IT in Industry, vol. 9, no.3, 2021 Published online 3 -5 -2021

COMPUTER AIDED BREAST CANCER SEGMENTATION, FEATURE EXTRACTION, CLASSIFICATION AND DETECTION APPROACHES USING HISTOPATHOLOGICAL IMAGES: A REVIEW

I.Sofiya[1], Dr.D.Murugan[2]
[1]Research Scholar, [2]Professor,
Department of CSE, Manonmaniam Sundaranar University,
Abishekapatti, Tirunelveli.
***Corresponding Author:** sofiya21193@gmail.com*

Abstract
Breast cancer is one of the most common and lethal cancers in women. Since histopathological images provide adequate phenotypic information, they are essential in the diagnosis and treatment of breast cancers. Artificial Neural Network (ANN) methods are commonly used in the segmentation and classification tasks of breast histopathological images to increase the precision and objectivity of Breast Histopathological Image Analysis (BHIA). Histopathological photographs (HIs) are the gold standard for testing such forms of tumours for cancer diagnosis. Even for professional pathologists, analysing such images takes time and resources, and it is difficult, resulting in inter-observer and intra-observer disagreements. In this analysis, we provide a detailed overview of BHIA techniques based on ANNs. First and foremost, we divide the BHIA structures into classical and deep neural networks for further study. The related studies based on BHIA systems are then discussed. Following that, we study the current models to find the best algorithms. Finally, freely available datasets with download links are given for the convenience of potential researchers. In this article, we present a summary of ML and DL techniques with a focus on breast cancer.

Keywords: Breast cancer, histopathology, segmentation, classification, deep learning.

1. Introduction

Computers can now solve problems in a wide range of fields thanks to advances in hardware and computational technologies. The medical profession uses technology admirably to improve the health and quality of life of people. One appropriate example is medical computer-aided diagnosis. Among the diagnoses, image-based diagnoses such as magnetic resonance imaging (MRI), X-rays, computed tomography (CT), and ultrasound have piqued the interest of scientists and academics. Similarly, histopathological images (HIs) are another form of medical imaging obtained by microscopy of tissues from biopsies, which gives specialists the opportunity to analyse tissue characteristics on a cell-by-cell basis.

Cancer is a disease with high mortality rates in both developed and developing countries. In addition to causing mortality, the associated medical costs are high and have an effect on both public and private healthcare systems, penalising both the government and the community. According to Torre et al, the mortality rate in high-income countries is stabilising or even declining as a result of risk factor prevention interventions (e.g., smoking, over-weighting, physical inactivity) and treatment improvements. Mortality rates are increasing in low and middle-income countries due to a rise in risk factors. Early identification of tumours is one of the key points of success in treatment. In reality, breast cancer is the most common form of cancer among women in 140 of 184 countries. Mammography, ultrasound, and CT scans can detect the presence of masses developing in breast tissue, but only a biopsy can confirm the type of tumour. Biopsies, on the other hand, take longer to produce a result due to the acquisition technique (e.g., fine-needle aspiration or open surgical biopsy), tissue processing (creation of slide with staining process), and finally pathologist visual examination. Naturally, pathologist research is a highly technical and time-consuming task that is vulnerable to inter and intra-observer discordance.

Furthermore, the staining process may increase variation in the analysis process. While hematoxylin and eosin (H&E) are the most popular and accessible types of stain, they can produce varying color intensities depending on the brand, storage period, and temperature. As a result, computer-aided diagnosis (CAD) will boost pathologists' throughput and results trust by adding reproducibility to the diagnosis process and reducing observer subjectivity.

The examination of nuclei is a critical component of cancer diagnosis. Tumors such as ductal carcinoma and lobular carcinoma have an abnormal growth pattern on epithelial cells. A large number of nuclei or mitotic cells in a small area may indicate irregular tissue development, which may be a tumour. An HI will detect this function, but in addition to the nuclei, it will detect other healthy tissues visible in images of benign tumours. Stroma is a type of tissue that appears in both malignant and benign photographs. Selecting more appropriate patches can improve classification processes.

In recent years, we have seen an increase in the use of machine learning (ML) methods in CAD and HI research. ML procedures have been used to diagnose cancer in various tissues or organs such as the breast, uterus, skin, brain, bones, liver, and so on. ML methods can also be useful in HI analysis. ML methods have been widely used in the segmentation, feature extraction, and classification of HIs. HIs have rich geometric structures and complex textures that differ from the visual characteristics of macro vision images used in other machine learning tasks such as object recognition, face recognition, scene reconstruction, and event detection.

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

This review aims to capture the most important works from the last decade that use ML methods for HI research. We present a detailed overview of ML methods for HI analysis, including segmentation, feature extraction, and classification. The motivation is to comprehend the evolution and application of ML methods in HI analysis, as well as to discover ML methods' future potential in HI analysis. Furthermore, the following three research questions will be addressed in this review:

1. Which ML methods were used for HI classification, and how were HIs presented to the ML methods (raw images, preprocessed images, or extracted features)? This query seeks to identify which monolithic classifiers, ensembles of classifiers, or DL methods have been frequently used to classify HIs.
2. What are the most important HIs elements, and how are they obtained? This query seeks to determine which types of tissues or structures can be defined using ML methods.
3. What are the dominant patterns in HI analysis? This query seeks to classify the most promising ML methods for HI analysis in the near future.

The main contributions of this paper are: I it covers a period of exponential change in computer vision, from handcrafted features to representation learning methods; (ii) it is a comprehensive review that does not focus on HIs of specific tissues or organs; and (iii) it categorizes the works according to the task: segmentation, feature extraction, classification, and representation learning. Section 7 contains a number of survey and review papers on HI research. Unlike previous studies and surveys on HIs that only concentrate on HIs of particular tissues or organs or on a single learning modality (supervised, unsupervised, or DL techniques), this review covers a variety of methods, methodologies, databases, and experimental findings, allowing readers to recognize potential areas for future study in HI analysis.

