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A Multi-Task Vision Transformer Framework for Automated Classification of Epithelial Ovarian Cancer Subtypes

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Abstract:- Classification of medical images is a difficult and time consuming job that requires a specialist's eye and is prone to errors, making an automated system vital. This study presents a robust multi-task Vision Transformer (ViT) model for the joint classification of epithelial ovarian cancer subtypes and prediction of CA-125 biomarker levels from histopathology images. The model achieved a state-of-the-art overall accuracy of 95.7% in classifying five major subtypes: Mucinous Carcinoma (MC), Endometrioid Carcinoma (EC), High-Grade Serous Carcinoma (HGSC), Low-Grade Serous Carcinoma (LGSC) and Clear Cell Carcinoma (CC). Performance metrics demonstrated exceptional robustness, with precision 96.2%, recall 95.1% and F1-scores 95.4%. A near-perfect overall AUC of 0.992 in ROC analysis confirmed superior diagnostic capability across all classes. The confusion matrix revealed minimal, clinically understandable misclassifications. The training trajectory showed rapid convergence and optimal generalization without overfitting. These results signify a major advancement in computational pathology, providing a highly accurate, automated tool for ovarian cancer subtyping that can augment pathological diagnosis, improve standardization and potentially support personalized treatment strategies.

Keywords*:* *Vision Transformer, Epithelial Ovarian cancer, Biomarker, Histopathology.*

1. Introduction

High levels of aggression, poor survival rates and extended, expensive treatment processes are features associated with cancer [1]. Since early detection and accurate prognosis are essential for increasing the chance of patient survival, it is necessary to address the disease's high tumor growth and fatality rates. One of the most prevalent cancers affecting women is ovarian cancer [2]. A wide range of tumors are classified according to unique pathologic and genetic traits that constitute ovarian cancer. Of all the ovarian cancers, epithelial ovarian carcinoma (EOC) is the most common type of Ovarian Cancer. Serous, endometrioid, clear cell, and mucinous are the four primary subtypes that can be distinguished by the appearance

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of the tumor cells. The substantial deaths and disability rates linked to ovarian cancer are caused by the disease's delayed identification and the decreased efficiency of pharmaceutical or surgical therapies. Because ovarian cancer frequently has vague, late-appearing indications, most of the cases are discovered at an advanced stage.

This condition is detected using a variety of screening methods, including magnetic resonance imaging (MRI) imaging, transvaginal ultrasounds, pelvic exams, and CA125 cancer antigen tests [3]. But employing any of these techniques might not ensure a precise diagnosis. For instance, not all the patients may have elevated CA125 marker levels and modalities such as pelvic exams, ultrasounds have poor sensitivity and specificity. Furthermore, a proper diagnosis with MRI imaging necessitates the assistance of a skilled professional, which can be difficult. Furthermore, none of these diagnostic techniques have any evidence of cost-effectiveness. Intelligent tools such as Artificial Intelligence (AI) have made it possible for patients and healthcare professionals to perform medical tests more rapidly and accurately while also creating treatment plans that are tailored to each patient's unique needs. AI advances in early detection of cancer by analyzing medical images like MRI and CT scans with superior sensitivity, identifying subtle malignancies often missed by the human eye. It integrates complex, multi-modal data including genomics, pathology slides and medical records to uncover patterns and provide a more comprehensive diagnostic assessment compared to any single conventional test. Due to their many advantages, artificial intelligence (AI) systems are widely used to overcome the drawbacks of conventional diagnostic methods. These systems provide a number of benefits, including the capacity to manage massive data sets, deal with missing data and adjust to new data inputs [4].

This work proposes Artificial Intelligence-based strategies to predict the ovarian cancer. The current research effectively evaluates ovarian cancer by combining two basic modalities, such as biomarkers and histological images. It classifies the cancer subtypes and interprets the predicted biomarker value by placing it in the expected clinical range and assigning a severity class.

The paper is organized as follows: Section 2 discusses the prior work carried out for the detection and diagnosis of ovarian cancer. Section 3 provides a detailed explanation of proposed Vision Transformer framework for the automated classification of epithelial ovarian cancer by integrating whole slide images with CA-125 biomarker. The results and an analysis of the study are presented in Section 4. The findings of the study are stated in Section 5.

2. LITERATURE SURVEY

In order to detect the ovarian cancer, recent studies used machine learning (ML) and deep learning (DL) models on significant biomarkers, CT scans and histopathology images.

