer, showing that these models outperformed individual classifiers. Their research, which analyzed 49 risk factors across 349 patients, revealed that ensemble learning techniques improved AUC and accuracy by 19% and 16%, respectively [12].

Li and Wang utilized ML models to predict survival outcomes in ovarian cancer patients based on SEER database records. The Random Forest classifier achieved an accuracy of 88.72% and an AUC of 82.38%, while the XGBoost regressor attained an RMSE of 20.61% and an R^2 value of 0.4667. The study used SHAP analysis to identify crucial predictive features, such as histologic type, chemotherapy history, and tumor stage [13]. Zhang and Huang developed a predictive model using the LightGBM algorithm for early ovarian cancer diagnosis. Their model achieved an accuracy of 88% and was capable of detecting the disease approximately 17 days before clinical confirmation. The study identified key predictive features, including laboratory test results, imaging findings, demographics, and symptoms, with CA125 levels being one of the most significant indicators [14]. Huang and Liu employed the XGBoost classifier on whole-exome sequencing data from 47 ovarian cancer patients to predict driver genes associated with causative mutations. Their model achieved a classification accuracy of 94.6%, identifying 12 potential candidate genes, including LAMA3, LAMC3, COL6A1, and COL5A1, which may serve as clinical biomarkers [15].

Liu and Zhao proposed an integrated diagnostic framework combining clinical test indicators, imaging features, and genetic biomarkers using ensemble learning. Their model outperformed traditional statistical approaches, achieving an accuracy of 91.2% and demonstrating enhanced early detection capabilities [16]. Sun and Wu applied machine learning models, including Random Forest, KNN, and XGBoost, to classify ovarian cysts as benign or malignant using transvaginal ultrasound (TVUS) images. The study found that the XGBoost classifier performed best, achieving an accuracy of 94.3% and surpassing traditional radiological evaluations [17]. Yang and Chen introduced an interpretable AI framework utilizing SHAP (Shapley Additive Explanations) to identify key diagnostic features for ovarian cancer in both premenopausal and postmenopausal women. Their model achieved a diagnostic accuracy of 90.1% and highlighted age, CA125 levels, and genetic mutations as the most significant predictors [18]. Zhao and Lin integrated genomic, transcriptomic, and proteomic data

to predict chemotherapy responses in ovarian cancer patients. Their deep learning-based multi-omics model achieved an AUC of 0.85, outperforming single-modality predictive approaches [19].

Feng and Wang employed convolutional neural networks (CNNs) to analyze histopathology slides and predict ovarian cancer prognosis. Their model successfully stratified high-risk and low-risk patients, achieving a concordance index of 0.78 and identifying significant morphological features associated with survival outcomes [20]. Srinivasu et al. conducted a comprehensive review of machine learning applications in the healthcare industry, focusing on both supervised and unsupervised learning algorithms. They evaluated the performance of these algorithms in enhancing time-series healthcare metrics, with a particular focus on improving the accuracy and efficiency of heart rate data transmission. The study highlighted the potential of ML to enhance data accuracy and operational efficiency in healthcare settings [21]. Khalifa and Albadawy introduced ClinicalBench, a platform designed to compare the clinical prediction capacities of large language models (LLMs) against traditional ML models. The study evaluates predictive performance across various clinical scenarios, providing deeper insights into the strengths and limitations of various modeling approaches in healthcare, this analysis helps in understanding their effectiveness, applicability, and potential challenges in real-world medical scenarios [22]. Zhang et al. offered a comprehensive review of multimodal learning techniques in healthcare, covering various data modalities commonly utilized in clinical diagnosis. The review discussed how integrating multiple data sources can improve diagnostic accuracy and patient outcomes, while also addressing the challenges associated with multimodal data integration [23].

Ali et al. concentrated more on methods based on Explainable Artificial Intelligence (XAI) in healthcare, giving an overview on a comprehensive analysis of the existing tools and case studies. The study emphasizes the importance of interpretability in AI models to ensure transparency and trustworthiness in clinical decision-making processes [24]. Wang et al. conducted a systematic review on enhancing clinical trial outcome prediction with artificial intelligence. The study explores how AI can help in improving the accuracy in predictions of clinical trial, thereby aiding in the development of more effective therapeutic interventions [25].

The reviewed highlights how machine learning and deep learning models have significantly improved ovarian cancer prediction. Inspired by these advancements, a mix of traditional classifiers, ensemble methods, and deep learning models, ensuring both accuracy and interpretability are applied. Feature selection played a key role in refining our approach, aligning with studies that emphasize explainable AI. By integrating these techniques, this research aims to enhance early detection and support better clinical decision-making.

III. METHODOLOGY

The research methodology is meticulously structured to develop a highly efficient and accurate ovarian cancer prediction model by integrating machine learning (ML) and deep learning (DL) techniques. Given the complexity of medical data, each step in the research pipeline from data preprocessing to model evaluation is executed with precision to ensure meaningful results.

Figure 1 illustrates the step-by-step workflow followed in this study to develop an optimal ovarian cancer prediction model. The process begins with collecting raw data, which undergoes preprocessing, including handling missing values, removing outliers, applying Principal Component Analysis (PCA), and normalizing the dataset.

