Ovarian Cancer Prediction Using Deep Learning: A Comprehensive Review

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Abstract. This systematic study investigates the constraints impeding the implementation of Computer-Aided Diagnosis (CAD) systems in medical diagnostics, with a specific emphasis on Ovarian Cancer (OC). Our comprehensive analysis of existing literature revealed that a major limitation is the inadequate scale and variety of datasets, which negatively impacts the precision of predictive models. Prior research suffers from a lack of thorough testing on diverse datasets, leading to restricted applicability and reliability. Furthermore, there is a pressing requirement for progress in image segmentation and accurate identification of tumor size to improve the precision of (OC) categorization and early-stage prognosis. It is crucial to address these gaps to enhance the accuracy of diagnosis and, as a result, improve the survival rates of patients with (OC). This review highlights the need for stronger, more varied datasets and improved analytical methods to enhance computer-aided diagnosis procedures in (OC).

Keywords: CAD, Ovarian Cancer, Deep Learning, Region of Interest, Segmentation.

1 Introduction

Ovarian Cancer is a widespread type of cancer that predominantly impacts women. During the year 2018, a total of 295,414 women received a diagnosis of OC, which unfortunately led to 184,799 fatalities across the globe. Due to the lack of symptoms in early-stage tumours, the mainstream of women with (OC) is detected at a progressive stage, leading to reduced long-term survival rates [1]. Even though ovarian tumours are responsive to chemotherapy and show a good response to platinum/taxane therapy, patients with advanced cancer have a high recurrence risk of 60% to 80% within 5 years [2].

Mild symptoms distinguish it during the initial phases and a low chance of mortality. OC is the greatest prevalent and deadly form of gynecologic malignancy. Primary epithelial OC can be categorized into four distinct subtypes: serous, mucinous, endometroid, and clear cell [3]. Based on a prior study, the prevalence of OC among wom-

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en is estimated to be 1 in 54. An estimated 48.6% of patients with ovarian cancer will survive for five years [4]. The high mortality proportion can be attributed, in part, to the fact that cancer is often detected in its advanced stages, with 72% of patients being diagnosed with stage III or IV conditions. Timely identification is so essential. Blood markers and medical imaging methods have both been used in the past to identify early-stage OC. Nevertheless, these biomarkers show potential.

Although the Serum Carbohydrate Antigen (CA125) is widely used, its accuracy rate is low because of its high compassion. Early identification of any medical illness, including cancer, is crucial for enhancing survival rates. Research has shown that medical imaging is highly useful in diagnosing early-stage conditions, predicting brain imaging techniques, monitoring different stages of cancer, and doing post-cancer therapy follow-up operations. Furthermore, computer-aided diagnostic (CAD) technologies are commonly used to aid clinicians and pathologists in the more efficient analysis of medical pictures. A CAD medical imaging technology utilizes machine learning (ML) algorithms for cancer screening [5].

This study examines the existing limitations that restrict the utilization of CAD-based medical diagnostic techniques by conducting a literature analysis. Our findings indicate that the prediction results were largely inaccurate due to insufficient dataset availability. The varied dataset was not used to assess the implemented system's performance. Therefore, there is a continued requirement for enhancing image segmentation and precisely determining the precise size of ovarian cancer tumours. This will aid in the precise classification of ovarian cancer types and enable early-stage prediction. This will enhance the patients' survival rate.

2 Materials and Methods

A comprehensive literature analysis was conducted, first searching a total of 172 records on ovarian cancer disorders. A total of 56 duplicates were identified and subsequently eliminated. A total of 32 records were eliminated due to their lack of emphasis on Deep Learning or Artificial Intelligence technology. In conclusion, a total of 24 publications were selected to undertake a systematic review of previous research carried out on ovarian cancer.

The following is a comprehensive summary of the literature we have reviewed on this topic.

G. Wadhwa et.al sought to employ histopathology images to develop a deep learning approach for the identification of OC. The methodology utilizes a Convolutional Neural Network (CNN). The DenseNet-201 CNN model was employed to extract features. Cancer is classified as either malignant or benign. A maximum accuracy of 94.73%, precision of 0.91, and recall and f1-score of 0.90 and 0.95, respectively, were obtained during the characterization phase using the PLCO dataset [6].

