REVIEW ARTICLE

INTERNATIONAL RESEARCH JOURNAL OF MULTIDISCIPLINARY TECHNOVATION

Asian Research Association

DOI: 10.54392/irjmt2519

A Review of Deep Learning Models for Early Detection and Diagnosis of Ovarian Cancer

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DOI: https://doi.org/10.54392/irjmt2519

Received: 30-09-2024; Revised: 07-01-2025; Accepted: 17-01-2025; Published: 27-01-2025

Abstract: Ovarian cancer ranks seventh worldwide and is the third most common type of cancer diagnosed in women in India. Numerous studies have demonstrated that the number of people affected by ovarian cancer is expected to rise significantly in the future. Proactive measures for early cancer detection are essential to prevent death and recurrence. This paper attempts to review the various deep learning (DL) models in ovarian cancer diagnosis, including detecting risk factors, analyzing genomic data sets, predicting disease progression, recurrence, and mortality rates, and identifying correlations and patterns. The patient's electronic health records contain effective analytics on imaging and other types of data that may open the door to more accurate or early identification of ovarian cancer. The taxonomy of the several ways that DL aids in the diagnosis, early detection, and treatment of ovarian cancer will be compiled in this review article. As per the reviews, more research studies have examined the Convolutional Neural Networks (CNNs) approach for the Early Detection and Diagnosis of Ovarian Cancer. This is because CNNs are a popular and potent architecture for image classification tasks because of their capacity to learn spatial and hierarchical features from images effectively. The review article seeks to give future research topics and assess the state-of-the-art application of DL algorithms for ovarian cancer diagnosis.

Keywords: Healthcare Analysis, Ovarian Cancer Diagnosis, Machine Learning, Deep Learning, Early Detection

1. Introduction

The uterine side of the female reproductive tract has two ovaries that produce progesterone and estrogens as well as eggs for reproduction. Ovarian cancer is the name for cancer that begins to spread within the ovaries. Ovarian cancer is caused by non-susceptible cells growing out of control inside the ovaries. These cells might never die and build up to become a tumor. It is among the most serious cancers that can kill a woman worldwide. According to data, ovarian cancer is more common in women with high-risk characteristics between the ages of 50 and 65. Ovarian cancer has a very low patient survival rate compared to other gynecological cancers [1]. It is known as the "silent killer" disease because symptoms do not appear until the very end of the disease. The main risk factors for developing ovarian cancer are (i) a family history of ovarian or colon cancer; (ii) postmenopausal women; and (iii) genetic mutations. Although cancer cells can spread to other areas of the body and proliferate there, the process by which a cancer is identified when its cells move to another area of the body and begin to grow there is known as metastasis [2]. Ovarian cancer accounts for 2.5% of all gynecological cancer cases in women. There are three forms of ovarian cancer, which are distinguished by the type of cell they start in. These three categories are the root cause of over thirty different types of cancer. The cell covering the lateral surface of the ovaries is the source of ovarian cancer of the *epithelial type* [3]. More than 90% of cases of ovarian cancer fall into this group. The epithelial type of cancer does not exhibit any signs till the advanced stages. The cells in the ovary that generate eggs are the source of *germ cell* cancer [4]. These carcinomas typically impact young people and are easily curable. *Germ cell-type* cancer affects more than 5% of women. An uncommon condition called *stromal cell* ovarian cancer develops in the ovaries' connective tissues [5]. This category affects about 5% of women. In contrast to cancers of the epithelium and germ cells, stromal cancer presents with a multitude of symptoms, including irregular hormone production and changes in the menstrual cycle. Staging is a global approach that determines the patient's percentage of internal cancer spread. It aids in choosing the course of treatment for patients. Table 1 describes the staging classification along with its causes and symptoms. The remaining portion of the paper is divided into the following sections: section 2 covers the history of ovarian cancer; Section 3 discusses the stages of ovarian cancer diagnosis; Section 4 covers some related

works; Section 5 covers challenges; and Section 6 covers the paper's conclusions.

2. Background

Every year, more than 184,000 people die from ovarian cancer, the second most common gynecologic disease in the world [6]. The 70 % majority of cases occur in postmenopausal women, with an incidence of 40 occurrences per 100,000 women over 50 years. The 5-year survival rate rises dramatically with early identification of this disease, from 3% in Stage IV to 90% in Stage I. Results are closely correlated with the stage at diagnosis; UK women identified at stages I and IV had five-year survival rates of 90% and 4%, respectively. Globally, 313,959 women received an ovarian cancer diagnosis in 2020. This will have increased by 42% to 445,721 by 2040 [7]. Asia has seen the most Percentage increase in cases, but Africa has seen the largest absolute increase. Over the next 20 years, it is predicted that approximately twice as many women in Africa will be diagnosed with ovarian cancer [8]. One of the major cancers of the female reproductive system is ovarian cancer. In 2020, there were more than 0.3 million ovarian cancer cases worldwide, nearly 0.2 million fatalities, and more than 0.8 million women who are still alive five years after being diagnosed. By 2040, there would likely be 0.4 million more newly diagnosed cases per year, along with a similar increase in fatalities[9]. It is different from other cancers that are common in women in several respects. First, unlike other anatomical sites, there are no confirmed pre-malignant lesions of any kind at this site.(b) No standardized screening instrument is available for this cancer location. Furthermore, the cause of this malignancy is not as well known. According to a study on the global burden of illnesses, the age-standardized incidence rate of ovarian cancer in India rose by 286% between 1990 and 2016 [10]. Since 1981, India's National Cancer Registry Programme (NCRP) has been actively collecting cancer-related data [5]. The diversity of the Indian people is reflected in the statistics gathered. The National Centre for Disease Informatics and Research (NCDIR) of the Indian Council of Medical Research (ICMR; ICMR-NCDIR-NCRP) Bengaluru is responsible for coordinating the network of registries under NCRP. Consensus guidelines for the treatment of different malignancies based on evidence-based approaches and cancer control programs are developed using periodic NCRP reports [11].

