Early Diagnosis of Ovarian Cancer by the Integration of Whole Side Images and Deep Learning Models

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Abstract: The Ovarian cancer subtypes have been demonstrated to represent unique pathologic entities with varying prognosis and of Ovarian cancers have been shown to be diverse pathologic entities with different treatment outcomes and predictions. Even though pathologists are capable of performing the tissue biopsy process with reliability, there are some challenging situations that necessitate consulting with a specialist. We propose an automated approach for ovarian cancer classification to enhance pathologists' performance and satisfy the need for more accurate and reproducible diagnosis. Whole Slide Images (WSIs) tiled into accessible datasets are used in this study. For the diagnosis and prognosis of ovarian cancer, precise measurement of mitotic activity is essential. In order to identify two forms of mitotic activity, multipolar and caterpillar mitosis that are frequently seen in the histopathology of ovarian tumors, an average of more than 2000 tiles were taken from each of the WSIs using GPU-optimized tiling algorithms. To detect malignant mitotic activity, this paper's focus includes the detection and classification of the aforementioned kinds of mitosis using deep learning architectures. Following training, YOLO-based object detection models achieved accuracies of 78.20% and 89.33%, respectively. A trained ResNet-34 model yielded 86.25%. One important factor that makes it possible for strong deep-learning pipelines for cancer is the tiling technique, which reduces resource usage while preserving good image quality.

1 INTRODUCTION

It is currently acknowledged that ovarian tumors are a diverse group of multiple different histotypes rather than a singular illness (Kussaibi et al., 2024). These tumors vary not only at the cellular level but also in a wide range of other ways, including aggressiveness and how well they respond to therapy. Until recently, all ovarian cancers had the same treatment, which often had unsatisfactory outcomes. Depending on the stage of the disease, this included surgery and/or standard chemotherapy regimens (Suma et al., 2022). The identification and classification of cancer is among the most popular uses for automatic histopathology image analysis. Histopathology images can be analyzed using nuclear and textural features (Farahani et al., 2022). There are studies that describe the appearance of tissue component using segmentation-based characteristics. Ovarian cancer presents significant diagnostic challenges due to its heterogeneity across subtypes. Histopathological analysis, relying on mitotic activity, remains central to its assessment. However, manual quantification is prone to variability and significant time, motivating automated detection methods (Kasture et al., 2021). This paper is a part of a much wider study of "Ovarian Cancer Detection using Deep Learning Techniques" and explores the use of tiled WSIs, obtained from another study, part of the same wider pursuit ("A Novel Tile-Based Methods for Identifying Ovarian Cancer in Histopathological Images"), for training deep learning models to identify mitotic activity, leveraging GPU-accelerated tiling for efficient dataset creation. We compare various state-of-the-art models to determine the most reliable approach for mitosis detection in ovarian cancer. The models

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perform detection and classification for the mitosis subtypes: Multipolar and caterpillar. As a "translation" of pathologists' diagnostic process into a system of computer vision that chooses discriminative image characteristics to carry out an automatic diagnosis, we present our suggested automatic ovarian cancer classifier. In Figure 1, the suggested model is summarized. Four components comprise the design: feature extraction, machine learning-powered categorization, picture the process of segmentation and image pre-processing.

2 LITERATURE SURVEY

Mitotic detection in histopathology has advanced with machine learning. Recent works emphasize efficiency and scalability, addressing challenges like image resolution *and variability as per table I.*

Table 1: Study of Prior Work.