In their study work, A.S. Azhar et.al utilized the SEER dataset to construct machine learning algorithms for both classification and regression methodologies. We collaborated with a skilled clinician to collect the data and develop the courses to achieve clinically meaningful outcomes. This study was pioneering in its use of the regression technique to estimate the number of months that ovarian cancer patients will survive. XGBoost outperformed other models in classification, random forest, and regression tasks [7].

The study, conducted by He-Li Xu et al., presents a comprehensive analysis of the substantial skills of AI algorithms in precisely identifying Ovarian Cancer through the use of medical radiological imaging. However, it is recognized that the overestimation of the algorithm's performance resulted from an inadequate level of methodological rigour supporting this discovery. There is a need to improve research on AI-based approaches for diagnosing OC in terms of study design [8].

Dingdu Hu et al. investigated the viability of utilizing deep learning techniques for automating the segmentation process. According to the results, DL may be able to split EOC on T2-weighted MR pictures automatically. U-Net++ outperforms other models in terms of segmentation performance and requires fewer processing resources [9].

Using Machine Learning models and statistical techniques to do predictive analytics for early diagnosis was the primary goal of the study by Md. Martuza Ahamad et al. This was accomplished by scrutinizing clinical data collected from 349 patients. A range of machine learning models were utilized to build classification models that could discriminate between patients with benign and malignant OC. These models included RF, SVM, DT, XgBoost, LR and GBM. The results of the prediction study demonstrate that these Machine Learning models can reliably differentiate between malignant and benign patients, obtaining a precision rate of up to 91% [10].

L.K. Hema et.al introduced an innovative approach to categorising ovarian pictures by labelling them and employing ROI (region of interest) segmentation with FR-CNN (rapid region-based convolutional neural network). Three different types of cells were identified from the presented photographs: stroma, germ, and epithelial cells. The picture has undergone segmentation and pre-processing. Subsequently, the process of annotation was conducted with FR-CNN. The framework for region-based categorization utilizes a comparison between manually annotated and learned features in FRCNN. Utilizing machine learning-based categorization can enhance the accuracy of sickness diagnosis compared to manual annotation since previous research has shown that human annotation is less accurate. Therefore, the proposed work provides empirical evidence that machine learning-based categorization can achieve greater precision. The SVC-Support vector classifier and Gaussian distribution were combined in the classification process following region-based training in FR-CNN [11].

A computed tomography (CT)-based artificial intelligence (AI) model was created by Ya-Ting Jan and colleagues, and it can accurately and successfully differentiate between benign and malignant ovarian tumours. The ensemble model, which integrates radiomics, deep learning, and clinical feature sets, surpasses the performance of the other four models. The model attained a precision rate of 82%, a specificity rate of 89%, and a sensitivity rate of 68%. The model exhibited superior precision (82% vs. 66%) and specificity (89% vs. 65%) in comparison to the average performance of younger radiologists while keeping a comparable sensitivity (68% vs. 67%). The utilization of the model led to subordinate radiologists attaining superior average precision (81% vs. 66%), specificity (80% vs. 65%), and sensitivity (82% vs. 67%), which was on par with the presentation of the eldest radiologists [12].