Great investigations and studies have been carried out by scientists and clinicians to forecast the survivability of cancer patients [12, 13]. Indian women have less than 20% survival rates. Research states that 45–65 years old accounts for 50% of all ovarian cancer cases in India [14]. However, the median range in the majority of Western nations is greater than 60 [15]. Since most patients do not exhibit symptoms in the early stages, most are already in an advanced stage, and by the time of diagnosis, 70% of patients with advanced cancer already had distant metastases [16]. Vaginal ultrasonography, C.T. scans, biopsies, and the CA-125 blood test can all be used to detect the condition. A biopsy is a critical procedure that therapists typically carry out to establish the existence of malignant cells in the ovaries. The symptoms of cancer vary depending on the stage of the disease. Patients with Stage I cancer typically experience extremely minor or no symptoms at all. Later on, it may experience symptoms including bloating, constipation, and frequent urination.

3. Phases of Ovarian Cancer Diagnosis

Four steps are involved in the deep learning diagnosis of ovarian cancer, from data collection and preprocessing to model training and assessment. Figure 1 shows the overviews of phases such as types, input types, and diagnosis methods.

Table 1. Stages of OC disease

Stages	Details	Treatment	Survival Rate
I.	Cells are restricted to the ovaries and do not proliferate to other areas of the ovary	Removal of the fallopian tubes and both ovaries during an abdominal hysterectomy	90 %
II.	Cells may proliferate throughout the fallopian tubes, the uterus, and the ovaries	Tests for infection are performed on material surrounding the ovaries in addition to a hysterectomy	70 %
III.	The cancer cells have the potential to proliferate outside of the ovaries and begin accumulating on the liver's surface	The same care is given to this step as to stage II. If necessary, the patient may receive chemotherapy after the operation	40 %
IV.	Every body part has been affected by cancer. Fluids removed from other internal organs may contain malignant cells	Attempt to remove the areas where the tumor has spread by using radiation treatment and chemotherapy together	20 %

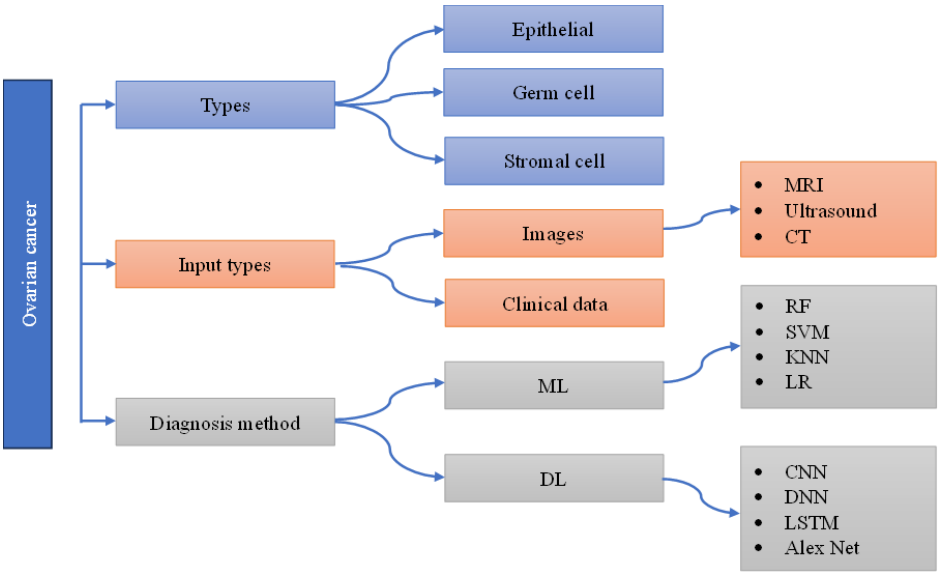

Figure 1. Overview of ovarian cancer

3.1 Data Collection

Compile a variety of dataset, such as imaging, and clinical data. Electronic health records (EHRs), genomic databases, biobanks, and medical imaging databases are a few examples of sources. Two types of inputs are considered for ovarian cancer diagnosis such as clinical information, and images.

- ***Clinical data:*** Clinical data, which offers important details about the patient's health, medical history, and symptom presentation, is essential for ovarian cancer prediction [17]. Early signs of ovarian cancer may include symptoms like bloating, altered urine habits, and abdominal pain. Early detection can be aided by analyzing the patterns and intensity of these symptoms. Abdominal palpation and pelvic exam results may show anomalies or masses that point to ovarian cancer. Testing blood for biomarkers such as CA-125 levels can aid in the early detection of disease. Although CA-125 is not specific and can also be raised in other illnesses, it is frequently linked to ovarian cancer. A higher genetic risk may be indicated by a family history of ovarian cancer or associated cancers (e.g., breast cancer). This data aids in the identification of those who pose a high danger.
- ***Images data:*** Imaging is essential for ovarian cancer diagnosis, staging, and follow-up. A thorough examination requires a variety of information kinds, which are provided by different imaging modalities. Various types of images are considered for ovarian cancer diagnosis such as Computed Tomography (CT)[18], Ultrasound (US)[19], Magnetic Resonance Imaging (MRI) [20], and Positron Emission Tomography (PET) [21]. Combining these imaging modalities offers a thorough method for ovarian cancer detection, staging, and treatment. Every imaging modality has advantages and disadvantages, and they are frequently combined to offer a comprehensive and precise evaluation that helps with treatment planning and enhances patient outcomes. Imaging is useful in determining whether ovarian masses are present, differentiating between benign and malignant lesions, and describing the type of tumors. Finding the stage of ovarian cancer requires evaluating the size of the main tumor, the involvement of local lymph nodes, and the existence of distant metastases. Accurate imaging is essential for this process.