Ref.	Dataset	Approach	Deliverables
(Farahani et al., 2022)	Not explicitly mentioned, likely publicly available histopathology datasets	Convolutional Neural Networks (CNNs) for histotype classification	High accuracy in histotype classification (up to 94%).
(Kasture et al., 2021)	Not explicitly mentioned, likely publicly available histopathology datasets	Convolutional Neural Networks (CNNs)	High accuracy in histological analysis.
(Cireşan et al., 2013)	Mitosis Detection dataset (breast cancer histology images)	Deep MaxPoolingCNN with data augmentation	High F1-score, winning the ICPR 2012 mitosis detection contest.
(li et al., 2019)	Publicly available breast cancer datasets (ICPR, AMIDA)	Weakly supervised learning with concentric loss function and CNNs (ResNet)	Achieves competitive performance with only image-level labels.
(alom et al., 2018)	Diverse medical image datasets (retinal blood vessels, skin lesions, lung segmentation)	Recurrent residual U-Net (R2U-Net) architecture for image segmentation	Improved segmentation accuracy compared to standard U-Net.
(Mousavi, 2023)	99 whole-slide images of canine mammary gland (CMG) tumors	First stage detects potential mitotic candidates; second stage classifies true mitoses using deep learning.	A two-stage framework using Mask R-CNN and ResNet-50 achieves an F1 score of 76.0%.
(Aubreville, 2020)	Laserendomicroscopy (CLE) images from 84 patients undergoing surgery for oral squamous cell carcinoma (OSCC)	ResNet-50 and ResNet-101for feature extraction and classification and Transfer learning from ImageNet, Data augmentation	High sensitivity, specificity, and accuracy for in vivo and ex vivo image datasets.
(Tellez et al., 2018)	Three public datasets (MITOS-ATYPIA-14, ICPR 2012, and AMIDA13) of breast cancer histology images	Two-stage approach: candidate detection using a deep learning model, followed by classification using another deep learning model	High performance across all three datasets, with an F1-score of 0.743 on MITOS-ATYPIA-14.
(Bertram et al., 20198)	Canine cutaneous mast cell tumor (CCMCT) dataset of 1,000 WSIs	Deep learning-based object detection (Faster R-CNN) to identify and classify mitotic figures	Mitotic count and spatial distribution of mitoses can be used to predict tumor grade and patient outcome.
(Aksac, 2019)	Histopathological images of papillary thyroid carcinoma (PTC)	Deep learning-based object detection models (YOLOv3, RetinaNet) to detect and classify nuclei and mitotic figures	High accuracy in detecting nuclei and mitotic figures, with potential for use in automated pathology diagnosis and grading.

(li et al., 2020)	Three public datasets of breast cancer histology images (ICPR 2012, ICPR 2014, and MITOS-ATYPIA-14)	Deep cascaded networks consisting of multiple CNNs to detect mitoses in a coarse-to-fine manner	Improved accuracy and efficiency compared to single-stage models, with an F1-score of 0.821 on ICPR 2012.
(Chen et al., 2016)	Breast cancer histology images from the ICPR 2012 mitosis detection challenge	Parallel computation using GPUs to accelerate mitosis detection algorithms based on feature extraction and classification	Significant speedup compared to CPU-based methods, enabling faster analysis of large histology images.
(Malon et al., 2013)	Breast cancer histology images from the AMIDA13 dataset	Evaluation of various mitosis detection algorithms based on feature extraction, classification, and deep learning	Comparison of different algorithms and identification of their strengths and weaknesses, providing insights for future algorithm development
(Veta et al., 2015)	Breast cancer histology images from a local hospital	Morphological operators and image processing techniques to detect mitotic cells	Simpler and faster compared to deep learning-based methods, but might not be as accurate.
(Paul and Mukherjee, 2013)	Various histopathology images, including breast, prostate, and colon cancer	Review of different methods for nuclei detection, segmentation, and classification, including traditional image processing and machine learning	Comprehensive overview of the field and discussion of various techniques, challenges, and future directions.
(Irshad et al., 2014)	Breast cancer histology images from the ICPR 2012 mitosis detection challenge	Deep cascaded networks with multiple stages for candidate detection and classificatio	High accuracy in mitosis detection, demonstrating the effectiveness of multi-stage approaches.

3 METHODOLOGY

3.1 Block Diagram

Numerous techniques have been put forth to identify nuclei in histological images. It is clear from the results of these studies that the current approaches work well for nuclei with consistent shapes but fall short when the nucleus's size and shape change. A straightforward method for categorizing mitotic nuclei is offered in the current study. The nucleus segmentation process is depicted in Fig. 1.