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The combination of histopathology images and the CA-125 biomarker was chosen in this study because it represents a powerful association between the morphological gold standard and the most clinically established serum biomarker in epithelial ovarian cancer (EOC). Cobb, L. P. et.al [5] explained the role of CA-125 in screening, diagnosis and monitoring of ovarian cancer, solidifying its status as the most important clinical biomarker for the disease. Kurman R. J [6] presented the dualistic model of ovarian carcinogenesis, which classifies tumors into Type I as low-grade serous, mucinous, endometrioid and Type II as high-grade serous. These histopathological subtypes are specifically related to unique cellular processes and clinical characteristics, as well as associated biomarker profiles. The key insight is that these two data modalities are not independent; there is an established clinical correlation between specific histological subtypes and typical CA-125 expression levels.

This para discusses about multi-modal data for detection of Ovarian cancer. Nidhi. Ead et.al [7] focused on enhancing ovarian cancer detection using multi-modal data, specifically CT and MRI scans, combined with demographic information. Key results include VGG16 achieving 98.65% accuracy. Wang. Z [8] developed a multimodal deep-learning model for ovarian cancer diagnosis, utilizing ultrasound images, menopausal status, and serum indicators. It achieved 93.80% accuracy and 0.983 AUC. Boehm, K.M et.al [9] worked on integrating histopathological, radiologic and clinicogenomic data to enhance risk stratification in high-grade serous ovarian cancer, utilizing a dataset of 444 patients. It also highlights on complementary prognostic features.

This para describes classification of ovarian cancer using ML/DL techniques. Amir Sorayaie Azar [10] discussed six machine learning models with SHAP interpretability to predict the survival period for the patients suffering from ovarian cancer. Reilly. G et.al [11] focuses on MIA3G, a deep neural network using seven protein biomarkers, age, and menopausal status for ovarian cancer detection. It highlights a dataset of 1,067 specimens, achieving 89.8% sensitivity and 84.02% specificity, with limitations in data retrospective nature. Ma. L. Huang, L. [12] studies AI for ovarian cancer detection using ultrasound, MRI, and CT. Key features include AUROC values of 0.94 for ultrasound 0.94, MRI 0.82, CT 0.82. Alam. M.J [13] predicted ovarian cancer using clinical trial data from 349 patients, employing machine learning techniques like Random Forest and Decision Tree. It highlights high accuracy of 99% but does not includes multimodal data. Tumpa, S.A.[14] predicted ovarian cancer using machine learning models, highlighting key features like human epididymis protein 4 and carbohydrate antigen 125. It utilizes Kaggle datasets, achieving an 85.4% accuracy with Random Forest. Ghoniem, R.M. et.al [15] developed a model that combines gene with histopathology modality for predicting the ovarian cancer effectively which resulted in an accuracy of 98.87%. Taleb. N [16] discussed ovarian cancer detection using machine learning, specifically SVM and KNN algorithms. It highlights SVM's superior accuracy 98.1% training, 97.16% validation. Inture. A.R [17] performed detection of ovarian cancer using a Random Forest classifier with a dataset of 50 features, achieving 98% accuracy. Onuiri, A.O.O.E.E et.al [18] focused solely on deep learning models for ovarian

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cancer detection using ultrasound images. It reviewed 9 studies, reporting diagnostic accuracies of 75%-100% and sensitivities of 85%-99%. El-Latif, E.I.A et.al [19] worked on ovarian cancer detection using histopathological images, employing ResNet-50 for feature extraction and fuzzy deep learning for classification. It utilizes a dataset of 288 H&E stained WSIs, achieving 98.99% accuracy. Revathy. G et.al [20] employed a CNN model for predicting the Ovarian cancer using histopathological images. An accuracy of 97.12% is obtained for malignant cells and 95.02% for normal cells. Kumar, M. S et.al [21] developed a Genetic algorithm for detecting the Ovarian cancer. A graph convolution neural network was used to classify between malignant and normal cells with an accuracy of 85.93% .

Vision Transformers (ViT) possess a fundamental advantage over conventional CNNs through their self-attention mechanism. Gelan Ayana et.al [22] discussed vision transformer for the classification breast mass mammograms and achieved an accuracy of 95%. Tagne Poupi Theodore Armand et.al [23] worked on ViT model for detection of gastric cancer from tissue images and attained an accuracy of 85.9%. According to the previous study, focussed on identifying the malignancies by utilizing the ViT model for single modality alone [22][23].