2. Related Works

2.1 Segmentation

Pathologists typically search for tissue regions that are important to disease diagnosis. HI segmentation usually aims to mark regions of pixels based on the structure they represent. For example, the identification of nuclei structures may be used to extract morphological features such as the number of nuclei per area, their size, and format, which may aid in the diagnosis of a tumour. The key problems in HI segmentation revolve around the separation of low-level and high-level structures. The former focuses on nuclei segmentation and was the subject of early works, which generally aimed to define mitosis and pleomorphism. Early research concentrated on low-level structures due to hardware limitations in loading and processing high-resolution HIs. Recent science, on the other hand, has concentrated on high-level segmentation, with the aim of identifying tissue types on high-resolution HIs. Furthermore, in recent years, there has been an increase in the number of large datasets based on high-level systems, such as the ICIAR BACH Challenge dataset. Finally, we can illustrate the segmentation using the stain color, which is typically accomplished by color space manipulation, image processing techniques, and low-cost machine learning algorithms. This section provides many techniques for segmenting HIs, the majority of which are focused on either supervised or unsupervised ML methods. The former includes HI datasets with area annotation, while the latter does not.

2.1.1 Unsupervised Approaches

The k-means algorithm is an unsupervised ML approach for clustering that has been used for pixel area segmentation. Fatakdawala et al [1] proposed a method for detecting lymphocyte nuclei based on the expectation-maximization of the geodesic active contour that can distinguish four structures: lymphocyte nuclei, stroma, cancer nuclei, and history. The method begins with segmentation using a k-means algorithm, which clusters pixels with identical intensities, and is then enhanced using an expectation-maximization algorithm. The magnetic interaction principle is used to determine the contours. Following the concept of contours, an algorithm looks for concavity, which indicates that nuclei are overlapping. The studies were carried out using a breast cancer dataset. Roullier et al. [2] investigate multiscale segmentation with k-means. The pathologist's concept is used in this work to examine an entire slide picture (WSI). The segmentation begins at a lower magnification factor and progresses to a higher magnification factor, where it is easier to distinguish mitotic cells. The clustering algorithm's output aims to classify regions of interest in each magnification.

Rahmadwati et al. [3] used the k-means algorithm to help classify HIs. Although the emphasis is on Gabor filters rather than k-means, this clustering approach is critical in the segmentation process. Peng et al. [4] used k-means and principal component analysis (PCA) to divide HIs into four types of structures: glandular lumen, stroma, epithelial-cell cytoplasm, and cell nuclei. Following that, morphological operations of closing and filling are carried out. He et al. [5] used a combination of local region-scalable fitting and k-means to segment cervix HIs. Fatima et al. [6] used k-means for segmentation, followed by skeletonization and shock graphs to classify nuclei in the previously segmented picture. If the shock graph gives a trust value less than 0.5 for nucleus detection, a multilayer perceptron is used in the second attempt (MLP). This hybrid method achieves 92.5 percent precision in nucleus detection.

Mazo et al. [7] have used k-means to classify cardiac images into three categories: connective tissues, light areas, and epithelial tissue. A flooding algorithm processes light areas in order to blend the results with epithelial regions and boost the final result. Finally, the plurality rule was used to categories cells as flat, cubic, or cylindrical. This approach had a sensitivity of 85%. Mazo et al. [8] expanded this work. Tosun et al. [9] suggested k-means segmentation, which divides all pixels into three categories (purple, pink, and white), which are further subdivided into three subcategories. Object-level segmentation based on clustering achieved 94.89 percent accuracy compared to 86.78 percent for pixel-level segmentation. Nativ et al. [10] proposed a k-means clustering based on morphological features of lipid droplets previously segmented using active contours models.

A decision tree (DT) was used to validate the rules that lead to the classes obtained by clustering. The association with pathologist assessments was 97 percent. Shi et al. [11] use a two-step k-means algorithm to segment follicular lymphoma HI. The first phase divides nuclei and other

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

forms of tissues into two clusters. The previous step's "another type tissue" region is then divided into three groups in the following step (nuclei, cytoplasm, and extracellular spaces). The final move is a watershed algorithm to obtain better nuclei contours. The discrepancy between manual and automatic segmentation was approximately 1%. Brieu et al. [12] proposed a k-means-based segmentation approach. The effect of k-means segmentation is improved and simplified by applying a series of thresholds that seek to maintain the shape of artefacts. The most important aspect of such a system is nucleus identification rather than segmentation. Shi et al. [13] used k-means to cluster pixels in the CIELAB color space using pixel neighborhood statistics.

A thresholding phase enhances contour identification of fat droplets, and human specialists examine morphological details relevant to the droplets to make a diagnosis. Shi et al. [11] suggested a segmentation approach that takes into account the local correlation of each pixel. A k-means algorithm-based first clustering produces a poorly segmented cytoplasm, and a second clustering is performed that does not take into account the nuclei found by the first clustering. Finally, a watershed transform is used to complete the segmentation.

2.1.2 Supervised Approaches

In this section, we present works on HI segmentation that are focused on supervised ML approaches. The majority of the works discussed in this section are focused on classification algorithms and thus involve labelled datasets with annotated pixels or pixel regions. Table 5 summarizes recent publications on supervised ML methods used for segmentation, with eight out of fourteen works focused on SVM classifiers. Yu and Ip [14] proposed a method for encoding HIs that uses a patching technique and a method called spatial hidden Markov model (SHMM). Each patch is defined by a function vector that combines Gabor energy and gray-level features. When compared to a secret Markov model, the SHMM showed changes ranging from 4% to 17% in multiple tissues. Arteta et al. [15] use the idea of external regions on grayscale images to distinguish nuclei on HIs. They used an SVM classifier to classify the threshold of external

regions arranged in an overlap tree. In terms of the number of cells detected after segmentation, this method obtained 88.5 percent of the F1-score, compared to 69.8 percent for the state-of-the-art. Janssens et al. [16] proposed a segmentation protocol for identifying muscular cells.

