

Optimization-Based Adaptive Hybrid Biomarker Selection with Explainable Attention 1D-CNN for Early Ovarian Cancer Prediction

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Optimization-Based Adaptive Hybrid Biomarker Selection with Explainable Attention 1D-CNN for Early Ovarian Cancer Prediction

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Abstract. Precise and interpretable biomarker selection is crucial for early diagnosis of diseases and precision medicine. Nonetheless, high-dimensional biomedical datasets are characteristically having redundant, noisy, and correlated features, thereby deteriorating classification performance and interpretability. A NEW Effective Optimization-Based Adaptive Hybrid Biomarker Selection Framework (O-AHBS) Integrated with an Attention-Enhanced Multi-Scale 1D Convolutional Neural Network for Diagnosing Biological Classification in Biomedical Applications is Proposed; the method gives input to AMS-1D-CNN robustly. We propose an open-source hybrid scoring approach called O-AHBS that uniquely combines statistical feature ranking, ensemble-based feature importance, and explainability-driven inference into a comprehensive scoring system. PSO learns the weights for scoring from data itself, which allows us to choose discriminative biomarkers. An attention-boosted multi-scale 1D-CNN that emphasises clinically relevant biomarker interactions is then used to classify the chosen biomarkers. We performed stratified 10-fold cross-validation and compared the framework with XGBoost, Support Vector Machine (SVM), and Multilayer Perceptron (MLP). Evaluation was done using accuracy, precision, recall, specificity, F1-score, balanced accuracy, and ROC-AUC. Statistical significance was ensured using the Wilcoxon signed-rank and Friedman tests, while global and local interpretability were facilitated by SHAP and LIME. Comparative experimental results validate the proposed framework to deliver higher predictive accuracy, robustness, and interpretability than state-of-the-art methods, thus ensuring its potential role as an effective decision-support tool for biomarker-driven disease diagnosis.

Keywords: Ovarian Cancer, Clinical Biomarkers, Tumour Markers, Deep Learning, One-Dimensional Convolutional Neural Network (1D-CNN), Feature Selection, Explainable Artificial Intelligence (XAI), SHAP Analysis, Clinical Decision Support System

1. Introduction

Ovarian cancer (OC) is a type of aggressive gynecologic malignancy and still the highest mortality cause among the female population worldwide. The disease is often termed a "silent killer," as its earliest symptoms are non-specific and vague, leading to diagnosis in advanced stages where treatment options are limited, and survival rates are significantly decreased [1]. As per recent global cancer statistics, the prognosis of ovarian cancer is highly dependent on early detection; therefore, a clinically interpretable diagnostic approach that is reliable and accurate is in

demand. Thus, the discovery of informative biomarkers capable of discriminating malignant from non-malignant cases at an early stage has gained prominence as a key research target for precision medicine.

Most clinical diagnoses of ovarian cancer are based on a combination of serum tumour markers, laboratory blood tests and/or biochemical indicators [2], imaging methods (ultrasonography or computerised tomography), and personal clinical factors. Cancer Antigen 125 (CA125), Human Epididymis Protein 4 (HE4), Carbohydrate Antigen 19-9 (CA19-9), and Carcinoembryonic Antigen (CEA) are biomarkers that have substantial clinical importance for screening and diagnosis of ovarian cancer. Ovarian cancer, however, is a heterogeneous disease in which multiple biomarkers interact through complex nonlinear algorithms. The clinical datasets in high dimensions usually have redundant, noisy, and correlated variables, which diminish prediction performance, increase computational overheads, and impair the clinical interpretation of diagnostic models. As a consequence, identifying the most relevant biomarkers is crucial for constructing robust and reliable computer-aided diagnostic systems.

The rapid advances in artificial intelligence (AI), machine learning (ML), and deep learning (DL) have enhanced the applicability of computerised disease diagnosis through data-driven feature extraction and predictive modelling. Clinical datasets have been used by several authors with conventional machine learning algorithms (e.g., Random Forest, Support Vector Machine (SVM), Extreme Gradient Boosting (XGBoost), Extra Trees, and Multilayer Perceptron (MLP)) for ovarian cancer prediction purposes. More recently, 1D-CNNs have been shown to achieve better performance than previously common multivariable models in modelling nonlinear relationships among numerical clinical biomarkers by automatically extracting discriminative feature representations. However, existing approaches mainly use a single feature-selection method, are sensitive to redundant biomarkers (such as features that are highly correlated with each other), have limited generalisation across heterogeneous clinical data from different studies or patient populations, and lack the interpretability that clinicians need to support decision-making in practice [3-4]. The reason that motivates an expert to implement a feature selection step when analysing biomedical data is that it reduces dimensionality by selecting only relevant variables improves model generalisation, and helps to identify clinically meaningful biomarkers [5-6]. In conventional statistical ranking methods, we look at each biomarker independently, and ensemble-based approaches estimate feature importance from predictive models. Explainable artificial intelligence (XAI) approaches like SHAP provide a way to quantify the contribution of each biomarker toward model predictions and can thus reveal clinically meaningful insights in the context of disease mechanisms. Dubbed Reel, this approach would work as optimal viewpoint aggregation that fuses very different complementary feature evaluation strategies within a single optimization framework capable of adaptively gauging the relation between relative importance. This denotes the necessity of a smart biomarker [7] selection approach providing flexibility to merge multiple feature assessment measures while maintaining predictive power and clinical interpretability. In this work, we developed a new optimization-based adaptive hybrid biomarker selection framework (O-AHBS) combined with the attention-enhanced multi-scale one-dimensional convolutional neural network (AMS-1D-CNN) for ovarian cancer

classification. In this study, we introduce the O-AHBS framework, which unifies statistical feature ranking with ensemble-based feature importance and explainability-driven relevance as a hybrid scoring approach. We utilise Particle Swarm Optimisation (PSO) [8] to automatically learn optimal weighting coefficients for each feature-scoring strategy and then adaptively choose discriminative biomarkers without introducing redundant clinical variables. The proposed AMS-1D-CNN architecture then processes the selected biomarkers through data flows, utilising parallel convolutional branches with varying kernel sizes to identify complementary local feature patterns. A second layer containing an attention mechanism improves feature learning, allowing for emphasis on clinically relevant biomarker interactions while downplaying more spurious contributions.

This research paper presents a framework that also provides Explainable AI (XAI) to help increase the transparency and clinical reliability of using machine learning (ML) with model predictions to provide both global and local explanations, sourced from SHAP and LIME [9]. These explainability approaches recognise the most relevant biomarkers for ovarian cancer diagnosis, gain clinicians' trust, and assist in evidence-based medical decision-making. To this end, the proposed framework has been evaluated using stratified 10-fold cross-validation in an environment where it is compared to most machine learning and deep learning classifiers, such as XGBoost [10], SVM, and MLP (Multilayer Perceptron). Performance is measured using accuracy, precision, recall, specificity, F1-score, Matthews Correlation Coefficient (MCC), balanced accuracy [11], and ROC-AUC. In addition, Wilcoxon signed-rank and Friedman tests are used to validate statistical significance, and a systematic ablation study examines the effects of adaptive hybrid biomarker selection, multi-scale convolution, and the attention mechanism.

The main contributions of this paper can be summarised as follows:

An adaptive hybrid biomarker selection (O-AHBS) framework that integrates statistical feature ranking, ensemble feature importance, and explainability-driven relevance of features in a single optimisation-based adaptively refined process.

Adaptive weight learning based on particle swarm optimisation for identification of consistent, validated, discriminative ovarian cancer biomarkers.

Attention-enhanced multi-scale 1D convolutional neural network [12] (AMS-1D-CNN) to learn multi-scale and hierarchical representation of clinical features, enhancing clinically important biomarker interactions through attention.

Integration of Explainable Artificial Intelligence (SHAP and LIME) to enable global and local explainability, along with clinically meaningful biomarker ranking. Extensive experimental validation, including stratified 10-fold cross-validations, multiple performance metrics used for evaluation, statistical significance analysis, and comprehensive ablation studies, shows higher predictive accuracy, robustness, and interpretability compared to existing machine learning and deep learning approaches.

2 Literature Review

Piedimonte et al. (2022) conducted one of the first systematic reviews investigating the application of machine learning techniques for ovarian cancer diagnosis and prognosis. The review analysed published studies employing machine learning algorithms, including Random Forest, Support Vector Machine (SVM), Artificial

Neural Networks (ANN), logistic regression, and Extreme Gradient Boosting (XGBoost). The authors reported that most machine learning models consistently outperformed conventional statistical approaches for predicting ovarian cancer outcomes. The authors concluded that future research should focus on larger multicenter datasets, standardised validation strategies, and explainable artificial intelligence (XAI) techniques to facilitate clinical adoption [1].

Huang et al. (2023) proposed an explainable machine learning framework for ovarian cancer biomarker discovery using the PLCO ovarian biomarker dataset. The study integrated supervised machine learning with SHAP (SHapley Additive exPlanations) to identify clinically meaningful biomarkers and quantify their contribution to prediction outcomes. Their framework demonstrated that SHAP explanations were highly consistent with conventional statistical analyses while providing improved transparency and accountability. The authors highlighted that integrating explainability into biomarker discovery could significantly improve clinician confidence and facilitate translation into clinical practice [2].

Aelgani and Vadlakonda (2023) developed an explainable ensemble machine learning framework using electronic health records and clinical biomarker data collected from 349 patients with ovarian tumours. The framework evaluated multiple machine learning algorithms, including Random Forest, XGBoost, AdaBoost, and Gradient Boosting, and demonstrated that ensemble learning achieved superior predictive performance compared with individual classifiers. SHAP analysis was incorporated to explain prediction outcomes and identify the most influential biomarkers contributing to ovarian cancer classification. Although the study improved prediction accuracy and interpretability, feature selection relied primarily on conventional preprocessing techniques without adaptive optimization of biomarker importance [3].

Newaz et al. (2023) proposed an explainable machine learning framework for ovarian cancer diagnosis that combines multiple machine learning classifiers with SHAP-based interpretation. The study introduced different biomarker subsets for premenopausal and postmenopausal women, demonstrating that population-specific biomarker selection improves diagnostic performance. SHAP explanations identified the relative contribution of each biomarker, thereby improving model transparency and clinical trust [4].

Huang et al. (2024) developed OvcaFinder, an interpretable multimodal framework that integrates ultrasound images, radiologists' O-RADS scores, and routine clinical variables for ovarian cancer diagnosis. The framework combines deep learning with clinical information to improve diagnostic accuracy while maintaining interpretability. Experimental evaluation demonstrated that OvcaFinder achieved superior diagnostic performance compared with conventional deep learning and clinical prediction models, with excellent generalization on both internal and external validation cohorts. [5].

