Efficient Mitosis Segmentation and Detection in Breast Cancer Histopathological Images Using YOLOv5 Model

Jithy Lijo [1,2,*] and Saleema J. S. [3]

[1] Department of Computer Science, Christ University, Bengaluru, Karnataka, India
[2] School of Computer Applications, Dayananda Sagar University, Bengaluru, Karnataka, India
[3] Department of Statistics and Data Science, Christ University, Bengaluru, Karnataka, India
Email: jithy.lijo@gmail.com (J. L.); saleema.js@christuniversity.in (S.J.S.)
*Corresponding author

***Abstract*—Mitosis count serves as a critical biomarker in breast cancer research, aiding in the prediction of aggressiveness, prognosis, and grade of the disease. However, accurately identifying mitotic cells amidst shape and stain variations, while distinguishing them from similar objects like lymphocytes and cells with dense nuclei, presents a significant challenge. Traditional machine learning methods have struggled with this task, particularly in detecting small mitotic cells, leading to high inter-rater variability among pathologists. In recent years, the rise in deep learning has reduced the subjectivity of mitosis detection. However, Deep Learning models face challenges with segmenting and classifying mitosis due to its intricate morphological variations, cellular heterogeneity, and overlapping structures. In response to these challenges, this study presents an Intelligent Mitosis Segmentation and Detection in Breast Cancer Histopathological Images Using Deep Learning (IMSD-BCHIDL) Model. The purpose of the IMSD-BCHIDL technique is to segment and classify mitosis in the histopathological images. To accomplish this, the IMSD-BCHIDL technique mainly employs YOLO-v5 model, which proficiently segments and classifies the mitosis cells. In addition, InceptionV3 is applied as a backbone network for the YOLO-v5 model, which helps in capturing extensive contextual details from the input image and results in improved detection tasks. For demonstrating the greater solution of the IMSD-BCHIDL method of the IMSD-BCHIDL technique, a wide range of experimental analyses is made. The simulation values portrayed the improved solution of the IMSD-BCHIDL system with other recent DL models.**

***Keywords*—breast cancer, histopathological images, segmentation, YOLO-v5, mitosis cells, deep learning**

I. Introduction

Breast cancer is a widespread type of cancer that affects women, making up approximately 25.1% of all cancers in women, according to the Global Cancer Project's (GLOBOCAN 2012) report [1]. The early detection of breast cancer is essential in minimizing mortality rates, as appropriate treatment plans can be recommended based on the grade and diagnosis of the cancer. The Nottingham grading system is commonly used to evaluate breast cancer, relying on three biomarkers found in Histopathological Images (HSI) to determine the grade of the cancer [2]. These biomarkers include nuclear atypia, tubule formation, and the mitotic cell count [3]. Of the three biomarkers, the mitotic cell count is particularly crucial since it directly affects tumor diagnosis. In real-time, mitotic cells can be identified through the visual analysis of HSI of the breast under a high-resolution microscope [4].

However, this technique is often subjective, time-consuming, and can lead to imprecise identification, especially when conducted by a diagnostician with limited experience. The imprecise identification of breast cancer can have significant consequences, such as delayed treatment, misdiagnosis, and ultimately, a poor prognosis.

To overcome these challenges, there is a need for objective and accurate methods to identify mitotic cells in HSI images. One promising approach is the use of machine learning algorithms, which can analyse the histopathological image dataset quickly and accurately. By training the algorithm on dataset of HSI images, it can learn to identify mitotic cells with high accuracy and consistency. This method can greatly increase the precision and effectiveness of detecting and grading breast cancer. The accurate identification of mitotic cells in HSI images is crucial in diagnosing and grading breast cancer. The use of machine learning algorithms can provide an objective and accurate approach to identifying mitotic cells, thereby improving the accuracy and efficiency of breast cancer diagnosis and treatment.

Artificial Intelligence (AI) models have made a significant impact on the healthcare sector, revolutionizing many procedures and enabling the development of innovative solutions [5]. In the field of breast cancer diagnosis and treatment, AI models have been developed that can serve as valuable second-opinion mechanisms, improving the accuracy of diagnoses and

Manuscript received December 14, 2023; revised February 11, 2024; accepted February 28, 2024; published October 23, 2024.

treatment plans [6]. However, the automation of mitotic-cell detection using AI approaches has its own set of challenges. One of the major difficulties in automatically detecting mitotic cells is the need for pathological knowledge and a high-resolution microscope to distinguish normal cells from mitotic cells. The morphology and texture of mitotic cells can resemble that of normal cells, and other organelles, such as apoptotic cells, can also resemble mitotic cells in appearance [7]. Additionally, the mitosis process has two distinct phases, each with its unique features, making it necessary to develop a robust method for detecting different types of mitotic cells.

Another challenge in the automated detection of mitotic cells is the need to maintain a standard environment for data preparation. The scanning procedures, biopsy, and slide preparation must be carried out carefully to avoid problems that can compromise the accuracy of the outcome. Any errors or inconsistencies in data collection or slide preparation can lead to inaccurate results, emphasizing the need for standardization and quality control measures. AI models have the potential to transform the field of breast cancer diagnosis and treatment, but the automated detection of mitotic cells presents several challenges. Overcoming these challenges will require the development of robust methods that can accurately distinguish normal cells from mitotic cells and maintain a standard environment for data preparation. With continued research and development, AI models have the potential to significantly increase the precision and efficacy of breast cancer diagnosis and treatment.