First, a segmentation focused on thresholding distinguishes connective tissues and cells. The segmented regions are then fed into an SVM, which categorizes them recursively into three groups (connective tissue, clump of cells, and cells) until only connective and cell tissues remain. This approach received an F-score of 62 percent, which was cutting-edge at the time. Saraswat and Arya [17] proposed a segmentation protocol based on a non-dominated sorted genetic algorithm (NSGA-II) and a threshold classifier. The NSGA-II produces the function value threshold from ground-truth pictures. The segmentation is created by comparing learned thresholds and feature values. The research by Qu et al. [18] focuses on breast cancer prognosis. They used an SVM to conduct pixel-wise classification to distinguish nuclei from stroma. A second step based on a watershed algorithm recognizes nuclei. Using pixel-level, object-level, and semantic-level features, the method achieved 72% accuracy. Salman et al. [19] proposed a k-NN-based segmentation approach for WSI analysis. The method generates histograms from patches of 6464 pixels extracted from the H&E channels obtained through color deconvolution. The highest accuracy was 73.2 percent when histograms of both H&E channels were used. Chen et al. [20] suggested a system for identifying stroma and tumour nests using pixel-wise SVM. A watershed algorithm is used to segment nuclei, producing 314 object-level features and 16 semantic-level features. The study of function value was used to minimise the feature dimensionality.

Geessink et al. [21] used a normal density-based quadratic discriminant classifier (QDA) to segment colorectal images. The segmentation employs the CIELAB color space with a threshold to exclude background pixels and the HSV color space to identify the remaining pixels. Following classification, errors are corrected based on histological constraints. According to the scientists, the algorithm created an error rate of 0.6 percent for tumour quantification, which is lower than pathologists' error (4.4 percent).

2.2 Feature Extraction

Image feature extraction is typically divided into three steps: preprocessing, feature extraction, and feature processing. The features are then segmented and classified using machine learning techniques. The aim of preprocessing is to remove interference factors and highlight characteristic information. The primary methods are as follows: image standardization [22] (adjust image size); image normalization [23]. (Adjust the image center of gravity to 0). The main goal of feature processing is to remove features with little details and reduce the amount of measurement. Principal components analysis is a common feature processing method [24]. Among them, feature extraction is a critical stage. The process of converting input data into a collection of features is known as feature extraction [25]. The main aim of feature extraction is to extract the most important information from the original data and display it in a lower-dimensional space [26]. As a result, in this section, we primarily summaries the features extracted in WSI for CAD. Until classification, supervised shallow methods rely on features extracted from raw data.

Feature extraction methods process images and provide a fair number of features summarizing the image's content. Such methods seek to minimize the dimensionality of the image and highlight relevant details related to the problem, such as the presence or absence of specific structures, the number of individual components, texture, and structure shapes. Ideally, features should be independent of translation, size, and rotation. The key challenges in extracting features from HIs are the extraction of morphological characteristics from structures present in such images and the quest for higher-level representations that allow capturing information relevant for medical diagnosis. The morphological features are associated with recognizing cellular changes, such as deformed nuclei due to a problem or mitotic processes, or tissue changes, such as density or an odd number of cells. The morphological features are similar to the way pathologists interpret HIs, searching for clear justifications for categorizing the HI. High-level features, on the other hand, are abstractions of all structures in HIs, not just the cell structures. As a result,

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

texture descriptors or frequency domain representations are often used by researchers. Form, scale, texture, fractal, or even a combination of these features have been used for HIs. Table 6 summarizes the papers on function extraction. Object-level and morphometric characteristics such as form and scale are critical for disease grading and diagnosis. Ballar et al. [27] suggested segmenting HIs to distinguish dysfunctional or stable megakaryocytes, structures from which morphometric features are derived. Petushi et al. [28] used the Otsu algorithm to highlight nuclei and then extracted various features such as inside radial contact, inside line contact, field, perimeter, area-perimeter ratio, curvature, aspect ratio, and major axis alignment.

Feature vectors are generated by concatenating the histograms of all these functions. Madabhushi et al. [29] proposed a method for predicting disease outcome using multiple modalities, including MRI, digital pathology, and protein expression. To represent the spatial arrangement of histopathology images, they used graph-based features such as Voronoi diagram (total area of all polygons, polygon area, polygon perimeter, polygon chord length), Delaunay triangulation (triangle side length, triangle area), minimum spanning tree (edge length), and nuclear statistics (density of nuclei, distance to the nearest nuclei in different pixel radii). Song et al. [30] used thresholding and the watershed transform to extract features such as cystic cytoplasm length, cystic mucin production, and cystic cell density. These three features are used to train various classifiers. The experimental results showed that these three features outperformed morphological features (shape and size), achieving 90 percent accuracy versus 64 percent. Furthermore, the combination of these features with morphological features achieved just 85 percent accuracy. Gorelick et al. [31] use a segmentation step to classify super pixels for prostate cancer detection and classification. Morphometric and geometric features are used to depict segmented images.

Filipczuk et al. [32] proposed a cytological analysis and breast cancer diagnosis system that included morphometric features. After isolating nuclei from photos, they measured area, perimeter, eccentricity, major and minor axis length, luminance mean and variance, and distance to the centroid for each nucleus. Ozolek et al. [33] classified follicular lesions on thyroid tissue. Following a preprocessing phase for nucleus segmentation, the chromatin texture of nuclei with linear optimal transport provides features for the final classification. Fukuma et al. [34] compared spatial-level and object-level descriptors such as Voronoi tessellation, Delaunay triangulation, minimum spanning tree, elliptical, convex hull, bounding box, and boundaries. In the best case, object-level features had an accuracy of 99.07 percent, while spatial features had an accuracy of 82.88 percent. Morphometric characteristics can also be present in other structures, such as glands, which are easier to distinguish due to the distinction between the lumen and other cellular structures. This is the focus of the work proposed by Loeffler et al. [35], who use inverse compactness and inverse solidity as indicators of gland alteration in prostate cancer. The features were derived from the area (object and convex hull area) and perimeter of threshold highlighted objects. Marugame et al. [36] used morphometric features derived from image artefacts indicating nuclear aggregations to represent three types of ductal carcinomas in breast HIs. The number of pixels, weight, and thickness of the objects represents their size and shape. Osborne et al. [37] used four geometrical features derived from nuclei after segmentation to diagnose melanoma in skin HIs. The four characteristics are the ratio of nuclei to cytoplasm, the perimeter of a nucleus to its area, the major axis length of a nucleus to its minor axis length, and the number of nuclei to the area of cytoplasm.