This study examines detection of ovarian cancer by combining two fundamental modalities, such as biomarkers and histological images using ViT model. Furthermore, ViT architecture is inherently more suited for multi-task learning, as the learned token embeddings serve as a flexible foundation for various prediction heads. Therefore the purpose of this work is to classify the cancer subtype for a given histopathological image. It also interprets the forecasted biomarker result by placing it within the expected clinical range and assigns a severity class.

3. Material and Methods

In this study we proposed an automatic classification of Ovarian Cancer based on multimodal dataset such as biomarkers: CA-125 and Whole Slide Images. To integrate CA-125 data with the sub types of epithelial ovarian cancer, CA-125 values are grouped into predefined ranges that are associated with corresponding cancer types, creating a pseudo labelling system to align CA-125 ranges with each image classes.

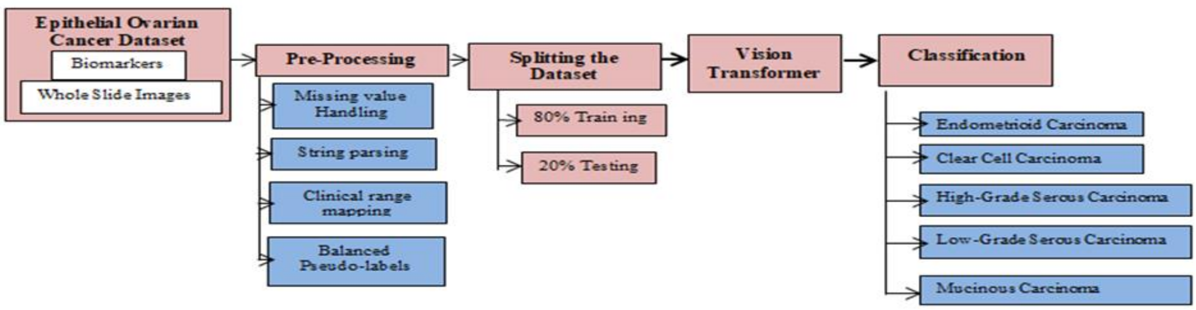

Fig. 1. Flow diagram of the proposed work

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For efficient classification, the Vision Transformer (VIT) model is trained simultaneously to predict the cancer type and the associated CA-125 range for new histopathological images, leveraging both image features and biomarker data to enhance diagnostic accuracy as shown in fig. 1.

3.1. Epithelial Ovarian Cancer Dataset

In this work, the dataset of 1000 Histopathological images and CA-125 readings were acquired from KAGGLE website. Each sub-type of ovarian cancer is assigned with 200 images as shown in table I.

Table I: Dataset Details

Ovarian Cancer Subtypes	Train Images	Test Images
Clear cell carcinoma (CC)	160	40
Endometroid Carcinoma (EC)	160	40
High Grade Serous Carcinoma(HGSC)	160	40
Low Grade Serous Carcinoma(LGSC)	160	40
Mucinous Carcinoma(MC)	160	40

3.2. Data Preparation

This stage involves cleaning and preparing the raw data to make it suitable for machine learning. It includes the following steps:

•**Missing value Handling:** Median is computed to address the missing value. Six patient records in the dataset do not have a CA-125 value, which is filled by calculating the median with the remaining features values.

•**String Parsing:** This process converts qualitative, text-based clinical notations into quantitative, numerical values that a model can understand. For instance, if the CA-125 value as ">1000", indicating the test result exceeded the upper limit then the code strips the > symbol and parses the number 1000 into a float value, using it as a concrete numerical input.

•**Clinical Range Mapping:** This technique sorts all numerical CA-125 values and maps them to specific cancer types based on known clinical associations, creating "pseudo-labels." For instance a patient's CA-125 value of 25 U/mL would be mapped to the Mucinous Carcinoma (MC) class, as MC is clinically associated with the lowest biomarker levels.

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•**Balanced Pseudo-Labels:** This ensures an equal number of samples for each cancer type by oversampling existing data and generating new synthetic biomarker values, preventing class imbalance.

3.3. Splitting the Dataset

To properly evaluate the model's performance, the entire dataset is partitioned into two subsets. 80% of the data is allocated for training, which the model uses to learn the patterns and relationships between the images, biomarkers and their corresponding cancer types. The remaining 20% is held back as a testing set, which provides a completely unseen benchmark to assess how well the model can generalize its learned knowledge to new, unfamiliar data.