Convolutional Neural Networks (CNNs) have emerged as a popular tool for detecting mitotic figures, a technique used in medical image analysis [8]. The widespread adoption of Graphics Processing Units (GPUs) has made CNNs more accessible and affordable for researchers in this field. By leveraging the power of GPUs, CNNs have proven to be an effective method for detecting mitotic figures in medical images. CNNs are particularly well-suited for studying strong structural representations of objects of interest in medical images, such as tissues or cellular entities [9]. Several studies have developed CNN-based techniques for the detection of mitotic figures in various tissues, including skin, breast, and stem cells [10]. To achieve strong performance on these datasets, CNNs have been complemented with various approaches, including better augmentation strategies and hand-crafted features. These techniques have shown promising results in accurately detecting mitotic figures in medical images, potentially reducing the subjectivity and variability associated with manual detection methods.

The aim of this study was to develop an automated technique called IMSD-BCHIDL technique for the segmentation and classification of mitosis in breast cancer histopathological images using deep learning. The technique involves several steps, starting with image pre-processing to ensure the images are compatible with deep learning analysis. Next, the pre-processed images are fed into, which is responsible for deep instance segmentation and classification of mitotic and non-mitotic nuclei. To extract the relevant features, the InceptionV3 model is used as the backbone network for the YOLO-v5 model.

The performance of the Intelligent Mitosis Segmentation and Detection in Breast Cancer Histopathological Images Using Deep Learning (IMSD-BCHIDL) approach was assessed by conducting a simulation analysis on two benchmark datasets. The IMSD-BCHIDL technique is a promising approach for automated mitosis segmentation and detection using deep learning on breast cancer histopathological images. This technique has the potential to significantly reduce the subjectivity and variability associated with manual detection methods, leading to more accurate and personalized diagnoses and treatment plans for breast cancer patients.

II. Related Works

Khan *et al.* [11] proposed SMDetector, a deep learning-based method for finding small objects, such as mitotic and non-mitotic nuclei. Dilated layers were added to the backbone to solve the problem of small objects becoming lost in the deep levels. The size difference between the photos and the recognised objects was something the authors tried to lessen. They also enhanced the Region Proposal Network (RPN) to recognise small objects more precisely. Mathew *et al.* [12] proposed a novel solution to address the challenges in effectively training Deep Neural Networks (DNNs) for cell classification tasks. They successfully addressed the problem of highly trained data requirements by augmenting the available data from multiple sources through the asset colour-normaliser procedure. Additionally, they tackled the issue of class imbalance through a context-preserving approach, which involved augmenting the mitotic instances. Finally, they utilized a modified CNN to accurately categorize the candidate cell into the targeted classes. Nateghi and Pourakpour [13] proposed two techniques for improving mitosis identification in histopathologic images. These techniques involve a domain-invariant two-stage approach and a stain-augmentation approach to achieve better generalization. Lei *et al.* [14] presented a precise and rapid methodology to mechanically identify mitosis through histopathology imageries. This technique can mechanically find mitotic candidates from histologic sections for screening mitosis. To be Specific, this technique availed VNN for extracting high-level features for detecting mitotic candidates.

Sebai *et al.* [15] modelled a new partially supervised framework related to 2 parallel deep fully convolutional networks. In the detection stage, to gain the final mitosis detections, the authors merge segmentation maps produced by 2 networks. Naik *et al.* [16] tackled the challenges of detecting mitotic nuclei in histopathological images by utilizing YOLOv4, a faster object detection technique. Their approach enabled the direct prediction of mitotic nuclei in a single step without the need for segmentation. The researchers trained the model using 506 examples of mitosis from the publicly available MITOS-ATYPIA14 grand challenge dataset, which

comprised H&E-stained breast histopathological images that were annotated by experts. Sohail *et al.* [17] developed a new CNN-based heterogeneous ensemble approach called "DHE-Mit-Classifier" to detect mitotic nuclei in breast histopathological images. The method involved three stages and identified candidate mitotic patches from the biopsy region. In Ref. [18], a deep learning-based image processing methods is proposed to identify mitoses in histopathological images of neuroendocrine tumors. The model utilized YOLOv5 by incorporating the YOLOv5 transform module for enhanced performance.

Albuquerque *et al.* [19] introduces a deep learning method for automating cell detection and quantification in the zebrafish xenograft cancer model. Using a fine-tuned Faster R-CNN with Inception ResNet V2, the approach addresses challenges like overlapped cells and a diverse dataset. Yu *et al.* [20] developed an automated model by using ResNet. Concurrently, an automatic mitosis detection algorithm was created using YOLOv5. Subsequently, a logical evaluation method was devised to create an automated diagnostic aid for UMT, capable of "studying and synthesizing" a pathologist's expertise. In Ref. [21], an IoMT-enabled CNN model is proposed. Hyper-parameter optimization using the HORD algorithm enhances the effectiveness of finding optimal values for the CNN model, ensuring precise leukemia feature identification and improved overall model performance. Huang *et al.* [22] suggests a deep learning framework to ascertain the count of lymph nodes and subsequently classify each node as benign or malignant. This framework comprises a network for lymph node detection and another for the benign and malignant classification of lymph nodes. In Ref. [23], a Deep Active Learning (DAL) model is proposed. Also, customized deep learning detectors are designed to directly identify mitotic cells within entire microscopic HEp-2 specimen images, eliminating the need for a segmentation step.

A notable research gap endures developing reliable method that address the intrinsic difficulties of overlapping structures, histological variations, and cellular heterogeneity within the images while considerable progress was made in the classification segmentation and of mitosis on breast cancer HSI. Existing methods consistently meet with limitations in capturing the morphological features of mitotic figures, particularly in the context of breast cancer subtype. In addition, the scarcity of publicly available annotated dataset designed especially for mitosis segmentation in breast cancer histopathology hinders the benchmarking and development of advanced algorithm. Bridging this research gap needs novel methods that consider the nuanced features of mitotic cells in different histopathological contexts, together with a comprehensive and standardized dataset to enable a more rigorous evaluation of segmentation and classification algorithms in the domain. Despite these developments, still there is a research gap in the automatic detection and classification of mitosis in breast cancer HSI analysis, including the need for increasing the generalization of the models, and enhancing the performance of mitotic nuclei detection, which address the problems of class disparity.