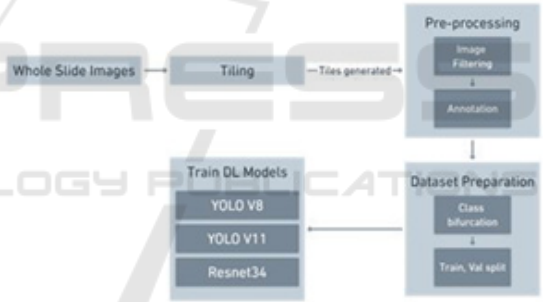

Figure. 1 Proposed model for detection of mitotic region in whole side images

3.2 Dataset

The dataset was created using GPU-based tiling as detailed in the referenced paper. Whole Slide Images (WSIs) of ovarian histopathology were sourced from the UBC-OCEAN dataset, comprising 538 WSIs scanned at 200× magnification. Each WSI is 30,000×23,000 pixels in resolution, on average.

3.3 Pre-Processing and Dataset Preparation

The whole slide images that make up the original dataset are too large in file size and image dimensions to use directly. The mitotic activity that is desired to be represented in the images are observed only at 200x zoom of the images. This makes the division of

the large images into tiles, required. Thus, the WSIs are tiled using the Tiling algorithm proposed as a part of the wider study. The Tiling algorithm proposed is a novel method, that uses a custom CUDA kernel implementing the DALI feature by Nvidia, to perform a GPU-based tiling which utilized the GPU at its fullest. This can be seen in table 1, where the proposed method outperforms the existing methods. The obtained tiles are then pre-processed, i.e. They are filtered for observable mitotic activity and annotated to the classes in context. These classes are then represented in a metadata file and the dataset is split into Training and Validation sets, Concluding the dataset preparation.

3.4 Tiling Process

Following section describes the tiling in detail:
Tile Size: Images were divided into tiles of 1024×1024 pixels using a CUDA-accelerated tiling algorithm.

Filtering: Empty tiles or tiles with non-relevant regions were identified using a thresholding algorithm and discarded to ensure informative datasets.

GPU Optimization: GPU acceleration via NVIDIA DALI and CuPy minimized data transfer between CPU and GPU, significantly reducing tiling time and memory usage. Processing metrics included execution time, resource utilization, and scalability. The tiling process was benchmarked on an AMD Ryzen 7600X CPU, NVIDIA RTX 4080 GPU, and 32 GB RAM.

Table 2: Tiling Performance

Method	Execution Time (min)	RAM Usage (GB)	Utilization (%)	
			CPU	GPU
CPU Only	28	12	67	0
GPU Acceleration	19	10	42	14
GPU with DALI and CUDA	6	6	12	32

3.5 Deep Learning Models

We investigated two deep learning architectures for mitosis detection:

YOLO-based Models: A Pretrained YOLO model were fine-tuned for mitotic detection. The purpose of YOLO model is to minimize the input image's dimension to half and enables the extraction of low-level parameters like patterns and edges. The initial level of the YOLO Model architecture includes a convolutional layer with 32 filters and a 3x3 kernel size. After each convolutional layer, Batch Normalization is applied. Pooling is not used directly in the first layers of YOLO model. Rather, the stride-2 convolution were used. SiLU activation, a computationally effective method for improving the cancer detection was applied.

ResNet: A pre trained ResNet model was incorporated to simplify the training of the system. In the beginning, there is a convolutional layer with 64 filters and a 7x7 kernel size. This is the first convolution layer and a max-pooling layer follows next. In all situations, the stride is set to 2. The pooling layer and the convolution layers follow in conv2_x. Due to the way in which the residuals are related, these layers tend to appear in pairs. Prior to the final output layer, fully connected layers were placed into position, and cancer variations were categorized using ReLU activation.

Hierarchical Framework for the process of mitotic detection :

Environment: Models were trained on NVIDIA RTX 4080 using PyTorch and TensorFlow frameworks. Training used cross-entropy loss for classification and IoU loss for bounding box predictions.

Data Augmentation: Augmentations included rotations, flips, color jitter, and noise addition to improve robustness.

Optimization: Learning rates and batch sizes were optimized through grid search. Early stopping prevented overfitting.

Evaluation Metrics: Models were assessed on accuracy, precision, recall and F1 score.

