Science World Journal Vol. 20(No 4) 2025 https://dx.doi.org/10.4314/swj.v20i4.24
www.scienceworldjournal.org
ISSN: 1597-6343 (Online), ISSN: 2756-391X (Print)
Published by Faculty of Science, Kaduna State University

Full Length Research Article

COMPARATIVE ANALYSIS OF SELECTED MACHINE LEARNING MODELS FOR THE PREDICTION OF OVARIAN CANCER

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ABSTRACT
Ovarian cancer is among the most common cancers and represents one of the top causes of cancer death in women. One of the main ways to enhance survival of patients with ovarian cancer is to catch it early, but this is difficult since ovarian cancer is asymptomatic in its early stages. Accurate and rapid prediction of ovarian tumors would be useful. Building a model based upon artificial intelligence methods could be one acceptable and accurate method of detecting and predicting this cancer. As previous research has shown, Machine Learning (ML) techniques can support early cancer detection efforts. However, the abilities of these techniques hindered by false positive rates and overfitting, and also by other challenges in generalizing a model. In this study, we will review the performance of six popular algorithms - Support Vector Machine (SVM), Random Forest (RF), Decision Tree (DT), Logistic Regression (LR), Naive Bayes (NB), and K-Nearest Neighbors (KNN) - for the prediction of ovarian cancer with a dataset of 349 patients, which includes 49 clinical and biochemical features from pathology diagnoses. In medicine, the accuracy of interpretation is vital, as misinterpretation could lead to adverse health outcomes. Therefore, all models were examined in terms of accuracy, precision, recall, and F1 score. The Naïve Bayes model performed best overall with the highest accuracy (87.14 %) and precision (87.58 %), whereas the Random Forest model demonstrated the strongest recall (87.56 %). Logistic Regression showed comparable performance across all metrics, whilst K-Nearest Neighbour performed the weakest in all metrics evaluated. These findings support the possibility for ML algorithms, Naïve Bayes in particular, and Random Forest, to be used in improving early detection of ovarian cancer. In conclusion, the study demonstrates the promise of ML for the advancement of the diagnosis of cancer and ultimately improving patient care.

Keywords: Artificial Intelligence, Ovarian cancer prediction, Machine learning, Early detection, Diagnostic models.

INTRODUCTION

Cancer results from uncontrolled development and spread of abnormal cells in the body. Usually, a cell that is damaged will undergo apoptosis (programmed cell death), and will be replaced by a healthy cell. If this process is disrupted, a damaged cell may stay alive and proliferate, eventually forming a tumor. Tumors can be benign (not cancerous), or malignant (cancerous), and malignant tumors have the potential to invade neighboring tissues and spread to other organs (Johariya et al., 2024; Hasan, 2024). Ovarian cancer, which develops from abnormal growth of cells in the ovaries, is one of the most lethal cancers in women. Ovarian cancer, if detected too late, can spread to other organs, reducing the probability of successful treatment (Pal et al., 2024). Ovaries are crucial structures in the female reproductive system, where eggs are produced and hormones such as estrogen and progesterone are generated. Ovarian cancer makes up approximately 4 % of all cancers in women, but it is one of the deadliest cancers in gynecology (Ali, Al-Ani & Al-Ani, 2023).

The initial symptoms of ovarian cancer can be vague and unspecific, which can complicate a timely diagnosis. The common symptoms include abdominal discomfort, bloating, nausea, alterations in bowel habits and/or unexplained weight loss (Keyvani et al., 2023). Risk factors include family history of ovarian or breast cancer, later menopause and older age of childbirth (Sideris, Menon & Manchanda, 2024). Diagnosis is mainly through imaging, genetic testing, pelvic exam, and biopsy, with ultrasound and the CA-125 blood test being the most commonly used. Due to the vague early symptoms, as well as no effective screening (unlike cervical and breast cancer), ovarian cancer presents at later stages when prognosis is much poorer (Gandhi, Zubair & Bhatt, 2024).

Survival rates of ovarian cancer differ largely due to stage at diagnosis. The five-year survival rate for stage 1 is as high as 92 % but drops to 22 % for stage 3 (Baker, 2024). Due to the vague early signs of ovarian cancer, and no regular screening tests, more than 50% of patients will be diagnosed with advanced stage cervical cancer (Fernandes, 2024)).