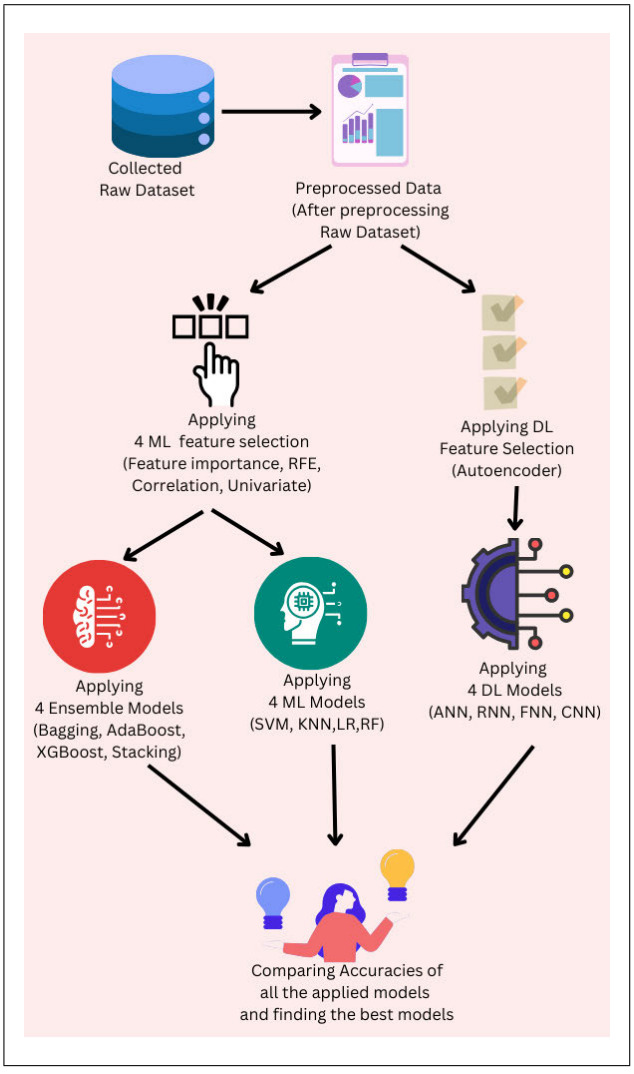

FIGURE 1. Study workflow for ovarian cancer prediction, from data preprocessing to model evaluation.

Next, four ML based feature selection techniques—Feature Importance, Recursive Feature Elimination (RFE), Correlation Analysis, and Univariate Selection—are applied

to identify the most relevant predictors. The refined dataset is then used to train four ML classifiers: Support Vector Machine (SVM), k-Nearest Neighbors (KNN), Logistic Regression (LR), and Random Forest (RF). To enhance predictive accuracy, ensemble models (Bagging, AdaBoost, XGBoost, and Stacking) are implemented.

Additionally, DL models, including ANN, FNN, RNN, and CNN, are explored. A DL based autoencoder is also used for feature selection which helps in improving the performance of classification methods. Finally, the accuracies of all models are compared to determine the best-performing approach for early ovarian cancer detection.

A. DATASET DESCRIPTION

The dataset considered in this study [26] comprises patient records with multiple clinical and biochemical features relevant to ovarian cancer diagnosis. It includes blood test parameters such as mean platelet volume (MPV), red blood cell count (RBC), hemoglobin (HGB), and white blood cell count (WBC), which provide insights into hematological conditions. Additionally, tumor markers like human epididymis protein 4 (HE4), alpha-fetoprotein (AFP) and cancer antigen 125 (CA125) are included, aiding in identifying malignancies. Metabolic indicators such as glucose, creatinine, calcium levels, and liver function enzymes further contribute to understanding patient health profiles. The dataset encompasses both pre- and post-menopausal cases, allowing for a comprehensive analysis of ovarian cancer risk factors. Given the critical nature of early detection, feature selection and model optimization play a significant role in improving predictive accuracy.

B. DATA PREPROCESSING

To ensure the reliability and accuracy of the machine learning models in prediction of ovarian cancer, a robust data preprocessing pipeline was implemented. The preprocessing steps, as illustrated in Fig 2, transformed the raw dataset into a structured and refined form suitable for classification. The major steps involved in preprocessing are as follows:

1) HANDLING MISSING VALUES

Medical datasets often have incomplete records due to data entry errors or unavailable test results [27]. Ignoring these missing values can introduce bias or reduce the sample size, which can negatively impact model performance [28]. To handle missing values, various strategies are employed depending on the proportion of missing data. There are different types of missing data: Missing Completely at Random (MCAR), which refer to a scenario where missing values occur randomly with no identifiable patterns or relationships; Missing at Random (MAR), refers when the missing value probability relies on observed data but not on the missing data itself; and Missing Not at Random (MNAR), where the missing values are influenced by unobserved data, making imputation more challenging [29].

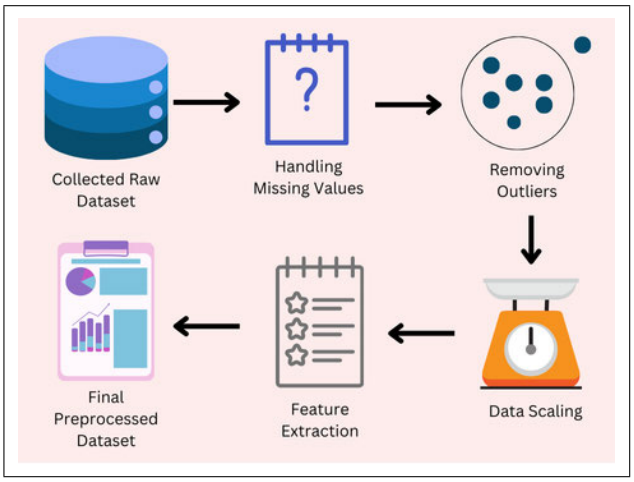

FIGURE 2. Data preprocessing pipeline.

Several methods are available for handling missing data [30]. Deletion methods involve removing rows with missing values, particularly when they are few, or removing entire columns if a significant proportion of values are missing, especially if the column is not essential for the analysis. On the other hand, imputation methods focuses on replacing all the missing values [31]. For numerical data, techniques such as mean or median imputation can be applied [32], where missing values are substituted with the mean or median of the corresponding column. Median imputation is preferred for skewed distributions. For categorical data, methods like mode imputation can be used, which uses the most frequent category to replace missing values. Methods like backward and forward fill are generally utilized in time-series data, where missing values are replaced by the last or next available value, respectively. More advanced imputation methods, like predictive imputation, models such as K-Nearest Neighbors (KNN), regression, or deep learning to calculate and fill missing values based on patterns in the data are used [33].

If the missing values themselves are significant, an indicator variable can be created, where a binary column is added to denote the presence of missing data (1 for missing and 0 for not). This can help retain the informative nature of missingness in certain situations.

In this study, median imputation was chosen because it handles missing values efficiently without being influenced by extreme values. In contrast to mean imputation, which can be distorted by outliers, the median is more robust, making it a better choice for medical datasets where some features may have skewed distributions. Deleting data is not an option since it would reduce the sample size [34], and while advanced methods like KNN or regression-based imputation could provide more precise estimates, they add unnecessary complexity [35]. Median imputation offers an optimal blend of simplicity, efficiency, and accuracy for our dataset [36].

