

## OVARIAN CANCER PREDICTION

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### ABSTRACT

Ovarian cancer is one of the most lethal gynecological malignancies worldwide due to its silent progression and late-stage diagnosis. Early detection significantly improves survival rates; however, conventional diagnostic approaches often fail to identify the disease at an initial stage. This study presents an Artificial Intelligence (AI)-driven Clinical Decision Support System (CDSS) designed to predict ovarian cancer risk using clinical and biochemical data. The proposed system integrates machine learning and deep learning algorithms to analyze multiple patient parameters, including age, menopausal status, hematological indicators, metabolic biomarkers, and tumor markers such as CA125, HE4, and AFP. The dataset is preprocessed through normalization, missing value handling, and feature selection to improve model accuracy. Various predictive models such as Logistic Regression, Support Vector Machines (SVM), Random Forest, and Deep Neural Networks are implemented and compared to identify the most reliable predictive model. Additionally, Explainable Artificial Intelligence (XAI) techniques, particularly SHAP (SHapley Additive Explanations), are employed to enhance transparency and interpretability by identifying the contribution of each biomarker in predicting cancer risk. The system architecture incorporates a scalable web-based platform with a FastAPI

backend, a React frontend, and integrated database support for clinical data storage and user management. This enables healthcare professionals to input patient parameters and receive real-time predictions along with interpretable insights. Experimental results demonstrate that the proposed model achieves improved predictive performance compared to traditional diagnostic approaches. The developed system has the potential to assist clinicians in early screening, risk assessment, and decision-making, thereby improving early diagnosis and patient outcomes in ovarian cancer management.

**Keywords:** Ovarian Cancer, Machine Learning, Deep Learning, Clinical Decision Support System, Explainable AI, Biomarkers, Early Detection

### I INTRODUCTION

Ovarian cancer is considered one of the most dangerous gynecological cancers due to its high mortality rate and difficulty in early detection. Globally, it represents a significant health challenge among women, particularly because symptoms often remain undetected until the disease reaches an advanced stage. According to global cancer statistics, ovarian cancer accounts for a large proportion of cancer-related deaths among women worldwide [1]. The survival rate significantly decreases when the disease is diagnosed at a later stage, emphasizing the importance of early

screening and accurate diagnosis [2]. Traditional diagnostic methods such as ultrasound imaging, biopsy, and blood tests are often expensive, time-consuming, and sometimes inconclusive in early detection [3]. Tumor biomarkers like CA125 and HE4 have been widely used in ovarian cancer diagnosis; however, their predictive capability alone is limited [4]. In recent years, researchers have focused on integrating multiple clinical parameters and biomarkers to improve prediction accuracy [5]. Advances in medical data analysis have enabled researchers to analyze large volumes of clinical data to identify patterns related to cancer risk [6]. Data-driven approaches have shown promise in detecting subtle patterns that may not be visible through conventional clinical analysis [7]. The integration of computational techniques into healthcare systems has significantly enhanced disease diagnosis and prediction capabilities [8]. Artificial Intelligence (AI) has emerged as a powerful tool in modern healthcare for predictive analytics and decision support [9]. Machine learning algorithms are capable of learning from historical medical data and predicting disease risks with improved accuracy [10]. Techniques such as Support Vector Machines, Random Forest, and Logistic Regression have been widely applied in medical diagnostics [11]. These algorithms can analyze complex relationships between clinical variables and disease outcomes [12]. Furthermore, deep learning methods have demonstrated superior performance in analyzing large and complex medical datasets [13]. The application of AI in oncology has significantly improved cancer detection, classification, and prognosis prediction [14]. Recent studies highlight the potential of machine learning in predicting ovarian cancer using patient demographics and laboratory data [15].