The prognosis for ovarian cancer varies greatly according to the stage at diagnosis. For stage 1, the five-year survival rate is up to 92 %. For stage 3, this rate drops significantly to 22 % (Baker, 2024). Unfortunately, owing to the insidious nature associated with early-stage ovarian cancer and the absence of routine screening methods, more than 50 % of patients with ovarian cancer are diagnosed at late stages (Fernandes, 2024). Ovarian cancer is divided into four stages; the earliest stage of development is simply when the cancer is localized in the ovaries - stage 1; and the final stage is stage 4, when the ovarian cancer metastasizes to distant organs, including the liver or lungs (Wang et al., 2024).

Recently, advancements made in artificial intelligence (AI) and machine learning (ML) have shown great promise for advancing healthcare, specifically for diagnosing and predicting the progression of diseases (Sarker, 2024). Machine learning, which is a category of AI, is particularly good at analyzing large-scale medical data, which can lead to the development of predictive models that can evaluate multiple factors at once (Ali & Mohammed, 2024; Naik et al., 2024). Machine learning has shown to be especially beneficial with regard to early detection and

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diagnostic of numerous diseases, including ovarian cancer (Fatima, 2024). If realized, these advancements will improve early detection, prognostication, and allow for more accurate and timely treatment of patients.

A variety of machine learning models (i.e., Decision Trees (DT), Support Vector Machines (SVM), Logistic Regression (LR), and Artificial Neural Networks (ANN) have been utilized to predict ovarian cancer (Ayyoubzadeh et al., 2024; Mysona et al., 2023; Liu et al., 2023). These models have achieved positive results, but their efficacy is impacted by issues of high false positives and false negatives, as well as some overfitting (Xu, Coen-Pirani & Jiang, 2023). The issue of overfitting arises when a model performs extremely well on training data, but greatly underplays its ability to generalize to new or unseen data, decreasing confidence in real-world applications, which clearly impacts efficacious use of such predictive models. Ensemble learning solutions have been introduced to address these concerns. Using ensemble learning, we take the opportunity to collectively learn from each model (not only an individual error) in order to combine models and minimize the errors that are susceptible to models of its nature (i.e. white-box versus black-box). Stacking in particular has been utilized as an ensemble learning where multiple models through a meta-learner, have the potential to leverage one another's strengths to increase predicting prediction accuracy (Mahesh et al., 2024). While the strength of stacking is dependent on its associative process of taking a variety of models, and limiting weaknesses of individual algorithms, the collective arrangement of how the combination of models work demonstrates how they work towards reliably and accurately finding a prediction (Jannat et al., 2023; Guo et al., 2020).

The growing use of machine learning algorithms for ovarian cancer diagnosis suggests that more research on an optimized machine learning model in this domain is warranted. This research compares six different machine learning algorithms: K-Nearest Neighbors (KNN), Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), Naive Bayes (NB), and Logistic Regression (LR) for predicting ovarian cancer.

MATERIALS AND METHODS

This study utilized a machine learning pipeline approach with multiple stages: dataset collection, data exploration and preprocessing, dataset splitting, model training, model testing, model performance evaluation, performance comparison, and conclusion. The overall pipeline design is illustrated in Figure 1. Each stage of the pipeline will be elaborated upon individually in the next sections to provide all-inclusive understanding of the processes in achieving the goal of the study.

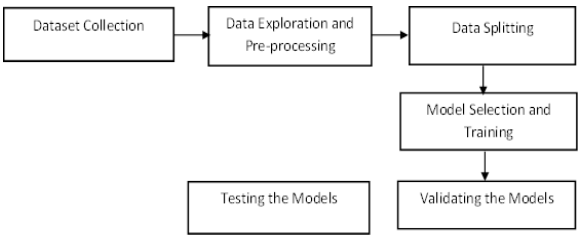

Figure 1: Research Design

Data Collection

This study utilized a dataset from July 2011 to July 2018 that included 349 patients from the Third Affiliated Hospital of Soochow University. The dataset from the Third Affiliated Hospital of Soochow University is considered reliable for research purposes as it is frequently used in studies published in reputable, peer-reviewed medical journals such as those indexed by The National Institute of Health (NIH). Patients with the following diagnoses were included in this dataset: 178 patients diagnosed with benign ovarian tumors; 171 patients diagnosed with ovarian cancer. (https://www.kaggle.com/datasets/saurabhshahane/predict-ovarian-cancer, accessed on October 27, 2023). A total of 49 clinical features were collected based on pathological diagnosis, including 22 from general chemical tests, 19 from blood routine tests, and 6 tumor markers, as well as age and menopause-related information. All patients were diagnosed postoperatively with no preoperative radiotherapy or chemotherapy. The histological diagnoses were classified with respect to the World Health Organization criteria.