3.2 Preprocessing

- *Data cleaning* is a serious step in ovarian cancer diagnosis, particularly when working with clinical, genetic, imaging, or histopathological data. Appropriate cleaning confirms data quality, constancy, and dependability, leading to more precise and healthy models for detection diagnosis. Identifying the missing values, removing duplicate, redundant, and outlier.
- *Handling imbalanced data:* class imbalance is a general issue in any disease including ovarian cancer datasets, as malignant (cancerous) cases are frequently outstripped by benign control cases. It directly influences the performance, consistency, and clinical applicability of extrapolative models. Ovarian cancer datasets characteristically suffer from imbalance because malignant cases are less common than benign case controls, particularly in large population-level studies. Addressing class imbalance is vital to avoid biased approaches that perform well on the majority class but poorly on the smaller class.

- *Data normalization is a* crucial preprocessing step in the identification of ovarian cancer, especially when working with varied datasets such as imaging, histopathology slides and clinical data. In order to improve accuracy, speed up convergence, and confirm equitable comparisons across numerous features or modalities, normalization makes sure that the data is in a reliable format.
- *Data augmentation* is used to boost the diversity of the training dataset and strengthen the robustness of the model, using methods like rotation, flipping, and cropping for image data [22]. The performance of ML and DL approaches employed for the diagnosis of ovarian cancer is significantly improved by data augmentation. Because of the lack of labeled datasets, class differences, and the high expense of data gathering, it is particularly significant in ovarian cancer research.

3.3 Feature Engineering

Extract pertinent features from unprocessed data using feature engineering. This could entail aggregating time-series data or computing risk scores for clinical data. This could involve obtaining texture, shape, and intensity information from image data. Particularly for high-dimensional data such as genomics, employ methods to minimize the number of features while maintaining critical information [23].

3.4 Model Development

Several phases and procedures are involved in the building of models for the diagnosis of ovarian cancer, utilizing conventional deep learning (DL) techniques. The objective of these models is to enhance the precision and efficacy of ovarian cancer early detection, which is essential for better patient outcomes. To forecast the risk of ovarian cancer, machine learning (ML) techniques like decision trees, support vector machines (SVM), and random forests can evaluate sizable dataset including genetic, imaging, and medical record data. By examining gene expression data and proteomics, machine learning can find possible biomarkers for ovarian cancer. However, compared with DL, ML approaches are complex to solve ovarian cancer diagnosis because ML approaches handle clinical information efficiently while some difficulties by using image dataset [24].

Hence, a more effective method for handling both dataset such as clinical and image dataset. The prediction and diagnosis of ovarian cancer is only one area in which DL has demonstrated great potential in the realm of medical imaging and diagnostics. Model Development is the process of selecting the right models for predicting, classification, and predicting ovarian cancer using various input data samples. The prediction and classification of ovarian cancer is greatly aided by DL, which also contributes to numerous aspects of patient management, therapy planning, and diagnosis [25]. High-dimensional dataset such as proteomics, metabolomics, and gene expression profiles are frequently used in ovarian cancer research. Compared to classical machine learning, which frequently calls for dimensionality reduction techniques or human feature engineering, deep learning is more efficient in processing and extracting patterns from such large, complicated dataset. Convolutional neural networks (CNNs), in particular, are excellent for automatically identifying minute patterns or abnormalities in medical pictures (such as CT scans, MRIs, or ultrasounds) that radiologists or conventional machine learning models could overlook.

3.5 Performance evaluations

To make sure that the models are accurate, dependable, and therapeutically valuable, ovarian cancer prediction models developed using DL must be evaluated using a variety of metrics and approaches. Accuracy, precision, sensitivity, specificity, Area Under the Receiver Operating Characteristic Curve (AUC-ROC), and F-Measures are the most significant performance measures. To predict ovarian cancer, the performance evaluation of DL models requires a thorough methodology that incorporates several criteria. This guarantees that the models are dependable, accurate, and comprehensible in clinical practice. Strong assessment frameworks aid in the selection of the most suitable models for implementation, which eventually improves patient outcomes and makes better use of technology in healthcare.

4. Ovarian Cancer with Deep Learning

Machine learning algorithms examine vast dataset of patient records, including genetic information, medical histories, and biomarkers, to uncover patterns that may suggest the early stages of ovarian cancer. DL algorithms can autonomously segregate ovarian cancers from surrounding tissues in medical imaging, permitting more accurate diagnoses and treatment planning. The most recent research methods have been discovered utilizing machine learning techniques for ovarian cancer classification, Tables 2 and 3, display the summary of the latest study with their proposed methods, dataset with their size and types, accuracy, merits, and demerits. An end-to-end pipeline, made possible by deep learning, maps input data—such as genetic information or medical images—directly to the intended output, such as risk assessment or cancer diagnosis. This lessens reliance on preprocessing or intermediary processes, which are typical in conventional ML workflows. By finding indicators in blood tests or imaging data that conventional techniques

might miss, DL-based algorithms can identify ovarian cancer in its early stages. Compared to conventional techniques, DL can identify cancer in its early stages and distinguish between benign and malignant diseases with fewer false positives or negatives. After training, DL models may analyze data in real-time, facilitating quicker and more effective diagnosis. They are appropriate for population-level screening programs because of their excellent scalability and capacity to manage huge dataset.