4 RESULTS AND DISCUSSION

The models trained for the aforementioned task are YOLO V8, YOLO V11, ResNet-34. The details pertaining to the models and their performance are mentioned in the upcoming section. The models were trained on the discussed dataset, to perform detection and classification. The classes trained in, i.e. Caterpillar and Multipolar mitosis are well represented and this is reflected upon inference.

4.1 Model Performance

The below table III details on the model's performance, followed by the confusion matrices and the validation set of each model from Fig. 2 to 7.

Table 3: Performance of Deep Learning Model

Model	Accuracy	Precision	Recall	F1 Score
YOLO V8	78.20%	78.57%	75.49%	76.20%
YOLO V11	89.33%	87.93%	89.28	88.60%
ResNet-34	86.25%	84.50%	86.22%	85.35%

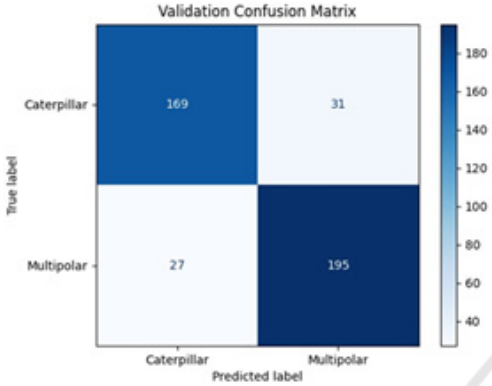

Figure. 2: Confusion matrix for validation of YOLO V8

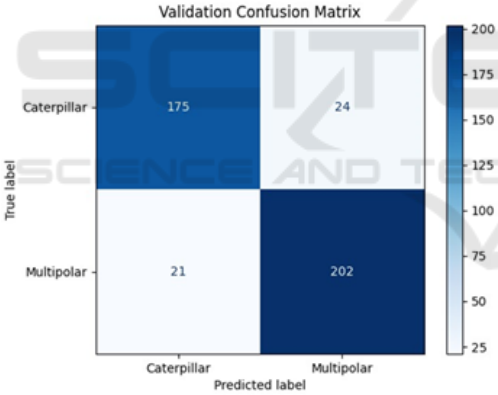

Figure. 3: Confusion matrix for validation of YOLO V11

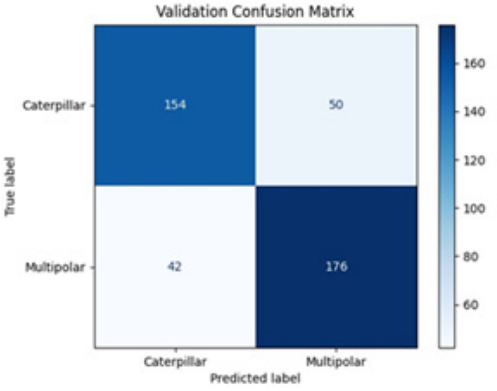

Figure. 4. Confusion matrix for validation of Resnet 34

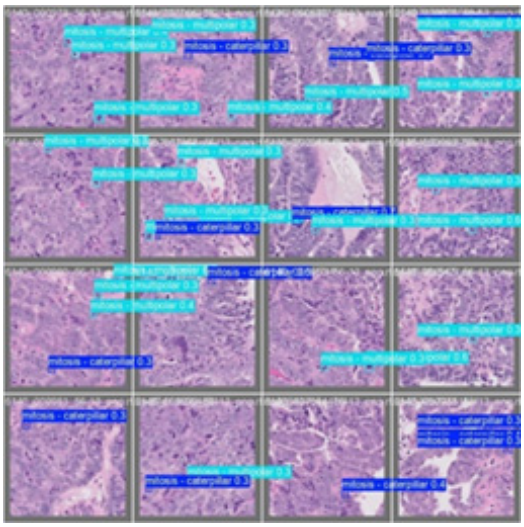

Figure 5: Validation set inference YOLO V8

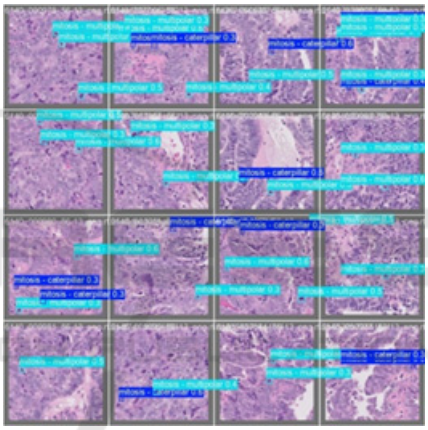

Figure 6: Validation set inference YOLO V11

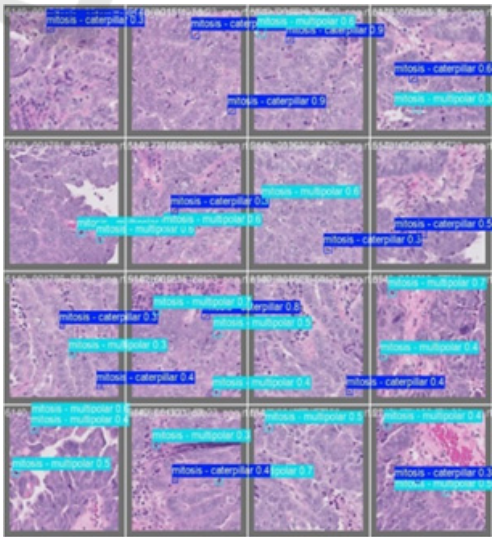

Figure.7: Validation set inference Resnet34

4.2 Discussion

This study successfully demonstrates the application of deep learning models, specifically YOLOv8, YOLOv11, and ResNet-34, for the detection and classification of mitotic figures in ovarian cancer histopathology images.

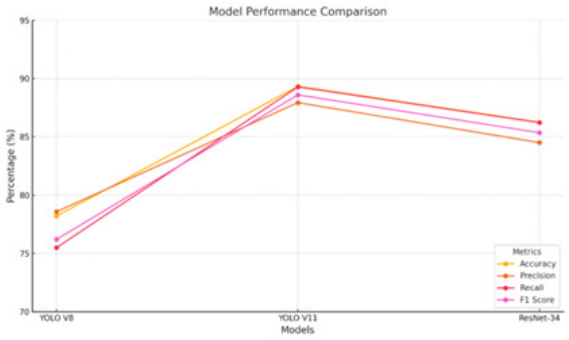

Figure . 8. Consolidated graph all models