Kwak and Hewitt [38] proposed a multi-view approach to detecting prostate cancer that derived morphological and intensity features from multiple resolutions. Area, compactness, smoothness, roundness, convex hull ratio, major-minor axis ratio, extent, bounding circle ratio, distortion, and shape background are derived from lumens and epithelial nuclei, as well as other relational features between them. Olgun et al. [39] proposed a feature extractor for HIs that is based on the local distributions of objects segmented by color intensity. The function extractor computes the distance between an object and its surroundings. The proposed method outperformed the other thirteen approaches that used textural and structural features.

2.3 Feature Selection

Lambrou et al [40] introduced a hybrid GA-based CPs, dubbed GA-CP, in 2011. The ability of rule-based GA to produce human-readable action was one of its primary advantages. The proposed model was tested using datasets collected from a fine needle aspirate of a breast mass, and the results showed that it outperformed the current model in terms of diagnosis accuracy and reliability. Beura et al [41] proposed two-dimensional DOST in 2015 in order to derive coefficients from optical mammograms. The most important DOST coefficients were chosen from a large collection of DOST coefficients using a novel feature selection algorithm based on the NHT and statistical "two-sample t test." The benign or malignant type of cancer was determined using ammographic image classification based on the selected features. The Ada Boost algorithm was used in conjunction with a random forest classifier to classify the mammographic images. The proposed model was validated using MIAS and DDSM datasets, and the results demonstrated an improvement in classification accuracy and AUC. Takemura et al [42] developed a novel algorithm to differentiate between ultrasonic breast tumour images using the Adaboost Algorithm, which was based on the log-compressed distribution parameter. Furthermore, the pattern in the spectrum-based features was created to measure the abnormalities in the tumor's form. The proposed multiclass Ada Boost learning algorithm, in conjunction with the sequential feature-selection method, was compared to conventional models such as the Mahalanob is, distance-based classifier, and multiclass support vector machine. In terms of the approximate parameters for tumour discrimination, the findings showed that the proposed model outperformed the current models.

Several machine learning methods for detecting breast cancer have been investigated in the literature. However, due to the absence of many features in the prediction process, the detection technique still needs development. The variance of diagnosis accuracy was reduced in WAUCE [43], however large datasets could be handled. Aside from these benefits, the detection technique has the disadvantage of requiring a long computation time due to the lack of parallel computation techniques. With SD-CNN, [44] there was no need for reprogramming for

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

each data feature, and each feature's processing time was kept to a minimum. However, there was a need to investigate the raw imaging characteristics derived from the first layers of extracted features. Furthermore, despite having no prior knowledge of the lesions, CNNIBCC4 was effective at automatically extracting cancer regions, with a high AUC of classification. CNNI-BCC, despite having a strong AUC, still had scalability issues. [45] Greater classification accuracy was achieved with GNRBA. The computational complexity, however, was lower. The failure of this approach was primarily due to its reliance on benign or malignant cases alone, as well as the lengthy processing time for the features. DMAS8 was very effective at detecting small tumours. In function classification, however, it had low sensitivity and specificity. The area where tumours are likely to form in the future was predicted using GA-CP [40]. Despite having a high degree of trust, it was unable to generate reliable results for large datasets due to errors. [41] In DOST, the accuracy of distinguishing tumour from non-tumor regions was good, as was the AUC. However, due to the method's ambiguity in estimating the likelihood of the null hypothesis, it cannot be used to its full potential. Furthermore, the Ada-Boost Algorithm [42] reduced both the cost and the number of human resources. This method had drawbacks such as a lack of successful feature set selection.

[47] Formalized paraphrase This paper created an intelligent breast cancer diagnosis model that includes (a) preprocessing, (b) segmentation, (c) feature extraction, (d) feature collection, and (e) classification phases. The CLAHE and median filtering models were used to perform preprocessing on the given input image in this case. Following that, the Region Growing algorithm was used to complete the segmentation procedure. Geometric, texture, and gradient features from the segmented tumour were extracted during the feature extraction process. Since the length of the feature vector was discovered to be high, this proposal sought to pick the best features using a new hybrid algorithm called VU-LA, which was created by combining the LA and PSO algorithms. Finally, the NN classifier was used to classify the features that were optimally chosen. Furthermore, a new training algorithm was used, with the proposed VU-LA algorithm updating the weight of the NN to achieve maximum accuracy. According to the overall study, the VU-LA model is 5.8 percent more accurate than WOA, 29.4 percent more accurate than GWO, 30.7 percent more accurate than FF, 11.7 percent more accurate than PSO, and 8.2 percent more accurate than LA. As a result, the proposed breast cancer diagnostic model was discovered to effectively distinguish between benign and malignant images.

2.4 Classification

Image classification, as the name implies, is to have a fixed set of classification labels, and then for the input image, find a classification label from the classification label set, and eventually assign the classification label to the input image. It is at the core of computer vision and is the most basic concern that serves as the foundation for other computer vision tasks such as positioning, detection, and segmentation [47] [48]. It is commonly used in practice. Although it is a simple task for humans, it can be difficult for computer systems. Many seemingly disparate problems in computer vision (such as object recognition and segmentation) can be reduced to image classification. CAD is the most researched task of pathological image analysis. It also aids the pathologist in making a diagnosis. The diagnostic method entails assigning one or more WSIs to a disease group. Since the errors created by machine learning systems vary from those produced by human pathologists [49], the use of computer-aided design systems will boost classification accuracy [50]. Histopathological image classification has increasingly become a research hotspot in the field of medical image processing in recent years, owing to advances in computer technology. To the human anatomy area and the pathological changes area to continue the accurate classification, may the full degree doctor accurate, the rapid diagnosis state. This is critical for physicians' future diagnoses and patient care. There are approximately 54 publications from 2004 to 2020 on image classification using WSI techniques to assist pathologists in diagnosis in the papers we summarized.