M. A. Vázquez *et al.* (2018) [26] presented a quantitative analysis of the efficacy of two automated techniques for the early identification of ovarian cancer that can make use of various biomarker readings across time. The first approach makes use of a Bayesian hierarchical model to create links between variables that may be understood clinically. The second method uses a recurrent neural network (RNN) for the binary classification of the inputs, and it is entirely discriminative. M. Wu *et al.* (2018) [27] used a Deep Convolutional Neural Network (DCNN) based on AlexNet to automatically identify the various forms of ovarian tumors from cytological images. Two sets of input data are used to train DCNN: the first set contains the original picture data, while the second set contains enhanced and rotated image data. L. Zhu *et al.* (2021) [28] conducted an experiment that was to investigate how ovarian tumor analysis might use computed tomography (CT) pictures that were based on intelligent segmentation techniques. To segment CT diagnostic images of patients with ovarian cancers, a CNN algorithm model was built. Y. Wang *et al.* (2023) [29] create a DL model to help distinguish between epithelial ovarian cancer (EOC) and borderline ovarian tumors (BOT) using conventional magnetic resonance imaging. On the Picture Archiving and Communication Systems (PACS) server, every image data was examined. The lesion area was determined using both T1-weighted imaging (T1WI) and T2-weighted imaging (T2WI) magnetic resonance images. Using deep supervision, we trained a U-net++ model to identify the lesion area in MR images. Afterward, a DL network-based classification model was given to the segmented regions to automatically classify ovarian masses. M. M. Ahamad et al. (2022) [24] presented statistical techniques and machine learning models to apply predictive analytics to early diagnosis. To identify the important blood biomarkers in statistical analysis, the student's t-test and the log fold changes of the two groups are employed.

X. Guo *et al.* (2022) [30] investigate the development and validation of a logistic regression model for qualitative ovarian cancer diagnosis. H. Wang *et al.* (2021) [31] planned to assess the DCNN's ability to distinguish between benign, borderline, and malignant serous ovarian tumors (SOTs) on ultrasound (US) pictures. The ResNet34 model outperformed the other models overall, and it continued to perform better even after transfer learning. M. C. Comes *et al.* (2023) [32] suggested an explainable machine learning ensemble technique utilizing clinical data that is frequently obtained in clinical practice to accurately determine when to perform RRSO for BRCA-mutated patients who are at high risk of ovarian cancer. S. Althubiti *et al.* (2023) [33] offer a novel quantum black widow optimization for a smart healthcare system called QBWO-MLDSS ("quantum black widow optimization with a machine learning-enabled decision support system"), which is enhanced by machine learning. The QBWO-MLDSS technique's main goal is to quickly and precisely identify and classify the OC. In addition, the Z-score normalization strategy is used by the QBWO-MLDSS model to pre-process the data. Furthermore, a QBWO algorithm is constructed as a feature selection method to derive optimal feature subsets using the QBWO-MLDSS methodology. Additionally, the total classification performance is enhanced by applying symbiotic organisms search (SOS) with an extreme learning machine (ELM) classifier for detection and classification.

R. M. Ghoniem *et al.* (2021) [34] constructed a hybrid evolutionary DL model with multimodal data. The multi-modal fusion framework that has been built combines histopathological image modality with gene modality. We configured the deep feature extraction network according to the various forms and states of each modality, accordingly. To process gene longitudinal data, this combines an optimized short-term (LSTM) with a predictive ant lion algorithm (LOA). To handle histopathology images, an additional predictive LOA-optimized CNN is incorporated. P. H. Nagarajan *et al.* (2023) [35] created a model to categorize the different forms of ovarian tumors using DSSGL-EUNet with Multi-Scale DCNN (DSSGL-EUNet-MSDCNN). Initially, the DSSGL is used to enhance the training CT images, and the EUNet models are used to segment each ROI. Next, the segmented ROIs are input into the fused DCNN structure, where each DCNN uses the lion optimization algorithm (LOA) to select the hyperparameters of each DCNN, capturing the features from each segment at a scale level. D. Schwartz *et al.* (2022) [36] suggested an automated framework that uses optical coherence tomography (OCT) recordings to learn how to recognize ovarian cancer in transgenic mice. Three neural network-based techniques are used in the suggested method: an LSTM, a 3D CNN, and VGG.

Y. Jung *et al.* (2022) [37] created a CNN model with a convolutional autoencoder (CNN-CAE) to categorize ovarian tumors. This model takes out extraneous information from ultrasound pictures and divides ovaries into five groups. By removing markings from ultrasound pictures, CNN-CAE is a practical diagnostic method that can reliably classify ovarian cancers. X. Wang *et al.* (2022) [38] suggested YOLOv5-improved as the foundation for a new end-to-end network.

Table 2. Overview of recent studies for ovarian cancer

Ref.	Dataset (size)	Data type	Algorithm	Accuracy	Merits	Demerits
[26]	CA-125 (223)	Clinical	BCP and RNN	98 %	Accounting for the uncertainty	Overfitting
[27]	Customized (85)	Cytological	DCNN	78.20 %	Fast convergence	Lack inaccuracy
[28]	Customized (100)	CT	CNN	97.64 %	High accuracy	Less dataset used
[29]	Customized (123)	MRI	CNN	87.3 %	Fast convergence	Noisy
[24]	Customized (349)	Clinical	ML	91 %	Comparatively high accuracy	Imputation data
[30]	Customized (207)	MRI and ultrasonic	LR	88.5 %	Stability	Low accuracy
[31]	Customized (279)	Images	DCNN	75 %	Fast convergence	Low accuracy
[32]	Customized (184)	Clinical	ML	83.2 %	handle imbalanced data	Limited data
[33]	Kaggle dataset (349)	Images	QBWO-MLDSS	97.14 %	High accuracy	Lacks in outliers
[34]	TCGA-OV (578)	CT and Clinical	ALO-LSTM ALO-CNN	95.58 %	Stagewise analysis	Underfitting
[35]	TCGA-OV (350)	CT	MSDCNN	93.82 %	Moderately efficient	Low convergence rate
[36]	Customized	OCT	ANNs	0.98 (AUC)	Detecting radiographic signatures	Small dataset
[37]	Customized (1613)	US	CNN-CAE	97.2 %	Cleaning	Limited data only used
[38]	Customized (5100)	CT	YOLO-OCv2	-	More efficient	Complex structure
[39]	Customized (50,000)	Images	Hybrid CNN	0.99 (AUC)	Low computational time	Overfitting
[40]	Customized (720)	Clinical	Hybrid DL	92.05 %	Fast convergence	Underfitting
[41]	Gene dataset (6352)	Clinical	GAT-DNN	0.76 (AUC)	Feature extraction	Inefficient
[42]	Standford	Clinical	LRC-CNN	98.76 %	Handling large multi-modal data set	The convergence rate is slow
[20]	Customized (3663)	MRI	CNN	81 %	Borderline tumor detection	Fewer data
[43]	Customized (441)	Clinical and US		0.90 (AUC)	High performance	Lacks in dataset
[44]	TCGA-OV (141)	CT	RED-CNN	95%	Reduces CT radiation exposure	Less accuracy
[45]	Customized (93)	MRI and clinical	CNN	0.91 (AUC)	Fast convergence	Incomplete data due to retrospective nature