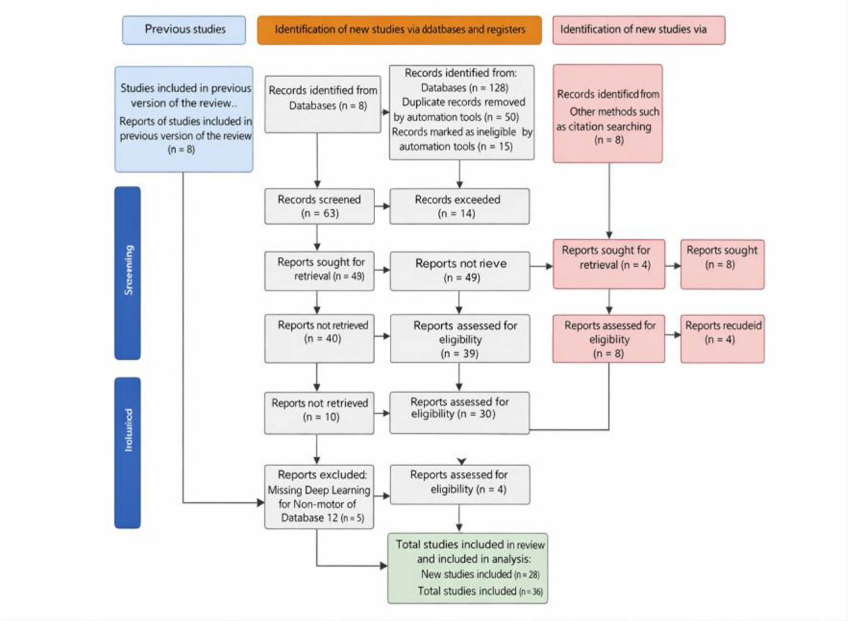

Fig. 1. Prisma Flow diagram for Literature Review

Filbert H. Juwono proposed an efficient method for simultaneously weighting features and optimizing parameters to detect the presence of cancer in the ovaries. Above Figure 1 represents Prisma Flow diagram for Literature Review diagrammatically for better understanding .The LASSO regularization and ADE with cross-validation error were used as the fitness functions to optimize the weights. Furthermore, they applied Occam's razor approach and implemented LASSO regularization using a weighted l1 norm to limit the number of features used. The results clearly showed a significant decrease and removal of characteristics from the subset of features. The mean precision of the KNN approach was 97.24%, whereas the SVM technique yielded a mean precision of 96.48% [13].

Laboni Akter and Nasrin Akhter utilized the PLCO dataset to examine the efficacy of TVUS screening through the application of three ML methodologies: RF, KNN, and XGBoost. Three target variables were examined in the study using these ML Techniques. With estimated values of 99.50%, 99.50%, 99.49%, and 99.50%, respectively, these algorithms showed excellent performance in terms of precision, recall, f1 score, and accuracy. The RF, KNN, and XGB procedures achieved AUC scores of 99.87%, 98.97%, and 99.88%, respectively, as reported in reference [14].

Three neural network approaches—a 3D CNN, a convolutional LSTM network, and a feed-forward network supported by VGG—were introduced by David Schwartz et al. Despite the substantial noise often associated with OCT photos, the testing results indicated that the proposed models achieved a favourable presentation without the need for physical changes or feature manipulation. A neural network based on convolutional LSTM was the best-performing model, with a mean area under the curve AUC of 0.81 ± 0.037 [15].

M. Kalaiyarasi et al. started the gene selection process with the ANOVA approach. They then used three transform-based feature extraction techniques and two approaches based on clustering, namely the DCT, Hilbert Transform, SDA, and Fuzzy C Means. The traits are then divided into normal and abnormal categories by six classifiers. The NLR classifier has the maximum precision rate of 92% while employing SDA features. On the other hand, the KNN classifier shows the lowest performance with an accuracy rate of 55% when utilizing SDA, Hilbert, and DCT features. When correlation distance feature selection is used, the NLR classifier only achieves a 53% accuracy rate, whereas the GMM classifier achieves an 88% accuracy rate [16].

Ziyambe et al introduced a novel CNN method for identifying and diagnosing OC. The project involved training a CNN using a dataset of histopathology pictures. The dataset was separated into subsets for training and validation purposes. The dataset was updated before training. With a 94% accuracy rate, the software successfully identified 93.02% of healthy cells and appropriately identified 95.12% of malignant cases. The importance of this work rests in its ability to tackle the difficulties linked to human expert evaluation, such as increased rates of misclassification, inconsistency across different observers, and lengthy analytic durations. This work demonstrated a more precise, efficient, and dependable method for predicting and detecting Ovarian Cancer [17].