2) REMOVING OUTLIERS

Outliers are data points that deviate considerably from the majority of the dataset [37]. They can deform statistical models, affect machine learning performance, and lead to misleading interpretations. The causes of outliers can include measurement errors, such as incorrect data entry or sensor faults, natural variations where rare but valid observations occur, and experimental errors resulting from inconsistent data collection methods [38].

There are various methods for detecting outliers. Statistical approaches such as the Z-Score method, it quantifies the number of standard deviations a value is away from the mean, with values beyond Â±3 standard deviations typically considered outliers [39]. The Interquartile Range (IQR) method detects outliers based on the 25th (Q1) and 75th (Q3) percentiles, flagging any value outside 1.5 times the IQR from Q1 or Q3 as an outlier. Visualization techniques, such as boxplots, scatter plots, and histogram or density plots, can also be used to reveal outliers by showing the distribution of data and highlighting extreme values [40]. ML based methods, like Isolation Forests, detect anomalies by isolating rare instances in a tree structure [41], while the Local Outlier Factor (LOF) method examines the density of a point relative to its neighbors [42], flagging points with lower density as outliers.

Once outliers are detected, they can be handled in various ways [43]. If an outlier is due to a clear data entry error, it can be removed. Alternatively, transformations methods, such as square root, log, or power transformations, can reduce the impact of outliers on the dataset. Capping, or Winsorization, replaces extreme values by the valid nearest values within an acceptable range [44]. Binning, which involves converting continuous variables into categorical bins, can also help mitigate the effect of outliers by grouping extreme values into broader categories.

In this study, Z-score method was selected because it's a simple and efficient way to detect outliers without over-complicating the process [45]. Since many medical features follow a normal distribution, using standard deviations to flag extreme values works well. Unlike machine learning-based methods, which require more computation, or IQR, which is better for skewed data, Z-score is straightforward and effective for our dataset.

3) NORMALIZING DATA

A crucial step in data preprocessing that ensures numerical features are scaled consistently, preventing models from being biased toward features with larger magnitudes is normalization [46]. This is especially important because some algorithms in ML, such as SVM, KNN, and Neural Networks, are responsive to the variations in the magnitudes of features [47]. When features are not normalized, those features with larger ranges can overpower the learning process, resulting in inaccurate predictions. In addition to preventing feature domination, normalization also improves the convergence of optimization algorithms, particularly those based on gradient descent, and enhances the interpretability and visualization of data, allowing better recognition of patterns.

There are several common techniques for normalizing data. Min-Max Scaling adjust the data to a predefined range, usually between [0,1] or [-1,1]. While this technique preserves the relationships between values, it can be sensitive to outliers [48]. Z-Score Standardization modifies the data to have a mean of 0 and a standard deviation of 1, making it well-suited for normally distributed data [49]. Log Transformation is often used to reduce skewness, especially in right-skewed distributions such as financial data [50]. Lastly, Robust Scaling is a method that uses the median and interquartile range for scaling, making it more resistant to outliers and providing a better fit for datasets with significant extreme values.

Choosing the right normalization technique relies on the nature of the data and the algorithms being used [50]. Min-Max Scaling is useful when the data has a known range and when algorithms like KNN or Neural Networks are being applied. Z-Score Standardization is more appropriate when the data is normally distributed and when using algorithms such as SVM or Linear Regression. For highly skewed data, like financial data, Log Transformation is often the best choice to handle extreme values and bring the data into a more manageable form.

In this study, Z-Score Standardization is implemented because it scales features consistently without being affected by outliers [49]. It works well for models like SVM and Neural Networks, which are sensitive to feature magnitudes. In contrast to Min-Max Scaling, it doesn't require a fixed range and is ideal for medical data that often follows a normal distribution, ensuring better model performance.

4) FEATURE SCALING

High-dimensional datasets often contain redundant or highly correlated features, which can increase computational complexity and negatively affect model performance [51]. To address this, Principal Component Analysis (PCA) is an effective method to reduce dimensionality while retaining essential information [52]. PCA transforms the data to a lower-dimensional space, while retaining as much variability in the data as possible [53]. This process not only improves computational efficiency but also enhances performance of the model by noise removal and prioritizing on the most important features [54].

PCA begins by identifying the features that contribute most to the variance in the data [55]. Variance indicates how spread out the data points are, and features with higher variance have a greater impact on the overall distribution of the data. These features are considered more important for capturing the underlying structure of the data. The next step involves calculating the covariance matrix, which captures the relationships between different features.

Strong correlations between features are reflected in a high covariance value, helping to identify redundant features that can be combined or removed [56].

Next, PCA does the computation of values in covariance matrix such as eigenvalues and eigenvectors [57]. The eigenvectors represent the directions of the new axes, known as principal components, in the transformed space. Eigenvalues represent the significance of each principal component, with higher eigenvalues indicating components that capture a greater portion of the data's variation. The top principal components, corresponding to the largest eigenvalues, define the new feature space [53]. Finally, the original data is mapped onto these newly defined axes, producing a lower-dimensional representation [56]. This transformation allows the dimensionality of the dataset to be reduced while maintaining most of the original variability, making the data more manageable and improving model performance.

In this study, PCA is used to reduce redundancy and focus on the most important patterns in our data. This helps improve model efficiency, speed up processing, and remove noise while retaining key information for accurate predictions [51].

C. FEATURE SELECTION

Feature selection is crucial for improving model performance, interpretability, and computational efficiency by identifying the most relevant predictors from high-dimensional datasets [58]. In this study, multiple feature selection techniques were employed to assess their impact on ovarian cancer prediction. The goal was to eliminate redundant, noisy, or irrelevant features that could degrade classifier performance or introduce bias.