III. The Proposed Model

In this study, we have concentrated on the development and design of the IMSD-BCHIDL method for the segmentation and classification of mitosis on breast Histopathological Images. The major intention of the IMSD-BCHIDL technique is to exploit DL model for segmenting and classifying mitosis in the histopathological images. To accomplish this, the IMSD-BCHIDL technique comprises three major components: data pre-processing, YOLO-v5, and InceptionV3 model. Fig. 1 represents the entire procedure of IMSD-BCHIDL algorithm.

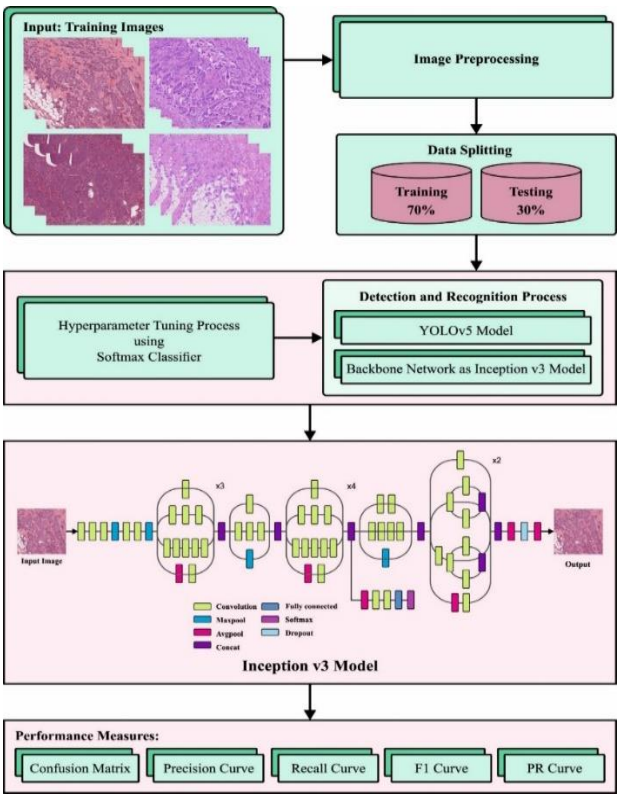

Fig. 1. Overall process of IMSD-BCHIDL algorithm.

A. Data Pre-processing

Mitosis detection and classification are essential tasks in medical image analysis, contributing to the diagnoses and treatment of different diseases, including cancer. Data pre-processing is an important step in preparing the annotated information for training DL model, including YOLO (You Only Look Once), which is a conventional object detection method. This stage includes converting annotation into YOLO format and splitting the dataset into training and validation sets.

Converting Annotation to YOLO Format: Annotations for mitosis detection are usually provided in the form of labelled bounding boxes, indicating the location of mitotic figures within image. YOLO is an effective real-time object detection method, which needs annotation in a certain format for training. The YOLO format consists of:

- Class Index: An index allocated to all the classes (for example, mitosis).
- Bounding Box Coordinates: The coordinate of top-left and bottom-right corners of the bounding box (normalized in the range of zero and one).
- Image Dimensions: The dimension of the image where the object is located.

Converting annotations to YOLO format includes associating the appropriate class index and transforming the bounding box coordinates.

B. *Creating Training and Validation Data:*

It is important to split the annotated dataset into training and validation sets for efficient model training and evaluation. A common practice is to use a 70:30 or 80:20 ratio for these splits, with 70% (or 80%) of the data utilized for training and the residual 30% (or 20%) for validation. This avoids overfitting and ensures that the model generalizes well to unseen data. This process includes the following steps:

- Shuffle the dataset: Randomly shuffle the annotated data to ensure that the training and validation sets are representative of the overall distribution.
- Calculate split points: Define the number of samples to assign to all the sets based on the selected ratio.
- Assign data to sets: Allocate sufficient number of samples to the training and validation sets according to the calculated split points.

C. *YOLO-v5-Based Mitosis Detection and Classification*

For the segmentation, detection, and classification of mitosis, the YOLOv5 model is used. YOLOv5, an advanced version of the YOLO architecture [16]. The YOLOv5 framework has fast detection rate and great performance and meets the requirements of real-time applications. Using a single neural network, it can easily reach the steps required to identify an object. Both detection accuracy and speed are imperative in UAV detection. Therefore, YOLOv5 achieves real-time speed and obtains excellent detection accuracy in UAV detection. Furthermore, it can be trained easily to identify distinct objects and has outstanding performance. YOLOv5 was established in Pytorch that is an open-source platform for DL dependent upon Python. There are three main components in the YOLOv5 model, as follows.

The backbone network has been composed of revolutionary core block named the CSPNet (cross-stage partial network). CSPNet is used to resolve distinct gradient-related problems. It not only decreases the amount of Floating-point Operations Per Second (FLOPS) and parameter count of the algorithm. While reducing the size of architecture, it increases the accuracy and inference speed. Moreover, the backbone contains 1 Spatial Pyramid Pooling Rapidly (SPPF), multiple convolution layers, and 4 CSP bottlenecks with 3 convolutions. The primary goal of backbone is to extract varying-size mapping feature in the input image through several rounds of pooling and convolution. For that reason, the backbone layer in YOLOv5 works as a feature extractor. It is used to save and send features in deep layer to the detection head.

Consequently, it generates the outcome feature map of 3 varying sizes and extracts feature information. The output or head part carries out object detection. In the head section, there are upsampling and concatenate layers, several convolutions, and 4 CSP bottlenecks with 3 convolution layers. The head portion is used to determine the class, predict visual characteristics, and draw bounding box around the target object and this can be computed by:

$$\sigma_r^g = O_{r,g} \times \mho_T^p \quad (1)$$

In Eq. (1), the confidence score of r bounding boxes is σ_r^g and the bounding box of g grid is r. $O_{i,j}$ implies the Intersection over Union (IoU), an assessment metric in image detection. $O_{r,g}$ indicates the target once it is within the g box. If the target is in g box, then the $O_{i,j}$ value is 0; or else, 1. The $IOU\ score$ is based on the accuracy of accurate position of the bounding boxes nearby the target.

