A REVIEW FOR DETECTING CANCER FROM HISTOPATHOLOGY IMAGES

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Abstract
Strong computer-assisted analytical approaches to radiological data have been developed during the past ten years thanks to huge advances in computational capacity and advancements in image analysis algorithms. Tissue histopathology slides can now be scanned and preserved as digital images thanks to the recent development of entire slide digital scanners. Hence, the use of computerized image analysis and machine learning techniques to digital tissue histopathology is now possible. Similar to how CAD algorithms are used in medical imaging to support the judgment of a radiologist, CAD algorithms are now being developed for disease detection, diagnosis, and prognosis prediction to support the judgment of a pathologist. Medical regulations and the law both hold pathological examinations to a standard that requires specific action during the diagnosis procedure. Hematoxylin and eosin stained photos can now be used as a source of information for image analysis thanks to developments in digital pathology.An overview of tissue preparation, an examination of stained images, and a prognosis for cancer patients are presented at the outset of this study. Sensitivity and specificity are reduced by the high accuracy findings that were recorded. Rarely are the issues of the missing loss function and class imbalance addressed, and most frequently the chosen performance measures are out of place in the given context. The difficulty lies in analyzing entire slide images for the necessary content imaging, diagnostic biomarkers, and prognosis support backed by digital pathology.

Keywords: Histopathology, Segmentation, Digital pathology, Image processing.

Introduction
Histopathology dealt with the concept of diagnosing the disease of tissues. It was the study of the signs and symptoms of the disease using the microscopic exam of a biopsy or surgical specimen that was processed and fixed onto glass slides. Histopathology images could be received using specialized cameras with a microscope, wherein an automated automatic method could be achieved. To take a look at numerous structures and constituents of tissues below a microscope, the biopsy specimen was embedded in wax and dyed with one or more stains. The diagnosis of breast cancer could be used by Medical image processing technique [1]. For diagnosing the disease, a piece of sample was taken from the human for testing, and the way of this procedure was called a biopsy. The process of testing the sample tissue or specimen was called pathology. Histopathology was also called the study and brief analysis of biopsy samples. It was done by a pathologist. For the histopathology process, the first step was to take the sample that was to be processed, and it was placed on the glass slides. The second step was to examine the biopsy sample by intrusive or minimal intrusive methods. The process was performed by a pathologist under an instrument like a microscope. It could be performed for the study of cancer, tumors, and so on.
In Paper [2], the concept of various techniques used for histopathology images of breast cancer detection and classification was discussed. The focus was mainly on the efforts of pathologists and examining the biopsy samples by using computer-aided techniques. The conclusion drawn was that biopsy is the most accurate method for diagnosing histopathology images.

Researcher [3] studied the preparation of tissue, stained image analysis, and cancer patients' analysis. It also delved into machine learning and deep learning techniques to detect breast cancer. Furthermore, it addressed the segmentation, detection, and classification of histopathology images.

Sample Beast cancer images are shown from various dataset are shown in fig (1)
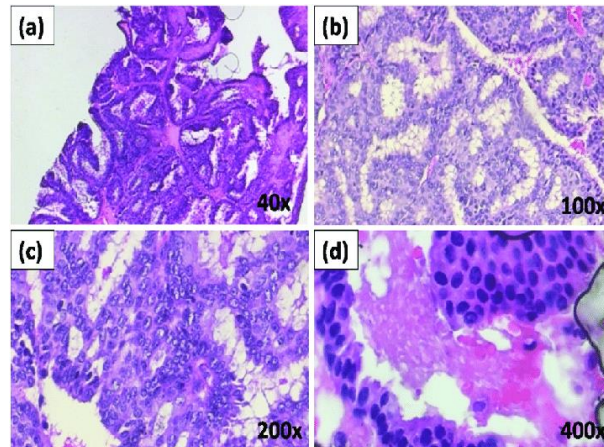

Fig (1) Sample Breast Cancer Histopathology images

This paper provides an overview of the survey on the use of histopathology images for detecting different types of cancer. The paper highlights various techniques utilized for the detection and classification of histopathology images.

Literature survey

It seems that the work described in [4] is focused on the analysis of histopathology images, specifically using Whole Slide Imaging (WSI) scanners as a primary tool for pathologists. WSI scanners allow for high throughput digitization of histopathology slides, which is cost-effective and efficient.In [5], the focus is on digital pathology and the advantages it brings to the analysis of hematoxylin and eosin histopathology images. These types of images are commonly used to evaluate tumor grade and predict cancer. The work summarizes the use of hematoxylin and eosin histopathology images for breast cancer, including the image acquisition process, pre-processing, detection and segmentation, and feature extraction. Finally, the study evaluates the values of image features and image feature-based prognostic models.

The article [6] discusses the potential of computer-aided pathology for early diagnosis of diseases such as breast cancer and brain tumors. The paper primarily focuses on the automatic segmentation of cell nuclei, which is a crucial feature for detecting such diseases. However, one of the main challenges in automatic segmentation is the separation of clustered nuclei. To address this problem, the paper proposes a new method for analyzing histopathological images stained for different proteins.

In another study [7], machine learning algorithms are employed for digital pathological image analysis, showcasing the benefits of this technology for disease diagnosis. Additionally, a review paper [8] delves into the fundamental concepts of deep learning and explores various applications, such as image registration, detection of anatomical and cellular structures, tissue segmentation, and computer-aided disease detection and diagnosis. The paper also suggests avenues for further improvement in these areas.