Ucuzal and Kivrak (2025) proposed an explainable artificial intelligence framework for discriminating malignant and benign ovarian masses using routine demographic information, haematological indices, tumour markers, liver function tests, and biochemical laboratory parameters collected from 309 patients. The Boruta feature selection algorithm identified 19 significant biomarkers, after which five ensemble machine learning algorithms were evaluated using repeated stratified cross-

validation. Gradient boosting achieved the best overall performance with approximately 89% accuracy and an AUC-ROC of 0.934. SHAP analysis identified HE4, CA125, CEA, globulin, and age as the most influential predictors. Despite its strong explainability, the framework relies on a single feature-selection algorithm and does not incorporate adaptive hybrid optimization [6].

Kucukakcali et al. (2025) introduced an explainable machine learning framework for the early clinical detection of ovarian cancer using demographic variables and routine laboratory biomarkers. Unlike conventional explainability methods, the study employed the Contrastive Explanation Method (CEM) to improve transparency by explaining why individual predictions differed from alternative diagnostic outcomes. The proposed framework improved clinician interpretability and demonstrated promising diagnostic capability. However, the study employed conventional machine learning classifiers and did not explore deep learning architectures, adaptive feature weighting or multi-scale feature extraction mechanisms [7].

Chekini et al. (2025) developed a machine learning and explainable AI framework for identifying novel biomarkers associated with epithelial ovarian cancer using transcriptomic (RNA-seq) data. Multiple machine learning and deep learning models were trained for stage-specific ovarian cancer prediction, while SHAP analysis was employed to identify biologically significant hub genes. Experimental validation using patient tissue and peripheral blood samples confirmed several important biomarkers involved in estrogen signalling, vesicle trafficking, and cell-cycle regulation. Although the study successfully integrated machine learning with molecular validation, it focused primarily on genomic biomarkers rather than structured hospital-based clinical biomarker datasets [8-9]

Machine-Learning-Assisted Clinical Biomarker Analysis (2025)

Recent work on machine-learning-assisted analysis of patient clinical biomarkers investigated multiple machine learning algorithms for improving ovarian cancer diagnosis using routine clinical laboratory measurements. The study demonstrated that combining multiple blood biomarkers with advanced machine learning significantly improved diagnostic performance compared with conventional statistical models. Feature importance analysis identified clinically meaningful biomarkers contributing to disease prediction and highlighted the importance of integrating heterogeneous laboratory information for early diagnosis [10-11]

Table 1. Comparative Analysis of Recent Studies on Ovarian Cancer Prediction Using Clinical Biomarkers (2022–2025)

Ref	Dataset	Feature Selection	Classification Model	Explainability	Major Limitation
[1]	Multiple datasets (systematic review)	Various	Various ML Models	No	Review paper; no unified framework
[2]	PLCO Ovarian Biomarker Dataset	SHAP Biomarker Ranking	XGBoost	SHAP	No adaptive feature optimization (cdas.cancer.gov)

[3]	Electronic Health Records	Ensemble Feature Selection	Ensemble ML	SHAP	Fixed feature weighting
[4].	Clinical Ovarian Dataset	Biomarker Selection	Explainable Ensemble ML	SHAP	No optimization-based biomarker fusion (arXiv)
[5]	Multiple Public Datasets	Various	Deep Learning Models	Partial	Systematic review only
[6]	Multimodal Clinical Dataset	Integrated Multimodal Features	Gradient Boosting Ensemble	SHAP	Limited adaptive optimization (PMC)
[7]	Hospital Clinical Biomarkers	Boruta	Gradient Boosting	SHAP + LIME	Single feature-selection strategy (PMC)
[8]	Hospital Clinical Dataset	Embedded Selection	Explainable ML	Contrastive Explanations	No adaptive hybrid biomarker selection (MDPI)
[9]	Gene Expression Dataset	ML-Based Biomarker Discovery	Machine Learning	XAI	Genomic data only
[10]	Clinical Biomarker Dataset	Biomarker Analysis	Machine Learning	Partial	Limited explainability

3. Proposed Methodology

3.1 Global Structure of the O-AHBS-AMS-1D-CNN

This study proposes a new optimization-based adaptive hybrid biomarker selection and attention-enhanced multi-scale one-dimensional convolutional neural network (O-AHBS-AMS-1D-CNN) framework to solve the challenges of high-dimensional clinical data, redundant biomarkers, nonlinear feature interactions, and weak interpretability in ovarian cancer diagnosis [12]. Compared with the traditional machine learning analysis framework, which employs a single feature selection technique and an independent classifier, the proposed method integrates optimization of both feature selection and classification into one procedure to achieve increased prediction accuracy, model robustness, and clinically interpreted properties [13].

What sets the proposed framework apart is its ability to incorporate advanced biomarker ranking methods using an optimization-based adaptive weighting approach. Instead of treating every feature selection algorithm equally, we propose a PSO-based framework that finds the best importance of each method [14]. Thus, the selected biomarker subset is statistically significant and optimized with respect to the target classification. With an eye towards minimization of feature redundancy, our adaptive optimization dramatically decreases the number of features while preserving clinically significant biomarkers useful for prediction of ovarian cancer [15]. We have developed the Optimization-Based Adaptive Hybrid Biomarker Selection and Attention-Enhanced Multi-Scale One-Dimensional

Convolutional Neural Network (O-AHBS–AMS-1D-CNN) framework to identify an accurate, reliable, and interpretable solution for predicting ovarian cancer using multidimensional clinical biomarker data. This framework combines adaptive hybrid biomarker selection, optimization-based feature weighting, multi-scale feature extraction, attention-guided representation learning, and explainable artificial intelligence (XAI) into a single end-to-end diagnostic framework compared to conventional machine learning [16] approaches that either rely on one feature-selection strategy or use a common deep learning classifier. Through integration, it automatically identified the most discriminative clinical biomarkers, learned non-linear correlations between the model, and aimed to use its predictive ability to guide clinical interpretability [17].

The overall architecture of the proposed framework is composed of nine consecutive stages: (i) clinical data acquisition; (ii) data preprocessing; (iii) Optimization-Based Adaptive Hybrid Biomarker Selection(O-AHBS); (iv) Pso-based strategy-weighted optimization; (v) hybrid score fusion & biomarker selection; (vi) Attention-enhanced Multi-Scale One-Dimensional Convolutional Neural Network(AMS-1D-CNN); (vii)Explainability (XAI); (viii)Clinical decision support; (ix) Model evaluation and validation.

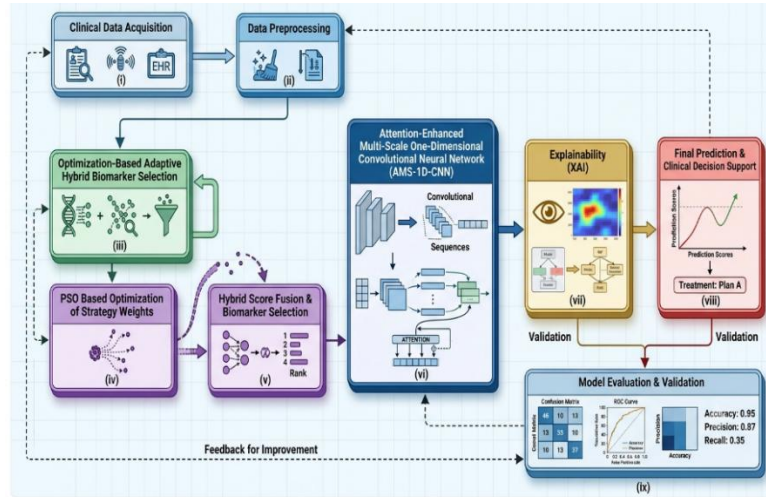


Fig. 1. Flow chart of the proposed system.

3.2 Clinical Dataset Description

The effectiveness of any computer-aided diagnosis (CAD) system is quite reliant on the content, variety, and quality of the clinical dataset used to create a model. A novel Optimization-Based Adaptive Hybrid Biomarker Selection (O-AHBS) method combined with the proposed Attention-Enhanced Multi-Scale 1D Convolutional Neural Network (AMS-1D-CNN) was developed and validated on a multi-dimensional clinical dataset of ovarian cancer [18]. Data are routinely collected for

haematological measures, biochemical parameters, tumour biomarkers and demographic characteristics after the diagnosis of ovarian cancer. This proposed approach aims to combine heterogeneous clinical characteristics into a single analysis framework, carefully distinguishing between ovarian cancer and non-cancer subjects as well as identifying the clinically most relevant signals.

The data set for this study was downloaded from a publicly available ovarian cancer dataset in the Kaggle repository [18]. Ovarian cancer dataset for classification which includes anonymised clinical and biomarker-related data. The authors did not collect any patient data prospectively or directly; they also did not create a clinical cohort at their institution for this study. The dataset was public, and we only used it for secondary analysis in relation to biomarker selection, model building, validation and performance evaluation.

In comparison to imaging-based datasets, clinical biomarker datasets are generally structured numerical variables that describe the physiology and biochemistry of a patient. These factors provide crucial data to help in the diagnosis of organ function, inflammatory response, and metabolic problems as well as tumour growth. Unfortunately, clinical datasets often display important aspects such as high complexity, duplicate variables, missing observations and non-linear correlation between biomarkers. Such characteristics make predictive modelling harder, and thus you need even more powerful preprocessing and adaptively selected features.[19]

Mathematical Representation of Clinical Dataset

Let the ovarian cancer clinical dataset be represented as

$$D = \{(X_i, y_i)\}_{i=1}^N \quad (1)$$

where: N = total number of patients,

X_i = feature vector of the i^{th} patient,

y_i = class label.

The feature vector is defined as

$$X_i = [x_{i1}, x_{i2}, x_{i3}, \dots, x_{im}] \quad (2)$$

where m denotes the total number of clinical biomarkers and patient attributes.

Table 2. Summary of the Clinical Dataset Used for Ovarian Cancer Prediction

Category	Description	Examples
Dataset Type	Structured clinical biomarker dataset	Tabular numerical data
Prediction Task	Binary classification	Ovarian Cancer (1), non-Cancer (0)
Patient Information	Demographic characteristics	Age, menopausal status*
Tumor Biomarkers	Cancer-associated serum markers	CA125, HE4, CA19-9, CEA
Hematological Parameters	Complete blood count measurements	HGB, WBC, RBC, PLT, Neutrophils, Lymphocytes
Biochemical Parameters	Routine laboratory measurements	Albumin, Total Protein, Creatinine, ALT, AST, ALP, Urea, Glucose*

Data Quality Processing	Data cleaning	Missing-value imputation, duplicate removal, outlier handling
Normalization	Feature scaling	Min-Max normalization
Feature Selection	Proposed O-AHBS	Statistical ranking + Ensemble importance + SHAP relevance + PSO optimisation
Classification Model	Proposed deep learning model	AMS-1D-CNN
Validation Strategy	Performance estimation	Stratified 10-fold cross-validation

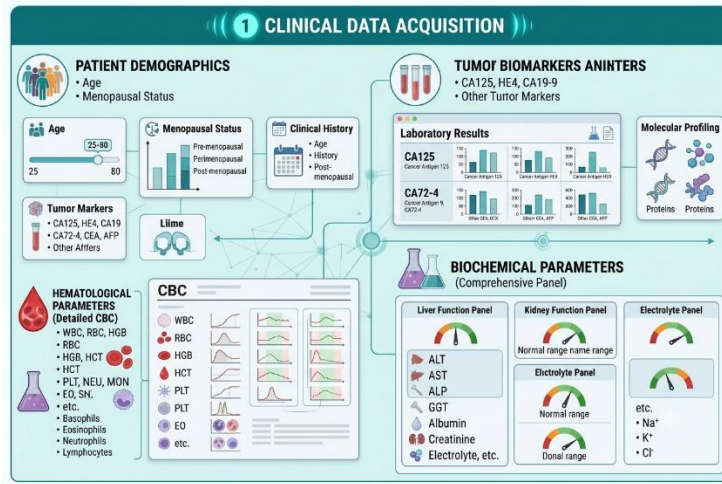


Fig 2. Proposed Clinical Decision Support System for Ovarian Cancer Diagnosis.