YOLOv5x, YOLOv5s, YOLOV51, and YOLOV5m are different versions of YOLOv5. Fig. 2 illustrates the framework of YOLOv5. The study used YOLOv5x in this framework. Amongst them, YOLOv5x is the biggest model. It contains 476 layers. Nearly 87 million parameters were created using this layer.

The feature maps of convolution layer can be evaluated by Eq. (2):

$$R = L * W + b \quad (2)$$

$$L * W = \sum_{n,m} W(n,m) x L(x-n, y-m) \quad (3)$$

Now the activation function has been used on the outcome mapping feature R, $*$ which denotes the convolution operator. Next, the resultant mapping feature $*$ analyses the features identified from the input. n and m symbolize the weighted kernel index. L refers to the input volume that convolves $*$ with the trained weighted W and the b bias term. X signifies the elementwise multiplication between the input and the weight.

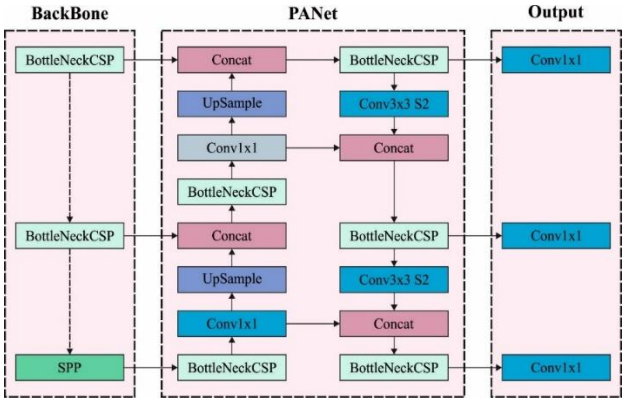

Fig. 2. Structure of YOLOv5.

The Loss Function (LF) of YOLOv5 is the sum of regression functions for classification loss, bounding boxes, and confidence loss. It has been computed by the following expression:

$$LP = l_{bx} + l_s + l_j \quad (4)$$

In Eq. (4), the loss function for the confidence is l_j, the regression function for bounding boxes is l_{bx}, the loss function for classification is referred to as l_s and the computation process can be given as follows:

$$l_{bx} = \lambda_{cd} \sum_{i=0}^{s^2} \sum_{m=0}^{b} I_{i,m}^{j} bj(2 - W_i \times h_i)[(x_i - x_i^{\mathrm{m}\prime})^2 + (y_i - y_i^{\mathrm{m}\prime})^2 + (w_i - w_i'^m)^2 + (h_i - h_i'^m)^2] \quad (5)$$

In Eq. (5), the correct coordinate of the target is denoted as y_i and χ_j. The indicator function of whether the cell i has an object is λ_{cd}. The height and width of the target is represented as h' and w',

$$l_s = \lambda_s \sum_{i=0}^{s^2} \sum_{m=0}^{b} I_{i,m}^{j} \sum_{C \in cl} V(c) log\big(VV_i(c)\big) \quad (6)$$

$$l_j = \lambda_{noj} \sum_{i=0}^{s^2} \sum_{m=0}^{b} I_{i,m}^{noj} (c_i - c_l)^2 + \lambda_j \sum_{i=0}^{s^2} \sum_{m=0}^{b} I_{i,m}^{j} (c_i - cc_l)^2 \quad (7)$$

where the classification loss function is λ_s, cl is the class, cl denotes confidence score, and the category loss coefficient is λ_{noj}.

D. InceptionV3-Based Backbone Network

In this work, the InceptionV3 model can be applied as the backbone network of the YOLOv5 model. The inception model aims to reduce the impact of computation efficacy and lower parameters in application situations [17]. The number of pixels in the image inputted into InceptionV3 was 299×299. Even though the size is 78% greater than VGGNet 244×244, the running speed of InceptionV3 is greater than VGGNet. The major cause for this greater effectiveness of InceptionV3 are given as follows: the amount of parameters of InceptionV3 is less than one-fourth that of VGGNet (140,000,000) and below half that of AlexNet (60,000,000) compared to AlexNet; in addition, the amount of floating-point computation of the entire InceptionV3 is around 5,000,000,000, which is considerably greater than InceptionV1 (around 1,500,000,000). This makes InceptionV3 better, viz., it is easy to implement in a typical server to deliver fast response service.

A convolutional kernel of varying sizes was adopted by InceptionV3, which allows it to own receptive field of dissimilar areas. A modular system and final joining were adopted to decrease the design space of networks, thus recognizing the fusion of features of different scales. In InceptionV3, a Batch Normalization (BN) layer has been introduced as regularize among the Fully Connected (FC) layers and the auxiliary classifiers. In BN, the batch gradient descent algorithm is used for accelerating the model convergence and training speed of the DNN. The formula of BN is formulated by the following equations:

$$B = \{x_{1\ldots m}\}, \gamma, \beta \quad (8)$$

$$\{y_i = BN_{y,\beta}(\mathrm{x_i})\} \quad (9)$$

$$\mu_B \leftarrow \frac{1}{m} \sum_{i=1}^{m} x_i \quad (10)$$

$$\sigma_B^2 \leftarrow \frac{1}{m} \sum_{i=1}^{m} (x_i - \mu_B)^2 \quad (11)$$

$$\hat{x}_i \leftarrow \frac{x_i - \mu_B}{\sqrt{\sigma_B^2 + \varepsilon}} \quad (12)$$

$$y \leftarrow \gamma \hat{X}_i + \beta = BN_{\gamma,\beta}(x_i) \quad (13)$$

where Y and β refer to learnable parameters (γ is used to adjust the variance from the value distribution and β is used to adjust the location of average value), and ε is a constant. The average value in 1D space is μ_B, the minimal activation value of batches B is indicated as x, the count of activation values is m, the standard deviation in every size of mapping features is σ_B^2.