In the field of medical imaging, image segmentation and classification are currently the most popular techniques used for diagnosing and treating cancer[9]. One proposed method for achieving this involves classifying images based on the handcrafted and shape features of bag visual words (BoW).

In [10], the detection of mitosis in pathology plays a crucial role in the diagnosis and prognosis of cancer. Traditionally, pathologists manually examine Hematoxylin and Eosin (H&E) stained histopathology sections on glass slides through a microscope to identify mitotic cells. However, with the development of computational techniques, automating the detection of mitotic cells using image processing algorithms has garnered significant research attention. Mitotic cell count is an important parameter in the assessment of breast cancer and glaucoma, unlike other types of cancer.

The research article [11] discusses computer-aided analysis and outlines three main steps:

Segmentation, Feature Extraction, and Classification. By utilizing computer algorithms to analyze and evaluate histology images, this approach assists pathologists in diagnosing diseases and reduces the potential for human error. The article proposes a tumor-based segmentation method based on Persistent Topology Profiles (PHPs). These profiles are derived to distinguish tumor regions from normal regions. The framework consists of two steps: one focuses on speed, while the other emphasizes high accuracy. The study conducts experiments on various datasets containing adenoma, adenocarcinoma, signet, and normal tissues [12].

In reference to [13], the paper proposes a set of broad strategies for cancer segmentation. It summarizes a specific pipeline for tumor segmentation and investigates the use of hard model mining in this context. The proposed technique is evaluated through tests to demonstrate its effectiveness and the impact of hard example mining.

Moving onto [14], the paper focuses on using histopathology images for carcinoma detection and classification. The article highlights relevant information about slide preparation and emphasizes image segmentation techniques for feature extraction and disease classification. The study focuses on four significant carcinomas, namely cervix, prostate, breast, and lung, to showcase the capabilities of existing computer-aided design frameworks. In [15], a systematic literature review is conducted on histopathology images of different types of carcinoma. The paper provides an in-depth analysis of the most recent methods reported for the diagnosis of carcinoma using histopathological images. Overall, the review highlights the necessity of an AI-based carcinoma diagnostic system.

The paper [16] introduces the DenseRes-Unet model, which improves upon the traditional Unet architecture by incorporating dense blocks in the encoder's final layers. This approach enhances the model's ability to focus on relevant features, leading to improved segmentation results. In contrast to standard skip connections, the DenseRes-Unet model uses residual connections with Atrous blocks, which effectively bridge the semantic gap between the encoder and decoder paths. The model's performance is evaluated on four publicly available datasets for Nuclei segmentation, demonstrating its effectiveness.

A study on the classification of breast cancer utilizes effective techniques such as grayscale and edge detection, coupled with supervised machine learning algorithms like RF, SVM, and KNN. The analysis is based on histopathological images (HI) and is presented in [17].In [18], a novel method for breast cancer classification is proposed, which employs a dense dual-task network (DDTNet). This network comprises a backbone network, also known as a feature pyramid network, for extracting multi-scale morphological characteristics of TILs. Additionally, it includes a detection module for locating TIL centers and a segmentation module for drawing TIL boundaries.

We introduce a multi-scale conditional GAN[19] for the generation and segmentation of large-scale, high-resolution histopathology images. Our model is composed of a pyramid of GAN structures, where each is responsible for generating and segmenting images at a different scale. Using semantic masks, the generative part of our model is capable of producing visually realistic histopathology images.

A novel deep learning approach has been proposed in [20] for accurately detecting peripheral nerve invasion (PNI) regions across multiple types of cancer. The proposed method leverages the U-Net architecture to effectively capture the boundary regions between different features. By using a boundary dilation method and a loss combination technique, the performance of PNI detection can be significantly enhanced without the need for full segmentation maps. The proposed approach has demonstrated promising results, offering a more efficient and effective alternative to existing PNI detection methods.

This article presents a comparative analysis of two feature extraction techniques for the classification of lung and colon cancer [21]. One approach discusses six handcrafted feature extraction methods based on color, texture, shape, and structure. Another strategy presents seven deep learning frameworks for deep feature extraction from histopathological images of lung and colon cancer, utilizing transfer learning.The extracted deep features are utilized as input attributes in conventional

GB, SVM-RBF, MLP, and RF classifiers to classify lung and colon cancer.

Our hypothesis is that fine-tuning pre-trained models using histopathological images [22] can improve feature extraction and downstream prediction performance. To test this hypothesis, we employed a two-step process where we fine-tuned a pre-trained Xception model using 100,000 colorectal cancer (CRC) HE image patches that had been annotated. This approach can potentially improve the accuracy of CRC diagnosis and prognosis.

Breast cancer can be detected through various imaging techniques, with histopathology being one of the most reliable methods, as explored in this paper [23]. The proposed CAD system utilizes deep feature transfer learning as its feature extractor. In this study, we utilize sixteen different pre-trained networks and concentrate on the classification phase, which has not received enough attention.

In this study, we aimed to classify breast cancer using the BreakHis dataset. To achieve this, we employed both handcrafted feature extraction methods, including Hu moment, Haralick textures, and color histogram, as well as Deep Neural Network (DNN) techniques.Our approach involved training DNN classifiers with four dense layers and Softmax using features extracted from the handcrafted methods. Additionally, to mitigate the problem of overfitting, we utilized data augmentation techniques.Overall, our methodology involved a combination of traditional feature extraction methods and modern deep learning techniques to accurately classify breast cancer in the BreakHis dataset.