The dataset used in this investigation contains records from two diagnostic categories: ovarian cancer patients (positive class) and non-cancer participants (negative class). For each patient, various clinical features derived from routine laboratory tests and cancer marker studies are available. Target variable: 1 for ovarian cancer and 0 for not having it, which is the diagnostic result. This binary classification framework facilitates the development of an automated decision-support system for early diagnosis of diseases [20].

The collected clinical variables can be categorised into four main categories: Demographic Characteristics: These comprise patient-specific variables, such as age and other relevant demographic characteristics that may influence disease onset and progression. Tumour Biomarkers: This is one of the most helpful feature classes used during the diagnosis of ovarian cancer. Biomarkers such as Human Epididymis Protein 4 (HE4) and Cancer Antigen 125 (CA125) are recognised to be some of the important biomarkers of ovarian cancer. Some other biomarkers that can offer

additional diagnostic information related to the underlying biology of tumours include Carbohydrate Antigen 19-9 (CA19-9) and Carcinoembryonic Antigen (CEA). Conventional Haematological Parameters: The measurements of complete blood count (CBC), including haemoglobin (HGB), white blood cells and differentiated WBC counts, platelet count (PLT), red blood cells, neutrophil cell number, lymphocyte cell number and other relevant haematology indices provide indirect evidence of immune response and inflammation or systemic immunophysiological changes associated with cancer progression[21].

3.2.1 Ethics Statement

A secondary analysis of an open-access dataset obtained from the Kaggle retrieval site was performed. This study did not recruit participants, biosamples or identifiable personal information from the authors directly. The data set was de-identified and incorporated into a publicly available repository for use in our analyses. This study was restricted to secondary analysis of a publicly available dataset, and the authors did not directly interact with human participants or collect new human-subject data.

3.3 Data Preprocessing

This preprocessing framework is unique as it encompasses six interconnected processes: data quality assessment, missing value imputation, removal of duplicate records and inconsistencies, outlier detection and treatment, normalisation-encoding, and class imbalance handling. Establish the complete preprocessing of both these processes as shown in Fig. 3.

In the first preprocessing phase, missing clinical values, contradictory observations, and duplicate patient records are detected. Either inconsistent records are removed or improved as per certain quality-control measures defined beforehand, and duplicate entries are removed to avoid unnecessary information. Imputation methods, which can restore any salient patient information while minimising the introduction of systematic bias, are employed to address missing data. All number-based characteristics are subsequently standardised via min-max normalisation to ensure uniform contributions from every biomarker during model training, regardless of the values derived from their measurement scale. [21]

3.3.1 Evaluation of Data Quality

First, we inspect the ovarian cancer clinical dataset for completeness, consistency and reliability. Each patient record is checked for inconsistent clinical data, clearly wrong feature values, unobserved features and duplicate records.

Let the raw clinical dataset be represented as

$$\mathcal{D} = \{(\mathbf{x}_i, y_i)\}_{i=1}^N \quad (3)$$

where

N denotes the number of patient records,

$\mathbf{x}_i = [x_{i1}, x_{i2}, \dots, x_{im}]$ represents the clinical biomarker vector,

m is the total number of features,

$y_i \in \{0,1\}$ denotes the class label.

The dataset is evaluated according to four quality indicators.

$$Q = \{Q_{\text{miss}}, Q_{\text{dup}}, Q_{\text{out}}, Q_{\text{cons}}\} \quad (4)$$

Where Q_{miss} : Missing-value ratio

Q_{dup} : Duplicate records

Q_{out} : Outliers

Q_{cons} : Clinical consistency

The missing-value ratio of feature j is

$$MR_j = \frac{N_j^{\text{miss}}}{N} \quad (5)$$

Where N_j^{miss} = number of missing observations.

Overall dataset completeness becomes

$$C = 1 - \frac{\sum_{j=1}^m N_j^{\text{miss}}}{Nm} \quad (6)$$

Min-Max Normalization

To eliminate scale variations among biomarkers, min-max normalization is applied:

$$x'_{ij} = \frac{x_{ij} - x_j^{\min}}{x_j^{\max} - x_j^{\min}} \quad (7)$$

Where $x_j^{\min}$ = minimum value of feature j

$x_j^{\max}$ = maximum value of feature j

Thus, $0 \leq x'_{ij} \leq 1$ for all normalized features.

Categorical Encoding

Categorical variables are transformed into numerical representations:

Label Encoding:

$$C = \{c_1, c_2, \dots, c_k\} \quad (8)$$

$$ic_i \rightarrow i$$

or One-Hot Encoding:

$$c_i = [0, 0, \dots, 1, \dots, 0] \quad (9)$$

where the position of 1 indicates the category index.

Class Imbalance Measurement

Let N_{pos} denote ovarian cancer cases and

N_{neg} denote non-cancer cases.

The imbalance ratio is

$$IR = \frac{\max(N_{\text{pos}}, N_{\text{neg}})}{\min(N_{\text{pos}}, N_{\text{neg}})} \quad (10)$$

An ideal balanced dataset satisfies.

$$IR \approx 1$$

These are categorical variables and are encoded into numerical representations, which deep learning algorithms can process.

Another crucial characteristic of biomedical datasets is class imbalance, where the discrepancy in numbers between positive and negative cases can be quite large [22].

This imbalance can potentially bias the learning towards information from the majority class, leading to poor sensitivity for minority-class prediction. To resolve this problem, appropriate resampling methods are applied whenever required to balance class distribution and improve the performance of the model in correctly identifying ovarian cancer patients.

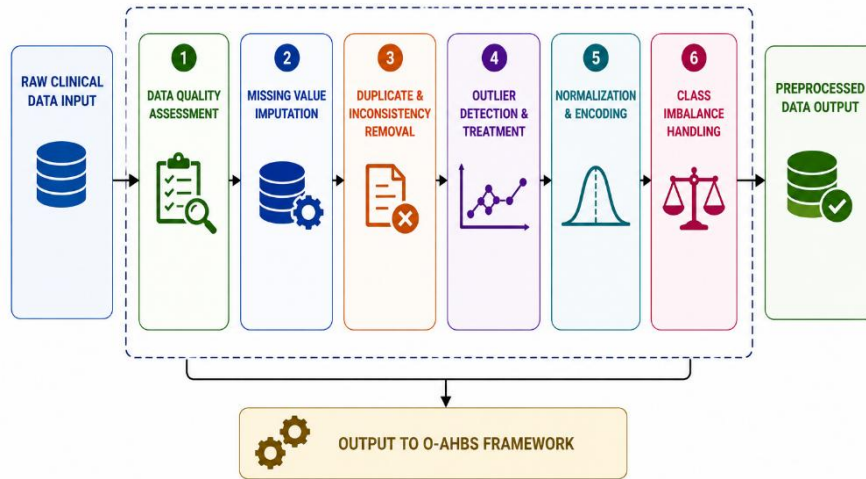


Figure 3. 3 Data Preprocessing Pipeline of the O-AHBS Framework for Ovarian Cancer Biomarker Analysis.

3.4 Optimization-Based Adaptive Hybrid Biomarker Selection (O-AHBS)

One major challenge in clinical data analysis is the representation of high-dimensional biological data, which is why feature selection is performed at an early stage. Normally, clinical datasets contain a diverse number of characteristics such as biochemical, histological and tumor markers. However, most of these features are noisy, redundant or only weakly informative. Collinearity and irrelevant variables increase the computational burden while reducing generalizability and fostering over-fitting of predictive models, meaning that their classification performance is compromised. While many markers correlate with the progression of ovarian cancer, very few have diagnostic utility. It is therefore important to discover the most informative biomarkers in order to improve predictive power and clinical reliability of decision-support systems, while keeping them simple.[8]

Traditional feature selection techniques can generally be divided into statistical, wrapper, embedding and optimisation-based approaches. Wrapper methods determine the best feature subsets using a classifier performance metric, and statistical techniques like ANOVA, Chi-square analysis, and Mutual Information analyse

features independently of their discriminative capacity. Embedded approaches perform feature selection as part of the model training process. Although these methods have been found useful in biological applications, reliance on a single evaluation criterion may exclude complementary and diagnostically beneficial biomarkers while keeping redundant or clinically unimportant features[8].

To address these issues, this paper proposes an Optimization-based Adaptive Hybrid Biomarker Selection (O-AHBS) framework that integrates multiple feature evaluation methods with an adaptive optimization model. O-AHBS features a comprehensive evaluation of biomarker importance using statistical feature ranking, ensemble-based feature importance, and feature relevance derived using SHAP. The benefit of using these methods collectively is that the feature selection quality will be improved and subsequently the predictive performance of the downstream AMS-1D-CNN model by having identified a more useful and clinically relevant biomarker subset for prediction [9].

Unlike general hybrid feature-selection methods, where many approaches apply fixed weights (instead of adaptive ones) to different high-saving-rate feature scores with some specific sizes, the suggested O-AHBS framework [12] applies particle swarm optimization (PSO) for adaptively learning how much weight each feature evaluation strategy should be given as weighing coefficients or resistors. PSO focuses on optimizing the combination of weights which achieves minimum repetition while maximizing classifier performance. The optimized hybrid scores are used to rank all the biomarkers, and only the most discriminative ones for classification. This adaptive optimization technique, aside from lessening the computational burden, also facilitates automatic selection of clinically relevant biomarkers, thus providing some dimensionality reduction.[14]

This biomarker subset is then input into the proposed attention-enhanced multi-scale one-dimensional convolutional neural network (AMS-1D-CNN) for automated feature learning and ovarian cancer classification. The O-AHBS framework, designed to score all features based on their causal inference stages, integrates highly informative biomarkers into predictive clinical applications by pruning less informative features and augmenting the deep neural network's learning capacity, model generalization, and diagnostic accuracy. Moreover, with its goal of delivering interpretable biomarker rankings that assist clinical decision making, SHAP attached to the feature-selection framework can also enhance model interpretability. Thus, using the proposed O-AHBS framework, a strong optimization-based interpretability-driven biomarker selection method might be developed for personalized diagnosis of ovarian cancers.[15]

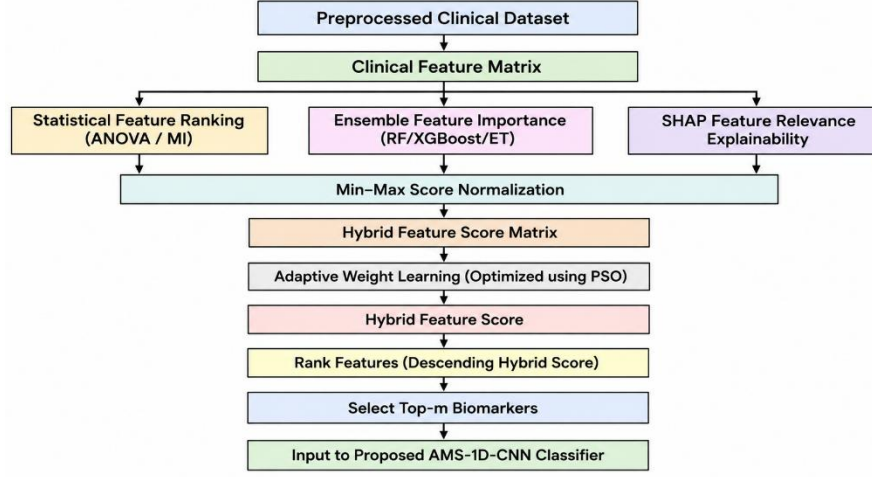


Figure 4. Mathematical workflow of the proposed Optimization-Based Adaptive Hybrid Biomarker Selection (O-AHBS) framework.