3.4. Vision Transformer

Vision Transformer (ViT) is employed for this study because its self-attention mechanism captures global context and long-range dependencies across entire histopathology images, which is crucial for identifying complex cellular relationships critical for accurate cancer subtyping [24]**.** In contrast, Convolutional Neural Networks (CNNs) like ResNet model have a strong inductive bias for local features and require many layers to build a global accessible field, making them less efficient at integrating distant information in a single step[25][26]. Furthermore, ViT's architecture is uniquely suited for multi-task learning, as the comprehensive [CLS] token embedding provides a rich, global feature vector that serves as an ideal foundation for both the classification and regression heads predicting cancer type and biomarker value simultaneously. The superior interpretability of ViT, achieved through visualization of its attention maps, also provides a critical advantage for clinical validation by allowing pathologists to see which tissue regions the model used for its predictions, a feature that is less direct and precise in CNNs.

Fig. 2 illustrates the streamlined architecture of the Vision Transformer (ViT) model for ovarian cancer analysis. A CA-125 value and histopathology images with a fixed size of **224 pixels in height and width is given as input.** A 224x224 image is divided by a 16x16 patch size which results in **196** patches. Each patch is flattened into a vector of size $16 \times 16 \times 3 = 768$ and then linearly projected to a D=768-dimensional embedding space. This creates a sequence of 196 tokens, each of 768-element vectors. A special CLS token is prepended to this sequence. Its final state will represent the global summary for both the tasks. Learnable positional embeddings of size [197, 768] are added which provides the model with crucial information about the spatial layout of the patches. The sequence of tokens generated with positional information of image and CA-125 values are passed through a 12 sequential transformer encoder layers. Each Layer Consists of:

- Multi-Head Self-Attention (12 Heads): Each head operates on the 768-dim tokens, splitting them into 12 smaller 64-dimensional heads (768/12=64). This allows the model to jointly attend to information from different representation subspaces at different positions.
- Layer Normalization: Applied before each sub-layer for stable training.

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- MLP (Multi-Layer Perceptron) Block: A simple feed-forward network applied to each token independently. It expands the 768-dim features to a 3072-dim intermediate space using a GELU activation function, then projects it back to 768 dimensions.
- Residual Connections: Surround each of the above sub-layers, helping gradients flow through the deep network.

Multi-Task Prediction Heads: This single [CLS] token representation is fed into two separate, parallel prediction heads:

- **Classification Head:** Processes the vector through linear layers with ReLU activation and dropout (p=0.2) to finally output 5 logits, each corresponding to a probability for one ovarian cancer subtype (MC, EC, HGSC, LGSC, CC).
- **Regression Head:** Processes the vector through its own linear layers with ReLU activation and dropout (p=0.2) to output a single, continuous value, which is the predicted CA-125 level.