This paper [25] focuses on detecting mitosis in breast cancer cells. The study aims to develop a new framework that utilizes neural network-based concepts, reduced feature vectors, and multiple machine learning methods to classify cells as mitotic or non-mitotic. Texture features were found to be crucial for accurate mitosis detection, so the study uses cells' textures to create effective reduced feature vectors. During the feature engineering process, specific characteristics were identified that distinguish cancer cells from normal cells.The proposed architecture draws inspiration from neural networks and assigns different weights to various features, enhancing the model's efficiency. This study aims to bridge the gap in knowledge by introducing a new methodology for detecting mitosis in breast cancer cells.

A new segmentation method [26] has been proposed, which offers several advantages over existing methods. In addition, a classification approach has been developed for breast cancer detection, which utilizes a weighted feature selection method and a Convolutional Neural Network Classifier. An improved version of the Genetic Algorithm has also been implemented in this approach. By incorporating these advanced algorithms into a CAD framework, the number of incorrect diagnoses can be reduced, and classification accuracy can be improved. Therefore, the proposed segmentation and classification algorithms hold promise for practical implementation in breast cancer detection.

This paper examines the use of machine learning-based techniques for analyzing whole slide images (WSI) [27]. It begins by discussing the current state of development in WSI and computer-aided detection (CAD) methods. The paper then goes on to discuss evaluation metrics and publicly available datasets that can be used for segmentation, classification, and detection tasks. The latest advancements in machine learning techniques for WSI segmentation, classification, and detection are also reviewed. These techniques have demonstrated that pre-trained Xception models are capable of accurately classifying histopathological images of breast cancer at different magnifications, unlike traditional handcrafted methods. The accuracy of the Xception model and SVM classifier with the "radial basis function" kernel was found to be the best and most consistent [28].

This study introduces a novel approach for classifying histopathological haematoxylin and eosin (H&E) images using the innovative dual-stage AlexNet-HHO-DrpXLM architecture [29]. The classification of images of hepatocellular carcinoma is performed using the Dropout Extreme Learning Machine (DrpXLM) classifier, while the performance is enhanced by the Horse Herd Optimization (HHO) mechanism. The proposed method achieves higher accuracy rates for the classification of benign and malignant images, namely 25.70%, 37.48%, 9.99%, 33.32%, 25.70%, and 7.31% respectively.Convolutional neural networks (CNNs) are the most prevalent classification

architecture utilized to address numerous image classification problems. This advanced review delves into the utilization of CNN-based architectures in digital histological image analysis, examines some of the challenges associated with such analysis, and offers potential solutions. [30] Figure 2 Deep Learning in Histopathology.
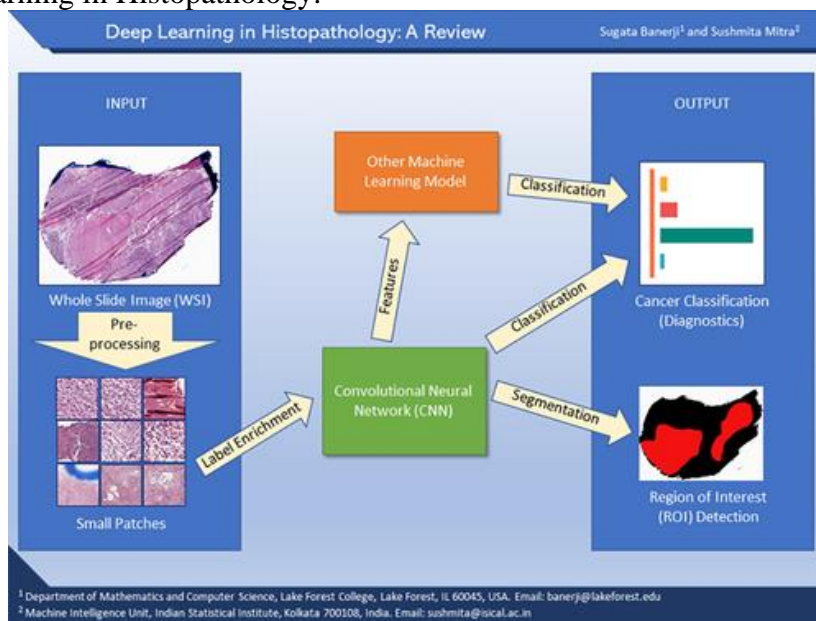

Figure (2) Deep Learning in histopathology

The majority of cases of malignant MedulloBlastomas (MBs) in children were studied using three cutting-edge deep learning models trained with textural images produced by two texture analysis techniques. In addition to the original histopathological images, this approach allowed for the integration of spatial and textural information.This study utilized a large dataset of lung and colon histopathology images for training and validation purposes. Prior to training, the four layers of a pre-trained neural network (AlexNet) were modified, and the contrast enhancement technique was used to improve the quality of images from the underperforming class, while still maintaining computational efficiency and improving overall accuracy. The proposed fractional rider gradient descent was used for U-Net training, which combines the rider optimization algorithm (ROA) and fractional order gradient descent. This advanced approach enhances the accuracy of the model and enables it to effectively analyze the textural features of the images.