3.5 PSO-Based Optimization of Strategy Weights

The application of various feature evaluation methods greatly influences the performance of hybrid biomarker selection. Usually, traditional hybrid feature selection approaches implicitly consider that every method of ranking each feature contributes the same to biomarker discrimination by assigning fixed or empirically determined weights for each technique. Nevertheless, fixed weighting methods are generally not appropriate for complex biomedical prediction problems because their importance varies from clinical dataset to clinical dataset.[13].

This study aims to overcome the limitations of traditional feature selection methods by proposing an Optimization-Based Adaptive Hybrid Biomarker Selection (O-AHBS) framework (Fig. 5) learning method; 2) a hybrid approach that uses Particle Swarm Optimization (PSO) to adaptively learn appropriate weights for multiple feature-ranking strategies. The pre-processed dataset and clinical data are used for four complementary analysis: Correlation Analysis (CA), Mutual Information (MI), XGBoost Feature Importance (XFI), and SHAP Feature Relevance. – Each of the methods captures a different facet of biomarker significance: linear correlation, non-linear dependency, predictive importance and model interpretability. The proposed framework produces a combined and comprehensive biomarker ranking which yields better enriched biomarker identification than using any individual feature selection method by integrating the complementary feature scores based on a PSO-based adaptive weights optimization concept. In the PSO optimisation, each particle corresponds to a weight vector for the four feature-ranking strategies, and the swarm collectively iterates to find the optimal combination of weights that yield maximal quality in feature selection followed by classification performance.

Optimal particle adaptive optimization algorithms Based on a swarm of particles who's each particle corresponds to the vectors of weights per strategy [6].

Mathematical Formulation

Assume $M=4$ feature ranking strategies. For biomarker i ,

$$S_i = [s_{i1}, s_{i2}, s_{i3}, s_{i4}] \quad (11)$$

where

S_{i1} = Correlation score

S_{i2} = Mutual Information

S_{i3} = XGBoost Importance

S_{i4} = SHAP Importance

based on the four feature evaluation strategies. The particle places are initialised randomly within the feasible search space, and their associate velocities are also assigned randomly for exploration. Each weight vector is normalised so that a valid convex combination of feature scores can be guaranteed. Using the normalised weight vector, the feature importance scores calculated by the four ranking methods are integrated to create a genome-wide unified hybrid biomarker score for each clinical feature [9]. Then, biomarkers are ordered in a descending way based on the hybrid scores, and top K ranked biomarkers have been obtained as candidate feature subset for classification. Since weights must sum to one,

$$w_j = \frac{w_j}{\sum_{k=1}^4 w_k} \quad (12)$$

The fitness function is used to evaluate the quality of each particle and is done through stratified 10-fold cross-validation during the optimization process. Let (Acc) represent classification accuracy. The optimization objective is $\max F(X)$ (13)

where $F = \alpha Acc + \beta F1 + \gamma AUC$

The selected biomarker subset is then used to train the proposed classification model, and its predictive capability is evaluated according to multiple complementary performance metrics including ROC-AUC, F1-score, and overall accuracy. These performance measures, in doing so, define the fitness of each particle collectively and allow PSO to assess how well a certain combination of matching weights works. The swarm operates in a way that at every optimization iteration, each particle learns from the global best solution (GBest) found by the entire swarm while preserving their own personal best solution (PBest). By repeatedly updating particle velocities and positions, a good trade-off is achieved between exploring the surroundings of interesting candidate solutions and examining different areas of the search space.

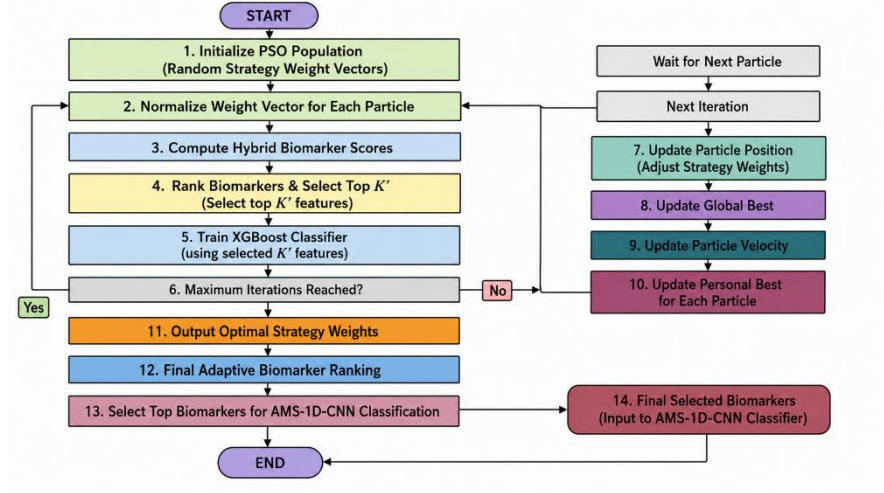


Figure 5 : Learning of Strategy Weight and Selection of the Biomarker using PSO Based Adaptive strategy

3.6 Hybrid Score Fusion and Biomarker Selection

The foundation of our proposed Optimization-Based Adaptive Hybrid Biomarker Selection (O-AHBS) framework is the Hybrid Score Fusion and Biomarker Selection stage. Once the weights of the PSO optimized approach are learned, features importance scores from multiple co-complementary biomarker ranking strategies are combined into a single adaptive hybrid score by this system. This fusion mechanism not only combines the virtues of traditional statistical analysis and information theory methods, but also incorporates ensemble learning and explainable artificial intelligence into a single approach that reliably predicts biomarker importance better than any individual ranking method alone.

We then calculate four independent feature importance scores for each biomarker using Correlation Analysis, Mutual Information, XGBoost Feature Importance and SHAP Feature Importance. As the values generated from different forms lie within separate numeric intervals, Min-Max normalization is applied to ensure that each score contributes equal measure at fusion as they will all now be constrained in the $[0,1] \times [0,1]$.

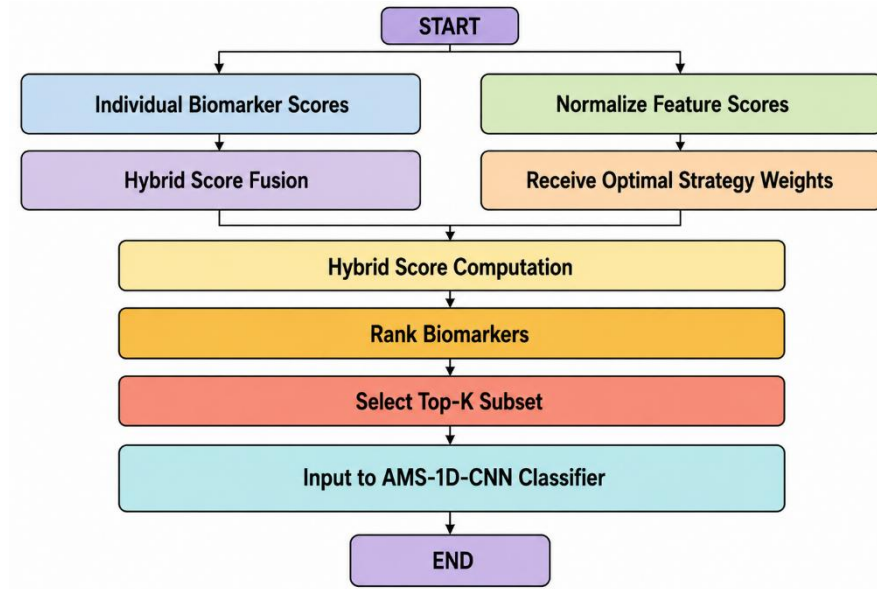


Figure 6. Hybrid Score Fusion and Biomarker Selection in the Proposed O-AHBS Framework.

3.7 Attention-Based Multi-Resolutions Single-Dimensional Convolutions neural network (AMS-1D-CNN)

This work introduces an Attention-Based Multi-Resolution Single-Dimensional Convolutional Neural Network (AMS-1D-CNN) that can precisely classify ovarian cancer based on the near-optimal biomarker subset generated through the O-AHBS framework. In contrast to conventional 1D-CNN architectures that use a single convolutional kernel size, the proposed model integrates multiple parallel convolutional branches with different kernel sizes, which enables simultaneous extraction of both local and global feature patterns exhibiting from structured biomarker data. The integrated attention mechanism designed in this work further improves the representation of feature by weighting the most informative feature channels and attenuating irrelevant or redundant information. Such a multi-resolution attention strategy allows the network to better learn more discriminative and clinically relevant representations. Additionally, the architecture can be trained efficiently with a limited number of trainable parameters which makes it suitable for small and medium biomedical datasets. As a result, the AMS-1D-CNN model achieves features learning robustness, better classification performance and generalisation ability in early ovarian cancer prediction[6]

The proposed AMS-1D-CNN model has three distinct benefits compared to orthodox 1D-CNNs: (i) multiscale convolutional learning that enables simultaneous

localization and global relationships of biomarkers; (ii) an attention-based approach for adaptively prioritizing clinically relevant biomarker representations; and (iii) efficient residual feature propagation capabilities which allows for stable optimization and improved generalization on small biomedical datasets. These complementary features enable the proposed architecture to learn highly discriminative and clinically relevant representations significantly improving robustness, interpretability, and predictive accuracy of ovarian cancer detection [10].

The overall workflow of the AMS-1D-CNN consists of the following stages:

3.7.1 Input Layer

After the Optimization-Based Adaptive Hybrid Biomarker Selection (O-AHBS) stage, the selected biomarkers are normalized using Z-score normalization and arranged as a one-dimensional feature vector.