1) Feature Importance Graph
   Feature importance methods from tree-based models like Random Forest (RF) and XGBoost assign importance scores based on how often a feature is used for splitting and its role in minimizing impurity (e.g., entropy or Gini impurity). This method provided an intuitive ranking of features but can be biased toward features with higher cardinality. Results were validated using other selection methods [58].
2) Recursive Feature Elimination (RFE)
   RFE is a wrapper-based technique that progressively eliminates the least important features according to classifier performance. It ensures that only the most informative features remain, but it can be computationally expensive, especially for high-dimensional datasets [59].
3) Univariate Feature Selection
   Univariate methods like ANOVA F-tests and chi-square tests measure the statistical relationship between each feature and the target variable. Features with higher significance are retained. This method is effective for filtering irrelevant features but does not account for interactions between features, which is why it was combined with other techniques [58].
4) Correlation-Based Feature Selection
   Pearson's correlation coefficient is used to eliminate highly correlated features that may lead to multicollinearity. While this method reduced redundancy, it presumes linear relationships and might fail to detect non-linear dependencies, which was addressed with other methods [58].

Each feature selection method was evaluated for its impact on classification accuracy, computational cost, and generalizability. Tree-based feature importance and RFE provided robust rankings but were computationally expensive. Univariate selection was efficient but lacked interaction detection, while correlation-based selection reduced redundancy but required threshold tuning. Combining these methods resulted in a comprehensive feature selection strategy that enhanced model performance while maintaining interpretability.

By applying these techniques before classification, the selected features were predictive and non-redundant, improving ovarian cancer prediction. The comparative analysis also highlighted the relative effectiveness of each strategy, contributing to a more optimized predictive framework.

D. ML CLASSIFICATION MODELS

ML classifiers are essential in medical diagnostics, especially for ovarian cancer prediction from high-dimensional data. In this study, K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Logistic Regression (LR), and Random Forest (RF) are implemented due to their varied mathematical foundations and generalization abilities. Each classifier is assessed based on predictive performance, robustness, and computational efficiency.

1) K-NEAREST NEIGHBORS (KNN)

KNN assigns classifications by determining the majority class among a sample's K nearest neighbors, based on the *Euclidean distance metric*.. It is *non-parametric*, making it adaptable to complex patterns. KNN's strength is in modeling *non-linear decision boundaries*, but it is *computationally inefficient* with large datasets. Optimizing K through cross-validation balances overfitting and underfitting [60].

2) SUPPORT VECTOR MACHINE (SVM)

SVM separates classes by finding an optimal *hyperplane*, using *linear* or *non-linear (RBF kernel)* approaches. It performs well on high-dimensional data and is *insensitive to overfitting* with correct hyperparameter tuning. However, training with non-linear kernels is computationally expensive, requiring careful selection of C and γ parameters to optimize performance [61].

3) LOGISTIC REGRESSION (LR)

LR predicts probabilities using the *sigmoid function*, providing useful probabilistic interpretations for medical diagnoses. It is chosen for its *efficiency, interpretability, and robustness to noise*, though it assumes *linear decision boundaries*. Feature engineering, such as polynomial transformations and

L1 (Lasso) and *L2 (Ridge)* regularization, supports to improve flexibility and prevent overfitting [61].

4) RANDOM FOREST (RF)

RF is an ensemble approach that builds multiple *decision trees* using *random feature selection* and bootstrapping, improving accuracy and generalization. RF excels at modeling complex, *non-linear relationships* and is resistant to overfitting, though it is *computationally intensive* and less interpretable than simpler models. A higher number of trees improves accuracy but also extends inference time [61].

E. ML ENSEMBLE LEARNING TECHNIQUES

Ensemble learning combines multiple classifiers to improve performance, reduce variance, and enhance generalization [62]. In this study, ensemble classifiers such as Stacking, Bagging, AdaBoost, and XGBoost are used to evaluate their effectiveness in ovarian cancer prediction, with each method optimizing performance based on dataset characteristics.

1) STACKING

Stacking combines predictions from multiple base classifiers using a higher-level meta-model. KNN, SVM, Logistic Regression, and Random Forest are used as base models, with a Logistic Regression as meta-model [63]. This method captures complementary strengths of different models, improving generalization. However, it is computationally expensive, requiring careful model selection to avoid overfitting. Cross-validation is employed to ensure the meta-model generalizes effectively.

2) BAGGING

Bagging builds multiple instances of the same classifier, where each model is trained on bootstrapped subset of data, and combines predictions by voting or averaging. Random Forest is used as an extension of Bagging with decision trees. Bagging reduces variance and enhances stability [64], making it ideal for high-variance models like decision trees. Its main drawback is increased computational complexity, which was addressed by tuning the number of base estimators.

3) AdaBoost

AdaBoost is a sequential ensemble method that focuses on misclassified samples by reweighting them in each iteration. Decision stumps are used as weak learners [65]. AdaBoost performs well on imbalanced datasets, crucial for ovarian cancer prediction, but it is sensitive to noisy data. This was mitigated by tuning the learning rate and the number of estimators to balance adaptability and avoid overfitting.

4) XGBoost

XGBoost is an advanced boosting method that incorporates *regularization* and *parallelized computation*, making it efficient for large datasets. It reduces overfitting through *L1 (Lasso)* and *L2 (Ridge)* regularization, which is vital for high-dimensional data. However, it requires careful hyperparameter tuning, such as adjusting the learning rate and tree depth. Cross-validation and grid search were employed to optimize these parameters [66].

F. AUTOENCODER-BASED FEATURE SELECTION

Autoencoders are a type of DL framework utilized for unsupervised feature learning. Input data is compressed into a lower-dimensional space (encoding), and then reconstructing it (decoding), they are able to identify and retain the most relevant features [67]. The key advantage of using autoencoders for feature selection is their ability to acquire complex, non-linear relationships within the data that traditional methods might miss [68].

In the context of ovarian cancer prediction, autoencoders are trained to learn a concise representation of the input features. Features that have contributed the most to the reconstruction accuracy are selected, while less important features are discarded. This approach not only reduces the dimensionality of the data but also helps in removing noisy or redundant features, which can improve the performance of ML models [69]. The primary benefit of using autoencoders for feature selection is their ability to retain essential patterns while ignoring irrelevant noise. However, the method requires significant computational resources and careful tuning of the architecture (like the count of hidden layers and neurons) to prevent overfitting [70]. Despite these challenges, autoencoders offer a powerful tool for extracting meaningful features from complex datasets like those used in medical diagnostics.