Moreover, large convolution kernel is separated as to smaller convolution kernels from the sequences; pooling and convolution are linked in parallel, and based on the smoothing criteria, LSR label is added for regularization. Additionally, the distribution inconsistency between input and output in a classical DNN is considered, which causes major problems for feature extraction, BN is introduced into InceptionV3. The learning effect can be enhanced by normalizing the input into all the layers.

IV. Results and Discussion

The proposed model is simulated using Python 3.8.5 tool with different Python Packages. The proposed model is experimented on Windows 11, i5 10th gen, 32GB RAM, and NVIDIA 1060ti 4GB.

In this section, the simulation validation of the IMSD-BCHIDL technique is tested on the MIDOG Challenge 2022 dataset (https://imig.science/midog/download-dataset/). The database is available as sqlite (SlideRunner format) and as json (MS COCO format). The dataset contains two subfolders: training dataset and validation dataset. In addition, the dataset hold images under two classes namely Mitotic and Non-Mitotic. The training dataset holds 2,714 mitotic samples and 1,721 non-mitotic samples. Besides, the testing dataset holds 743 mitotic samples and 577 non-mitotic samples. Fig. 3 demonstrates the sample images from the MIDOG Challenge 2022 dataset.

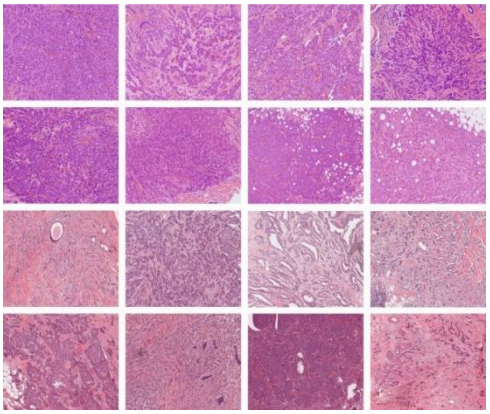

Fig. 3. Sample images.

A set of measures used to analyse the performance are precision, recall, F-Score [24]. Fig. 4 illustrates the sample

recognition results of the IMSD-BCHIDL technique on the validation dataset. The figures highlighted that the IMSD-BCHIDL technique properly recognized the mitotic and non-mitotic cells. In addition, the proposed IMSD-BCHIDL technique properly identifies least to maximum number of cells. Moreover, these figures outlined the enhanced detection performance of the proposed model.

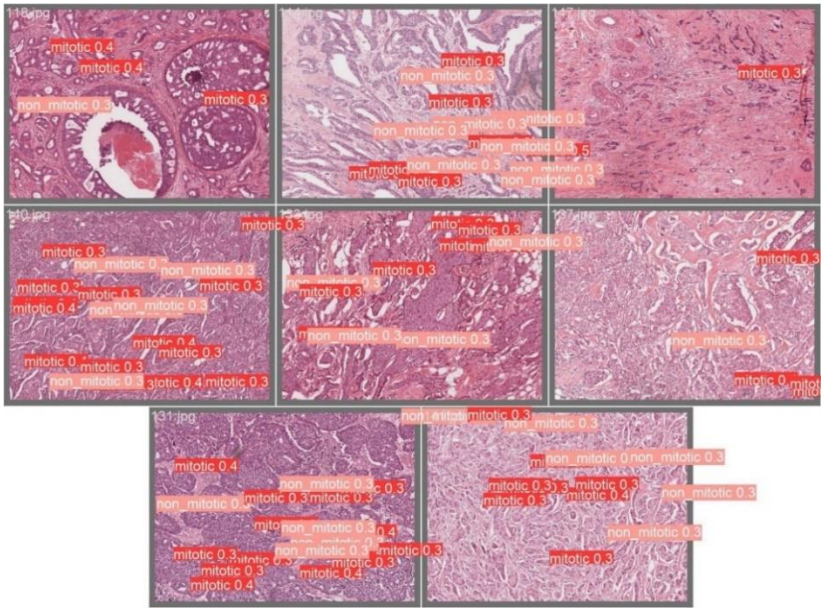

Fig. 4. Results on recognition of validation dataset.