In this study [34], we have developed the Dense Residual Dual-Shuffle Attention Network (DRDA-Net) as a deep learning model guided by dual-shuffle attention. The model incorporates the ShuffleNet architecture and has been specifically designed for this purpose. Despite being trained on a very small dataset, the DRDA-Net demonstrates remarkable performance.

In this research [35], a patch selection method was utilized to classify breast histopathological images through transfer learning. Discriminative patches were chosen and utilized as input to the Efficient-Net architecture, while an SVM classifier was also trained with Efficient-Net architecture features. The proposed model exhibited better performance metrics compared to baseline methods.In another study [36], feature extraction techniques based on deep learning and conventional methods were compared and contrasted. A convolutional neural network architecture was proposed for the deep learning approach, aiming to extract features of small cellular structures, such as mitotic cells. The random under-sampling boosting (RUSBoost) technique was employed as a result. The proposed framework was tested through mitosis detection in breast cancer histopathological images from the International Conference on Pattern Recognition (ICPR) 2014 contest.

In this paper [37], a new method utilizing knowledge distillation (KD) was presented. The approach involves providing the student model with the decomposed feature maps of intermediate layers from

a teacher model as dark knowledge. The experimental findings demonstrate that the student model, which was trained using 40X images, achieved high accuracy rates of 99.41%, 99.26%, 99.14%, and 99.09%.

In this paper, we introduce the BRACS dataset, which contains a vast collection of annotated Hematoxylin and Eosin (H&E)-stained images. The dataset has been developed to facilitate the advancement of artificial intelligence (AI) in the automatic characterization of breast lesions.The BRACS dataset comprises three types of lesions: benign, malignant, and a typical. Each of these types is further divided into seven categories, resulting in a comprehensive dataset for subtyping breast cancer at both the whole slide image (WSI) and region of interest (ROI) levels. To the best of our knowledge, the BRACS dataset is currently the largest annotated dataset for subtyping breast cancer using H&E-stained images. This dataset is expected to be an essential resource for the development and evaluation of AI algorithms designed to aid in the accurate diagnosis and classification of breast cancer.

In this study, a method was proposed to detect benign or malignant breast cancer using the BreaKHis dataset. The method utilized a convolutional neural network (AlexNet) to extract deep features. Another modified residual neural network-based method was proposed to detect breast cancer using histopathology images [40]. The same convolutional neural network (AlexNet) method was used to extract deep features from the BreaKHis dataset [41].The proposed system was evaluated in four experiments at different magnifications (40X, 100X, 200X, and 400X). Results showed that the proposed system achieved an accuracy of 95 percent, sensitivity of 97 percent, specificity of 90 percent, and AUC of 99.36 percent.

This study proposes a novel patch-based deep learning technique named Pa-DBN-BC for the detection and classification of breast cancer in histopathology images using the Deep Belief Network (DBN). The method employs an unsupervised pre-training phase and a supervised fine-tuning phase to extract features. The proposed model achieved an accuracy of 86% when trained and tested on the entire slide histopathology image dataset, consisting of images from four distinct data cohorts.

In the field of medical image analysis, deep learning methods such as CNN and CapsNet have shown great potential for the classification of histological images of breast cancer. In a recent paper [43], a novel method called "FE-BkCapsNet" has been proposed which combines deep feature fusion and enhanced routing. This method has been found to be highly effective in clinical settings for the accurate classification of breast cancer. Furthermore, in another study [44], two deep learning-based automatic systems have been proposed for grading nuclear atypia in breast cancer histopathological images. In the first proposed system, a three-hidden-layer convolutional neural network (CNN) is designed and trained for feature extraction and patch classification. The most significant patches of the image are identified using this system. The second proposed system combines a CNN for feature extraction with a two-layer Long short-term memory (LSTM) network for classification. In addition to breast cancer, deep learning methods have also been applied to the diagnosis of skin diseases. A light-weight attention mechanism-based deep learning framework called DRANet has been proposed in a recent study [45] to differentiate 11 types of skin diseases based on real histopathological images. The experimental results have shown that DRANet performs significantly better than baseline models such as InceptionV3, ResNet50, VGG16, and VGG19 with the same number of model parameters and comparable accuracy. Despite the progress made in the field of digital image-based AI solutions for the diagnosis of skin cancer, there are still challenges and opportunities for improvement, as discussed in a recent paper [46]. Melanoma, the most aggressive type of skin cancer, remains a significant challenge. Another recent paper [47] has focused on enhancement, segmentation, and classification of skin histopathological images. The proposed method uses bilateral filtering for image enhancement, Fuzzy C-Means for initial segmentation, and a local region recursive algorithm for final segmentation results.Overall, deep learning methods have shown great promise for the accurate diagnosis and classification of various types of cancer and skin diseases. Continued research in this field will lead to further advancements in medical image analysis and

ultimately benefit patients and medical professionals alike.

In this study, the aim is to develop an automated method for identifying the margins of squamous cell carcinoma in histopathology microscopic images, using deep learning techniques. The selected models were fine-tuned by adjusting hyper-parameters, and the images were preprocessed and trained using transfer learning pre-trained models.In addition, we propose a transfer learning-based approach for classifying breast histology image subtypes into four categories: normal, benign, in situ carcinoma, and invasive carcinoma. The Inception-V3 network achieved an average test accuracy of 97.08% for all four classes, which was slightly better than the ResNet50 network's average accuracy of 96.66%.