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Data Exploration and Pre-processing

Data preprocessing played an essential part in this study, improving data quality and preparing the data for machine learning. Critical elements of preprocessing in this work were the removal of duplicates to limit noise in the dataset, the resolution of mislabeled data to ensure accuracy of the analysis, and the conversion of categorical variables to numerical form to be in line with the algorithms. Any instances of missing values and infinite values were treated by either imputing or omitting missing values and replacing infinite values with zero to maintain consistency. In addition, the data underwent feature scaling using a Min-Max scaler to ensure normalized data (0 to 1). Finally, the dataset was separated into training and test sets for an unbiased evaluation of the model.

Data Splitting

Typically, data splitting consists of splitting the dataset into two sets—one set for training and the other for testing. In this study, the dataset was split in the way that was specific to the study's purposes. Here the models learn patterns that it can draw upon from the training set that performs well on the test set of data. A common split ratio of 70 % - 30 % was applied to ensure there was enough data for training the models, while also maintaining a sufficiently large testing set for evaluating the predictive performance of each model.

Model Validation Technique

The goal of model validation is to provide a more accurate estimate of a model's ability to perform on new or unseen data. This process is crucial to ensure that the model is accurate, reliable, and generalizes well.

A predominant validation method employed in this work is the K-fold cross-validation technique, with a value of K set to 10, signifying a 10-fold cross-validation.

Model Selection and Training

Machine Learning (ML) has demonstrated significant potentials in the area of healthcare, especially in predicting and diagnosing disease, including cancer. In ovarian cancer, machine learning algorithms can assess large datasets of patients to find patterns and characteristics that could ultimately identify women with ovarian cancer sooner and more accurately. To accurately train an ML model, it is essential to have high-quality, representative, and properly pre-processed data, and then tune the hyperparameters

of the algorithm to optimize performance. In this study, a total of six ML techniques were included: K-Nearest Neighbors (KNN), Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), Naive Bayes (NB), and Logistic Regression (LR). The hyperparameters used for each ML model, as shown in Table 1, were tuned by GridSearchCV, which evaluates the ML hyperparameters across a pre-defined range of values to determine the setting for optimally trained algorithms. The specified ranges for hyperparameter tuning were taken from the existing literature, and customized to fit the specifics of the dataset used in this study.

Table 1: Hyperparameter Details for Classifiers

Classifier	Hyperparameter
SVM	n_estimators = 120, learning_rate = 0.2, max_depth = 45
RF	n_estimators = 120, criterion = 'entropy', max_depth = 45
DT	learning_rate = 'optimal', epsilon = 0.2
LR	n_estimators = 120, max_depth = 45, criterion = 'entropy'
NB	n_estimators = 120, learning_rate = 0.2, max_depth = 45
KNN	n_neighbors = 5, leaf_size = 45

Testing the Models
Following successful validation, the models are evaluated using a test dataset to demonstrate their ability to generalize to new, unseen data. This is where the models are evaluated: Support Vector Machine, Decision Tree, Logistic Regression, K-Nearest Neighbors, and Naïve Bayes.

Performance Evaluation
The models' performance is evaluated using Scikit-learn's accuracy score and confusion matrix. These metrics offer valuable insights into how effectively the models classify ovarian cancer cases correctly.

Performance Comparison
The last step involves comparing the performance of the models to determine which model is best at predicting ovarian cancer. The model with better overall accuracy and good performance on other criteria will be selected for further development and possible deployment.

Performance Evaluation Metrics
Various criteria are commonly used to assess the effectiveness of a classification model, including metrics such as accuracy, precision, recall, and F1-score.