2.4.1 SVM-based Classification Method

SVM is a type of supervised machine learning technique. It was first published in 1963 by Vladimir N. Vapnik and Alexander Y. Lerner [51]. It employs the hypothesis space of linear functions in hyperspace [52] and trains with the learning algorithm of optimization theory, which realizes the learning bias derived from statistical learning theory. The aim of SVM classification is to find an efficient computational method for learning good separation hyperplanes in hyperspace [53]. SVM is intended for binary classification. When an SVM is applied to a multi-class classification problem, it internally divides the challenge into several binary classification problems and solves them using several SVMs [54] [55]. In our analysis, SVMs are used for WSI classification in ten articles.

2.4.2 Random Forest-based Classification Method

RF is a common machine learning algorithm that is frequently used in classification tasks in a variety of fields [56] [57]. RF is a list of tree structure classifiers [58]. Each tree is dependent on the value of a randomly chosen vector that is distributed uniformly over all trees in the forest [59]. Each tree in the forest will vote once, assigning each feedback to the most probable category mark. This method is fast and noise-resistant, and it is an effective ensemble that can detect nonlinear patterns in data. It can easily manage numerical and categorical data [57]. One of the key benefits of RF is that it causes overfitting even as more trees are added to the forest [60]. There are five articles in the papers we summarized that use RF classifiers for similar WSI classification.

In [61], WSI is classified for neuroblastoma biopsy. An automated classifier community extracts and processes the texture features derived from the tissue segmentation components. Multiple Classifiers: kNN, linear discriminant analysis (LDA) & kNN, LDA & nearest mean (NM), correlation LDA (CORRLDA) & kNN, CORRLDA & NM, LDA & Bayesian, and SVM with a linear kernel The performance of multiple classifiers is then chosen using a basic two-step classifier combination method comprised of voting and weighting processes. The automatic classifier community is trained in a multi-resolution frame with different levels of differentiation. The qualified classification system is checked on 33 WSIs. Finally, the classification accuracy is 87:88 percent. Prostate cancer regions in WSIs are defined in [62]. WSIs

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

are first decomposed into a picture pyramid of several resolution levels. Areas classified as cancer by a Bayesian classifier at a lower resolution are then identified at a higher resolution. The AdaBoost integration method is used to pick 10 image features from over 900 first order statistical, second order co-occurrence, and Gaborfilter feature groups at each resolution level. The experimental results show that, as compared to other classifiers, the Bayesian classifier produces higher AUC and precision.

2.5 Deep Learning based Classification Method

Because of recent advances in solving complex machine learning problems on large datasets, deep learning approaches are gaining traction in the scientific community. In a single optimization step, a convolutional neural network (CNN) can learn both a representation and a decision boundary. However, in order to prevent overfitting issues, CNNs typically need a large amount of data for sufficient training. Nonetheless, most HI databases have just a few patients and hundreds of images, which limits the use of DL. Data augmentation [63, 64] and transfer learning [65] are two approaches to overcoming the shortage of data in HI datasets. ImageNet, which contains over 14 million images, is one of the most commonly used datasets for training CNNs for object recognition.

Data augmentation creates new HIs from existing ones using affine transformations or morphological operations. Patching HIs is another popular method of data augmentation. Patching has the effect of choosing parts of an HI that have the same structure but belong to different groups. The transfer learning process, on the other hand, re-trains CNNs that have previously been trained in broad datasets that are typically from a different domain than the target problem. The pre-trained CNNs can be used in two ways: to extract features from HIs and use these features with shallow classifiers, as defined in Sections 4 and 5; and to fine-tune such CNNs on an HI dataset, which means that filters learned on a large dataset will be adapted to the HI dataset. Despite the success of DL methods in image classification, the literature has shown that CNNs are not well suited to classifying textures and achieve only moderate accuracy. HIs exhibit a variety of structures, one of which is texture. Several recent works have attempted to address these difficulties in order to use DL methods in HI analysis. Table 9 summarizes the works discussed in this section in terms of network architecture, tissue or organ from which the HI was collected, and publication year. Malon et al. [78] is among the first to use DL methods in HI analysis. They used a classic LeNet-5, a 7-layer CNN architecture proposed by Lecun et al. [66] in 1998 to learn a representation from HIs previously segmented with an SVR. An SVM was used to classify the features extracted by the CNN in order to find mitotic nuclei. The comparison between machines and three pathologists is the most impressive part of this work. The pathologists had Cohen Kappa factors of 0.13 and 0.44 in the best case, emphasising the inter-observer problem. Kainz et al. [67] proposed two CNNs based on the LeNet-5 architecture for segmentation and classification of glands in benign and malignant colorectal cancer tissue.

The first CNN distinguishes glands from the context, while the second CNN recognizes gland-separating structures. The tissue classification accuracy for the Warwick-QU colon adenocarcinoma and GlaS@MICCAI2015 challenge datasets was 98 percent and 95 percent, respectively. Some works used CNNs based on the AlexNet architecture proposed by Krizhevsky et al. [68] in 2012. AlexNet is similar to LeNet-5, but it has 12 layers, more filters per layer, and stacked convolutional layers. Stanitsas et al. [69] used the AlexNet CNN to describe breast cancer HIs. They compared the CNN findings to some handcrafted feature extractors and shallow classifiers and concluded that the CNN did not outperform the shallow methods. Spanhol et al. [70] investigated architectures based on AlexNet CNN for the issue of breast cancer HI classification. The experimental findings on the BreaKHis dataset revealed that the CNN achieved mean accuracy rates at patient-level ranging from 81.7 percent to 88.6 percent, depending on magnification, which is better than other shallow ML approaches with textural features. Sharma et al. [71] have used an AlexNet CNN and other custom CNN architectures to distinguish benign and malignant tumours. Because of the limited sample size, the authors had to use patching and affine transforms to supplement the results.11 WSIs produced 231,000 images for cancer classification. Four WSIs provided 47,130 images for training in necrosis detection. The AlexNet and custom CNN architectures outperformed most handcrafted features and an RF classifier.

Budak et al. [72] suggested an end-to-end model for detecting breast cancer in HIs based on a pre-trained AlexNet CNN and a bidirectional LSTM (BLSTM). Convolutional layers are used to encode HIs into a high-level representation, which is flattened and fed into the BLSTM. The proposed model achieved the best average accuracy of 96.32 percent for the magnification factor of 200 in experiments on the BreaKHis dataset. Furthermore, for magnification factors of 40, 100, and 400, the average accuracy was 95.69 percent, 93.61 percent, and 94.29 percent, respectively.