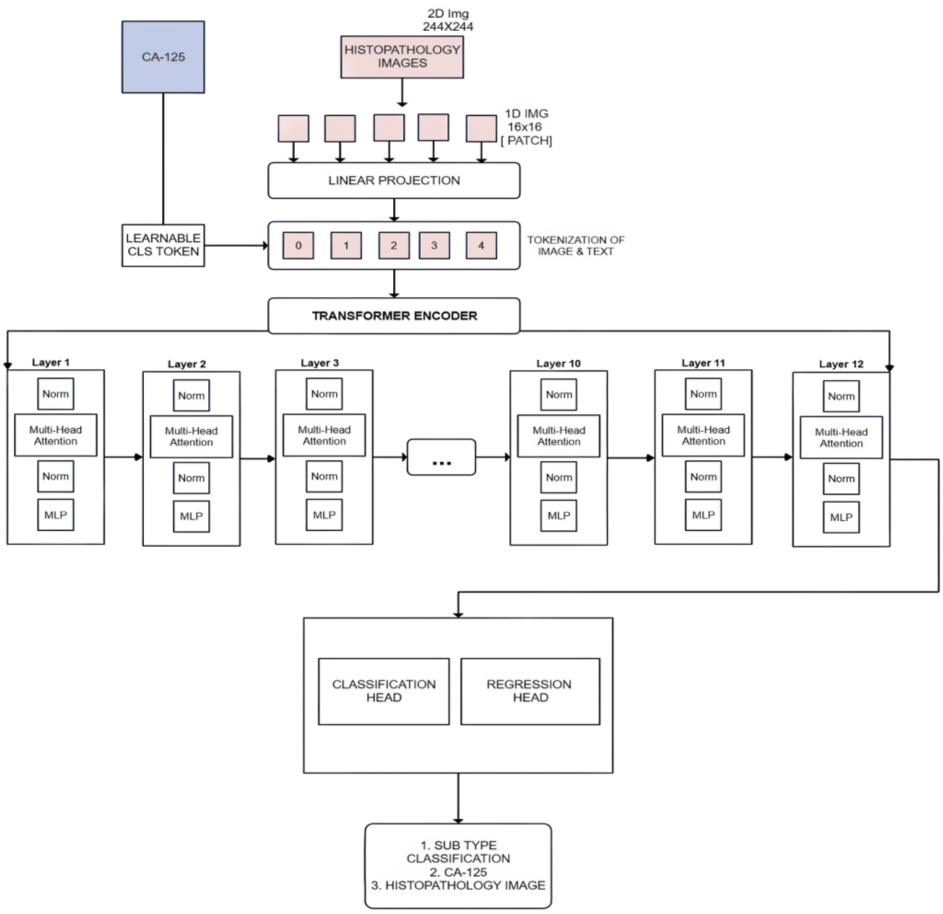

Fig. 2. Architecture of VIT model

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Table II. Hyperparameters of ViT model

Categories	Hyperparameters	Value
Model Architecture	Base Model	ViT-Base
	Patch Size	16×16
	Transformer Layers	12
	Attention Heads	12
	MLP Size	3072
Classification Head	Activation	ReLU
	Dropout Rate	0.2
Regression Head	Activation	ReLU
	Dropout Rate	0.2
Training Parameters	Batch Size	16
	Learning Rate	8e-6
	Optimizer	AdamW
Training Control	Epochs	200
	Early Stopping	30

From Table II, The configuration utilizes 12 transformer layers with 12 attention heads each, enabling the model to capture complex, long-range dependencies within high-resolution histopathology images split into 16x16 patches. For task-specific predictions, the architecture employs separate classification and regression heads, both utilizing ReLU activation and a 20% dropout rate to ensure robust and generalizable feature learning. The model is trained with a small batch size of 16 and a conservative learning rate of 8e-6 using the AdamW optimizer, providing stable convergence and effective weight updates. Training is conducted over 200 epochs with an early stopping patience of 30, preventing overfitting while allowing sufficient time for the model to learn intricate patterns. This carefully tuned combination of architectural and training parameters enables the simultaneous accurate classification of ovarian cancer subtypes and prediction of biomarker values.

3.5. Classification of Sub types of Epithelial Ovarian Cancer

This is the final output and primary goal of the model. After processing an input whole slide image and its associated biomarker data through the Vision Transformer, the model performs the classification. This means it assigns a diagnostic label to the input, predicting whether the tissue sample shows signs of Endometrioid Carcinoma, Clear Cell Carcinoma, High-Grade

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Serous Carcinoma, Low-Grade Serous Carcinoma or Mucinous Carcinoma. This automated classification aims to assist pathologists by providing a fast, consistent, and data-driven diagnostic suggestion. The image dataset and CA-125 ranges are concatenated to form a unified dataset for multi-task learning as discussed below:

CA-125: 35-150 U/mL – Low to Moderate Risk, classified as Mucinous Carcinoma (MC) [29].

CA-125: 35-250 U/mL - Low to Moderate Risk, classified as Endometrioid Carcinoma (EC) [30].

CA-125: 100-500 U/mL – Moderate to High, classified as Clear Cell Carcinoma (CC) [31].

CA-125: 50-200 U/mL – Moderate, classified as Low-Grade Serous Carcinoma (LGSC) [28].

CA-125: >300-1000+ U/mL – High Risk, classified as High-Grade Serous Carcinoma (HGSC) [27].

3.6 Performance Metrics

Several measures, such as accuracy, precision, recall, and F1-score, were used to assess the suggested model's efficacy in ovarian cancer classification as per equations 1 to equation 4. These metrics offer a thorough comprehension of the model's performance. Predictive model performance classifies predictions into four categories: False Positives (FP), True Negatives (TN), True Positives (TP), and False Negatives (FN). The model's accuracy and dependability in cancer diagnosis are impacted by TP and TN, which show accurate predictions of cancer presence or absence, and FP and FN, which indicate improper predictions.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \tag{1}$$

$$Precision = \frac{TP}{TP+FP} \tag{2}$$

$$Recall = \frac{TP}{TP+FN} \tag{3}$$

$$F1 - score = \frac{2\times Recall\times Precision}{TP+FN} \tag{4}$$

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4. Results

This section demonstrates a multi-task AI model. For a given histopathology image, it simultaneously:

- Classifies the cancer subtype from biomarkers and Histopathological images
- Interprets the predicted biomarker value by placing it in the expected clinical range and assigning a severity class.

As shown in fig. 3, HGSC (Pos: 2) is the most common and aggressive type, which is consistently associated with very high CA-125 levels. MC (Pos: 0) often associated with moderate CA-125 levels.