Accuracy
Accuracy is the percentage of correct predictions produced by the algorithm to the overall quantity of projections made.

$$\text{Accuracy } (\%) \frac{TP+TN}{TP+TN+FP+FN} \times 100 \quad (1)$$

Precision
Precision is determined as the ratio of true positives to the total of true positives and false positives. The equation representing precision is as follows:

$$Precison = \frac{TP}{TP+FP} \quad (2)$$

Recall
Recall is a numerical measurement that defines the percentage of accurately identified positive cases that were falsely marked as negative by the model. It is also known as the true positive rate. It is mathematically defined as the ratio of the number of true positive (TP) cases divided by the sum of all true positives + false negatives (FNs)

$$Recall = \frac{TP}{TP+FN} \quad (3)$$

RESULTS AND DISCUSSION
In this research, several machine learning (ML) models are utilized for ovarian cancer detection. The dataset is split into training and testing data in a 70:30 form, which is a standard practice in classification projects to limit the risk of overfitting. Performance is defined and evaluated using different metrics that are appropriate for ML classifiers. All of the experiments are created in a Python environment (3.12.0) with libraries, on a Dell PowerEdge T430 GPU (Chongqing, China), with 2 GB of memory, dual Intel Xeon 8-Core processors running at 2.4 GHz, and 32 GB DDR4 of RAM

Results of the Machine-Learning Models
The performance evaluation of the machine learning models listed in Table 2 was assessed with four metrics: Accuracy, Precision, Recall, and F1 Score. The four metrics expressed a holistic ability for each model to predict cases of ovarian cancer. The Naive Bayes (NB) models performed the best overall across all four metrics, with an accuracy of 87.14 % and well-aligned precision, recall, and F1 scores indicating a balanced and reliable performance. The following classification model was Logistic Regression (LR), which also performed competitively to the NB model at 86.89 % for accuracy. The Random Forest (RF) model performed better than all models on recall (87.56 %), but was slightly lower than the NB model on accuracy. Lastly, the K-Nearest Neighbor (KNN) model performed the lowest in this analysis of the four models at 77.94 % accuracy, suggesting limitations for the model in this use case.

Table 2: Performance Evaluation of the Machine Learning Model

Model	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)
SVM	85.52	85.42	85.43	85.42
RF	85.66	86.35	87.56	86.22
DT	84.94	85.72	85.87	85.65
LR	86.89	86.52	86.52	86.52
NB	87.14	87.58	87.53	87.19
KNN	77.94	77.43	78.36	77.98

The accuracy chart in Figure 2 demonstrates the proportion of instances that were accurately classified by each of the models out of all samples. The Naïve Bayes (NB) model had the highest accuracy with 87.14%. This represents a noteworthy degree of efficacy in differentiating between ovarian cancer and benign cases, indicating that this model has a strong ability in this data set. K-Nearest Neighbors (KNN) had the lowest level of accuracy of 77.94% indicating that KNN may exhibit difficulty in generalizing with datasets with diverse or overlapping features.

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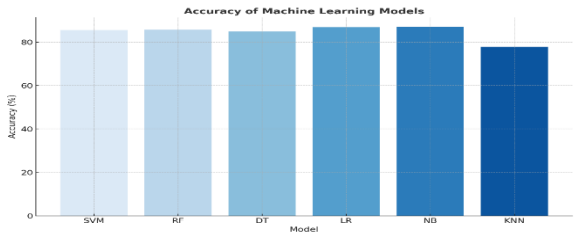

Figure 2: Accuracy Score of the Selected Models

Precision is an important metric for evaluating a model's ability to minimize false positives, which is especially critical in medical diagnostics. As shown in Figure 3, the NB model leads with a precision of 87.58 %, demonstrating its effectiveness in accurately identifying positive cases without misclassifying negatives as positives. In contrast, KNN achieved the lowest precision at 77.43 %, indicating that it may mistakenly label benign cases as ovarian cancer, potentially leading to unnecessary treatments or interventions.