Some works employ CNNs based on the inception architecture suggested by Szegedy et al. [73]. The inception modules have parallel paths where the image is passed through filters of various dimensions (1, 33, and 55). Additionally, max pooling is used. The outputs are concatenated and sent to the next inception module. GoogleLeNet, also known as Inception-V1 [73], has 9 such inception modules stacked linearly. It has 27 layers and employs global average pooling at the end of the last inception module. Inception-V2 and Inception-V3 [75] used an improved inception module and auxiliary outputs, which increased accuracy while decreasing computational complexity. Architecture is the Inception-ResNet, which blends the inception model with the ResNet model [75]. Li et al. [76] compared AlexNet and Inception-V1, handcrafted features and SVM, and features extracted by CNNs to identify regions of colon histology images as gland or non-gland. The best results were obtained by combining handcrafted features with an SVM and the estimation of a CNN. They used data augmentation with rotations and mirroring for handcrafted features and CNNs. Yan et al. [77] combined a pre-trained Inception-V3 with a BLSTM to identify breast cancer HIs as normal, benign, in situ carcinoma, or invasive carcinoma. The method divides HIs into 12 small patches on average. Following that, a fine-tuned Inception-V3 CNN extracts features from the patches, where a 5,376-dimensional feature vector is formed by concatenating the weights of the CNN's last three layers. Such feature vectors are fed into a 4-layer

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

BLSTM, which fuses features from 12 small patches to produce an image-wise classification. Experiments show that such a method achieved an average accuracy of 91.3 percent. de Matos et al. [65] proposed a classification method for breast cancer HIs that uses transfer learning to extract features from HIs using an Inception-V3 CNN pre-trained with the ImageNet dataset. The proposed method increased classification accuracy by 3.7 percent using feature extraction transfer learning and an additional 0.7 percent using irrelevant patch removal.

3. CONCLUSION

Image analysis approaches for CAD based on machine learning and WSI technologies are summarized in this paper. The datasets, assessment methods, feature extraction, segmentation, classification, and detection used in the task are evaluated and summarized. The two most widely used datasets in the general datasets summarized by us are TCGA [40] and Camelyon [41]. Color features, texture features, shape features, and deep learning features are the most widely used feature extraction techniques. In the segmentation work, it was divided into thresholding-based segmentation, region-based segmentation, graph-based segmentation, clustering-based segmentation, deep learning-related segmentation, and other methods. These conventional methods are easy to calculate but susceptible to noise, so they are not robust. In recent years, the U-net segmentation approach has become the de facto norm. Classification work is the most researched. In the classification work, the combination of ensemble learning for the conventional classifier, MIL, and neural network has better recognition ability. The majority of the research is done in tandem with the classification work. Furthermore, the deep learning system based on CNN has achieved excellent success in segmentation, classification, and identification tasks, which will aid in the early detection, diagnosis, and treatment of patients.

REFERENCES

[1] Fatakdawala, H.; Xu, J.; Basavanhally, A.; Bhanot, G.; Ganesan, S.; Feldman, M.; Tomaszewski, J.E.; Madabhushi, A. ExpectationMaximization-Driven Geodesic Active Contour With Overlap Resolution (EMaGACOR): Application to Lymphocyte Segmentation on Breast Cancer Histopathology. IEEE Trans. Biomed. Eng. 2010, 57, 1676–1689.

[2] Roullier, V.; Lézoray, O.; Ta, V.T.; Elmoataz, A. Multi-resolution graph-based analysis of histopathological whole slide images: Application to mitotic cell extraction and visualization. Comput. Med. Imaging Graph. 2011, 35, 603–615.

[3] Rahmadwati.; Naghdy, G.; Ros, M.; Todd, C.; Norahmawati, E. Cervical Cancer Classification Using Gabor Filters. In Proceedings of the IEEE 1st International Conference on Healthcare Informatics, Imaging and Systems Biology, San Jose, CA, USA, 26–29 July 2011; pp. 48–52.

[4] Peng, Y.; Jiang, Y.; Eisengart, L.; Healy, M.A.; Straus, F.H.; Yang, X.J. Segmentation of prostatic glands in histology images. In Proceedings of the IEEE International Symposium on Biomedical Imaging: From Nano to Macro, Chicago, IL, USA, 30 March–2 April 2011; pp. 2091–2094.

[5] He, L.; Long, L.R.; Antani, S.; Thoma, G.R. Multiphase Level Set Model with Local K-means Energy for Histology Image Segmentation. In Proceedings of the IEEE 1st International Conference on Healthcare Informatics, Imaging and Systems Biology, San Jose, CA, USA, 26-29 July 2011, pp. 32–39.

[6] Fatima, K.; Arooj, A.; Majeed, H. A New Texture and Shape Based Technique for Improving Meningioma Classification. Microsc.Res. Tech. 2014, 77, 862–873.

[7] Mazo, C.; Trujillo, M.; Alegre, E.; Salazar, L. Automatic recognition of fundamental tissues on histology images of the human cardiovascular system. Micron 2016, 89, 1–8.

[8] Mazo, C.; Alegre, E.; Trujillo, M. Classification of cardiovascular tissues using LBP based descriptors and a cascade SVM. Comput. Methods Programs Biomed. 2017, 147, 1–10.

[9] Tosun, A.B.; Kandemir, M.; Sokmensuer, C.; Gunduz-Demir, C. Object-oriented texture analysis for the unsupervised segmentation of biopsy images for cancer detection. Pattern Recognit. 2009, 42, 1104–1112.

[10] Nativ, N.I.; Chen, A.I.; Yarmush, G.; Henry, S.D.; Lefkowitch, J.H.; Klein, K.M.; Maguire, T.J.; Schloss, R.; Guarrera, J.V.; Berthiaume, F.; et al. Automated image analysis method for detecting and quantifying macrovesicular steatosis in hematoxylin and eosin-stained histology images of human livers. Liver Transplant. 2014, 20, 228–236.