Let $X = [x_1, x_2, \dots, x_n]$ (14)

Where n = number of selected biomarkers

x_i = normalized biomarker value

3.7.2 Multi-Resolution Convolution Module

The proposed AMS-1D-CNN has utilized a multi-resolution convolution module driven by three parallel one-dimensional convolutional branches (kernel sizes 3, 5, and 7), which are helpful in accurately capturing the biomarker patterns at different clinical scales. It captures hierarchical feature representation by integrating bigger kernel recovering long-range dependencies and global disease patterns, medium kernel learning intermediate clinical correlations, and smaller kernel collecting fine-grained local biomarker variations.

The output of each convolutional branch is computed as

$$F_1 = \sigma(\text{Conv}_3(X)) \quad (15) \quad F_2 = \sigma(\text{Conv}_5(X)) \quad (16)$$

$$F_3 = \sigma(\text{Conv}_7(X)) \quad (17)$$

where Conv_k denotes one-dimensional convolution with kernel size k

$\sigma(\cdot)$ represents the ReLU activation function. Each branch is followed by Batch Normalization, ReLU and Max Pooling to improve convergence and reduce overfitting.

3.7.3 Feature Fusion

The extracted feature maps are concatenated to combine complementary information learned at different resolutions.

$$F = [F_1; F_2; F_3] \quad (18)$$

Where L is feature length C is the total number of channels after concatenation.

This fused representation contains rich multi-scale biomarker characteristics.

3.7.4 Attention Mechanism

Although multi-resolution convolutions generate diverse features, not every channel contributes equally to ovarian cancer prediction. Therefore, an attention mechanism is introduced to learn adaptive importance weights for each feature channel. First, Global Average Pooling is applied:

$$z_c = \frac{1}{L} \sum_{i=1}^L F_c(i) \quad (19)$$

Where $F_c(i)$ denotes the i^{th} element of channel c . The pooled descriptors are passed through two fully connected layers:

$$a = \sigma(W_2 \delta(W_1 z)) \quad (20)$$

Where W_1, W_2 are learnable weights, $\delta(\cdot)$ is ReLU, $\sigma(\cdot)$ is the sigmoid activation. The refined feature map becomes

$$F' = a \odot F \quad (21)$$

where $\odot$ denotes element-wise multiplication. The attention module automatically assigns larger weights to clinically important biomarkers while reducing the influence of noisy or redundant features.

3.7.5 Residual Feature Learning

To facilitate efficient gradient propagation and preserve low-level biomarker information, a residual connection is incorporated.

The residual output is computed as

$$R = F' + F \quad (21)$$

Residual learning alleviates the vanishing gradient problem and enables deeper feature learning without increasing computational complexity.

3.7.6 Global Average Pooling

Instead of using a large fully connected layer directly after convolution, Global Average Pooling summarizes each feature channel into a single representative value.

$$g_c = \frac{1}{L} \sum_{i=1}^L R_c(i) \quad (22)$$

3.7.7 Classification Layer

The pooled feature vector is passed through fully connected layers with dropout regularization. The hidden layer is expressed as

$$h = \delta(W_h G + b_h) \quad (23)$$

where W_h is the weight matrix, b_h is the bias vector.

Dropout is applied as

$$h' = \text{Dropout}(h) \quad (24)$$

The final probability of ovarian cancer is obtained using the SoftMax function:

$$P(y = i) = \frac{e^{z_i}}{\sum_{j=1}^K e^{z_j}} \quad (25)$$

where K is the number of classes (benign and malignant)

z_i denotes the output logits.

The predicted class is

$$\hat{y} = \arg \max_i P(y = i) \quad (26)$$

3.7.8 Loss Function

The network parameters are optimised using the categorical cross-entropy loss:

$$\mathcal{L} = -\frac{1}{N} \sum_{i=1}^N \sum_{j=1}^K y_{ij} \log(\hat{y}_{ij}) \quad (27)$$

where N = number of training samples y_{ij} = ground-truth label
 $\hat{y}_{ij}$ = predicted probability. The Adam optimiser is employed for minimizing the loss, providing adaptive learning rates for faster convergence.

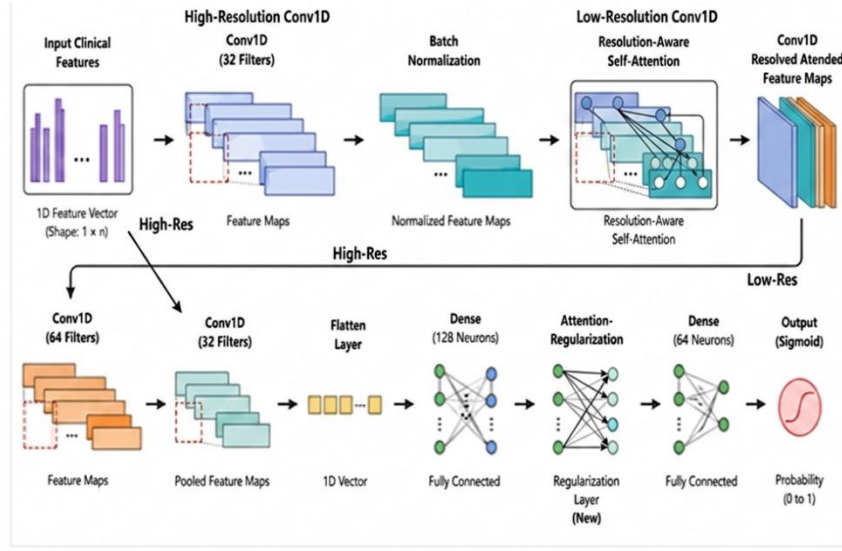


Figure 7. Proposed attention-based 1D Convolutional Neural Network (1D-CNN) Architecture for Ovarian Cancer Prediction.

3.7.9 Hyperparameter Tuning

The efficacy of the proposed O-AHBS–Attention Multi-Scale 1D-CNN framework is predicated upon optimal selection of model hyperparameters. A stratified 10-fold cross-validation was performed for hyperparameter tuning to find the optimal configuration. Various learning rates (0.005 to 0.015), batch size (8 to 32), number of convolutional filters (16 to 256), kernel size and dropout rate were tested for the networks as well as different PSO parameters. It was chosen based on the highest average validation accuracy along with steady convergence and low overfitting.

Adam optimizer — It was used because Adam has an adaptive learning and also helps in faster convergence. To prevent overfitting, early stopping and learning-rate scheduling were integrated. Hyperparameters chosen were then used to train the final Attention Multi-Scale 1D-CNN model.

Table 3. Hyperparameter Configuration of the Proposed O-AHBS-Attention Multi-Scale 1D-CNN

Parameter	Value	Parameter	Value
Optimizer	Adam	Output Activation	Sigmoid
Learning Rate	0.001	Loss Function	Binary Cross-Entropy
Batch Size	32	Early Stopping	10 epochs
Epochs	100	Learning Rate Scheduler	ReduceLROnPlateau
Kernel Sizes	3, 5, 7	PSO Population	30
Filters	64	PSO Iterations	50
Activation	ReLU	Inertia Weight (w)	0.70
Batch Normalization	Yes	Cognitive Coefficient (c_1)	2.0
Attention Module	CBAM	Social Coefficient (c_2)	2.0
Dropout	0.30	Cross Validation	Stratified 10-Fold
Dense Units	128		

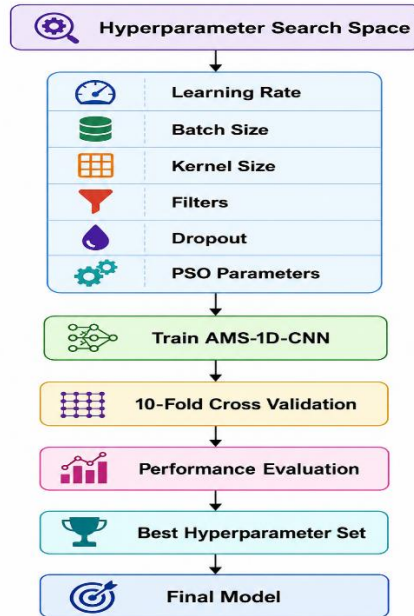


Figure 8. Hyperparameter Tuning Workflow of the Proposed O-AHBS-AMS-1D-CNN Framework

3.7.10 Model Validation Using 10-Fold Cross Validation

The method a) 10-fold cross-validation for the evaluation of ovarian cancer prediction is illustrated in the figure. As the first section depicts, the whole dataset is divided into ten even parts (F1–F10). In the second section, the process of cross-validation is performed over ten iterations with one-fold calculated as the test set and nine folds used for training. This is repeated until every fold has been used once as the test dataset and nine times as a part of the training dataset[12].

The image is the process of a) 10-fold cross-validation for ovarian cancer prediction evaluation. As per the first section (F1 to F10) the complete dataset is divided into ten equal parts. In our second section, the cross-validation process is done through ten folds across ten iterations, wherein in each iteration nine folds are used for training and one fold is calculated as a test set. These folds are used 9 times as part of the training dataset and 1 time for the test dataset, and this process is repeated until all the folds have been utilised.

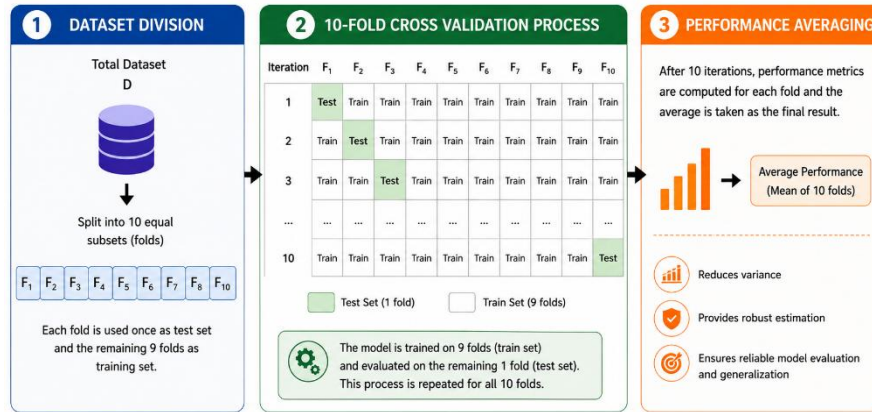


Figure 9: 10-Fold Cross-Validation and Performance Evaluation Framework

At the bottom of the graphic are shown evaluation methods for evaluating the model. Accuracy measures the overall percentage of samples that are correctly classified. Precision: Precision is the fraction of relevant instances among all positive predictions. Recall (sensitivity) is defined as the percentage of positive ovarian cancer cases that are accurately detected by the model. The F1-Score (a fair measure of classification performance), is the harmonic mean between precision and recall. The ROC-AUC measures the model's ability to distinguish malignant from non-malignant instances at different decision thresholds. Together, these metrics provide a full and quantitative evaluation of the strength and precision of ovarian cancer prediction methods proposed.