Kokila R. Kasture et al. developed and applied an improved DCNN-based structure for the identification of both benign and malignant cells. The researchers utilized 500 histopathological images from The Cancer Genome Atlas (TCGA-OV) collection that had been previously published to generate a total of 24,742 fresh pictures. The proposed classification network, called KK-Net, improved the training data quality and thus enhanced the accuracy from 75% to 91%. The AUC-ROC curve, short for Area under the Curve - Receiver Functioning Appearances, was utilized to assess the model's presentation through statistical analysis. The mean AUC-ROC curve value obtained was 95%. In addition, they employed Alex Net, VGG-16, VGG-19, and Google Net to evaluate the efficacy of the suggested model in comparison to state-of-the-art techniques [18].

Yuyeon Jung et.al devised a CNN model that integrates a convolutional autoencoder CNN-CAE to categorize ovarian tumours. Pre-processed and enhanced ultrasound pictures of 1613 ovaries with verified medical diagnoses were used for deep learning analysis. Annotations and callipers were removed from ultrasound pictures, and ovaries were divided into five different categories using a CNN-CAE model. Afterwards, the author performed a fivefold cross-validation to assess the precision, sensitivity, specificity, and area under the receiver operating characteristic curve AUC of the CNN-CAE model. The visual representation and confirmation of the CNN-CAE model's results were achieved through the use of Gradient-weighted class activation mapping, or Grad-CAM. The CNN-CAE model, which makes use of the DenseNet121 CNN architecture, successfully distinguished between normal and ovarian tumours with a precision of 97.2%, 97.2% sensitivity, and 0.9936 AUC. The CNN-CAE model, developed using the DenseNet161 CNN architecture, produced impressive results in discriminating malignant ovarian tumours. It attained a precision of 90.12%, 86.67% sensitivity, and an AUC of 0.9406 [19].

Lamin A and Lamin B, which are types of Nuclear Lamins, are located at the outside edge of the nucleus and function as guardians of the nuclei, controlling their form and structure. Therefore, alterations in their manifestation or dispersion are impacted by the configuration and dimensions of the nucleus. This method has been employed for the detection and diagnosis of OC. Confocal imaging of tissue tasters revealed a significant increase in both the size and boundary of OC nuclei. This discovery corresponds with the knowledge that cell nuclei in ovarian tumour tissues frequently display an increase in size in comparison to cell nuclei in healthy tissues. A study by Duhita Sengupta et al. evaluated the viability of extracting and characterizing quantitative aspects of nuclei using a novel deep hybrid learning network. The objective was to determine whether nuclear morphology might be utilized as a means of distinguishing between tissues from ovarian cancer and healthy tissues [20].

Booma P M et.al introduced the Enhanced Max Pooling (EMP) methodology for the identification and categorization of ovarian cancer utilizing sophisticated machine learning algorithms. This methodology examines the advantages and disadvantages of using machine learning to classify images [21].

In this study, Long-Yi Guo et al. devised an innovative deep-learning framework that utilizes a denoising autoencoder to integrate multi-omics data and identify different subtypes of ovarian cancer. The researchers identified two distinct molecular subtypes of ovarian cancer, indicating that the proposed approach was both effective and reliable. Any p-value below 0.05 signifies that the disparities between the cancer groupings are statistically significant. The author identified 34 unique genes linked to ovarian cancer by integrating the results of DEG and WGCNA analysis. Furthermore, the analysis revealed that the 34 discovered genes were associated with 19 KEGG pathways, such as the PI3K-Akt signalling network and the human papillomavirus infection pathway. Based on classification subgroups, the literature analysis discovered that 19 biomarkers (56%) and 8 KEGG pathways (42.1%) have been identified as being related to ovarian cancer [22]. Table 1 given below represents Contribution of major authors in OC research field.

Table 1: Literature Review Analysis

Author	**Year**	**Dataset Size**	**Methodologies**	**Results (Accuracy %)**	**Limitations**
G. Wadhwa	2021	PLCO Dataset 256 images	DenseNet-201 CNN	94.73%	1. Lesser Accuracy 2. Feature extraction to improve
A.S. Azhar et.al	2022	SEER Dataset 42827 images	RF, XGBoost	88.72	Accuracy can be improved
Dingdu Hu et al	2023	339	U-Net ++ Deep Learning	85.1%	Small dataset size and accuracy are lesser
Md. Martuza Ahamad et al	2022	349 patients	Light Gradient Boosting Machine	91%	Small size dataset
L.K. Hema et.al	2022	Cancer Imaging Archive database	FR-CNN	98.69	Hyperparameter tuning is missing
Ya.Ting Jan et.al	2023	149	Deep Learning	82%	The dataset is limited and the accuracy is low.
Filbert H. Juwono	2022	234+114	SVM	96.48%	The dataset is characterized by its limited size.