[11] Shi, P.; Zhong, J.; Huang, R.; Lin, J. Automated quantitative image analysis of hematoxylin-eosin staining slides in lymphoma based on hierarchical Kmeans clustering. In Proceedings of the 8th International Conference on Information Technology in Medicine and Education, Fuzhou, China, 23–25 December 2016; pp. 99–104.

[12] Brieu, N.; Pauly, O.; Zimmermann, J.; Binnig, G.; Schmidt, G. Slide-Specific Models for Segmentation of Differently Stained Digital Histopathology Whole Slide Images. In Proceedings of the SPIE Medical Imaging 2016: Image Processing, San Diego, CA, USA, 21 March 2016; Volume 9784.

[13] Shi, P.; Chen, J.; Lin, J.; Zhang, L. High-throughput fat quantifications of hematoxylin-eosin stained liver histopathological images based on pixel-wise clustering. Sci. China Inf. Sci. 2017, 60.

[14] Yu, F.; Ip, H.H.S. Semantic content analysis and annotation of histological images. Comput. Biol. Med. 2008, 38, 635–649.

[15] Arteta, C.; Lempitsky, V.; Noble, J.A.; Zisserman, A. Learning to Detect Cells Using Non-Overlapping Extremal Regions; Lecture Notes in Computer Science; Medical Image Computing and Computer-Assisted Intervention: Nice, France, 2012; Volume 7510, pp. 348–356.

[16] Janssens, T.; Antanas, L.; Derde, S.; Vanhorebeek, I.; den Berghe, G.V.; Grandas, F.G. Charisma: An integrated approach to automatic H&E-stained skeletal muscle cell segmentation using supervised learning and novel robust clump splitting. Med. Image Anal. 2013, 17, 1206–1219.

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

[17] Saraswat, M.; Arya, K.V. Supervised leukocyte segmentation in tissue images using multi-objective optimization technique. Eng. Appl. Artif. Intell. 2014, 31, 44–52.

[18] Qu, A.; Chen, J.; Wang, L.; Yuan, J.; Yang, F.; Xiang, Q.; Maskey, N.; Yang, G.; Liu, J.; Li, Y. Two-step segmentation of HematoxylinEosin stained histopathological images for prognosis of breast cancer. In Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine, Belfast, UK, 2–5 November 2014; pp. 218–223.

[19] Salman, S.; Ma, Z.; Mohanty, S.; Bhele, S.; Chu, Y.T.; Knudsen, B.; Gertych, A. A machine learning approach to identify prostate cancer areas in complex histological images. Adv. Intell. Syst. Comput. 2014, 283, 295–306.

[20] Chen, J.M.; Qu, A.P.; Wang, L.W.; Yuan, J.P.; Yang, F.; Xiang, Q.M.; Maskey, N.; Yang, G.F.; Liu, J.; Li, Y. New breast cancer prognostic factors identified by computer-aided image analysis of HE stained histopathology images. Sci. Rep. 2015, 5.

[21] Geessink, O.G.F.; Baidoshvili, A.; Freling, G.; Klaase, J.M.; Slump, C.H.; Van Der Heijden, F. Toward automatic segmentation and quantification of tumor and stroma in whole-slide images of H&E stained rectal carcinomas. In Proceedings of the Progress in Biomedical Optics and Imaging—Proceedings of SPIE, Orlando, FL, USA, 17 March 2015; Volume 9420.

[22] S. Shen, W. Sandham, M. Granat, in 4th International IEEE EMBS Special Topic Conference on Information Technology Applications in Biomedicine, 2003. (IEEE, 2003), pp. 149-152, 3.

[23] A.M. Khan, N. Rajpoot, D. Treanor, D. Magee, IEEE Transactions on Biomedical Engineering 61(6), 1729 (2014) 3

[24] S. Jhajharia, H.K. Varshney, S. Verma, R. Kumar, in 2016 International Conference on Advances in Computing, Communications and Informatics (ICACCI) (IEEE, 2016), pp.1896-1901

[25] D. ping Tian, et al., International Journal of Multimedia and Ubiquitous Engineering 8(4), 385 (2013)

[26] G. Kumar, P.K. Bhatia, in 2014 Fourth international conference on advanced computing & communication technologies (IEEE, 2014), pp. 5{12 3

[27] Ballarò, B.; Florena, A.M.; Franco, V.; Tegolo, D.; Tripodo, C.; Valenti, C. An automated image analysis methodology for classifying megakaryocytes in chronic myeloproliferative disorders. Med. Image Anal. 2008, 12, 03–712.

[28] Petushi, S.; Zhang, J.; Milutinovic, A.; Breen, D.E.; Garcia, F.U. Image-based histologic grade estimation using stochastic geometry analysis. In Proceedings of the Progress in Biomedical Optics and Imaging- Proceedings of SPIE, Orlando, FL, USA, 9 March 2011; Volume 7963.

[29] Madabhushi, A.; Agner, S.; Basavanhally, A.; Doyle, S.; Lee, G. Computer-aided prognosis: Predicting patient and disease outcome via quantitative fusion of multi-scale, multi-modal data. Comput. Med. Imaging Graph. 2011, 35, 506–514.

[30] Song, J.W.; Lee, J.H.; Choi, J.H.; Chun, S.J. Automatic differential diagnosis of pancreatic serous and mucinous cystadenomas based on morphological features. Comput. Biol. Med. 2013, 43, 1–15.

[31] Gorelick, L.; Veksler, O.; Gaed, M.; Gomez, J.A.; Moussa, M.; Bauman, G.; Fenster, A.; Ward, A.D. Prostate histopathology: Learning tissue component histograms for cancer detection and classification. IEEE Trans. Med. Imaging 2013, 32, 1804–1818.

[32] Filipczuk, P.; Krawczyk, B.; Wo´zniak, M. Classifier ensemble for an effective cytological image analysis. Pattern Recognit. Lett. 2013, 34, 1748–1757.

[33] Ozolek, J.A.; Tosun, A.B.; Wang, W.; Chen, C.; Kolouri, S.; Basu, S.; Huang, H.; Rohde, G.K. Accurate diagnosis of thyroid follicular lesions from nuclear morphology using supervised learning. Med. Image Anal. 2014, 18, 772–780.