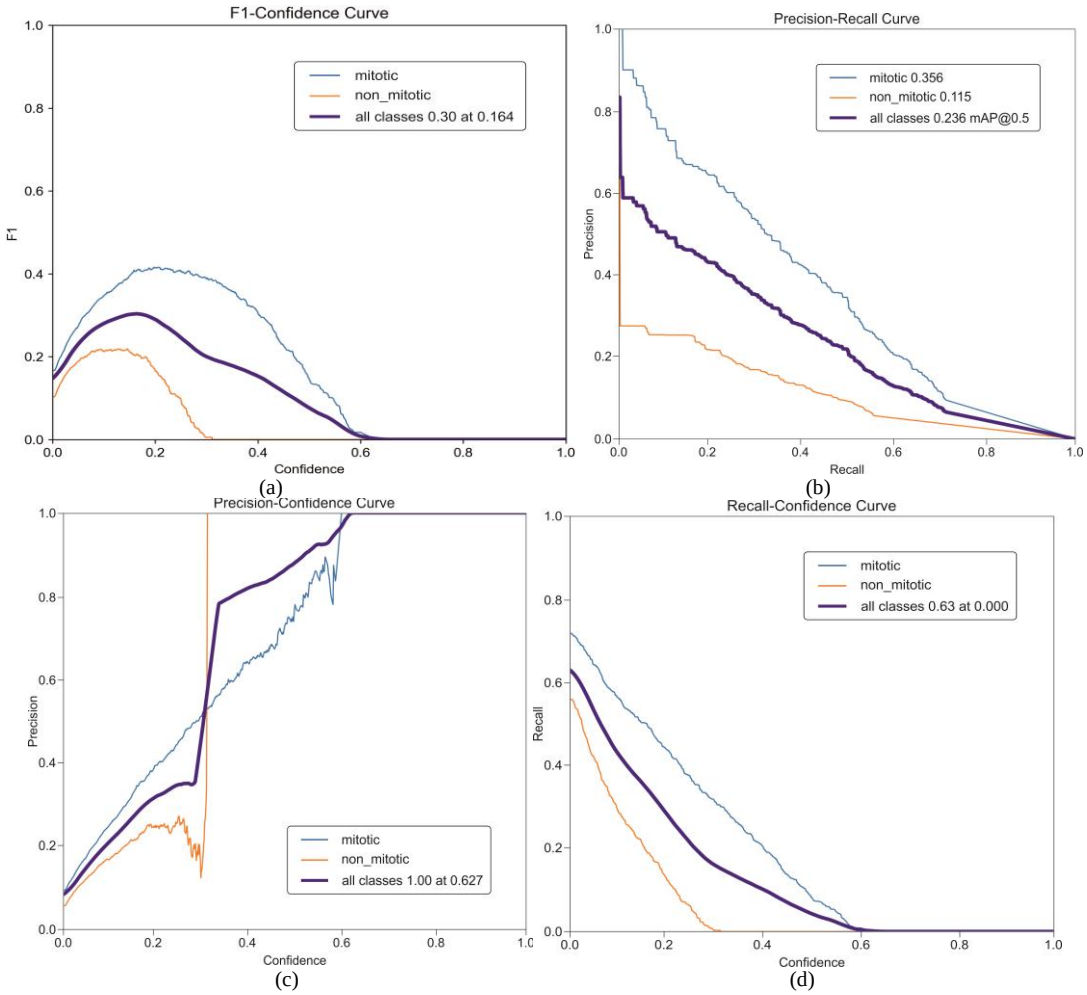

Fig. 5. Results on training dataset, (a) F1 Curve, (b) PR Curve, (c) Precision Curve, (d) Recall Curve.

A detailed PR curve of the IMSD-BCHIDL algorithm is defined on training database in Fig. 5. The simulation outcomes inferred that the IMSD-BCHIDL algorithm outcomes in enhanced PR values. Afterward, it can be clear that the IMSD-BCHIDL system achieves better performances of PR on 2 classes.

A comprehensive PR outcome of the IMSD-BCHIDL methodology is depicted on validation database in Fig. 6. The simulation values implied that the IMSD-BCHIDL system performs in higher outcomes of PR. Next, it can be obvious that the IMSD-BCHIDL methodology gains improved values of PR on 2 classes.

Table I state the comparative results of the IMSD-BCHIDL method with recent DL models [14, 15, 25, 26]. The results highlighted the enhanced characteristics of the IMSD-BCHIDL technique. Based on $accu_y$, the IMSD-BCHIDL technique illustrates improved $accu_y$ of 92.26% while the Multi-Phase Deep CNN model, PartMitosis, ResNet 50 and YOLOv5 model, Deep Mitosis model suggested by various authors accomplish decreased $prec_n$ of 85%, 76%, 71%,80%, correspondingly. Furthermore, based on $reca_l$, the IMSD-BCHIDL methodology outperforms higher $reca_l$ of 90.01% while the Multi-Phase Deep CNN model, PartMitosis, ResNet 50 and YOLOv5 model, Deep Mitosis model achieve reduced $reca_l$ of 81%, 81%, 76%, 77% correspondingly. When we compare the F1-Score of the various deep learning models suggested by different authors the proposed model outperforms all other models with a F1-Score of 91%.