The enhanced features include a decoupled detecting head and balanced mosaic data augmentation. Then, a multitask model that can finish the segmentation and detection tasks at the same time is suggested, based on the detection model. D. Sengupta *et al.* (2022) [39] created a revolutionary deep hybrid learning model, albeit one that was based on conventional CNN and traditional ML techniques. The created technology carried out comprehensive imaging of ovarian cancer in comparison to normal tissue and created a dual pipeline architecture that combines DL techniques for auto feature extraction from pre-processed pictures with morphometric parameter matrices. C.-W. Wang *et al.* (2022) [40] created poorly supervised DL models and a hybrid DL framework for every putative biomarker. The experimental findings demonstrate that the suggested model, when used in conjunction with AIM2, achieves good accuracy. L. Ye *et al.* (2021) [41] suggested a unique gene prediction technique to find the OC causative genes, using several omics data and dl approaches. The authors used a deep neural network (DNN) to predict genes related to OC after initially using a graph attention network (GAT) to create a compact representation of gene features. Z. Zhang *et al.* (2020) [42] Among all L techniques, CNNs and developed Advanced DL procedures are particularly interesting since they use LR to map a raw input image to the desired output image. In addition, we have applied the Internet of Medical Things (IoMT) to the segmentation of obstetric tumor images and the detection of tumors for medical professionals. According to the experimental results, the LRC based on CNN can be used to forecast the obstetric ultrasound's output when there is a higher-than-average rate of maternal and perinatal mobility.

T. Saida *et al.* (2022) [20] created a CNN-based technique for detecting ovarian cancer. When it came to MRI diagnosis of ovarian carcinomas, the CNNs performed diagnostically on par with radiologists. H. Chen *et al.* (2022) [43] created a novel detection technique using two fusion methodologies, such as feature and decision fusion, and a modified residual network (ResNet). K. R. Kasture *et al.* (2021) [46] created a novel DCNN-based prediction technique to identify subtypes of ovarian cancer and make predictions utilizing input from histopathology images. Pre-trained AlexNet Model serves as inspiration for the design and implementation of a novel architecture, which aims to achieve improved accuracy. The Rectified Linear Unit (ReLU) is the activation function in the basic AlexNet architecture, which consists of five convolutional layers, three Max pooling layers, and three fully connected layers. It has been modified by adding a Maxpooling layer after each pair of convolutional layers, four such iterations, four fully connected layers, and changing the architectural parameters. B. Ziyambe *et al.* (2023) [47] created a CNN-based-ovarian cancer diagnosis approach that was supplemented before training, and trained on a dataset of histopathology images that had been split between training and validation subsets.

H. Zhuang *et al.* (2024) [48] suggested a DL-based technique that uses multimodal positron emission tomography (PET) / CT images to assess a patient's platinum resistance. By combining an SESPP with a DCNN, an end-to-end Squeeze-Excitation-Spatial Pyramid Pooling (SESPP)–DCNN model was constructed. Experiments with single-modality data and ablation studies demonstrated the significance of taking multimodal data into account and integrating the SESPP into the DL model. L. Bote-Curiel *et al.* (2022) [49] proposed two analyses: (1) an autoencoder, a kind of neural network that may be used as a feature extraction technique to represent a dataset in three-dimensional latent space, is utilized in a nonlinear exploration of an OC dataset. (2) the use of a modification of the informative variable identifier to identify pertinent variable associations (IVI). A. Kodipalli *et al.* (2023) [50] developed A new novel deep learning model by author is used to analyze ovarian CT scan pictures. After several pre-processing methods were applied to the pictures, the UNet model was used to segment the tumor. After that, the cases were divided into two groups: benign and malignant tumors.

M. Mukhedkar *et al.* (2023) [51] created an optimized Bi-LSTM model that is incorporated into the CNN layers to improve learning. To further improve the accuracy and efficiency of the classifier, a feature selection technique based on Lion with Grey Wolf Optimization (LGWO) is used. Ovarian tumors are classified as benign or malignant using the Bi-LSTM method. C. Ch *et al.* (2023) [52] developed a method for forecasting the existence and stage of the disease based on a specially designed LSTM over Multi-Layer Perceptron (MLP). The researcher analyzes different medical ovarian cancer colposcopy images. In the SPSS investigation, about 15 medical samples were used to evaluate, compare, and understand the accuracy of the proposed algorithms.