Despite these advancements, one of the major challenges associated with AI-based healthcare

systems is the lack of interpretability and transparency in prediction models [16]. Many machine learning models function as “black boxes,” making it difficult for clinicians to understand how predictions are generated [17]. This limitation reduces trust and acceptance among healthcare professionals when using automated systems for clinical decision-making [18]. To address this challenge, Explainable Artificial Intelligence (XAI) techniques have been introduced to provide insights into model predictions [19]. Methods such as SHAP and LIME allow researchers to interpret how individual features contribute to the final prediction outcome [20]. Explainability is particularly important in healthcare applications where understanding model decisions can influence patient treatment strategies [21]. Another challenge in developing predictive systems for ovarian cancer is the integration of heterogeneous medical data from different sources such as laboratory reports, clinical history, and imaging results [22]. Effective data preprocessing, feature selection, and model optimization are essential to improve predictive accuracy [23]. Additionally, the development of user-friendly platforms is necessary to ensure that clinicians can easily interact with predictive systems [24]. Web-based healthcare platforms are increasingly being used to integrate AI models with hospital information systems [25]. Such platforms allow real-time analysis and decision support for medical professionals [26]. The integration of scalable backend architectures and interactive user interfaces further improves system usability and accessibility [27]. With the increasing availability of clinical data and advanced computational techniques, AI-driven diagnostic systems have the potential to revolutionize cancer prediction and screening [28]. Early detection of ovarian cancer through predictive modeling could significantly

improve treatment outcomes and survival rates [29]. Therefore, developing an intelligent, interpretable, and scalable ovarian cancer prediction system is an important step toward improving clinical decision-making and patient care [30].

## II LITERATURE SURVEY

Recent research has explored the use of machine learning techniques for predicting ovarian cancer using clinical and biochemical parameters. Early studies primarily focused on statistical models for identifying cancer risk based on tumor biomarkers and patient demographics [1]. Logistic regression models were widely used for medical diagnosis due to their simplicity and interpretability [2]. Researchers later introduced machine learning algorithms such as Support Vector Machines and Decision Trees to improve classification accuracy in cancer prediction tasks [3]. These models demonstrated better performance in identifying complex relationships between clinical variables and disease outcomes [4]. Random Forest algorithms have also been applied to ovarian cancer datasets to enhance predictive accuracy through ensemble learning techniques [5]. Studies have shown that ensemble methods often outperform individual machine learning algorithms in medical classification problems [6]. Additionally, feature selection techniques have been employed to identify the most relevant biomarkers associated with ovarian cancer [7]. Biomarkers such as CA125, HE4, and AFP have been widely studied as key indicators for ovarian cancer detection [8]. However, relying solely on these biomarkers has been shown to produce inconsistent results in early-stage detection [9]. To address this limitation, researchers have integrated multiple clinical features such as age, blood parameters, and metabolic indicators into predictive models [10].

This multi-feature approach has improved the reliability of cancer risk prediction systems [11]. Deep learning techniques have also been explored for cancer detection due to their ability to learn complex data representations [12]. Neural networks have been used to analyze large clinical datasets and identify patterns associated with cancer development [13]. Recurrent neural networks and Long Short-Term Memory models have demonstrated promising results in analyzing time-series medical data [14]. Furthermore, hybrid models combining machine learning and deep learning techniques have been proposed to enhance prediction accuracy [15].

In addition to predictive accuracy, recent studies have emphasized the importance of model interpretability in healthcare applications [16]. Many advanced machine learning models lack transparency, which limits their practical implementation in clinical environments [17]. Explainable Artificial Intelligence techniques have therefore been introduced to provide insight into model decisions [18]. Methods such as SHAP and LIME allow researchers to evaluate the contribution of each feature to the prediction outcome [19]. These techniques help clinicians understand the reasoning behind model predictions, increasing trust in AI-based systems [20]. Several studies have integrated XAI frameworks into cancer prediction systems to improve interpretability [21]. Another important aspect highlighted in the literature is the role of data preprocessing and feature engineering in improving model performance [22]. Handling missing values, data normalization, and outlier detection are essential steps in building reliable predictive models [23]. Researchers have also explored the use of large-scale healthcare databases to train predictive models for cancer detection [24]. The integration of electronic health records with

machine learning systems has enabled the development of more accurate and scalable healthcare solutions [25]. Additionally, web-based clinical decision support systems have been proposed to assist healthcare professionals in disease diagnosis and risk assessment [26]. These platforms enable clinicians to input patient data and obtain real-time predictive insights [27]. Modern healthcare systems increasingly rely on cloud computing and distributed databases to manage large volumes of medical data [28]. This technological advancement allows predictive systems to process complex datasets efficiently [29]. Overall, the literature highlights the growing importance of AI-driven healthcare systems in improving disease prediction and clinical decision-making [30].