By employing GPU-accelerated tiling, the methodology overcomes the challenges associated with analyzing large Whole Slide Images (WSIs), enabling efficient resource utilization while maintaining high image quality. The results indicate that YOLOv11 achieved the highest accuracy (89.33%) and F1-score (88.60%), outperforming both YOLOv8 and ResNet-34. The confusion matrices further reveal the efficacy of the models in distinguishing between the two targeted classes: caterpillar and multipolar mitoses. These subtypes, known to be critical in ovarian cancer characterization, were accurately identified.

The significance of this work lies in its potential to provide pathologists with an automated tool that can greatly aid in diagnosis and prognosis. The study's focus on the crucial mitotic activities and subtypes is an important step in enhancing diagnostic accuracy.

5 CONCLUSION AND FUTURE WORK

This work presents a robust deep learning-based framework for the detection and classification of malignant mitotic activity in ovarian cancer using tiled WSIs. The implemented GPU-optimized tiling and model architecture achieved high performance, with the YOLOv11 model demonstrating superior detection capabilities. This methodology offers a significant contribution towards developing automated diagnostic tools, reducing the time and subjectivity associated with manual pathological analysis. This work validates the use of deep learning architectures for accurately detecting mitotic figures and provides a strong foundation for future research and clinical applications.

Future research will focus on expanding the dataset to include a broader range of ovarian cancer subtypes and exploring methods to improve the robustness and of the models.

Contribution of authors – Suma P, Ananya D Hedge and Rakshith R are involved in the data analysis and paper structure. Suma K V is involved in the comprehension and critical review of the manuscript for conceptual substance. Each author pledges to be accountable for every aspect of the work.

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