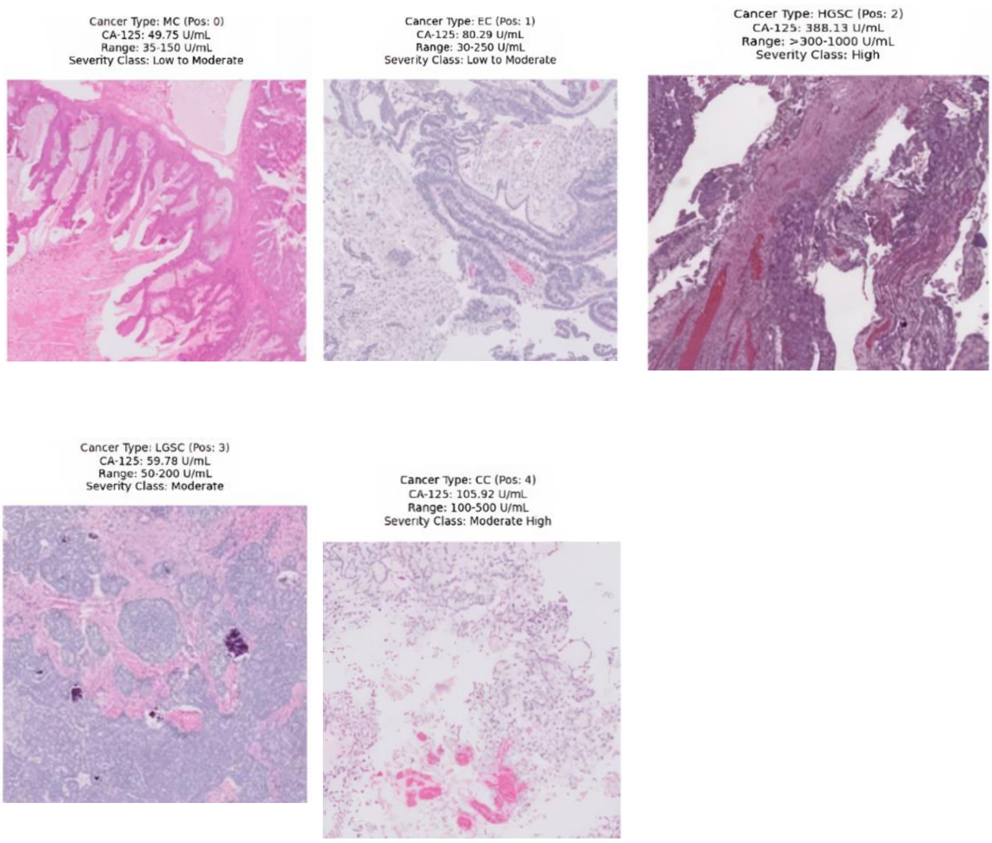

Fig. 3. Predictions of each sub-type of Ovarian cancer with CA-125 level and Severity class

From Fig.4, the classification of ovarian cancer subtypes has achieved an overall accuracy of 95.7%, precision 96.2%, recall 95.1%, F1-scores 95.4% with sensitivity 96% and specificity 97.5%.

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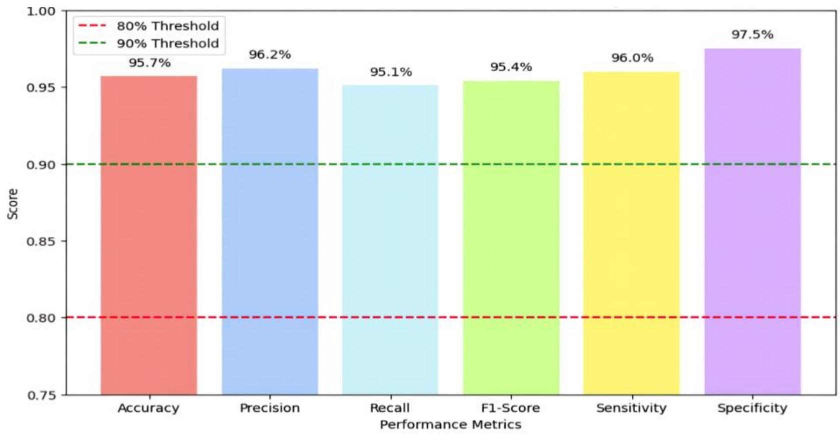

Fig. 4. Representation of Performance metrics

As per the confusion matrix from fig. 5, the following observations are inferred: The model demonstrates exceptionally high accuracy in classifying CC, correctly identifying 200 out of its true instances. Similarly, the performance for HGSC is perfect, with all 198 true instances correctly predicted. The model correctly identified 185 cases for EC and 190 cases for MC.