A. Boyanapalli *et al.* (2023) [53] developed the ensemble deep optimized classifier-improved Aquila optimization (EDOC-IAO) classifier for identifying various forms of OC. During pre-processing, the image is scaled and filtered with the modified Wiener filter (MWF). The IAO is used to reduce overfitting and increase precision. The picture characteristics are retrieved and the fusion is completed using average weighted fusion (AWF). Ultimately, the softmax layer identifies several ovarian tumor classes and carries out the OC classification. M. Xi *et al.* (2024) [54] aimed to select the five DCNNs to develop the OC prediction model such as MobileNet, Xception, Inception, ResNet, and DenseNet. S. Srivastava *et al.* (2020)[55] developed a new OC prediction model based on a fine-tuned VGG-16 model.

Table 3. Overview of recent studies for ovarian cancer

Ref.	Dataset (Size)	Input type	Algorithm	Accuracy	Merits	Demerits
[46]	TCGA (200)	Image	DCNN	83.25 %	Fast convergence	Overfitting
[47]	TCGA (200)	Image	CNN	94 %	Low computational	Low accuracy
[48]	Customized (289)	PET/CT	SE–SPP–DenseNet	92.6 %	Fast convergence	Low accuracy
[50]	Customized (4970)	CT	CNN	95.7 %	Low computational time	Insufficient accuracy
[51]	Kaggle	CT	Bi-LSTM	98 %	Fast learning process	Insufficient dataset
[52]	Customized	colposcopy	LSTM+MLP	92.67 %.	High accuracy	Small data samples
[53]	TCGA-OV dataset	CT	EDOC-IAO	96.53 %	Fast convergence	High computation time
[54]	Customized (1103)	US	DenseNet	97.05 %	Fast convergence	Overfitting
[55]	Customized (240)	US	VGG-16	97.11 %	Low computational time	Small dataset
[56]	Mass spectroscopy (216)	Clinical	LM-ERNN	100 %	High accuracy	Overfitting
[57]	Customized	US	KHO-CNN	98.57%	High accuracy	High computational time
[58]	Customized	CT	DNN	98.96 %	High accuracy	Overfitting
[59]	CLAM	Gigapixel histopathological		73.50 %	Fast learning	Insufficient accuracy

A 16-layer DNN trained on the ImageNet dataset is called a VGG-16 model. The final four layers of the VGG-16 network are modified to fine-tune the network. H. R. Farhan *et al.* (2024) [56] developed an excellent method for diagnosing ovarian cancer (OC) based on ERNN which can identify cancer via mass spectrometry data. The network's topology consists of two output nodes that show the status, five neurons for the hidden and context layers, and 100 input neurons for data reception. Reduced-size characteristics, such as ion concentration levels at particular mass/charge values, are used in the suggested method. These features are trained using different learning algorithms to identify the optimal one that produces the best results. The most accurate and fastest algorithm is the Levenberg Marquardt (LM) algorithm, which converges after six epochs. S. R. Kongara *et al.* (2024) [57] developed a new optimized method based on the krill herd optimization-based convolutional neural network (KHO-CNN) mechanism to identify ovarian tumors. Additional noise is also present in the obtained real-world ultrasound images of ovarian cancer, which is eliminated with the Wavelet Transform. The segmentation procedure has made use of an improved KHO model. A local binary pattern was utilized to extract features. The KHO-CNN classifies ovarian tumors as benign, malignant, or normal. This model was created and used with a series of deep learning approaches that make use of optimized convolutional neural networks to identify ovarian tumors.

A. Kodipalli *et al.* (2024) [58] developed an ensemble DNN model for the automatic binary classification of ovarian cancer.