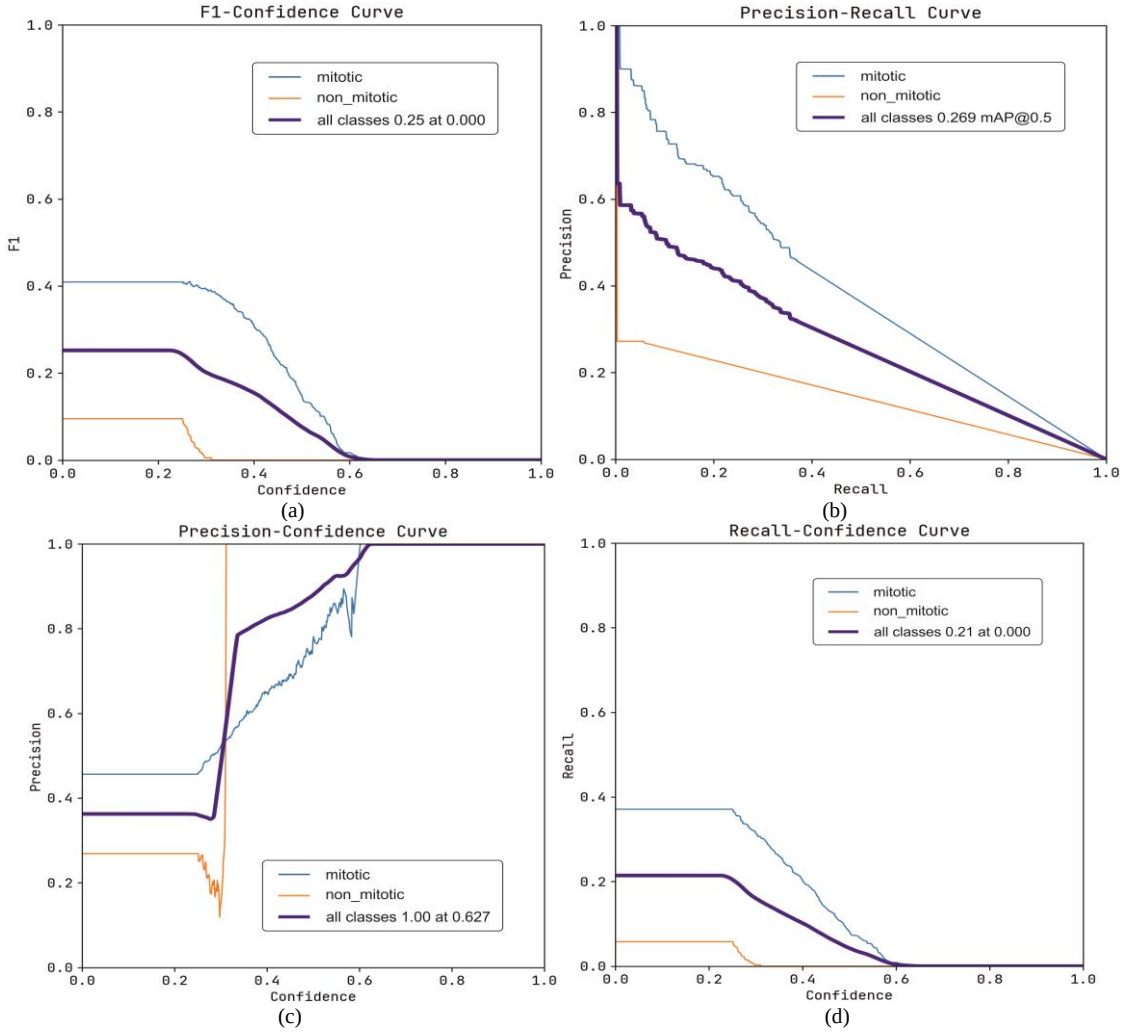

Fig. 6. Results on validation dataset, (a) F1 Curve, (b) PR Curve, (c) Precision Curve, (d) Recall Curve.

TABLE I. COMPARATIVE OUTCOME OF IMSD-BCHIDL ALGORITHM WITH OTHER FEW DL APPROACHES

References	Dataset	Method	Precision	Recall	F1-Score
Sohail *et al.* [19]	TUPAC16	Multi-Phase Deep CNN	0.71	0.76	0.75
Sewbai *et al.* [15]	ICPR 2014	Part Mitosis	0.76	0.81	0.78
Zorgani *et al.* [21]	ICPR 2012	ResNet 50 and YOLOv5	0.80	0.77	0.79
Li *et al.* [14]	ICPR 2012	Deep Mitosis	0.85	0.81	0.83
Proposed Model	MIDOG	YOLOv5 and InceptionV3	0.91	0.90	0.91

These outcomes demonstrated the enhanced performance of the IMSD-BCHIDL methodology with other approaches. Therefore, the IMSD-BCHIDL technique can be employed for automated mitosis segmentation and detection.

V. Conclusion

In this study, we have concentrated on the development and design of the IMSD-BCHIDL algorithm for the segmentation and classification of mitosis on breast cancer Histopathological Images. The major intention of the IMSD-BCHIDL technique is to exploit DL model for segmenting and classifying mitosis in the histopathological images. To accomplish this, the IMSD-BCHIDL technique comprises three major components: data pre-processing, YOLOv5, and InceptionV3 model. Here, the YOLOv5 model is mainly applied to segment and classify the mitosis cells with InceptionV3 as a backbone network. The design of InceptionV3 model helps in capturing extensive contextual details from the input image and results in improved detection tasks. Besides, the application of InceptionV3 model as a backbone network aids YOLOv5 to manage objects at various scales more effectively, contributing to improved detection performance.

To illustrate the better results of the IMSD-BCHIDL technique of the IMSD-BCHIDL methodology, a wide-ranging set of simulation values can be executed. The simulation results showcase the superior results of the IMSD-BCHIDL algorithm with other recent DL models with maximum precision of 0.91, recall of 0.90, and F1 score of 0.91. In the future, the IMSD-BCHIDL algorithm could benefit from advancements in deep learning architectures, exploring more sophisticated models or ensembles to enhance mitosis segmentation and classification accuracy. Additionally, refining the data pre-processing stage to accommodate a broader range of histopathological variations and incorporating transfer learning techniques may further improve the model's robustness across diverse datasets.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

All authors contributed to the study conception and design. Material preparation, data set selection and analysis were performed by Jithy Lijo. Manuscript review was done by Saleema J.S. All authors had approved the final version.

References

[1] I. O. Sigirci, A. Albayrak, and G. Bilgin, "Detection of mitotic cells in breast cancer histopathological images using deep versus handcrafted features," *Multimedia Tools and Applications*, pp. 1–24, 2022.

[2] T. Mathew, J. R. Kini, and J. Rajan, "Computational methods for automated mitosis detection in histopathology images: A review," *Biocybernetics and Biomedical Engineering*, vol. 41, no. 1, pp. 64–82, 2021.

[3] S. Ponnuru and L. S. Nair, "Feature extraction and selection with hyperparameter optimization for mitosis detection in breast histopathology images," in *Proc. Data Intelligence and Cognitive Informatics: Proceedings of ICDICI 2022*, 2022, pp. 727–749.

[4] X. Pan, Y. Lu, R. Lan, Z. Liu, Z. Qin, H. Wang, and Z. Liu, "Mitosis detection techniques in H&E stained breast cancer pathological images: A comprehensive review," *Computers & Electrical Engineering*, vol. 91, 107038, 2021.

[5] H. Hussain, O. Hujran, and K. P. Nitha, "Mitosis detection from histological images using handcrafted features and artificial neural network," *International Journal of Computer Aided Engineering and Technology*, vol. 16, no. 2, pp. 240–256, 2022.