### **III METHODOLOGY**

The methodology of the proposed ovarian cancer prediction system involves multiple stages, including data collection, preprocessing, feature selection, model development, evaluation, and deployment. Initially, a clinical dataset containing patient demographic information, hematological parameters, metabolic indicators, and tumor markers was collected. Key features considered in the dataset include age, menopausal status, white blood cell count, red blood cell count, hemoglobin level, platelet count, glucose level, creatinine, calcium, and tumor biomarkers such as CA125, HE4, and AFP. Data preprocessing is performed to ensure data quality and reliability. This step includes handling missing values, removing duplicate entries, detecting outliers, and normalizing feature values to ensure uniform data distribution. Feature selection techniques are then applied to identify the most relevant attributes that significantly influence ovarian cancer prediction. After preprocessing, the dataset is divided into

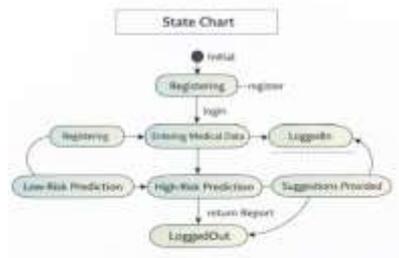
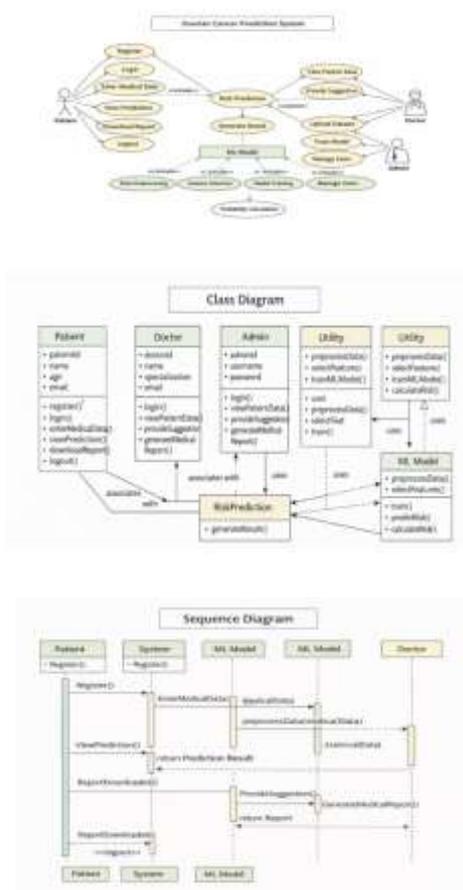
training and testing subsets to evaluate model performance. Various machine learning algorithms such as Logistic Regression, Support Vector Machines, and Random Forest are implemented to classify patients into cancer risk categories. In addition to classical machine learning models, deep learning techniques including Feedforward Neural Networks are also implemented to capture complex nonlinear relationships among clinical variables. The performance of these models is evaluated using standard evaluation metrics such as accuracy, precision, recall, F1-score, and confusion matrix. The best-performing model is selected based on its predictive performance and generalization ability. To improve interpretability, Explainable Artificial Intelligence techniques such as SHAP are integrated into the system to determine the contribution of each clinical parameter toward the prediction result. Finally, the trained model is deployed within a web-based clinical decision support system that enables healthcare professionals to input patient parameters and obtain real-time predictions. This integrated methodology ensures accurate, interpretable, and scalable ovarian cancer prediction.