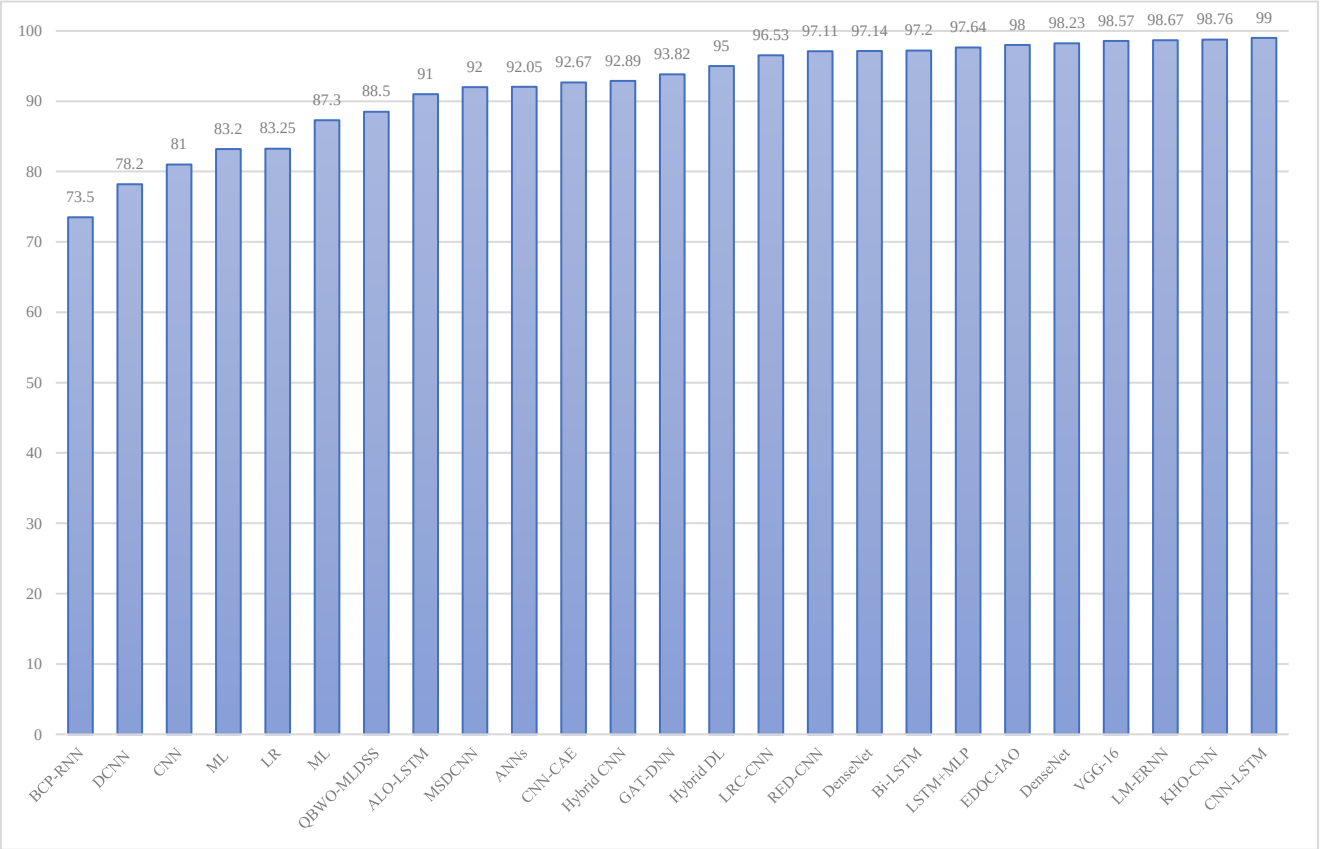

Figure 2. Comparative analysis-based accuracy

Four CNN models are incorporated into the suggested model, and transformers are used to extract features. Our suggested ensemble multi-layer perceptron model for classification uses these extracted characteristics as input. During model training, preprocessing and CNN tuning methods such as data augmentation, hyperparameter optimization, and fine-tuning are applied. Compared to single classifiers and machine learning techniques, our ensemble model performs better. I. Rasool *et al.* (2024) [59] developed a ground-breaking approach based on CLAM ("CLAM (Clustering-constrained Attention Multiple Instance Learning")architecture that uses slide-level labels alone, negating the requirement for in-depth annotations, to analyze gigapixel histopathology images in the context of OC treatment response prediction. To achieve this goal, several state-of-the-art methods have been employed, such as CNN models such as Inception V3, CNN-LSTM hybrid models, and the novel Vision Transformer (ViT) model. Furthermore, several preprocessing strategies have been carefully used to improve the procedure. Figure 2 shows the comparative analysis based on accuracy.

Deep learning holds promise for the identification of ovarian cancer, but there are still a number of unanswered questions that prevent its broad use and efficacy. Closing these gaps is essential to enhancing results and increasing the dependability and accessibility of these methods. Further, the following remarkable points are identified when using DL method of ovarian cancer detection.

- Due to the rarity of ovarian cancer, there aren't many dataset available for DL model training. Biased models may also result from dataset imbalances, such as more benign instances than malignant ones.
- The models' generalizability across various demographics and geographical locations is diminished by the majority of the current dataset lack of diversity in terms of population groups, imaging modalities, and clinical situations.
- Expert radiologists, pathologists, or physicians are needed to annotate medical imaging or omics data, which takes time and money.
- Early-stage ovarian cancer is difficult for DL models to detect because of modest biomarkers and imaging characteristics that can be mistaken for benign illnesses.
- Many healthcare facilities, especially those in low-resource regions, may lack the computational resources necessary to train DL models.

5. Challenges

Despite having the potential to completely transform medical diagnostics, applying DL to the diagnosis of ovarian cancer has several drawbacks. Data-related problems, model-related difficulties, interpretability issues, and ethical and regulatory

considerations are some categories into which these challenges might be divided.

- ***Data quality:*** Compared to other malignancies, ovarian cancer is less prevalent, which means there are fewer dataset available for model training. This may hinder the model's capacity to effectively generalize to fresh data. Biased models that underperform in minority classes are frequently caused by an imbalance in the class distribution, where non-cancerous samples greatly outnumber cancerous ones. Heterogeneous data is information that comes from a variety of sources, such as imaging, clinical records, and genetic data, and is frequently in a variety of forms and quality levels. It is difficult to integrate this disparate data.
- ***Privacy:*** Sensitive patient data is governed by stringent privacy laws and it is difficult to maintain data privacy when utilizing it for model training. Restrictions on data sharing imposed by laws and regulations may make it more difficult for institutions to collaborate.
- ***Methods:*** DL may overfit and record noise rather than significant patterns when a model is trained on a tiny dataset. Poor performance on fresh, untested data is the outcome of this. A substantial amount of memory and processing power is needed to train DL models, particularly when dealing with high-dimensional data such as imaging and genomics. Hyperparameters of DL are difficult and computationally costly to determine the optimal hyperparameters setting.
- ***Applicability:*** Due to variations in clinical procedures, genetics, and demography, models trained on data from one community may not generalize well to different populations.

Although DL holds great promise for enhancing the diagnosis of ovarian cancer, these obstacles must be overcome to fully utilize their potential. Enhancing data gathering and exchange procedures, creating more comprehensible models, making sure regulatory requirements are met, and seamlessly incorporating these technologies into clinical workflows are some of the solutions. Overcoming these challenges and maximizing the potential of machine learning and deep learning for ovarian cancer diagnosis will require sustained research, cooperation, and creativity.

6. Discussions

This article presents a thorough evaluation of a variety of articles that demonstrate the significant improvements made by machine and deep learning algorithms in medical imaging, particularly in ovarian cancer. Various machine learning and deep learning algorithms demonstrated impressive results in binary classification, prognosis, diagnosis, prediction, identification, type differentiation, and OC grading. This article covers the wide range of machine/deep learning techniques and technologies in detail. Various DL algorithms exhibit distinct behaviors when applied to diverse dataset, such as microarray, transcriptome profiling, gene expression, micro-RNA, cysts, protein profiling, and many more. The medical image analysis computer-aided diagnosis system was improved by DL techniques. DL techniques have been used in recent research to help populations handle enormous dataset quickly. Several papers describe the use of DNN, CNN, LSTM, and various models, including AleXnet, VGG-16, MeTylnet, and multilayer feedforward, to predict ovarian cancer.