[6] I. Selvamani and N. Umamaheshwari, "Automatic mitosis detection in histopathology images & grading using SVM classifier," in *Proc. AIP Conference*, 2021, vol. 2407, no. 1, 020027.

[7] R. Nateghi, H. Danyali, and M. S. Helfroush, "A deep learning approach for mitosis detection: application in tumor proliferation prediction from whole slide images," *Artificial Intelligence in Medicine*, vol. 114, 102048, 2021.

[8] M. Z. Naser, "Machine learning for civil and environmental engineers: A practical approach to data-driven analysis, explainability, and causality," *John Wiley & Sons*, 2023.

[9] M. Z. Naser, "An engineer's guide to explainable artificial intelligence and interpretable machine learning: Navigating causality, forced goodness, and the false perception of inference," *Automation in Construction*, vol. 129, 103821, 2021.

[10] A. Sohail, A. Khan, N. Wahab, A. Zameer, and S. Khan, "A multi-phase deep CNN based mitosis detection framework for breast cancer histopathological images," *Scientific Reports*, vol. 11, no. 1, pp. 1–18, 2021.

[11] H. U. Khan, B. Raza, M. H. Shah, S. M. Usama, P. Tiwari, and S. S. Band, "SMDetector: Small mitotic detector in histopathology images using faster R-CNN with dilated convolutions in backbone model," *Biomedical Signal Processing and Control*, 81, 104414, 2023.

[12] T. Mathew, B. Ajith, J. R. Kini, and J. Rajan, "Deep learning-based automated mitosis detection in histopathology images for breast cancer grading," *International Journal of Imaging Systems and Technology*, vol. 32, no. 4, pp. 1192–1208, 2022.

[13] R. Nateghi, and F. Pourakpour, "Two-Step domain adaptation for mitotic cell detection in histopathology images," in *Proc. Biomedical Image Registration, Domain Generalisation and Out-of-Distribution Analysis: MICCAI 2021 Challenges: MIDOG 2021, MOOD 2021, and Learn2Reg 2021, Held in Conjunction with MICCAI 2021*, 2021, pp. 32–39.

[14] H. Lei, S. Liu, A. Elazab, X. Gong, and B. Lei, "Attention-guided multi-branch convolutional neural network for mitosis detection from histopathological images," *IEEE Journal of Biomedical and Health Informatics*, vol. 25, no. 2, pp. 358–370, 2020.

[15] M. Sebai, T. Wang, and S. A. Al-Fadhli, "PartMitosis: A partially supervised deep learning framework for mitosis detection in breast cancer histopathology images," *IEEE Access*, vol. 8, pp. 45133–45147, 2020.

[16] M. D. Naik, S. Adarsh, S. Vijayakumar, A. P. Nambiar, and L. S. Nair, "Hybrid feature set based mitotic detection in breast histopathology images," in *Proc. 2022 International Conference on Inventive Computation Technologies (ICICT)*, 2022, pp. 281–290.

[17] J. Cao, M. Yan, Y. Jia, X. Tian, and Z. Zhang, "Application of a modified InceptionV3 model in the dynasty-based classification of ancient murals," *EURASIP Journal on Advances in Signal Processing*, vol. 1, pp. 1–25, 2021.

[18] Z. Yücel, F. Akal, and P. Oltulu, "Mitotic cell detection in histopathological images of neuroendocrine tumors using improved YOLOv5 by transformer mechanism," *Signal, Image and Video Processing*, pp. 1–8, 2023.

[19] C. Albuquerque, L. Vanneschi, R. Henriques, M. Castelli, V. Póvoa, R. Fior, and N. Papanikolaou, "Object detection for automatic cancer cell counting in zebrafish xenografts," *Plos One*, vol. 16, no. 11, e0260609, 2021.

[20] H. Yu, S. Luo, J. Ji, Z. Wang, W. Zhi, N. Mo, P. Zhong, C. He, T. Wan, and Y. Jin, "A deep-learning-based artificial intelligence system for the pathology diagnosis of uterine smooth muscle tumor," *Life*, vol. 13, no. 1, 2022.

[21] J. B. Awotunde, A. L. Imoize, O. B. Ayoade, M. K. Abiodun, D. T. Do, A. Silva, and S. N. Sur, "An enhanced hyper-parameter optimization of a convolutional neural network model for leukemia cancer diagnosis in a smart healthcare system," *Sensors*, vol. 22, no. 24, 9689, 2022.
[22] Y. Huang, Y. Xue, J. Lan, Y. Deng, G. Chen, H. Zhang, M. Dang, and T. Tong, "Deep learning framework for detecting positive lymph nodes of gastric cancer on histopathological images," in *Proc. the 2021 6th International Conference on Biomedical Imaging, Signal Processing*, 2021, pp. 14–23.
[23] A. Anaam, M. A. Al-Antari, J. Hussain, N. Abdel Samee, M. Alabdulhafith, and A. Gofuku, "Deep active learning for automatic mitotic cell detection on HEp-2 specimen medical images," *Diagnostics*, vol. 13, no. 8, 2023.
[24] A. Botchkarev, "A new typology design of performance metrics to measure errors in machine learning regression algorithms," *Interdisciplinary Journal of Information, Knowledge, and Management*, vol. 14, pp. 045–076, 2019.
[25] A. Sohail, A. Khan, N. Wahab, A. Zameer, and S. Khan, "A multi-phase deep CNN based mitosis detection framework for breast cancer histopathological images," *Scientific Reports*, vol. 11, no. 1, pp. 1–18, 2021.
[26] C. Li, X. Wang, W. Liu, L. J. Latecki, B. Wang, and J. Huang, "Weakly supervised mitosis detection in breast histopathology images using concentric loss," *Medical Image Analysis*, vol. 53, pp. 165–178, 2019.