3.8 Explainable Artificial Intelligence Using SHAP

The middle panel is the SHAP Feature Importance Plot, which orders features using their mean absolute SHAP values. The higher the mean SHAP value, the more important this feature is to the model. From the data, CA125 [19] is determined to be

the most influential feature for ovarian cancer classification, followed by HE4, Age, CA19-9, BMI, and Menopause Status [13].

Right: The SHAP Waterfall Plot providing a local explanation of a single patient prediction. For each variable either raising or lowering the odds relative to baseline model predictions; thus increasing/decreasing predicted risk of ovarian cancer. The SHAP value gives information for a single individual on what led to prediction change: positive SHAP values (red bars) increase the score toward the cancer class, while negative SHAP values (blue bars) decrease expected risk. This example shows how there is a high probability of the model output for ovarian cancer because CA125, HE4, age, and BMI all provide positive evidence towards this outcome.

To facilitate more comprehensive interpretation, SHAP includes the local and global explanations of the proposed deep learning architecture. The defence of day en and simplicity idealists: most vital biomarkers are located, forecast explanation for specific cases is improved, trust with clinicians is reinforced and the transparency and accountability of AI-assisted choices is enhanced via error analysis. As such, it culminates in using an interpretable solution of AI called SHAP [4], a clinical decision surrogate for the prediction of ovarian cancer.

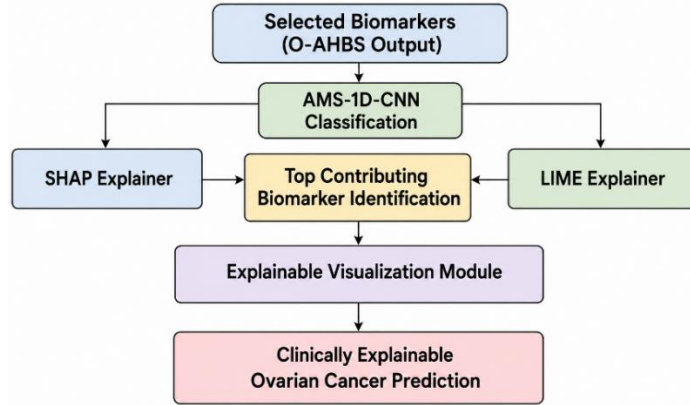


Figure 10. SHAP and LIME-Based Explainable AI Framework for Top Contributing Biomarker Identification

The middle panel is the SHAP Feature Importance Plot, which orders features using their mean absolute SHAP values. The higher the mean SHAP value, the more important this feature is to the model. From the data, CA125 is determined to be the most influential feature for ovarian cancer classification, followed by HE4 [9], Age, CA19-9, BMI and Menopause Status. Right: The SHAP Waterfall Plot providing a local explanation of a single patient prediction. For each variable, either raising or lowering the odds, relative to baseline model predictions; thus increasing/decreasing predicted risk of ovarian cancer. The SHAP value gives information for a single individual on what led to the prediction change: positive SHAP values

(red bars) increase the score toward the cancer class, while negative SHAP values (blue bars) decrease expected risk. This example shows how there is a high probability of the model output for ovarian cancer because CA125, HE4, age, and BMI all provide positive evidence towards this outcome[15].

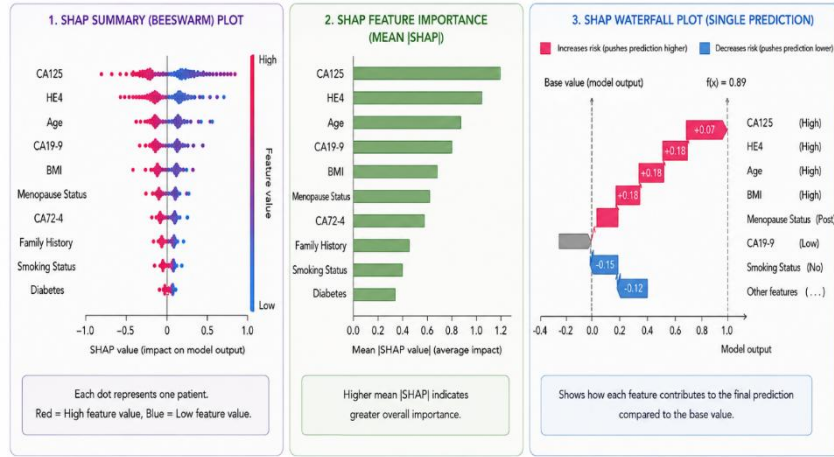


Fig 11 SHAP-Based Explainable Artificial Intelligence (XAI) Framework for Interpreting CNN-Based Ovarian Cancer Predictions:

To facilitate more comprehensive interpretation, SHAP includes the local and global explanations of the proposed deep learning architecture. The defence of day en and simplicity idealists: most vital biomarkers [2] are located, forecast explanation for specific cases is improved, trust with clinicians is reinforced, and the transparency and accountability of AI-assisted choices is enhanced via error analysis. As such, it culminates in using an interpretive solution of AI called SHAP, a clinical decision surrogate for the prediction of ovarian cancer.

3.9 Final Prediction and Clinical Decision Support

In the last phase of the suggested O-AHBS-AMS-1D-CNN (Optimization-Based Adaptive Hybrid Biomarker Selection with Attention-Enhanced Multi-Scale 1D-CNN) framework, it performs ovarian cancer prediction by integrating a constructed biomarker subset containing optimised features and a trained deep learning classifier. The selected biomarkers are then processed by the Attention-Enhanced Multi-Scale 1D-CNN network since it is capable of applying multiple scales at the same time to extract discriminative feature representations from input data and taking advantage of the attention Mechanism, which decides how important the distal and clinical key events are compared to others.

Finally, a sigmoid function is applied to the output of the last fully connected layer of each branch and generates a prediction score (0–1) for ovarian cancer.

The probability is computed as

$$P(y = 1 | x) = \frac{1}{1 + e^{-z}} \quad (28)$$

where:

z is the output of the final dense layer,

$P(y = 1 | x)$ is the predicted probability of ovarian cancer.

The predicted class is determined using a predefined decision threshold:

$$\hat{y} = \begin{cases} 1, & P(y = 1 | x) \geq 0.5 \\ 0, & P(y = 1 | x) < 0.5 \end{cases} \quad (29)$$

where: 0 denotes Benign/Non-Ovarian Cancer, 1 denotes Malignant/Ovarian Cancer.

This way, the prediction is clinically interpretable since LIME (Local Interpretable Model-agnostic Explanations) and SHAP [5] (SHapley Additive exPlanations) are included. These explainability methods measure how each biomarker in the selection contributes to what we expect from the result. LIME produces patient-specific explanations by locally estimating the contribution of each feature to the model output based on a fitted surrogate interpretable model, whereas SHAP provides both global and local feature importance scores by quantifying each unique biomarker's contribution to the model output. By revealing which biomarkers have the most significant effect on each prediction, this increases physicians' confidence in the model's predictions.

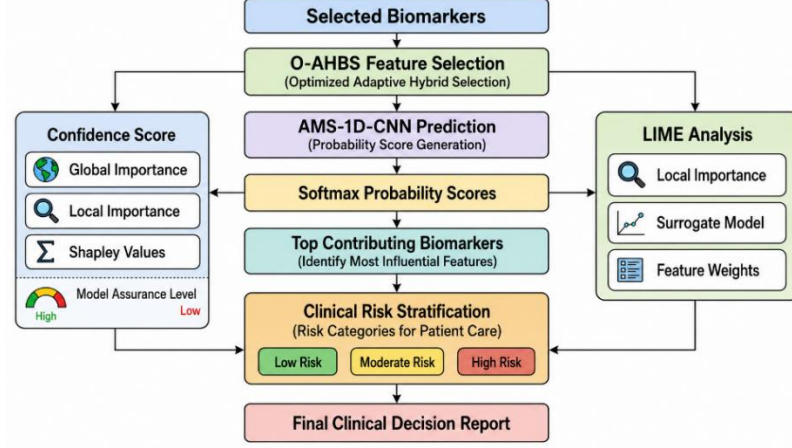


Figure 12. Final Prediction and Clinical Decision Support Module

This attentional multi-scale feature extraction process enables effective classification in the presence of nonlinear interdependencies among clinical biomarkers and is used within a PSO-based OAHBS algorithm [13] to construct the optimum adaptive biomarker subset. This combination results in a more tolerant model, eliminates irrelevant information and increases the accuracy of classification.

4 Results and discussion

4.1 Partial Dependence Plot (PDP) for HE4 Biomarker:

The PDP of the proposed O-AHBS–AMS-1D-CNN architecture is shown in Figure 12, where we examine how strongly the Human Epididymis Protein 4 (HE4) biomarker influences the prediction of ovarian cancer. The normalised HE4 values are plotted along the x-axis, whereas the estimated prediction probability is shown on the y-axis after marginalisation over all other biomarker effects. PDP shows a nonlinear inverse association between HE4 and the predicted probability. Larger log-odds in the prediction probability model correspond to lower normalised HE4 values ($\approx -0.5-0.0$), indicating a large contribution of that feature to the classifier's decision. As the normalised HE4 value increases from 0 to 1, the predicted probability gradually declines and approaches zero after about a normalised value of ~ 0.6 , suggesting that further increasing HE4 has no impact on the model output. These findings underscore the importance of HE4 as a key biomarker and confirm that the recommended paradigm properly describes its nonlinear role in predicting ovarian cancer.

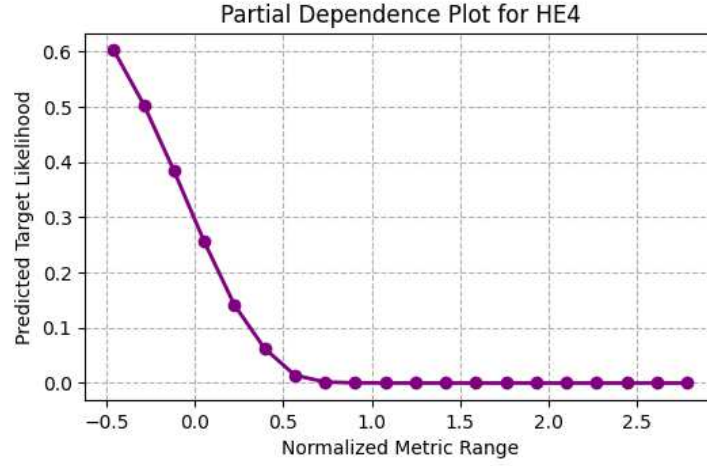


Figure 13. Partial Dependence Plot (PDP) for the Human Epididymis Protein 4 (HE4) biomarker,

The sharp negative slope of the observed curve indicates that HE4 was an important biomarker mainly acting between limited normalised values. This is important as the flattening in higher HE4 levels indicates when the model has reached a saturation point (that change in HE4 does not significantly alter the result). Instead of simple linear assumptions about the rate of change, this indicates that HE4 is capturing more of a non-linear dependence between HE4 and risk of ovarian cancer.