G. DL-BASED NEURAL NETWORKS

DL models, especially neural networks, have transformed the way of analyzing complex data, especially in fields like medical diagnostics [71], [72]. These networks comprise layers of interconnected neurons, each layer learning different patterns from the data. Depending on the current task, various types of neural networks are used. Below are some of the most popular types employed in ovarian cancer prediction:

1) ARTIFICIAL NEURAL NETWORKS (ANN)

ANNs are the foundational models in DL, influenced by the way the human brain processes information. In ANNs, each neuron in a layer is linked to all neurons in the preceding and subsequent layers, forming a dense network. ANNs are highly impactful for tasks like classification because they can recognize complex patterns in the data by modifying the connection weights between neurons during training [73]. However, they demand a large amount of data and computation to train properly, making them resource-intensive. Their ability to generalize from complex datasets makes them particularly useful for ovarian cancer prediction.

2) RECURRENT NEURAL NETWORKS (RNN)

RNNs are designed for sequence data, where the order of inputs matters, like time-series data or sequential information [74]. Unlike standard ANNs, RNNs are designed with looping connections, enabling them to retain and recall past inputs. This feature makes RNNs perfect for tasks like predicting trends or analyzing patterns in medical time-series data, such as patient health records over time. RNNs, however, can struggle with long-term dependencies and may suffer from issues like vanishing gradients, but variations like Long Short-Term Memory (LSTM) networks help overcome these challenges.

3) CONVOLUTIONAL NEURAL NETWORKS (CNN)

CNNs are specialized for analyzing spatial data, including images. By using convolutional layers, CNNs are able to automatically detect important features, like edges, shapes, and patterns, in images without manual feature extraction. In ovarian cancer prediction, CNNs can be applied to medical imaging, such as histopathological slides or MRI scans, where they can identify abnormalities or tumors with high accuracy [75], [76]. CNNs are highly effective in handling image-based data but require large datasets to train, which can be computationally expensive.

4) FEEDFORWARD NEURAL NETWORKS (FNN)

FNNs are a basic type of neural network in which information moves in a single direction, from input to output, through hidden layers. They are commonly used for simple classification tasks, where the input data is structured (e.g., numerical or categorical data) [73]. FNNs are computationally efficient and easy to implement, but they are less effective than more specialized networks like CNNs or RNNs for tasks involving complex data like images or sequences.

H. PERFORMANCE EVALUATION METRICS

Evaluating the performance of a predictive model is crucial to understanding its effectiveness in detecting ovarian cancer. In this study, accuracy is used as the primary metric to assess how well the models classify cases correctly. While accuracy provides a straightforward measure of overall correctness, it is important to interpret it carefully, especially when dealing with imbalanced datasets like ours.

I. ACCURACY

Accuracy represents the proportion of correctly classified cases out of the total instances in the dataset. It is calculated using the formula:

$$\text{Accuracy} = \frac{(T+) + (T-)}{(T+) + (T-) + (F+) + (F-)} \tag{1}$$

where: T+ (True Positives): Correctly identified ovarian cancer cases.

T− (True Negatives): Correctly identified non-cancer cases.

F+ (False Positives): Non-cancer cases misclassified as cancer.

F− (False Negatives): Cancer cases misclassified as non-cancer.

Although accuracy provides a general measure of classification performance, it may not fully capture a model's ability to distinguish between classes when the dataset is imbalanced. In medical diagnostics, minimizing false positives is crucial to preventing unnecessary treatments and reducing patient anxiety [77]. Despite these challenges, accuracy remains a fundamental metric for evaluating predictive models, particularly when combined with appropriate preprocessing techniques and model optimization strategies to enhance classification performance [76].

IV. RESULTS AND DISCUSSION

This section presents a structured analysis of the predictive models used for ovarian cancer classification. The evaluation follows a step-by-step approach, starting with baseline classifier performance, followed by the impact of data preprocessing and feature selection, a comparison of ensemble learning techniques, and finally, an assessment of deep learning models. The study provides accuracy improvements at each stage and identifies the most effective techniques for optimal performance.

To maximize model performance, hyperparameters were carefully chosen, as detailed in Table 1. SVM was configured with linear kernel to create effective decision boundaries, while KNN used three neighbors to strike a balance between bias and variance. Neural networks were trained using standardized settings for epochs and batch sizes, along with the Adam optimizer to ensure efficient learning and smooth convergence. These carefully selected parameters helped enhance the model's accuracy and reliability.

TABLE 1. Hyperparameter settings for machine learning and neural network models.

Hyperparameter	Value	Applicable Model	Description
SVM Kernel	Linear	SVM	Defines the decision boundary for SVM
KNN Neighbors	3	KNN	Number of nearest neighbor for classification
Logistic Regression Max Iterations	500	Logistic Regression	Number of base estimators
Random Forest Estimators	10	Random Forest	Number of trees in the forest
Optimizer	Adam	All Neural Networks	Optimization algorithm for weight updates
Epochs	10	All Neural Networks	Number of passes through training data
Batch Size	32	All Neural Networks	Number of samples processed at once
Loss Function	Binary Crossentropy	All Neural Networks	Loss Function for classification
Train Size	0.7	All Models	Proportion of dataset used for training
Test Size	0.3	All Models	Proportion of dataset used for testing

A. PRINCIPAL COMPONENT ANALYSIS (PCA) VARIANCE ANALYSIS

Understanding how much information each principal component retains is crucial in reducing dimensionality while preserving important patterns in the dataset. The PCA variance table provides insights into how much variance each component captures, helping us determine the optimal number of components to keep.

From our results, PC1 has the highest eigenvalue of 6.202, explaining 12.84% of the total variance. This means that PC1 holds the most significant patterns in the dataset. Following this, PC2 has an eigenvalue of 5.157, contributing 10.68% of

the variance, bringing the cumulative variance covered by the first two components to 23.51%.

TABLE 2. PCA variance table.