### **IV SYSTEM DESIGN**

The system design of the ovarian cancer prediction platform follows a modular and scalable architecture that integrates data processing, predictive modeling, and user interaction components. The architecture consists of three primary layers: the presentation layer, the application layer, and the data layer. The presentation layer represents the user interface through which healthcare professionals interact with the system. This interface is developed using modern web technologies to provide an intuitive and responsive environment for entering patient data and viewing prediction results. The user

interface includes forms for inputting clinical parameters such as patient age, blood test results, and tumor marker levels. Once the data is entered, it is transmitted securely to the backend server for processing. The application layer is responsible for implementing the machine learning models and processing user requests. This layer contains the core predictive engine that analyzes the input data and generates cancer risk predictions. The backend system is implemented using a high-performance API framework that handles user requests, processes input data, and communicates with the database. The predictive engine integrates various machine learning algorithms trained on historical clinical datasets. The application layer also includes modules for data preprocessing, feature scaling, and model inference to ensure consistent prediction results. Additionally, explainability modules are incorporated to provide interpretability of predictions through feature importance analysis.

The data layer serves as the storage and management component of the system architecture. This layer stores patient records, clinical datasets, and prediction results in structured databases. Relational databases are used to manage user accounts, authentication, and administrative data, while NoSQL databases are utilized to handle large volumes of clinical data and prediction logs. The system ensures data privacy and security through authentication mechanisms and secure communication protocols. When a clinician enters patient data into the system, the information is temporarily processed and then stored in the database for future analysis and auditing. The predictive model processes the data and returns a risk prediction score indicating the likelihood of ovarian cancer. The results are displayed on the user interface along with explanatory insights that highlight which clinical factors influenced the prediction. This design allows healthcare professionals to quickly interpret the results and make informed decisions regarding patient diagnosis or further testing. The modular architecture also enables easy integration of additional machine learning models, datasets, or analytical tools in the future. Overall, the system design ensures scalability, efficiency, and reliability in delivering real-time ovarian cancer prediction and decision support for healthcare providers.



## V PROPOSED SYSTEM

The proposed system introduces an advanced Artificial Intelligence-based Clinical Decision Support System designed to improve early

detection and risk prediction of ovarian cancer. The system leverages machine learning and deep learning techniques to analyze patient clinical data and predict the likelihood of ovarian cancer development. Unlike traditional diagnostic approaches that rely primarily on individual biomarkers or imaging results, the proposed system integrates multiple clinical features to generate more accurate predictions. The system utilizes a dataset consisting of demographic information, hematological indicators, metabolic parameters, and tumor markers. These features provide a comprehensive representation of patient health conditions that may influence ovarian cancer risk. The predictive models are trained using supervised learning techniques where historical patient records with known outcomes are used to train classification algorithms. The system implements several machine learning models, including Logistic Regression, Random Forest, and Support Vector Machines, to evaluate their predictive performance. Additionally, a deep learning-based Feedforward Neural Network is implemented to capture complex nonlinear relationships between the features. During training, the models learn patterns associated with cancer-positive and cancer-negative cases, enabling them to classify new patient data accurately. Model evaluation is conducted using cross-validation techniques to ensure that the selected model generalizes well to unseen data.

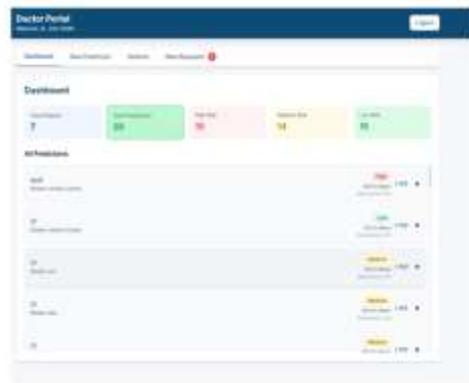
Another key component of the proposed system is the integration of Explainable Artificial Intelligence to enhance model transparency. In many healthcare applications, clinicians require clear explanations of how predictions are generated before they can rely on automated systems. To address this issue, the proposed system incorporates SHAP-based explainability techniques that analyze the influence of each feature on the final prediction. When a