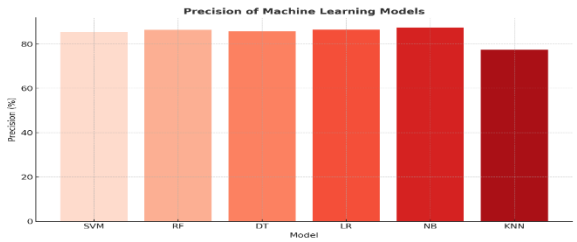

Figure 3: Precision Score of the Selected Models

Recall is an essential metric for ensuring that all actual positive cases are identified, reducing the likelihood of missing ovarian cancer diagnoses. As shown in Figure 4, the Random Forest (RF) model achieved the highest recall of 87.56%, demonstrating its effectiveness in minimizing false negatives. This makes RF particularly useful in situations where failing to detect a diagnosis could have serious consequences. On the other hand, KNN achieved a recall of 78.36%, indicating its limitations in identifying all true positive cases.

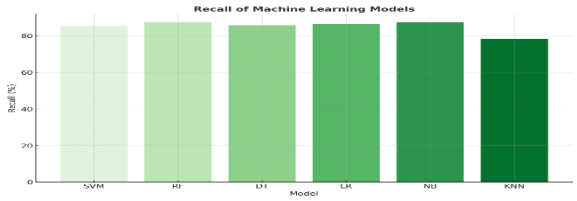

Figure 4: Recall Score of the Selected Models

The F1 Score is so valuable as it provides a balance of both precision and recall. This is especially critical in contexts such as medical applications, where both false positives and false negatives may have implications. As demonstrated in Figure 5, the NB model produced the highest F1 Score of 87.19 %, demonstrating its capacity to perform well in classifying ovarian cancer data. The KNN model produced an F1 Score of 77.98 %, demonstrating that it is less capable of appropriately balancing precision and recall, limiting its usefulness in this context.

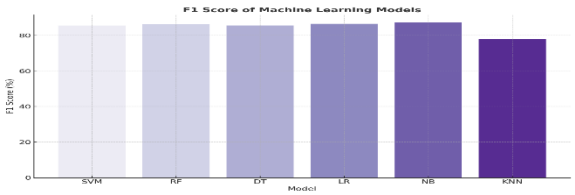

Figure 5: F1 Score of the Selected Models

DISCUSSION

This research examined the use of machine learning (ML) algorithms for predicting ovarian cancer using clinical and biochemical data from a dataset in the public domain. The primary aim was to evaluate the performance of six popular ML algorithms: Support Vector Machine (SVM), Random Forest (RF), Decision Tree (DT), Logistic Regression (LR), Naive Bayes (NB), and K-Nearest Neighbors (KNN) based on their accuracy, precision, recall, and F1 Score. These metrics are important for determining the predictive performance and trustworthiness of the models, especially in the critical field of medical diagnostics.

Performance Evaluation

The comparative analysis shown in Figure 6 of six machine learning models—SVM, Random Forest (RF), Decision Tree (DT), Logistic Regression (LR), Naïve Bayes (NB), and K-Nearest Neighbors (KNN)—demonstrates notable variations in their performance across four key metrics: Accuracy, Precision, Recall, and F1 Score.

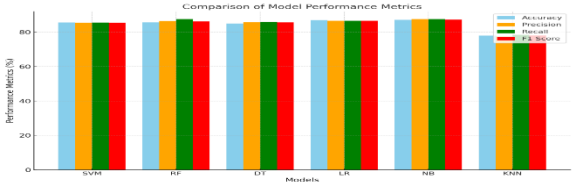

Figure 6: Comparison of Model Performance Metrics

The results indicated that Naive Bayes consistently outperformed each of the other models in all metrics, producing the highest accuracy (87.14 %), precision (87.58 %), and F1 Score (87.19 %). This robust performance suggests that NB can effectively account for the data's distribution and feature interactions, thus making it a solid choice for a predictive model for ovarian cancer. Random Forest also performed strongly, recording the highest recall (87.56 %) of all of the models. Capturing complex relationships is inherent in the model's ability to employ an ensemble of decision trees, which can predict positive cases; this is important for minimizing false negatives in a medical context. Logistic Regression showed powerful performance with an accuracy of 86.89% and a good balance between precision and recall. Its straightforwardness and interpretability make it a good baseline model for predicting ovarian cancer. Decision Tree and SVM both had similar performance with class accuracies of 84.94 % and 85.52 %, respectively. However, these models may struggle to capture complex relationships in high-dimensional datasets, as indicated by their slightly lower scores compared to Random Forest (RF) and Naive Bayes (NB).