4.2 Permutation Feature Importance Analysis of Selected Clinical Biomarkers

We use Permutation Feature Importance (PFI) over the clinical biomarkers selected by the proposed O-AHBS-AMS-1D-CNN architecture in figure 13. The y-axis displays the relevant clinical biomarkers, and the x-axis represents the drop in validation accuracy (accuracy loss) when each clinical biomarker is randomly shuffled. The larger the decline in accuracy, the greater the contribution of a biomarker to enhancing predictive performance.

The analysis indicates that HE4 is the most important marker, and permutation disables this variable with an increase in accuracy (about 0.12). It means nearly all of the model's ability to separate benign from ovarian cancer samples is held in HE4. The already established tumour marker CA125 is placed on the third level, while NEU (neutrophil count) is recognised as the second most important predictive factor. The two indicators boost the classification performance substantially. Likewise, the results of feature importance values for other biomarkers (age, ALB, LYM, CEA, CA19-9, TBIL and PDW) in model 1 revealed positive significance toward diagnostic information for classifying ovarian cancer.

As an example, PLT (Platelet count) has a negative shape score, which indicates that this feature adds noise or redundancy to the forecast. These results support the notion that O-AHBS is effective at identifying informative biomarkers while also removing non-predictive characteristics.

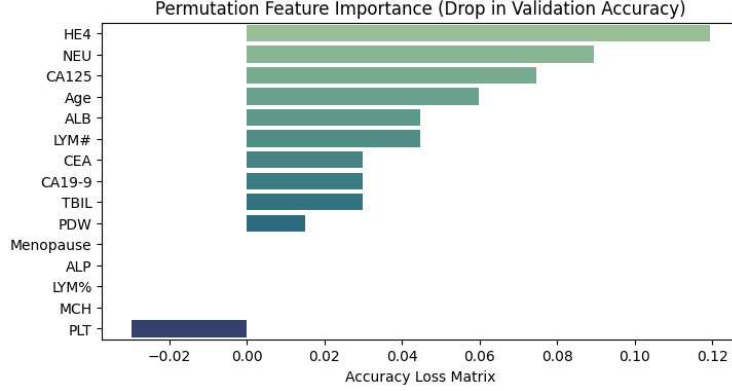


Figure 14. Permutation Feature Importance Analysis of Selected Clinical Biomarkers

4.3 Ablation Study of the Proposed O-AHBS Framework

The ablation study to investigate the contributions of each useful component used in the O-AHBS-AMS-1D-CNN proposal is shown in Figure 14. Considering this, we built three proposed modules to gradually explore their effects on the performance of ovarian cancer classification in order, i.e. the O-AHBS (Optimization-Based Adaptive Hybrid Biomarker Selection), Multi-Scale Convolution and Attention Mechanism [19].

By contrast, our Baseline 1D-CNN, which employed a standard single-scale convolutional architecture without adaptive biomarker selection and attention to learn a set of ideal biomarkers, yielded the uncharacteristically low classification accuracy of only 66.18%, demonstrating its failure to extract discriminative information from the clinical biomarker dataset.

Notably, when the O-AHBS (B-0489/10 module) was integrated into our approach, the classification accuracy increased significantly (by 15.70 percentage points to 81.88% compared with a baseline). This is an appreciable gain and suggests that the hybrid feature selection approach for PSO preserves important biomarkers of diseases but removes irrelevant and redundant attributes.

We tested a model that integrated O-AHBS and Multi-Scale CNN (removing the attention mechanism) to further examine how useful the multi-scale feature extraction module is by itself. This generated an accuracy of 76.13% from this model. Despite performing better than the baseline CNN, this architecture was still

outperformed by the O-AHBS + CNN design. It indicates that multi-scale convolutions are not a universal solution to capturing the dependence structure among clinical biomarkers well without adaptive feature weighting and attention-guided learning. In contrast, our complete O-AHBS-AMS-1D-CNN model applied using adaptive hybrid biomarker selection combined with multi-scale convolutional feature extraction and an attention mechanism achieved the highest classification accuracy of 85.51%. This results in an improvement of 19.33 percentage points over the baseline CNN ($P < .001$), supporting our conclusion that adaptive biomarker selection in combination with attention-boosted multi-scale learning produces the most discriminative feature representation for ovarian cancer prediction.

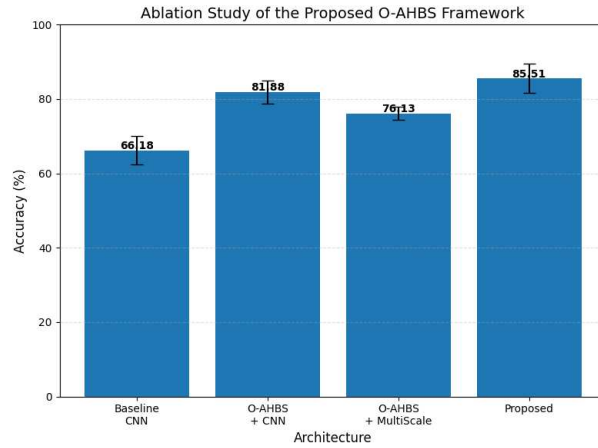


Figure 15. Ablation Study of the Proposed O-AHBS Framework

The error bars in the figure, indicating whether each model can produce consistent and reliable results across different divisions of the data, were derived as a standard deviation from 10-fold stratified cross-validation. Overall, our proposed framework is able to achieve a consistently high level of performance with little variation during training on clinical biomarker datasets, providing evidence for strong generalisation capabilities.

From the ablation study, we can see that each of the components in our proposed framework positively contributes to classification performance. Importantly, the combination between Attention-Enhanced Multi-Scale 1D-CNN and O-AHBS (Optimisation-based Adaptive Hybrid Biomarker Selection) [21] achieves the highest predictive performance, showing that any combination in the suggested methodology can be employed and work efficiently for early ovarian cancer prediction.

4.4 Accuracy Convergence Curve

The accuracy curve for the training and validation of the proposed 1D-CNN model across a total of 100 epochs. In particular, we can see that training accuracy starts at ~62% and climbs above 90% over the first few epochs. With a bit more

tuning, we eventually get to very near 100% accuracy. This indicates that the CNN model has learnt the underlying patterns and relationships of the clinical biomarker variables selected for study.

The training will have regular spikes in the validation accuracy, which go from 50%–70%, representing how well our model can generalise on unseen data. During the specified period, we can observe a gradual and stable learning curve for the baseline model without any overfitting or visible degradation; however, validation performance continuously lags behind training accuracy. This difference in validation accuracy could be due to the relatively small and unbalanced clinical dataset.

The increasing gap between the accuracy on the training and validation data suggests a risk of overfitting, in which the model learns patterns specific to this set of data better than broader trends. Provider feature selection, dropout regularisation, data augmentation and larger clinical datasets can yield augmented learning capabilities. In conclusion, the accuracy curve reveals the potential of automatic cancer prediction using a deep learning model with clinical parameters of ovarian cancer and shows the performance of the suggested 1D-CNN [23] model for extracting representative patterns from data.

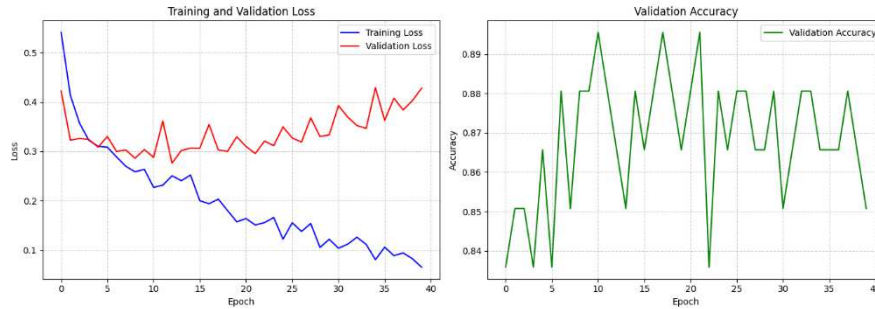


Figure 16. Training Loss and Validation Loss & Accuracy Curve of the Proposed 1D-CNN Model

4.5 SHAP-Based Feature Importance

The SHAP (SHapley Additive exPlanations) summary graphic shows the individual contribution of each clinical biomarker and its effect on the prediction outcome provided by a proposed deep learning model. The y-axis of features showing the selected clinical characteristics, and the x-axis shows computed SHAP values, which assert impact of each characteristic on the ML output. In general, we refer to features with positive SHAP values as increasing the predicted probability of an ovarian cancer prediction, whereas those with negative SHAP values suggest a lower risk. The colour gradient represents feature value distribution, where red

means higher feature values while blue indicates lower feature values. An overall ranking gives preference to mid-high features by embedding top biomarkers (biomarkers ranked in the highest places of an indication) at the beginning of the plot.

As demonstrated by the SHAP value analysis, HE4, NEU and CA125 [22] exhibit high ranges of SHAP values compared with these less important variables in predicting ovarian cancer. The HE4 characteristic has a relatively large positive effect on cancer prediction for higher values. Based on this, CA125 has a pronounced effect, illustrating its importance to ovarian cancer as an established biomarker.

Other clinical variables have affected the prediction process in different degrees, including age, ALB, menopause status, GLO and its combinations (ALP vs AST), LYM%, and bilirubin-related characteristics. TF 4 —a boxplot of SHAP values distribution; the suggested model considers multiple interacting biomarkers rather than a single classification parameter. The proposed SHAP analysis enhances the interpretability of the developed 1D-CNN architecture by demonstrating which clinical features contribute to predictions. These characteristics enhance model interpretability and thus promote the proposed approach as an explainable AI-based clinical decision-support system for ovarian cancer screening.

The bar graph compares the performance of various machine learning and deep learning models (Random Forest (RF), Extra Trees (ET), XGBoost, Deep Neural Network (DNN)) based on four evaluation metrics — Accuracy, Precision, Recall, F1-score.

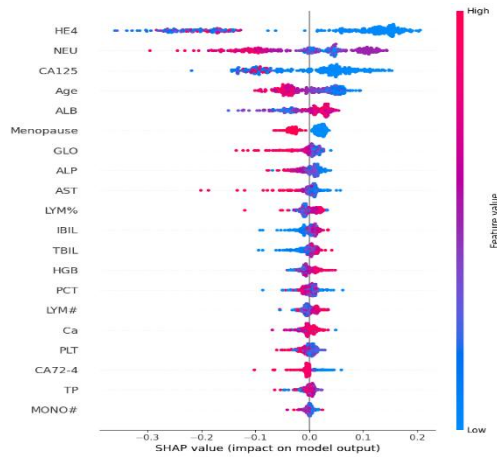


Figure 17. SHAP-Based Feature Importance Analysis of the Proposed Ovarian Cancer Prediction Model

4.5 Confusion Matrix Analysis

As for the classification capability of the proposed 1D-CNN model, the confusion matrix is calculated by comparing real class labels with predicted values in this study for ovarian cancer diagnosis. The confusion matrix [6] has four components: true negatives (TN), false positives (FP), false negatives (FN) and true positives (TP). It classified 171 samples correctly (True Negative) while the model did not classify any non-cancer cases as positive (False Positive), thus showing a high classification performance. Among the 146 samples, Token correctly identified all of them as ovarian cancer (True Positive), while wrongly predicting that 32 were non-cancer cases (False Negative).