After reading a variety of publications, it is evident that DL not only improves the ability to make correct predictions but also offers important new directions. Several machine learning techniques are examined through the use of medical imaging. These techniques primarily analyze complications related to epithelial ovarian cancer, which accounts for nearly 70% of all OC cases. These algorithms are used with feature selection strategies to increase classification accuracy. As technology in OC continues to advance, numerous researchers are using image dataset for their various publications. When used in huge dataset for disease evaluation and prognosis, DL outperformed other methods. Images from medical research, histological studies, and cytology are utilized to categorize the many forms of ovarian cancer. DNNs are effective in predicting epithelial ovarian cancer based on clinic-pathological data. CNN and the AleXnet model were effectively used to predict OC from computed tomography preoperative data. Preprocessing and data-augmentation approaches have also been the subject of several studies. These strategies have improved performance and yielded good accuracy, as data augmentation of tiny picture dataset is a useful contributor to superior solutions. However, there are some difficulties with using DL methods for ovarian cancer analysis. The application of DL models has very strong implications for the appropriate prescription of OC drugs. It was pointed out that these research fields ensure improved patient care and reduce the death rate. DL techniques, however, make it possible to list, categorize, and classify the disease patterns in the OC's medical image analysis. DNNs are thriving and developing quickly in the fields of medical imaging and healthcare. With the use of end-to-end DL algorithms, the classification and resolution of ovarian cancer problems became quite simple. In medical image analysis of OC, DL applications have attracted a lot of attention since they typically make use of practitioners' and researchers' mindsets.

According to the literature, CNN and LSTM are mostly developed to diagnose ovarian cancer. CNNs are essential for the accurate analysis of medical imaging data and the detection of patterns that may point

to the presence of ovarian cancer. This is a thorough examination of CNNs' function in ovarian cancer prediction. By automating feature extraction and learning from large dataset, CNNs improve the accuracy and efficiency of ovarian cancer diagnosis, ultimately assisting in early detection and better patient outcomes. CNNs are a powerful tool for ovarian cancer prediction, capable of analyzing complex imaging data to detect and classify tumors.

On the other hand, LSTMs are perfect for assessing time-series data, such as changes in tumor markers (like CA-125 levels) over time, because they are made to handle sequential data. If sequential or time-series data is present, LSTM networks perform exceptionally well in ovarian cancer prediction. LSTMs can offer important insights into the course of an illness, how a treatment responds to it, and how well a patient does by utilizing their capacity to record temporal dependencies. LSTMs enhance the overall predictive accuracy and usability of AI-driven healthcare solutions when they are coupled with other data modalities, such as imaging data evaluated by CNNs. This holistic approach to ovarian cancer diagnosis and prognosis is enhanced. LSTMs can forecast future results based on past patient data and track the course of an illness by evaluating longitudinal clinical data. When CNNs and LSTMs are combined, hybrid models that blend sequential and imaging data can be produced (for example, by combining time-series biomarker data with MRI scan results). Combining data from CNNs (imaging features) and LSTMs (temporal features) allows these hybrid models to combine features, which produces predictions that are more thorough and precise. Further, we identified some of the research gaps, and the following remarkable points are mentioned on how to fill the research above-mentioned research gaps:

- Creating a more extensive, varied, and well-annotated dataset to detect ovarian cancer.
- Developing explainable AI methods to improve the interpretability of DL models.
- Promoting inter-institutional cooperation for data exchange while upholding moral principles.
- Establishing uniform frameworks for the integration of multimodal data.
- An increasing computational effectiveness to enable DL solutions in environments with constrained resources.

7. Conclusions

The goal of this review was to clarify and evaluate the efficacy of several DL techniques in the detection of ovarian cancer. The taxonomy of genomic and imaging data for the prognosis of ovarian cancer is described. We specifically compared the patterns found about the kind of model being used, the kind of cancer that was diagnosed, the type of data used in the prediction and overall accuracy of the different methods with their validation techniques, and the efficacious analytics in the diagnosis of ovarian cancer. The survey highlighted a significant bias in the previous prediction of this fatal illness toward DL models. We discussed how DL models performed in this review, showing that they outperformed machine learning models in terms of accuracy. The major challenges of the existing method are handling the noise and complex dataset which disturb the performance of DL approaches. Future studies should focus on early detection of ovarian cancer as follows,

- An assembling of a variety of high-resolution dataset to enhance the generalizability of the model.
- Addressing data shortage by producing synthetic ovarian cancer imaging or omics data using Generative Adversarial Networks (GANs).
- Sophisticated augmentation methods to mimic real-world unpredictability, like random cropping and elastic deformations.
- Combining clinical, genomic, and proteomic data with imaging data, such as CT, MRI, and US, to provide a comprehensive analysis.
- Employing hybrid architectures or transformer-based models to successfully integrate these modalities.

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Authors Contribution Statement

Both the authors equally contributed to the Conceptualization, Methodology, Investigation, Validation, Formal analysis, Data Curation, Writing - Original Draft and Writing - Review & Editing. The final manuscript has been read and approved by all authors.

Funding

The authors declare that no funds, grants or any other support were received during the preparation of this manuscript.

Competing Interests

The authors declare that there are no conflicts of interest regarding the publication of this manuscript.

Data Availability

The data supporting the findings of this study can be obtained from the corresponding author upon reasonable request.

Has this article screened for similarity?

Yes

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