Principal Component	Eigenvalue	Attained Variance (%)	Cumulative Attained Variance (%)
PC1	6.202	12.84	12.84
PC2	5.157	10.68	23.51
PC3	3.464	7.17	30.69
PC4	2.775	5.74	36.43
PC5	2.699	5.59	42.02
PC6	2.314	4.79	46.81
PC7	2.167	4.49	51.30
PC8	2.037	4.21	55.52
PC9	1.783	3.69	59.21
PC10	1.686	3.49	62.70
PC11	1.425	2.95	65.65
PC12	1.358	2.81	68.46
PC13	1.250	2.58	71.05
PC14	1.180	2.44	73.50
PC15	1.131	2.34	75.84

As we move forward, we notice that the cumulative variance steadily increases with each added component. By the time we reach PC10, the dataset's explained variance rises to 62.70%. This suggests that these first ten components retain a significant portion of the dataset's structure, making them highly valuable for classification. Looking further, PC15 captures 75.84% of the cumulative variance, meaning these 15 components together retain most of the meaningful information needed for our analysis.

The cumulative variance in Table 2 confirms that the first 10 components alone account for nearly 60% of the dataset's variability, reinforcing the importance of dimensionality reduction. Components beyond this threshold contribute less variance, meaning they add minimal value to our predictive models.

By applying PCA, we successfully removed noise and irrelevant correlations, improving the overall generalization of our models. This step not only enhances computational efficiency but also ensures that our classification models focus on the most informative features, ultimately improving prediction performance.

B. CLASSIFIER PERFORMANCE EVALUATION

A direct comparison between model performance on raw and preprocessed data, as depicted in Figure 3, highlights significant shifts in classification accuracy across different machine learning models. Notably, SVM, which initially performed well with an accuracy of 83.10%, experienced a substantial drop of 25.96% after preprocessing, reducing its effectiveness. This suggests that SVM, a margin-based classifier, is highly sensitive to feature transformations, particularly scaling techniques that may alter its decision boundary.

Similarly, KNN's accuracy declined by 11.52%, from 78.87% to 67.35%, likely due to preprocessing-induced distortions in the distance metric, which is essential for nearest neighbor classification. Since KNN relies on distance calculations to classify new data points, certain preprocessing methods may have disrupted its ability to group similar instances effectively.

In contrast, Logistic Regression exhibited a notable improvement of 10.43%, increasing from 73.24% to 83.67%,

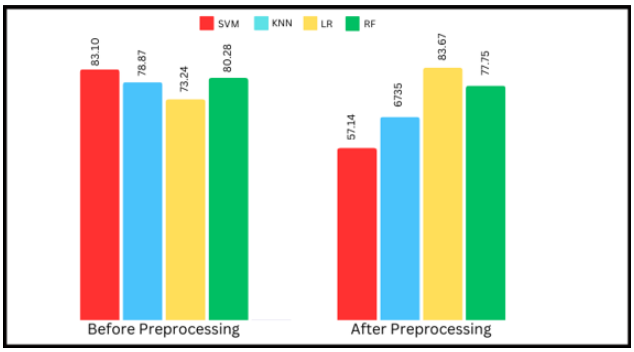

FIGURE 3. Accuracy graph for raw dataset and preprocessed dataset.

demonstrating that preprocessing can enhance the linear separability of features. The transformation of data likely refined the decision boundary, making it easier for Logistic Regression to classify data points accurately.

Random Forest, being inherently robust to feature scaling and transformations, only experienced a minor accuracy decline of 2.73%, dropping from 80.28% to 77.55%. This suggests that while preprocessing slightly altered the distribution of feature values, its impact on tree-based models remained minimal.

These findings underscore the importance of selecting preprocessing strategies based on the classifier in use. While some models, like Logistic Regression, benefit significantly from preprocessing, others, such as SVM and KNN, may require careful selection of scaling techniques to avoid performance degradation.

C. KNN ACCURACY FOR DIFFERENT k

The KNN classifier's accuracy, as shown in Figure 4, fluctuates across different values of k, demonstrating the importance of selecting an optimal neighborhood size. The highest accuracy (77.55%) was observed at k=3, indicating that smaller neighborhood sizes better capture local patterns in the dataset. However, as k increased beyond this point, accuracy showed inconsistent trends.

Notably, at k=5, accuracy dropped to 67.35%, suggesting that larger neighborhoods dilute the impact of local variations. Interestingly, at k=10, accuracy stabilized at 75.51%, showing that for certain values, the model maintains strong generalization. However, with k=15, performance declined again, reinforcing that excessively large neighborhoods lead to overly smoothed decision boundaries, reducing sensitivity to local structures.

D. EFFECT OF KERNEL SELECTION IN SVM

A comparative analysis of different SVM kernel functions reveals their impact on classification accuracy, as shown in Figure 5. The linear kernel achieved the highest accuracy of 77.55%, demonstrating that the dataset exhibits a strong linear separability. This suggests that linear SVM effectively

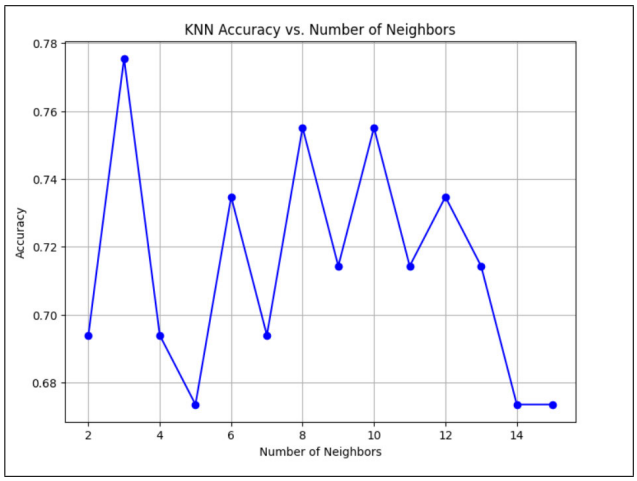

FIGURE 4. Accuracy of KNN for different values of K.

captures decision boundaries without overfitting to complex feature interactions.