prediction is generated, the system displays not only the risk score but also the contribution of individual biomarkers such as CA125, HE4, and other clinical parameters. This information enables clinicians to understand which factors significantly contributed to the prediction outcome. The proposed system is implemented as a web-based platform that allows healthcare professionals to access the prediction system through a user-friendly interface. The backend infrastructure manages data processing, model inference, and database communication, while the frontend provides interactive visualization of prediction results. The system also maintains patient records and prediction histories for future reference and analysis. By integrating predictive analytics with interpretable AI techniques, the proposed system provides a reliable and efficient tool for early ovarian cancer risk assessment. This approach has the potential to support medical professionals in clinical decision-making, reduce diagnostic delays, and improve patient outcomes through timely detection and treatment.

## **VI RESULTS & DISCUSSION**

The experimental evaluation of the proposed ovarian cancer prediction system demonstrates promising results in terms of predictive accuracy and reliability. Multiple machine learning models were implemented and evaluated using standard performance metrics such as accuracy, precision, recall, and F1-score. Among the tested models, the Random Forest and Neural Network models achieved the highest accuracy in predicting ovarian cancer risk. The results indicate that combining multiple clinical features significantly improves prediction performance compared to using individual biomarkers alone. The integration of Explainable Artificial Intelligence techniques further enhanced the interpretability of the model

predictions. SHAP analysis revealed that tumor markers such as CA125 and HE4 contributed significantly to the prediction outcomes, along with other clinical indicators such as age and blood parameters. The system successfully generated interpretable risk predictions that can assist healthcare professionals in identifying high-risk patients. Overall, the results demonstrate that the proposed AI-based system can serve as an effective tool for supporting early ovarian cancer detection.



The screenshot shows a 'Patient Registration' form with several sections: 'Account Information', 'Personal Information', and 'Medical History'. Each section contains various input fields for text, dates, and checkboxes. At the bottom, there are buttons for 'Request', 'Family History of Disease?', and 'Register'.

Ovarian Cancer Risk Assessment Report

**Patient Information**

Patient Name	John
Age	55 (2 years)
Marital Status	Married
CA 125	200 U/ml
HE4	1.5 U/ml
CA 158	1.2 U/ml
CA 199	0.8 U/ml
CA 229	0.5 U/ml
CA 242	0.3 U/ml
CA 272	0.2 U/ml
CA 319	0.1 U/ml
CA 349	0.1 U/ml
CA 359	0.1 U/ml
CA 373	0.1 U/ml
CA 394	0.1 U/ml
CA 415	0.1 U/ml
CA 450	0.1 U/ml
CA 486	0.1 U/ml
CA 500	0.1 U/ml
CA 549	0.1 U/ml
CA 577	0.1 U/ml
CA 615	0.1 U/ml
CA 629	0.1 U/ml
CA 645	0.1 U/ml
CA 675	0.1 U/ml
CA 724	0.1 U/ml
CA 750	0.1 U/ml
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CA 9948	0.1 U/ml
CA 9978	0.1 U/ml
CA 10008	0.1 U/ml

**Prediction Results**

Risk Level	High
Risk Probability	85.5%
Model Used	Support Vector
Date	2024-03-18 10:30:00

This report is generated by an AI system and should be used as a decision support tool. Final diagnosis should be made by qualified medical professionals.



VII CONCLUSION

Ovarian cancer remains a major health concern due to its high mortality rate and the challenges associated with early diagnosis. Traditional