Breast cancer is one of the most prevalent and lethal types of cancer affecting women worldwide. A recent study proposes using the Inception Recurrent Residual Convolutional Neural Network (IRRCNN) model for accurately classifying breast cancer [50]. The IRRCNN model outperforms existing methods in terms of sensitivity and global accuracy for both datasets.Another study [51] introduces a productive approach for automated examination and diagnosis of skin tissue using whole-slide images. The proposed method consists of five modules, including epidermis segmentation, melanocyte detection, keratinocyte segmentation, feature construction, and classification. Experimental results demonstrate that the method achieves an accuracy of approximately 90% and can assist pathologists in skin tissue analysis and diagnosis.

In this article [52], the authors introduce DenTnet, a method that utilizes DenseNet as a backbone model to address the issue of extracting features from the same distribution. Transfer learning is employed to achieve this. DenTnet outperforms various popular deep learning techniques in terms of detection accuracy.The main objective of another study [53] is to employ a deep learning model to classify skin cancer. The authors propose a hybrid context-aware convolutional neural network and recurrent neural network (CA-CNN-RNN) model based on skin cancer histology images.Furthermore, this paper [54] presents a new computer-aided method for breast cancer classification (binary and multi-class). Deep neural networks such as ResNet 18, ShuffleNet, and Inception-V3Net are used, along with transfer learning on the publicly available BreakHis dataset.

In this study [55], a deep learning model was proposed for the multiclass classification of invasive ductal carcinoma (IDC) in hematoxylin and eosin-stained histological images. The model distinguished IDC into different grades (G-1, G-2, and G-3). The focus of the approach was the Sequential Convolutional Neural Network Two-Dimensional (CNN2D), which identified the various grades of IDC. To address the same issue, a breast histopathology image classification technique called LPMF2Net [56] was proposed. This technique was based on the deep manifold fusion of multilayer features. The proposed LPMF2Net model was tested and its efficiency was demonstrated. The experimental findings were as follows: 94.91% at 40×, 96.12% at 100×, 95.51% at 200×, and 95.42% at 400×.

This paper (57) presents a novel deep learning-based system for automatically detecting osteosarcomas, a type of bone tumor, using whole slide images (WSIs). The system achieved an accuracy of up to 99.3% in tests on a large WSI dataset, which is a significant improvement over previous detection methods. The study's primary objective (58) was to explore the potential of convolutional neural networks in classifying images of skin lesions. Deep neural networks have shown great promise in image classification tasks, as they can handle the vast variability of the environment. In this study, the system classified images based on disease labels and trained images based on pixel values, achieving a highest level of model accuracy of over 86.65%.

Digital pathology has experienced significant growth due to the use of digital whole slide images (WSIs) in clinical practice. In this review, 26 studies were examined, and recommendations were made to improve the field of artificial intelligence (AI) in digital pathology. The review highlights the best ways to use AI as a diagnostic tool for WSIs and H&E stain, as well as the main limitations. The hope is that this study will improve the application of AI as a pathology diagnostic tool and assist future researchers in creating new projects and studies.One article in this field looked at 93

different references related to breast cancer diagnosis and categorization. The findings indicate that successful strategies largely focus on using deep learning techniques. In another study, a convolutional neural network-based approach was proposed to classify and identify metastatic cancer in histopathologic images of lymph node sections using the PatchCamelyon (PCam) data set. The accuracy rate was 0.94, indicating excellent performance in medical image classification and detection.Gastric cancer is the fourth leading cause of cancer-related death, and one study used image preprocessing to identify the Region of Interest (RoI) in histopathological images. The popular deep learning models VGG16, VGG19, and InceptionV3 were then used to find signet ring cell carcinoma (SRCC), and an experienced pathologist confirmed the algorithm's results. The VGG16 model performed better than the other models, with an accuracy of 95% and an F1-score of 95%.Overall, these studies provide valuable insights into the potential of AI in pathology diagnosis and highlight the need to continue exploring new methods and techniques to improve accuracy and reliability.

Osteosarcoma is the most commonly occurring primitive malignant bone tumor in humans, which can metastasize to other organs. Our proposed work involves preprocessing to improve image quality by reducing noise and removing false segments. This method benefits both the enhancement of image quality and the removal of false segments. Additionally, we utilize KNN, CNN, and ANN classification algorithms to classify image datasets.

This study aims to create a framework for classifying deep learning tumors using a proposed CNN model that consists of three stages and utilizes a deep learning approach. The first step is pre-processing, followed by feature extraction and classification. The article discusses detecting cancer cells in histopathology images, as well as the advantages and disadvantages of various detection methods. To overcome the limitations of these methods, the study employs a well-known swarm optimization (PSO) algorithm to obtain the near-optimal feature set. The results are compared to two cutting-edge CNN models, InceptionResNet and DenseNet, and MobileNet is found to be more effective.To segment tumor regions on breast histopathology images, this study proposes a straightforward global thresholding method, combined with partial contrast stretching and a median filter as pre-processing steps. The proposed method achieves 84.22% accuracy, 85.83% sensitivity, and 84.89% specificity, respectively. Effective deep learning-based methods for mitosis detection face the challenges of inadequate dataset size and class imbalance between mitotic and non-mitotic cells in slide images. To address these issues, the study proposes a novel strategy and utilizes the AlexNet-BC model, a novel framework for breast pathology classification, to alleviate overfitting and improve classification accuracy. This study also integrates channel and spatial attention into an ensemble of two CNN architectures, CSAResnet and DAMCNN, to extract features from histopathology images simultaneously.