K-Nearest Neighbors showed the weakest performance, scoring the lowest across all metrics. This underperformance could be attributed to its sensitivity to noisy or imbalanced data and its lack of advanced methods for handling feature weighting effectively.

Comparative Insights

The comparative analysis of the models emphasizes the trade-offs between simplicity and predictive power. Complex models like RF and NB utilize advanced techniques to capture intricate data patterns, while simpler models such as LR and DT strike a balance between computational efficiency and interpretability. In contrast, KNN, which relies on proximity metrics, may struggle with complex datasets, particularly when it comes to generalizing to unseen data.

Clinical Implications

The findings highlight the potential of machine learning models in enabling early detection of ovarian cancer, which is crucial for improving patient outcomes. Timely diagnosis facilitates early intervention, greatly enhancing survival rates. However, selecting an appropriate ML model requires consideration not only of its predictive accuracy but also of its interpretability and computational efficiency, especially for deployment in clinical settings.

Naive Bayes and Random Forest stand out as strong candidates for integration into decision-support systems due to their high performance and reliability. However, further validation on larger, more diverse datasets is needed to confirm their generalizability. Additionally, incorporating feature selection techniques and addressing class imbalances could further optimize the performance of these models.

Conclusion

This study aimed to evaluate the effectiveness of several machine learning (ML) models for predicting ovarian cancer, using a dataset of 349 patients with a total of 49 features, including patient demographics, pathology reports, blood tests, and tumor markers. Following pre-processing, the dataset was split into training and test datasets and was analyzed as part of a pipeline with model training, modeling, and test assessment. Model performance was evaluated utilizing key performance metrics such as accuracy, precision, recall, and F1 score for Support Vector Machine (SVM), Random Forest (RF), Decision Trees (DT), Logistic Regression (LR), Naive Bayes (NB), and K-Nearest Neighbors (KNN).

The findings indicated that Naive Bayes surpassed the other models on most metrics. With an accuracy (87.14%), precision (87.58%), recall (87.53%), and F1 score (87.19%), NB showed its ability to classify both ovarian cancer and benign cases correctly. The results are a testament of Naive Bayes's ability to capture the overall patterns of the data and balance the false positives and false negatives in the predictions. Logistic Regression and Random Forest were also close, with similar accuracy and precision scores, confirming they are promising models to use in the predictive analytics of ovarian cancer.

On the contrary, K-Nearest Neighbors exhibited the least performance on all metrics with an accuracy of 77.94 % and F1 score of 77.98 %. This implies KNN potentially struggles with the complexity or feature overlap within the data. While KNN is simplistic and interpretable, its performance limitations indicate that it is likely not the best modelling option for prediction tasks in ovarian cancer without additional augmentation or dimensionality reduction techniques.

This study emphasizes the need to choose appropriate models for medical diagnoses where both accuracy and recall are important components of the model. The Naive Bayes model emerged as the best balanced and most effective model for the analysis of the data. The Random Forest excelled in maximizing recall, making it particularly useful in situations where minimizing false negatives is crucial. Logistic Regression also proved to be a reliable and interpretable model.

Future research studies could investigate hybrid models or engage in ensemble modeling to improve predictive accuracy and robustness. The mathematical models can be evaluated using a larger and more diverse data set to improve their generalizability to a broader population. Lastly, previously discussed updated feature selection methods, including deep learning could also be included in the prediction of ovarian cancer diagnostics to improve prediction accuracy.

Conflict of Interest: The corresponding author, representing all the contributions, confirms the absence of any disputes of interest.

REFERENCES

Ali, A. M., & Mohammed, M. A. (2024). A comprehensive review of artificial intelligence approaches in omics data processing: evaluating progress and challenges. International Journal of Mathematics, Statistics, and Computer Science, 2, 114-167.

Ali, A. T., Al-Ani, O., & Al-Ani, F. (2023). Epidemiology and risk factors for ovarian cancer. Menopause Review/Przegląd Menopauzalny, 22(2), 93-104.

Ayyoubzadeh, S. M., Ahmadi, M., Yazdipour, A. B., Ghorbani-Bidkorpeh, F., & Ahmadi, M. (2024). Prediction of ovarian cancer using artificial intelligence tools. Health Science Reports, 7(7), e2203.