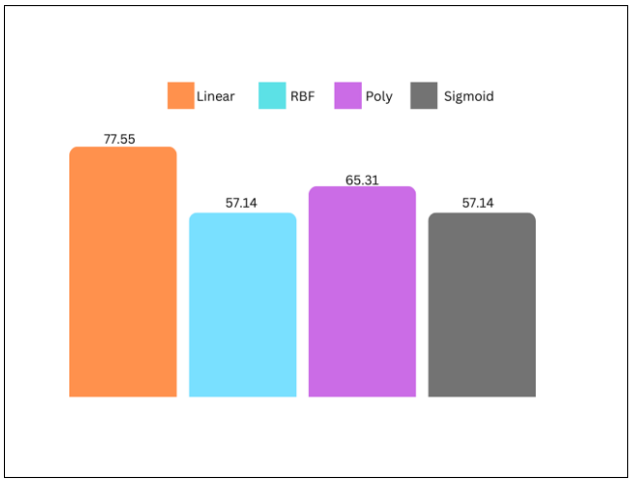

FIGURE 5. Accuracy of SVM with different kernels.

In contrast, the radial basis function (RBF) and sigmoid kernels both resulted in an accuracy of 57.14%, indicating that these non-linear transformations did not generalize well to the dataset. The polynomial kernel achieved an intermediate accuracy of 65.31%, suggesting that while some non-linearity exists in the data, excessive transformation complexity may reduce classification effectiveness. These findings emphasize the significance of choosing a suitable kernel function depending on the dataset's distribution and feature relationships, reinforcing the effectiveness of linear SVM for ovarian cancer prediction in this study.

E. FEATURE SELECTION ANALYSIS

A comparison of different feature selection techniques reveals their distinct impact on model performance, as illustrated in Figure 3. Using the Feature Importance method, SVM and Logistic Regression both achieved an accuracy of 81.63%, while KNN and Random Forest demonstrated the highest accuracy at 87.76%. This suggests that Feature Importance effectively retained key predictive features, leading to strong classifier performance. However, applying RFE resulted in a significant drop in KNN's accuracy to 63.27%, likely due to the removal of essential features affecting distance calculations. In contrast, Logistic Regression improved to 85.71%, indicating that RFE optimized the feature subset for linear classification.

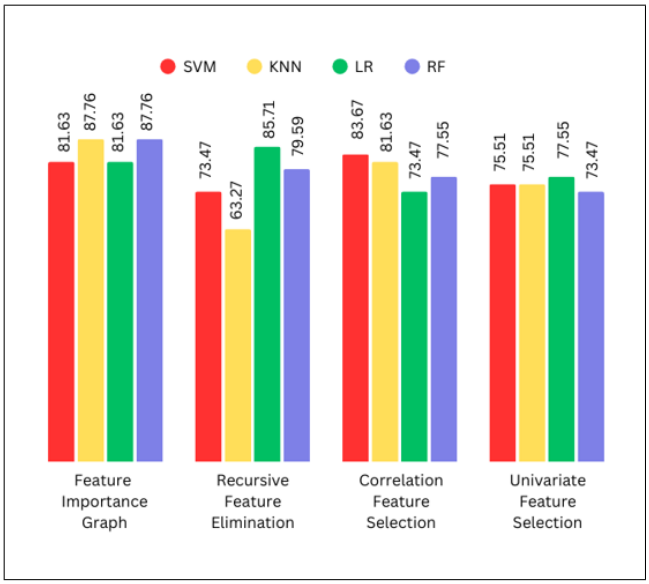

FIGURE 6. Basic classifier accuracy after feature selection.

The Correlation-based feature selection method produced stable results, with SVM reaching 83.67% accuracy, while KNN (81.63%) and Random Forest (77.55%) also maintained strong performance, suggesting that correlation-based selection preserved meaningful relationships in the dataset. In comparison, the Univariate feature selection method led to slight variations in classifier performance, with SVM and KNN both achieving 75.51% accuracy, while Logistic Regression (77.55%) and Random Forest (73.47%) exhibited minor declines. These findings, as shown in Figure 6, highlight that the choice of feature selection technique plays a crucial role in optimizing classification performance, reinforcing the need for model-specific selection strategies to enhance predictive accuracy.

F. ENSEMBLE CLASSIFIERS PERFORMANCE EVALUATION

Ensemble learning methods were applied after feature selection to improve classification performance, as illustrated in Figure 7. Among the tested feature selection techniques, RFE led to the highest accuracy across most ensemble classifiers, demonstrating its effectiveness in refining relevant features while removing redundant ones. Specifically, Bagging achieved the highest accuracy (87.51%) with

RFE, showing that the bootstrapped aggregation approach benefits from carefully selected feature subsets. Similarly, Adaboost and Stacking both performed well with RFE, each reaching an accuracy of 83.67%, reinforcing the role of adaptive boosting and meta-learning in leveraging optimal features. In contrast, XGBoost showed a lower accuracy of 71.43% with Feature Importance-based selection, indicating that its decision tree-based boosting method may not effectively utilize importance-ranked features. Additionally, when correlation-based feature selection was used, XGBoost achieved a moderate accuracy of 79.59%, suggesting that while it can leverage some statistically correlated features, it does not benefit as significantly from this approach as other classifiers.

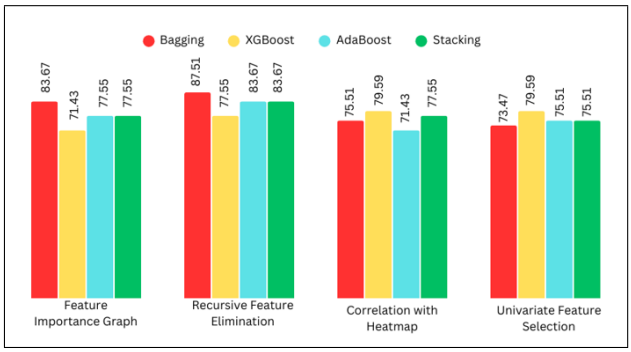

FIGURE 7. Performance of ensemble classifiers after feature selection.

The influence of different feature selection methods varied across ensemble models. For instance, Univariate selection resulted in lower performance across most classifiers, with Bagging (73.47%) and Adaboost (75.51%) performing slightly worse than their RFE-based counterparts. This suggests that filtering features based solely on their statistical significance may not capture the complex interactions that ensemble models rely on. Stacking, however, maintained relatively stable accuracy (75.51% with Univariate selection and 77.55% with Correlation selection), highlighting its ability to compensate for suboptimal feature selection by integrating multiple classifiers effectively. The performance gap across feature selection methods underscores the importance of selecting an approach tailored to the specific ensemble model. The strong performance of RFE across multiple classifiers suggests that its iterative elimination strategy is well-suited for complex ensemble learning.