diagnostic methods often detect the disease only after it has progressed to advanced stages, significantly reducing treatment success rates. In this study, an Artificial Intelligence-based ovarian cancer prediction system was developed to support early detection and clinical decision-making. The proposed system integrates machine learning and deep learning algorithms to analyze patient clinical data and predict cancer risk with improved accuracy. By utilizing multiple features including demographic data, hematological indicators, metabolic parameters, and tumor biomarkers, the system provides a comprehensive approach to ovarian cancer prediction. Various machine learning models were implemented and evaluated, and the results demonstrated that advanced algorithms such as Random Forest and Neural Networks provide reliable prediction performance. An important contribution of this study is the integration of Explainable Artificial Intelligence techniques to improve model transparency. By using SHAP-based interpretability methods, the system provides insights into the contribution of each feature in generating prediction results. This helps clinicians understand the reasoning behind model predictions and increases trust in AI-based healthcare systems. Additionally, the system is implemented as a scalable web-based platform, enabling easy interaction for healthcare professionals and real-time risk prediction. The proposed approach has the potential to assist doctors in identifying high-risk patients at an early stage, enabling timely diagnostic tests and treatment interventions. In the future, the system can be further enhanced by incorporating larger clinical datasets, integrating medical imaging data, and applying advanced deep learning techniques to improve prediction accuracy and reliability.

## REFERENCES

1. Siegel, R. L., Miller, K. D., & Jemal, A. (2020). Cancer statistics. CA: A Cancer Journal for Clinicians.
2. Torre, L. A., et al. (2018). Ovarian cancer statistics worldwide. *Cancer Epidemiology*.
3. Reid, B. M., et al. (2017). Ovarian cancer detection and treatment. *Nature Reviews Cancer*.
4. Bast, R. C., et al. (2005). CA125 biomarker in ovarian cancer. *Clinical Cancer Research*.
5. Moore, R. G., et al. (2014). HE4 biomarker for ovarian cancer detection. *Gynecologic Oncology*.
6. Kourou, K., et al. (2015). Machine learning in cancer prognosis. *Computational and Structural Biotechnology Journal*.
7. Cruz, J. A., & Wishart, D. S. (2006). Applications of machine learning in cancer prediction. *Cancer Informatics*.
8. Topol, E. (2019). High-performance medicine and AI. *Nature Medicine*.
9. Esteva, A., et al. (2019). AI in healthcare applications. *Nature Medicine*.
10. Kononenko, I. (2001). Machine learning in medical diagnosis. *Artificial Intelligence in Medicine*.
11. Cortes, C., & Vapnik, V. (1995). Support vector machines. *Machine Learning*.
12. Breiman, L. (2001). Random forests. *Machine Learning*.
13. LeCun, Y., et al. (2015). Deep learning. *Nature*.

14. Litjens, G., et al. (2017). Deep learning in medical image analysis. *Medical Image Analysis*.
15. Chen, H., et al. (2019). Deep learning for cancer prediction. *IEEE Access*.
16. Samek, W., et al. (2017). Explainable AI methods. *IEEE Signal Processing Magazine*.
17. Doshi-Velez, F., & Kim, B. (2017). Towards interpretable machine learning. *arXiv*.
18. Ribeiro, M. T., et al. (2016). LIME interpretability model. *KDD Conference*.
19. Lundberg, S., & Lee, S. (2017). SHAP explanations. *NeurIPS*.
20. Guidotti, R., et al. (2018). Explainable AI survey. *ACM Computing Surveys*.
21. Holzinger, A., et al. (2017). What do we need for explainable AI in medicine? *arXiv*.
22. Kuhn, M., & Johnson, K. (2013). *Applied Predictive Modeling*. Springer.
23. Han, J., et al. (2011). *Data Mining Concepts and Techniques*. Morgan Kaufmann.
24. Jensen, P. B., et al. (2012). Mining electronic health records. *Nature Reviews Genetics*.
25. Raghupathi, W., & Raghupathi, V. (2014). Big data analytics in healthcare. *Health Information Science*.
26. Shortliffe, E., & Cimino, J. (2013). *Biomedical Informatics*. Springer.
27. Bates, D. W., et al. (2018). Clinical decision support systems. *BMJ*.
28. Rajkomar, A., et al. (2019). Machine learning in healthcare systems. *New England Journal of Medicine*.
29. Beam, A. L., & Kohane, I. S. (2018). Big data in healthcare. *JAMA*.
30. Jiang, F., et al. (2017). Artificial intelligence in healthcare. *Stroke and Vascular Neurology*.