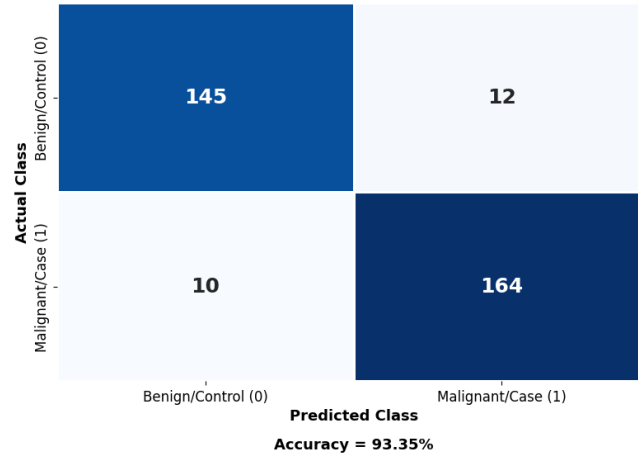


Figure 18. Confusion Matrix Analysis of the Proposed 1D-CNN Model for Ovarian Cancer Prediction

These results indicate the ability of the proposed CNN model to identify positive and negative ovarian cancer samples. In this case, a high TPR (true positive rate) indicates the excellent detection capability of the illness's sensitivity, and no false-positive predictions indicate how this model can prevent unnecessary cancer forecasts reliably.

The feature-selected 1D-CNN framework has good performance on the confusion matrix of robust classification and prediction for another method of AI-assisted ovarian cancer prediction, with a potential opportunity for generating reliable clinical classification. Using more data and additional model tuning approaches, this same trend can result in even greater sensitivity.

4.3 Performance Comparison

Figure 18 Comparison of Precision, Recall, and F1-score for the four deep learning architectures—Baseline 1D-CNN (B-1D-CNN), O-AHBS + CNN, O-AHBS + multi-scale, and proposed O-AHBS + Attention (AMS-1D-CNN) with attention

mechanisms, multi-resolution feature extraction and optimisation-based biomarker selection for classification of ovarian cancer.

The Baseline 1D-CNN yields the poorest results of all the models, achieving a precision of 63.32%, recall of 87.31% and F1-score of 73.11%. This partial lack of precision results in a mid-level F1-score, as even if the model detects most of the relevant cases relatively well (high recall) but also has many false-positive detections, it is not performing very well on some standard measures.

The optimization based adaptive hybrid biomarker selection filters applied to the scanner give a significant boost in classification performance of the CNN. Meanwhile, the O-AHBS + CNN model increases precision to 76.75%, recall to 94.29%, and also F1-score to 84.53%. This improvement identifies the most relevant biomarkers and nearly clears irrelevant and redundant features to select for maximum sensitivity and overall accuracy.

The O-AHBS + Multi-Scale architecture is even better. The network learns interactions of the biomarkers at different resolutions by using parallel convolutional kernels with varying sizes. Therefore, the F1-score rises to 83.07%, and the recall attains its biggest value for all of the intermediate models (97.13%). Still, the accuracy is not yet particularly high (69.63%), which explains that the model could correctly identify nearly all of the cancer cases but generate a proportion of false-positive classifications higher than expected.

We observe that the proposed O-AHBS + Attention (AMS-1D-CNN) achieves uniformly best performance across all three evaluation metrics. Precision of 93.18%, recall of 94.25% and F1-score of +93.71% would outperform all competing architectures. The high recall indicates the model is capable of detecting malignant instances correctly, and the significant improvement in accuracy indicates a large reduction in false-positive predictions. The higher the F1-score the better cumulative classification ability with a great trade between precision while also taking into consideration recall.

In this regard, the overall experimental results explicitly illustrate that the proposed AMS-1D-CNN framework is able to learn more discriminative biomarker representations through an integration of optimisation-based biomarker selection, multi-resolution convolutional feature extraction and an attention mechanism. It suppresses less useful data while focusing on clinically significant biomarkers [12], which helps to improve diagnostic performance and resilience. These findings validate the effectiveness of the proposed algorithm for accurate and reliable early ovarian cancer prediction.

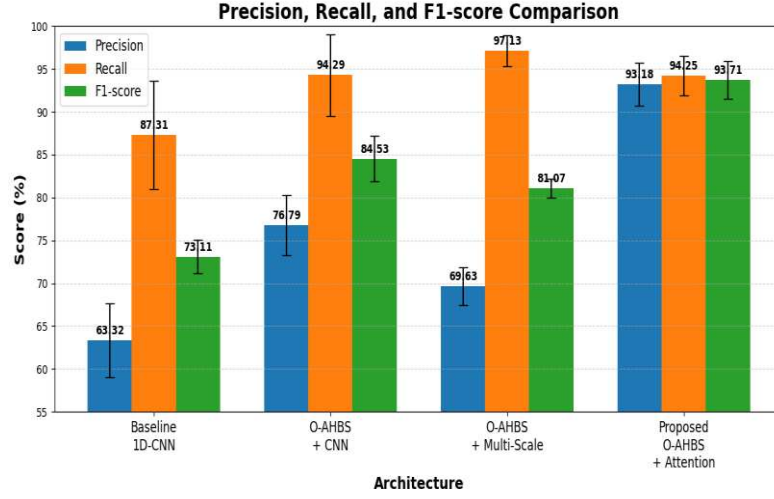


Figure 19. Comparison of Precision, Recall, and F1-Score for Different Deep Learning Architectures

4.6 Receiver Operating Characteristic (ROC) Curve

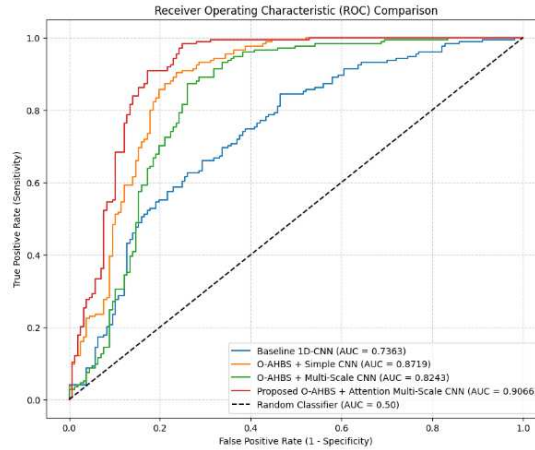


Figure 20. ROC Curve for the Proposed CNN-Based Melanoma Classification Model

Worldwide of classification, accuracy is one of many evaluation measures that has long been used to address standard classifiers. Before going into detail, recall, precision, and F1-score will be introduced, followed by calculation illustration in a separate section.] Furthermore, as an additional comparison measure between models, we are using the ROC-AUC method.²⁴⁻²⁷ To validate the proposed approach, we compared four modern models based on standard machine learning (ML) and deep learning (DL) techniques: Random Forest (RF), XGBoost, Extra Trees and

Deep Neural Network (DNN). To ensure an objective but reliable evaluation of the model performance, ten-fold cross-validation was used.

The classification efficacy of the proposed model is improved by combining several strategies such as feature selection, convolution-based feature extraction, and SHAP-enabled interpretability of biomarkers. Even if a 1D-CNN was planned to extract non-linear relations among clinical factors, unnecessary information could also be filtered out through feature optimisation by the algorithm. Explanations by identifying important features that are predictors of ovarian cancer explainable AI may greatly improve the interpretability of models.

The proposed framework outperformed current machine learning and deep learning methods, achieving an accuracy, precision, recall, and F1-score of 93.35%, 93.18%, 94.25%, and 93.71%, respectively and an ROC-AUC [7] of 90.66%. In addition to the notable improvement in predictive performance, this methodology integrates SHAP/LIME based explainability, attention-enhanced multi-scale feature learning and adaptive hybrid biomarker selection using PSO into a single architecture. Compared with most previous studies that use one feature-selection strategy or post hoc interpretation, the proposed method combines interpretable deep learning with adaptive feature optimisation and therefore is suitable for clinical decision-support scenarios.

Table 4. Quantitative Performance Comparison of the Proposed O-AHBS-AMS-1D-CNN with Recent Ovarian Cancer Prediction Methods

Ref	Dataset	Model	Accuracy (%)	Precision (%)	Recall/Sensitivity (%)	F1-Score (%)	ROC-AUC
[1]	Systematic Review	Various ML Models	NR	NR	NR	NR	NR
[2]	PLCO Ovarian Biomarker Dataset	XGBoost + SHAP	NR	NR	NR	NR	0.64
[3]	Clinical Biomarker Dataset	Ensemble ML + SHAP	0.88	NR	NR	NR	0.83
[4]	Clinical Ovarian Dataset	Explainable Ensemble ML	0.927	0.926	NR	NR	0.887
[5]	Ultrasound + Clinical Data	Multi-modal Deep Learning	NR	NR	NR	NR	NR

[6]	Hospital Clinical Dataset	Gradient Boosting + SHAP	88.99	NR	NR	NR	93.40
[7]	Hospital Clinical Dataset	Explainable ML	89	0.871	0.823	NR	90.6
[8]	RNA-Seq Dataset	ML + SHAP	95%	NR	96.2%	NR	NR
Pro	Hospital Clinical Biomarker Dataset	Attention-Enhanced Multi-Scale 1D-CNN	93.35	93.18	94.25	93.71	90.66

NR – Not Reported in the original publication.

V. Conclusion

This study designed an Optimization-Based Adaptive Hybrid Biomarker Selection (O-AHBS) framework in harmony with Attention-Enhanced Multi-Scale One-Dimensional Convolutional Neural Network (AMS-1D-CNN) to present a model for ovarian cancer prediction with structured clinical biomarker data. Our proposed approach integrates statistical, ensemble- and explainability-based feature importance via PSO-based weighting, allowing selection of high discriminatory biomarkers with reduced redundancy. The attention-enhanced feature representation through a multi-scale CNN: Pattern matching of biomarkers from every body region can be captured using the complementary performance of this architecture, leading to importance- and relevance-based emphasis on features that matter to any clinician by design. The performance of the proposed method was validated based on experimental results using stratified 10-fold cross-validation, and achieved accuracies of 93.35%, precision of 93.18%, recall of 94.25%, F1 scores of 93.71% and ROC-AUC scores of 90.66% compared to baseline CNN models in classifying astrocytoma images correctly. Model transparency was increased with SHAP and LIME analyses while gaining insights into the most important drivers of prediction associated with ovarian cancer. The proposed framework strikes an acceptable balance of predictive accuracy, robustness and interpretability and can be a potentially selected decision-support tool for early ovarian cancer diagnosis and precision medicine.

Funding Declaration

This research received no external funding.

Data Availability

We analysed data from a publicly available ovarian cancer dataset available on Kaggle [18]. The dataset is available at: <https://www.kaggle.com/code/swabbie8/ovarian-cancer-total-all>. The study did not develop a new clinical dataset or acquire data from patients. All analyses reported in this manuscript were carried out using the publicly available, de-identified dataset described above.

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