The study presents a hybrid model that can accurately detect lung, colon, and lung and colon cancer with respective rates of 99.05%, 100%, and 99.30%. This proposed model outperforms existing models and could be useful in clinics for cancer diagnosis. The primary objective of the study is to critically analyze various imaging modalities, such as mammography, histopathology, ultrasound, PET/CT, MRI, and thermography, for detecting and classifying breast cancer (BC). For the first time, the study includes relatively uncommon lung adenosquamous carcinoma (ASC) samples, resolving the issue of insufficient experimental subjects in computer-aided diagnosis of lung cancer subtypes. Additionally, the study proposes a computer-aided diagnosis technique based on histopathological images of ASC, LUSC, and SCLC. The study focuses on a computer-aided diagnosis system for automatically classifying lung tissue histopathological images. Two types of image feature extraction and machine learning techniques were used, namely homology-based image processing (HI) and conventional texture analysis (TA). To feed the features into well-known machine learning techniques, the structures of CNNs were modified. The study assesses 108 extractor-classifier mixes and finds that DenseNet169 with SVM (RBF) had the best results with an accuracy of 92.083% and an F1-Score of 92.117%. The study also proposes a deep learning-based

automated framework called HEAL for simple, adaptable, and comprehensive histopathological image analysis. Two case studies on colon cancer and lung cancer demonstrate its usefulness and functionality. The study further develops a deep learning system to classify histologic patterns in lung adenocarcinoma and predict TMB status. The model shows promising results with a patch-level area under the receiver operating characteristic curve (AUC) of 0.78–0.98 across nine histologic features when evaluated with an external data source. The study finds that the histologic subtype-based method performs similarly to a weakly supervised method (AUC of 0.72; 95 percent CI 0.64–0.80).

In this study, a model was developed to predict whether a patient with lung or colon cancer will survive long-term or short-term, using their survival time. The performance of this model was found to be superior to regression-based methods. Interestingly, the model was able to predict survival without the need for ROI annotations, using only histopathology images. The aim of the study was to develop a computer-aided diagnostic system that accurately classifies five types of colon and lung tissues based on their histopathological images. The dataset used was LC25000, which consisted of images of lung and colon cancer. The classification was performed using machine learning techniques, feature engineering, and image processing methods, with five different models being tested: XGBoost, SVM, RF, LDA, and MLP. The XGBoost model outperformed the other models, achieving an accuracy of 99% and an F1-score of 98.8%.

In this paper[80], a method for recognizing breast cancer histopathological images is proposed, which uses gray level co-occurrence matrix (GLCM) features and deep semantic features. The proposed approach is compared to seven baseline models, including AlexNet, VGG16, ResNet50, GoogLeNet, DenseNet201, SqueezeNet, and Inception-ResNet-V2, on the classification problems of magnification specific binary (MSB) and magnification independent binary (MIB) classification using the BreaKHis dataset. Experimental results demonstrate that the proposed approach outperforms the pre-trained baseline models in both MSB and MIB classification problems.Two methods for diagnosing breast cancer from single and multiple magnification histopathological images are presented in this paper[81]. The first method uses a pre-trained DenseNet201 CNN architecture, while the second method is trained solely from magnification images related to each of its four subsystems.Another work [82] aims to develop a computer-assisted OSF screening with improved classification accuracy based on textural features. This method divides histopathological tissue sections into normal, OSF without dysplasia (OSFWD), and OSF with dysplasia (OSFD), allowing oral onco-pathologists to quickly screen subjects. The combination of a fuzzy classifier and texture and higher-order statistics (HOS) features achieved an accuracy of 95.7%, sensitivity of 94.5%, and specificity of 98.8%. Furthermore, a brand-new integrated index known as the Oral Malignancy Index (OMI) is proposed, which uses the HOS, local binary patterns (LBP), and local ternary patterns (LTE) features to diagnose benign or malignant tissues with a single number.

This article provides an overview and summary of digital image processing techniques that are utilized for detecting breast cancer on histopathological images. Additionally, the potential applications of these techniques for the future are also discussed [83].

In this study, a novel framework for extracting features guided by nuclei in histopathological images is proposed. The approach is based on convolutional neural networks and involves using identified nuclei to train a three-hierarchy-structured neural network. By doing so, the network can extract image-level features such as the pattern and spatial distribution of the nuclei. Additionally, a fully automated stain normalization method is introduced in this paper. This technique addresses issues related to staining variability and helps to reduce batch effects. Ultimately, this approach supports research in digital pathology applications by enabling more accurate and reliable analyses of histopathological images.