Given that SVM and Logistic Regression demonstrated high accuracy in basic classification, they were selected for use in ensemble classifiers, excluding XGBoost, as shown in Figure 8. Stacking with SVM and Logistic Regression yielded the highest accuracy of 85.71% when combined with RFE, reinforcing the advantage of ensemble learning in aggregating diverse classifiers for improved generalization. Similarly, Adaboost performed well, reaching 83.67% accuracy with RFE, further demonstrating the effectiveness of boosting algorithms when applied to well-optimized feature subsets. Interestingly, Bagging recorded a lower accuracy (69.39%) with Feature Importance, indicating that bootstrapped aggregation may not be as effective when the features are selected purely based on their individual ranking rather than their contribution to model performance.

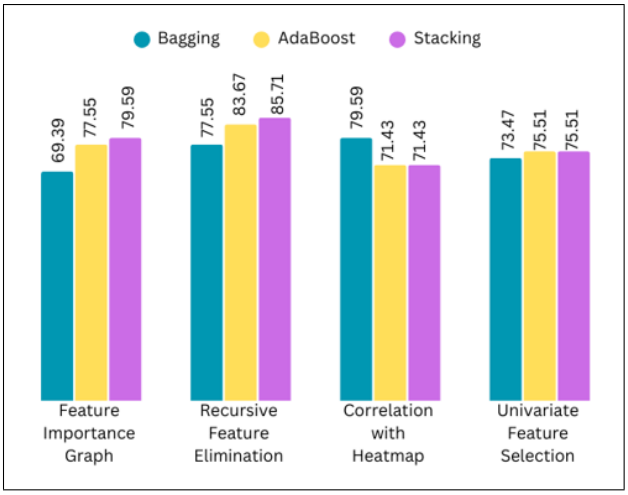

FIGURE 8. Ensemble classifier accuracy using SVM and logistic regression.

XGBoost was excluded from this specific ensemble combination, as its intrinsic feature selection capability within its gradient-boosting framework minimizes the need for additional external feature selection methods. This could explain why XGBoost's performance did not significantly improve with applied feature selection techniques. Since XGBoost inherently discards irrelevant features during training, externally applied feature selection methods may not always enhance its accuracy. The results highlight that while feature selection is essential for optimizing many ensemble models, certain algorithms like XGBoost might already be optimized to handle redundant features efficiently. The findings emphasize the need for an adaptive approach when selecting ensemble classifiers and feature selection techniques, ensuring that the combination maximizes model robustness and predictive performance for ovarian cancer classification.

G. DEEP LEARNING MODEL PERFORMANCE

Until now, we focused on ML classifiers for ovarian cancer prediction. To further enhance classification performance, we implemented deep learning models, including FNN, ANN, CNN and RNN. Their accuracy, both before and after autoencoder-based feature selection, is shown in Figure 9.

Prior to feature selection, ANN had achieved the best accuracy (81.63%) among all, followed by FNN (75.51%) and CNN (73.47%), while RNN had the lowest accuracy (48.98%). RNN's sequential nature, which makes it less useful for tabular data, is probably the cause of its poorer performance. CNN's relatively high accuracy shows that it can capture spatial and hierarchical patterns in the

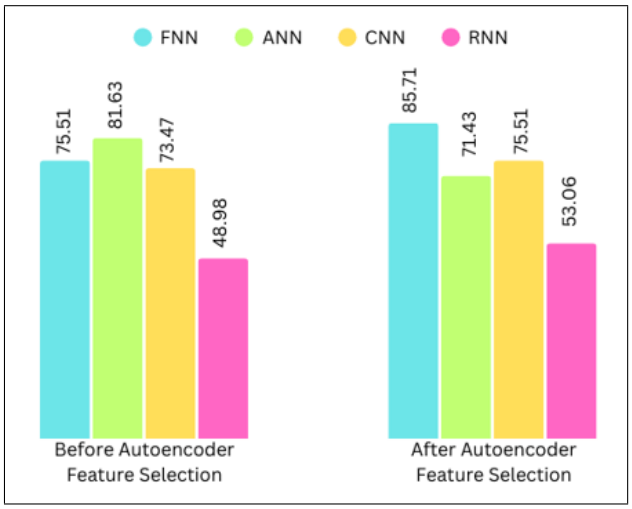

FIGURE 9. Comparison of deep learning model accuracy.

dataset, while ANN's strong performance indicates that fully connected networks can learn from raw features effectively.

Applying autoencoder-based feature selection significantly improved FNN (85.71%) and slightly boosted CNN (75.51%), confirming that reducing redundant features enhances model generalization. However, ANN's accuracy dropped to 71.43%, likely because the autoencoder removed certain features that ANN initially leveraged. RNN saw a marginal improvement to 53.06%, though it remained the weakest performer, reinforcing its limitations in structured datasets.

Overall, autoencoder-based feature selection proved beneficial, particularly for FNN and CNN, as it helped in extracting the most informative representations. However, its impact varies across models, as seen with ANN's drop in accuracy. These findings suggest that deep learning models, when optimized with proper feature selection techniques, can achieve high classification accuracy in ovarian cancer prediction [5], [9].

V. CONCLUSION AND FUTURE SCOPE

This study provides a comparative evaluation of traditional machine learning models and deep learning techniques for ovarian cancer prediction. Through extensive experimentation with preprocessing strategies, feature selection methods, and ensemble techniques, we identified that the Feedforward Neural Network (FNN) combined with autoencoder-based feature selection delivered the highest classification accuracy (85.71%). Logistic Regression and ensemble approaches like Stacking also demonstrated competitive performance. However, models such as RNN showed limited applicability to structured clinical datasets. Based on our findings, FNN is recommended for future predictive systems due to its balance of performance and computational efficiency. Future research can focus on integrating Explainable AI (XAI), expanding multimodal data inputs, and deploying these models in clinical decision support systems to enhance early diagnosis and patient care.

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