Baker, T. (2024). Early Detection, Symptoms, and Treatment Options for Ovarian Cancer. International Journal of Advanced Engineering Technologies and Innovations, 10(2), 332-343.

Fatima, S. (2024). PREDICTIVE MODELS FOR EARLY DETECTION OF CHRONIC DISEASES LIKE CANCER. Olaoye, G.

Fernandes, B. (2024). A Review on Emerging Biomarkers for Early Detection of Ovarian Cancer. Indian Journal of Pharmacy Practice, 17(1).

Gupta, S., Gupta, M. K., & Kumar, R. (2022). A Novel Multi-Neural Ensemble Approach for Cancer Diagnosis A Novel Multi-Neural Ensemble Approach for Cancer Diagnosis. Applied Artificial Intelligence, 36(1). https://doi.org/10.1080/08839514.2021.2018182

Hassan, M., Hassan, M., Yasmin, F., & Rakib, A. (2023). A comparative assessment of machine learning algorithms with the Least Absolute Shrinkage and Selection Operator for breast cancer detection and prediction. 7(May).

Jannat, N., Hasan, S. M., Efat, A. H., Taraque, M. F., Mitu, M., Al Mamun, M., & Faruk, M. F. (2023, February). Stacking ensemble technique for multiple medical datasets classification: A generalized prediction model. In 2023 International Conference on Electrical, Computer and Communication Engineering (ECCE) (pp. 1-6). IEEE.

Johariya, V., Joshi, A., Malviya, N., & Malviya, S. (2024). Introduction to Cancer. In Medicinal Plants and Cancer Chemoprevention (pp. 1-28). CRC Press.

Keyvani, V., Kheradmand, N., Navaei, Z. N., Mollazadeh, S., & Esmaeili, S. A. (2023). Epidemiological trends and risk factors of gynecological cancers: an update. Medical Oncology, 40(3), 93.

Liu, Y., Lawson, B. C., Huang, X., Broom, B. M., & Weinstein, J. N. (2023). Prediction of ovarian cancer response to therapy based on deep learning analysis of histopathology images. Cancers, 15(16), 4044.

Mahesh, T. R., Vinoth Kumar, V., Vivek, V., Karthick Raghunath, K. M., & Sindhu Madhuri, G. (2024). Early predictive model for breast cancer classification using blended ensemble learning. International Journal of System Assurance Engineering and Management, 15(1), 188-197.

Mysona, D. P., Purohit, S., Richardson, K. P., Suhner, J., Brzezinska, B., Rungruang, B., ... & Ghamande, S. (2023). Ovarian recurrence risk assessment using machine learning, clinical information, and serum protein levels to predict survival in high grade ovarian cancer. Scientific reports, 13(1), 20933.

Naik, K., Goyal, R. K., Foschini, L., Chak, C. W., Thielscher, C., Zhu, H., ... & Gobburu, J. (2024). Current status and future directions: The application of artificial intelligence/machine learning for precision medicine. Clinical Pharmacology & Therapeutics, 115(4), 673-686.

Pal, R. S., Pal, Y., Chaitanya, M. V. N. L., Babu, R., Mazumder, R., & Kumar, A. (2024). Multifaceted Understandings of Cancer: A Review of Disease Mechanisms and Therapies. Current Cancer Therapy Reviews, 20(5), 481-488.

Sarker, M. (2024). Revolutionizing healthcare: the role of machine learning in the health sector. Journal of Artificial Intelligence General science (JAIGS) ISSN: 3006-4023, 2(1), 36-61.

Sideris, M., Menon, U., & Manchanda, R. (2024). Screening and prevention of ovarian cancer. Medical Journal of Australia, 220(5), 264-274.

Wang, L., Wang, X., Zhu, X., Zhong, L., Jiang, Q., Wang, Y., ... & Zou, D. (2024). Drug resistance in ovarian cancer: from mechanism to clinical trial. Molecular Cancer, 23(1), 66.

Xu, C., Coen-Pirani, P., & Jiang, X. (2023). Empirical study of overfitting in deep learning for predicting breast Cancer metastasis. Cancers, 15(7), 1969.