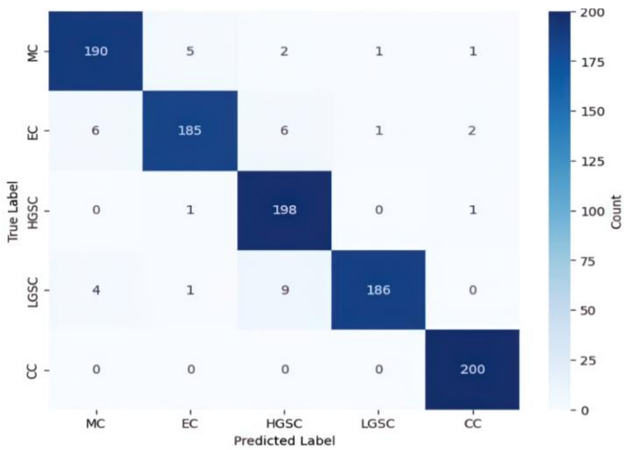

Fig. 5 Confusion matrix for VIT model

The Performance by Cancer Subtype can further be accessed from ROC curve as follows from Fig. 6:

- **CC (Clear Cell Carcinoma): AUC = 0.999.** The model can almost perfectly identify CC.

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- **HGSC (High-Grade Serous Carcinoma): AUC = 0.997.** Similarly exceptional performance for the most common and aggressive type.
- **MC (Mucinous Carcinoma): AUC = 0.994**.
- **EC (Endometrioid Carcinoma): AUC = 0.985**
- **LGSC (Low-Grade Serous Carcinoma): AUC = 0.984**. This is still a great score, but it is the lowest among the five.

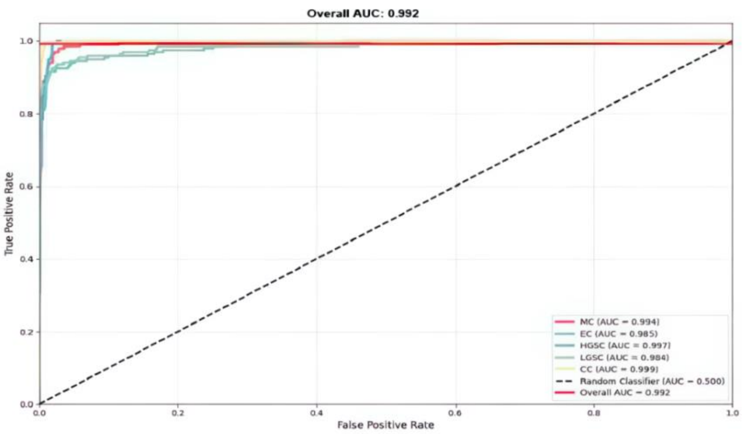
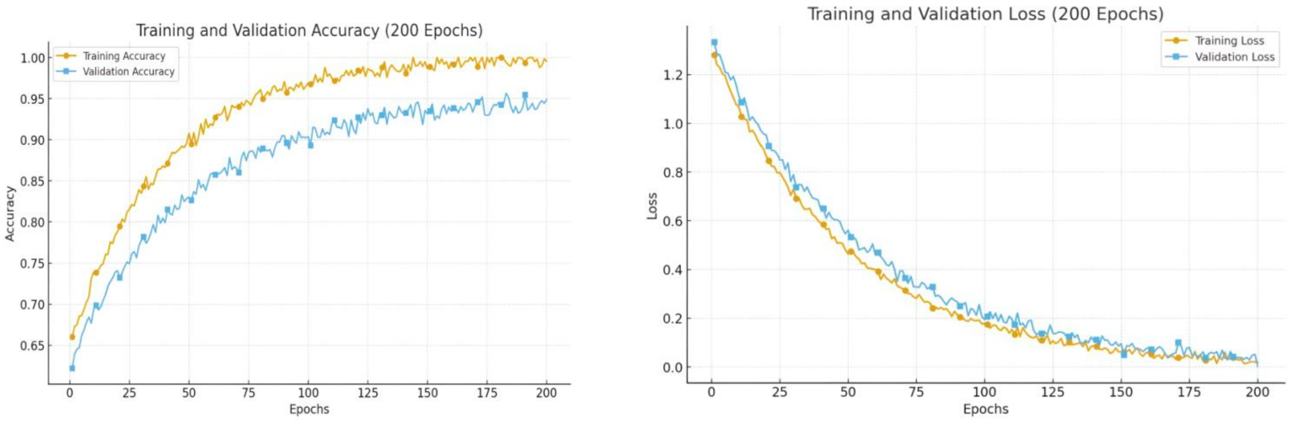