Laboni Akter and Nasrin Akhter	2022	PLCO	Random Forest	99.50%	Enhancing the efficacy of the selection process with deep learning methodologies
David Schwartz et al	2022	OCT Images	convolutional LSTM	81%	The region of Interest is not considered
Ziyambe et al	2023	200	CNN	94%	Accuracy to improve
Kokila R. Kasture	2022	500	CNN	91%	ROI not identified
Yuyeon Jung et.al	2022	1613	CNN-CAE	92.7%	Accuracy can be improved. ROI not identified

Nasser Taleb and his colleagues researched highly intricate and effective machine-learning techniques. SVM and KNN are two of the diagnostic techniques used for ovarian cancer. The proposed method can improve and establish a consistent format for data before diagnosing sickness. In terms of training and validation performance, the SVM algorithm fared better than the KNN approach. The SVM attained a training precision of 98.1% and a validation precision of 97.16%. If integrated into medical diagnostic systems, the suggested model has the potential to greatly enhance the accuracy of OC detection, resulting in more effective treatment and higher patient survival rates [23].

Robert Chen created a machine learning system that accurately predicts premature death in patients with malignant tumours of the left testis. The method has a precision rate of 76.1% and an AUC value of 0.621. Additionally, the model can detect clinical features that are indicative of early mortality [24].

3 Research Gap and Challenges

The subsequent research gap analysis delineates prevalent constraints and opportunities for enhancement derived from the presented studies:

3.1 Common Limitations

1. **Small Dataset Sizes :** Various research, including those conducted by Dingdu Hu et al. (2023), Ya-Ting Jan et al. (2023), Filbert H. Juwono (2022), and others, utilized relatively small datasets. This can restrict the capacity to apply and rely on the models in a wide range of scenarios and their overall effectiveness.
2. **Accuracy Concerns:** Several investigations, including those conducted by A.S. Azhar et al. (2022), Dingdu Hu et al. (2023), and Ya-Ting Jan et al. (2023), have reported accuracy rates that are deemed capable of improvement.
3. **Feature Extraction and Selection:** Research, such as the study conducted by G. Wadhwa in 2021, suggests that there is a requirement for better feature extraction techniques to increase the performance of models.
4. **Region of Interest (ROI) Identification:** Multiple investigations, such as those conducted by David Schwartz et al. (2022) and Kokila R. Kasture (2022), do not prioritize the identification of return on investment (ROI), a factor that has the potential to enhance accuracy.
5. **Hyperparameter Tuning:** In their study, L.K. Hema et al. (2022) emphasize the need for hyperparameter adjustment to optimize the performance of the model.

4 Discussion

This review highlights the growing impact of deep learning techniques in ovarian cancer diagnosis, particularly in enhancing accuracy and early detection. Despite notable advances, challenges such as limited datasets, inconsistent ROI selection, and lack of model generalizability remain significant. Addressing these gaps through standardized benchmarks and diverse clinical datasets is essential. Integrating AI with clinical workflows could revolutionize ovarian cancer care by supporting faster, more precise decision-making.

5 Conclusion

To diagnose (OC) using medical radiology imaging, the study gives a succinct summary of the enormous potential of AI algorithms. However, it is acknowledged that this finding is based on studies of rather low methodological quality, which inevitably causes an overestimation of the algorithm's efficiency. There is a need for further improvement in the study design of AI-based systems used in diagnosing OC. By addressing the existing gaps in research, it is possible to create prediction models that are more precise and dependable. Future research should prioritize the use of extensive datasets, sophisticated feature extraction techniques, precise determination of return on investment (ROI), meticulous model optimization, and the integration of different methodologies to improve the overall performance and applicability of the model.

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