This paper proposes a method for automatic quantitative image analysis of BCH images. The top-bottom hat transform is used for nuclei segmentation to improve image quality. Wavelet decomposition and multi-scale region-growing (WDMR) are combined to locate regions of interest

(ROIs) accurately. Overlapping cells are split using a double strategy splitting model (DSSM) with adaptive mathematical morphology and the Curvature Scale Space (CSS) corner detection method for improved accuracy and robustness.To classify cell nuclei, four shape-based features and 138 color-space-based textural features are extracted. The best feature set is produced by support vector machines (SVMs) and the chain-like agent genetic algorithm (CAGA). The proposed method was tested on 68 BCH images with more than 3600 cells, and the results indicate that the mean segmentation sensitivity was 91.53% (4.05) and the specificity was 91.64% (4.07). The classification accuracy for normal and malignant cell images is 96.19% (0.31%), sensitivity is 99.05% (0.27%), and specificity is 93.33% (0.81%).The study also looks at the use of AlexNet and Vgg16 models for feature extraction, and AlexNet is used for further fine-tuning. SVMs are then used to classify the obtained features. This study examines nuclei segmentation methods, feature extraction, and disease stage classification for brain tumor histopathological images using automated image analysis techniques. Automatic nuclei segmentation and labeling, as well as the K-S test, are used to determine the significance of feature descriptors and SVM and random forest (RF) classification accuracy for histopathology image data from The Cancer Genome Atlas (TCGA).

In this paper [89], a novel method for feature extraction called Local Binary Pattern (LBP) features, which uses a sliding window approach, is proposed. The method generates 25 sliding windows for each image, and a Support Vector Machine (SVM) classifier is trained using the features extracted from each window. The proposed approach achieved an accuracy of 91.12%, sensitivity of 85.22%, and specificity of 94.01%.Breast cancer is the leading cause of cancer-related deaths in females worldwide, making it a crucial area of research. In another study [90], statistical features were extracted from invasive ductal carcinoma histopathology images using the Histogram of Oriented Gradients (HOG) feature extractor. The performance of the algorithms was evaluated using various metrics such as specificity, accuracy, sensitivity, precision, F1_score, and AUC. When tested on a dataset of 100 images, the algorithms performed well and achieved the best performance.

This paper proposes a multi-scale visual transformer model called GasHis-Transformer for detecting Gastric Histopathological Images (GHID). This model enables the automatic detection of gastric cancer images globally. The GasHis-Transformer model comprises two key modules: a position-encoded transformer model and a convolutional neural network with local convolution. These modules extract global and local information, respectively [92]. The system evaluates the detection of early gastric cancer (EGC), one of the most common neoplastic diseases and the second most fatal tumor-based disease in humans, using the color threshold algorithm to extract color features by tuning the image's color bands. This technique is advanced by the deep Color-Net model (Deep CNET), which compares the training vector and test vector to find the maximum correlation. The system's performance is evaluated using F1-Score, accuracy, precision, and recall.Additionally, this paper [93] evaluates various algorithms for Mitosis detection, including CCIPD/MINDLAB, DTU, IDSIA, ISIK, MINES, NTSUT, PANASONIC, POLYTECH, and others. The methods are compared using various performance analysis techniques.

This paper presents a Stacked Sparse Autoencoder (SSAE), a type of deep learning approach, for the effective detection of nuclei on high-resolution histopathological images of breast cancer [94]. The SSAE learns high-level features from pixel intensities alone in order to identify the distinguishing characteristics of nuclei. Each image undergoes a sliding window operation to represent image patches using the high-level features obtained from the autoencoder. These features are then fed into a classifier, which determines whether each image patch is nuclear or non-nuclear. The SSAE was found to have an improved F-measure of 84.49 percent and an average area under Precision-Recall curve (AveP) of 78.83 percent.Additionally, this survey explores the latest materials and techniques for cancer detection using Computer Aided Design (CAD) on histopathology images [95].

This paper proposes an efficient machine learning-based nucleus detector [96] using color deconvolution to reconstruct each applied stain. The detector employs a substantial feature set and a modified AdaBoost algorithm to create two detectors that focus on distinct nuclei appearance

characteristics. This modified AdaBoost algorithm considers the computational cost of each feature during selection, leading to increased computational efficiency of the detectors.To automatically classify whole-slide images from the Cancer Genome Atlas as LUAD, LUSC, or normal lung tissue [97], a deep convolutional neural network (inception v3) was trained. The results demonstrate that deep-learning models can assist pathologists in identifying cancer subtypes or gene mutations. Transfer learning techniques like AlexNet, GoogleNet, and ResNet were used as foundations, with ResNet achieving the highest accuracy among all others, at 85 percent.The proposed improved design can be applied to automate other medical imaging techniques [98].

The paper[99] provides an overview of image preprocessing techniques, followed by a discussion of feature extraction approaches. The paper then delves into segmentation and classification methods, and concludes by presenting a systematic analysis of these techniques for the benefit of future researchers.In addition, this paper[100] comprehensively covers the computational steps involved in automated histopathology-based cancer diagnosis. These steps include image preparation to identify focal points, feature extraction to quantify focal area properties, and determination of cancerous areas and the level of cancer present. This process enables the creation of new features, identification of subsets of distinguishing features, and improves the accuracy of automated cancer diagnosis.

Methodology Reviews
a) Pre-Processing
This study proposes a novel hybrid method for diagnosing paratuberculosis using histopathology images taken from animals with an intact intestine. The hybrid approach combines image processing and deep learning to achieve improved outcomes.Reliable disease detection from histopathology images is a known open problem in medical image processing, and alternative solutions need to be developed. To address this issue, the study gathered 520 histopathology pictures in collaboration with Burdur Mehmet AkifErsoy College, Personnel of Veterinary Medication, and Branch of Pathology. However, manually detecting and interpreting these images requires expertise and a significant amount of processing time, making it challenging for veterinarians, especially newly hired physicians, to develop methods for detecting and treating this disease.Therefore, imaging and computer vision systems are urgently needed for developing methods for detecting and treating this disease. In this study, the proposed solution method combines the CLAHE method and image processing. The preprocessed images are classified using a VGG-16-supported convolutional neural network for making the diagnosis.