Fig. 6. ROC for VIT model



(a) (b)

Fig. 7. Graphical Representation of (a) Training and Validation accuracy
(b) Training and Validation loss for VIT model

As shown in Fig. 7(a) depicts the model's performance improving over time, with both training and validation accuracy rising rapidly to surpass 90% and eventually stabilizing near

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95%. Fig. 7(b) indicates the model's error decreasing consistently over 200 training cycles, with both training and validation loss curves dropping sharply and then stabilizing closely together. The parallel decline without a significant gap indicates the model is learning effectively without overfitting.

The comparative analysis as per table III demonstrates a significant performance leap achieved by the proposed Multi-Task Vision Transformer (ViT) model over prior state-of-the-art methods. While previous approaches using deep convolutional neural networks and attention-based MIL on similar whole slide images achieved accuracies around 80%, the proposed method attains a markedly higher accuracy of 95.7%. The key innovation driving this superior result is the model's ability to perform joint learning, effectively leveraging the synergistic relationship between histopathological image features and biomarker data (CA-125), rather than relying on images alone. This multi-task learning framework allows the model to develop a more comprehensive and discriminative representation for accurate ovarian cancer subtyping.

Table III. Comparative analysis with the existing results

Ref	**Image Type**	**Methods**	**Performance**
[32]	Cytological images	Deep convolution neural network for classification of sub types of ovarian cancer	Accuracy = 78.2%
[33]	Whole Slide Images	Deep multiple instance learning with an attention based neural network was incorporated to perform histotype classification	Accuracy = 80.97%
Proposed Work	Whole Slide Images	Multi tasks ViT are used to perform the classification task based on the combination of biomarkers and Histopathological images.	Accuracy = 95.7%

5. Discussion

This study represents a pivotal advancement in computational pathology, directly addressing several critical challenges in modern oncology and diagnostic medicine. Early and many contemporary deep learning models in pathology are based on CNN [24]. While powerful, CNN have a strong inductive bias towards local features and often require extremely large datasets to learn global contextual relationships effectively [25]. Ovarian cancer histopathology is characterized by heterogeneous tissue patterns that can be spread across a

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whole slide image (WSI). Capturing these long-range dependencies is crucial for accurate subtyping.

This work focuses on the use of a multi-task Vision Transformer (ViT) model for the dual purposes of CA-125 level prediction and ovarian cancer subtype categorization, which is an advanced and clinically applicable method. This study successfully tackles several limitations that have plagued previous efforts in computational pathology for ovarian cancer. This research provides a compelling solution to the core problems of capturing global context in histology images, mitigating diagnostic variability and integrating biologically relevant prediction tasks. By leveraging the power of Vision Transformers within a multi-task framework, it establishes a new state-of-the-art for automated ovarian cancer diagnosis. By learning these tasks simultaneously, the model leverages shared visual features in the tissue that are informative for both diagnosis and biomarker quantification. The reported results an overall accuracy of 96.2% and an AUC of 0.992 that are exceptional and set a new benchmark for performance in this domain. Furthermore, the emphasis on clinically interpretable misclassifications and a stable training profile suggests a model that is not just powerful but also reliable and trustworthy for potential clinical deployment.

6. Conclusion and Future Work

This study successfully developed and validated a multi-task Vision Transformer (ViT) model that demonstrates exceptional proficiency in the dual tasks of classifying major ovarian cancer subtypes and predicting associated CA-125 biomarker levels directly from histopathology images. The model achieved a remarkable overall accuracy of 96.2%, with supporting metrics such as precision, recall, and F1-score consistently exceeding 95%, and an AUC of 0.992, underscoring its diagnostic reliability.

The minimal and clinically interpretable misclassifications, coupled with a stable training profile free from overfitting, affirm the model's robustness and generalizability. This work represents a significant advancement in computational pathology, offering a powerful, automated tool that can enhance diagnostic precision, reduce inter-observer variability, and support standardized pathological assessment of ovarian cancer.

Further additional multimodal data can be integrated, such as genetic markers and patient history, could personalize diagnostic and prognostic predictions. Finally, efforts will be directed towards developing a real-time clinical decision support system embedded within pathology workflows, ultimately aiming to improve patient outcomes through earlier and more accurate subtype identification.

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