Contrast Limited Adaptive Histogram Equalization (CLAHE)
Adaptive Histogram Equalization (AHE) is a modified version of the standard histogram equalization technique that optimizes local image data. The process involves dividing the image into rectangular regions and applying standard histogram equalization to each sub-region. In this system, the image is first divided into small blocks or tiles, and AHE is applied to each tile to level the histogram. The limitation of contrast enhancement in homogeneous regions is then employed to prevent noise amplification.In the CLAHE method, any histogram splits that exceed the contrast limit are evenly distributed to avoid noise amplification. This technique can be used to increase contrast without introducing noise in various types of images, such as medical, hazy, underwater, satellite, and natural images.

b) Segmentation
This study [102] presents a new technique for generating pathology data for brain tumors by employing a generative model. Specifically, we utilized embedding features derived from a segmentation module to synthesize images in a general generative model. Our approach focuses on synthesizing ODG pathology data, and we utilized the PGGAN, one of the top-performing GAN models, as the basis for our model. By training the generator using embedding features and latent vector z, we were able to create realistic images. Our model is comprised of two modules. The process of reconstruction involves the extraction of significant features and creation of masked

images from reference images by the segmentation module. The generation module then utilizes a concatenation technique for embedding features to produce pathological images from the latent vectors and features obtained from the segmentation module.

The segmentation module comprises two networks: one for masking pathology images and reconstructing reference images. However, the ODG dataset used in the study presented an issue where generating labels for segmentation was not possible. To overcome this, k-means clustering was employed.The design of the generation module was based on PGGAN, which generally performs well but tends to produce poor visual quality in the pathology domain. To address this, embedding features were combined to create more realistic images. The output features from the segmentation module were also combined using this approach, along with the corresponding generator layer scale level. The result was the generation of high-quality and realistic ODG data.

c) Classification

The proposed MVMS-PFENet[103] algorithm was used to analyze high-resolution HE staining pathological images (2048 x 1536 pixels), dividing them into four categories: normal, benign, carcinoma in situ, and invasive carcinoma. The algorithm performed six view transformations (raw, 90∘, 180∘, 270∘, x-flip, y-flip) on each input image after preprocessing. Multi-scale key image patches were then extracted from regions with a high density of cell nuclei at three scales in each view. These patches were converted into vectors using PFENet and then fused together using a two-layer BiLSTM to generate category scores for each view. Finally, FDNet analyzed the scores from all six views and determined the type of cancer present based on majority votes. Based on the reviews the architecture can be designed as shown in figure 3.
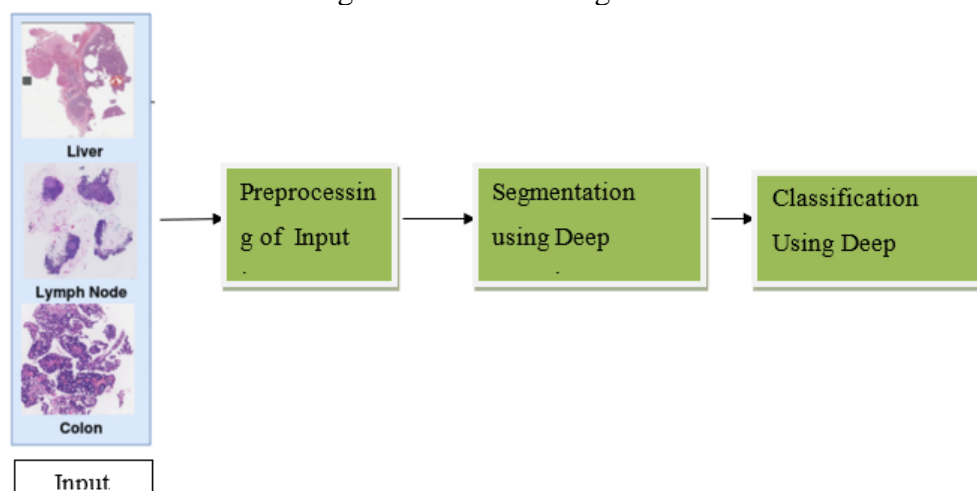

Fig (3) Overall Architecture for this review

Conclusion

In this paper, we review the research conducted in the field of medical science and technology, with a focus on cancer, which continues to be the leading cause of mortality worldwide. Early diagnosis is crucial, as the disease can be lethal. Unfortunately, there has been a lack of modern understanding and technology in the fight against cancer.To address this gap, we investigate the use of machine learning (ML) and deep learning (DL) architectures for the identification and classification of cancer in histopathology images. We cover the pre-processing, segmentation, and classification of these images in detail.Our study highlights the numerous approaches, algorithms, and ideas of feature extraction, selection, and classification used in histopathology images. We also evaluate the various merits and demerits of different methods, taking into account concerns such as accuracy, specificity, and sensitivity.Furthermore, we review the feature extraction and selection algorithms used for training data in cell images and propose incorporating suitable feature extraction and classification methods into big data analytics. This approach may prove useful for several histopathological analysis applications.In summary, our paper presents an overview of the state of the art in ML and

DL approaches for cancer diagnosis using histopathology images. We hope our findings will contribute to the development of more accurate and effective tools for cancer detection and treatment.

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