[34] Fukuma, K.; Prasath, V.B.S.; Kawanaka, H.; Aronow, B.J.; Takase, H. A Study on Nuclei Segmentation, Feature Extraction and Disease Stage Classification for Human Brain Histopathological Images. Procedia Comput. Sci. 2016, 96, 1202–1210.

[35] Loeffler, M.; Greulich, L.; Scheibe, P.; Kahl, P.; Shaikhibrahim, Z.; Braumann, U.D.; Kuska, J.P.; Wernert, N. Classifying Prostate Cancer Malignancy by Quantitative Histomorphometry. J. Urol. 2012, 187, 1867–1875.

[36] Marugame, A.; Kiyuna, T.; Ogura, M.; Saito, A. Categorization of HE stained breast tissue samples at low magnification by nuclear aggregations. In Proceedings of the IFMBE Proceedings, Munich, Germany, 7–12 September 2009; Volume 25, pp. 173–176.

[37] Osborne, J.D.; Gao, S.; Chen, W.b.; Andea, A.; Zhang, C. Machine Classification of Melanoma and Nevi from Skin Lesions. In Proceedings of the ACM Symposium on Applied Computing, TaiChung, Taiwan, 21–24 March 2011; pp. 100–105.

[38] Kwak, J.T.; Hewitt, S.M. Multiview boosting digital pathology analysis of prostate cancer. Comput. Methods Programs Biomed.2017, 142, 91–99.

[39] Olgun, G.; Sokmensuer, C.; Gunduz-Demir, C. Local object patterns for the representation and classification of colon tissue images. IEEE J. Biomed. Health Inform. 2014, 18, 1390–1396.

[40] Lambrou A, Papadopoulos H, Gammerman A. Reliable confidence measures for medical diagnosis with evolutionary algorithms. IEEE Trans Inf Technol Biomed. 2011;15(1):93-99.

[41] Beura S, Majhi B, Dash R, Roy S. Classification of mammogram using two-dimensional discrete orthonormal S-transform for breast cancer detection. Healthc TechnolLett.2015;2(3):46-51.

[42] Takemura A, Shimizu A, Hamamoto K. Discrimination of breast tumors in ultrasonic images using an ensemble classifier based on the AdaBoost algorithm with feature selection. IEEE Trans Med Imaging. 2010;29(3):598-609.

[43] Wang H, Zheng B, Yoon SW, Ko HS. A support vector machine-based ensemble algorithm for breast cancer diagnosis. Eur J Oper Res. 2018;267(2):687-699.

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

[44] Gao F, Wu T, Li J, Zheng B, Patel B. SD-CNN: a shallow-deep CNN for improved breast cancer diagnosis. Comput Med Imaging Graph. 2018;70:53-62

[45] Dora L, Agrawal S, Panda R, Abraham A. Optimal breast cancer classification using Gauss–Newton representation based algorithm. Expert Syst Appl. 2017; 85:134-145.

[46] Shivhare E, Saxena V (N). Breast cancer diagnosis from mammographic images using optimized feature selection and neural network architecture. Int J Imaging Syst Technol. 2020; 1–17.

[47] W. Rawat, Z. Wang, Neural computation 29(9), 2352 (2017)

[48] A. Karpathy, L. Fei-Fei, in Proceedings of the IEEE conference on computer vision and pattern recognition (2015), pp. 3128{3137

[49] D. Wang, A. Khosla, R. Gargeya, H. Irshad, A.H. Beck, arXiv preprint arXiv:1606.05718 (2016)

[50] D. Komura, S. Ishikawa, Computational and structural biotechnology journal 16, 34 (2018)

[51] V. Vapnik, A.Y. Lerner, Avtomat. i Telemekh 24(6), 774 (1963)

[52] S.T. Roweis, L.K. Saul, science 290(5500), 2323 (2000)

[53] S. Kumar, Z. Khan, A. Jain, International Journal of Advanced Computer Research 2(3),55 (2012) 5.1

[54] C.N. Kamath, S.S. Bukhari, A. Dengel, in Proceedings of the ACM Symposium on Document Engineering 2018 (2018), pp. 1-11

[55] G. Madzarov, D. Gjorgjevikj, I. Chorbev, Informatica 33(2) (2009)

[56] D.R. Cutler, T.C. Edwards Jr, K.H. Beard, A. Cutler, K.T. Hess, J. Gibson, J.J. Lawler, Ecology 88(11), 2783 (2007)

[57] J.I. Titapiccolo, M. Ferrario, S. Cerutti, C. Barbieri, F. Mari, E. Gatti, M.G. Signorini,Expert systems with applications 40(11), 4679 (2013)

[58] L. Breiman, Machine learning 45(1), 5 (2001)

[59] Z. Masetic, A. Subasi, Computer methods and programs in biomedicine 130, 54 (2016)

[60] A. Chaudhary, S. Kolhe, R. Kamal, Information Processing in Agriculture 3(4), 215 (2016)

[61] J. Kong, O. Sertel, H. Shimada, K.L. Boyer, J.H. Saltz, M.N. Gurcan, Pattern Recognition 42(6), 1080 (2009)

[62] S. Doyle, M. Feldman, J. Tomaszewski, A. Madabhushi, IEEE transactions on biomedical engineering 59(5), 1205 (2010)

[63] De Matos, J.; de Souza Britto, A., Jr.; de Oliveira, L.E.S.; Koerich, A.L. Texture CNN for Histopathological Image Classification. In Proceedings of the 32nd IEEE International Symposium on Computer-Based Medical Systems (CBMS), Cordoba, Spain, 5–7 June 2019; pp. 580–583.

[64] Ataky, S.T.M.; de Matos, J.; de Souza Britto, A., Jr.; de Oliveira, L.E.S.; Koerich, A.L. Data Augmentation for Histopathological Images Based on Gaussian-Laplacian Pyramid Blending. In Proceedings of the International Joint Conference on Neural Networks, Glasgow, UK, 19–24 July 2020; pp. 1–8.

[65] De Matos, J.; de Souza Britto, A., Jr.; Oliveira, L.E.S.; Koerich, A.L. Double Transfer Learning for Breast Cancer Histopathologic Image Classification. In Proceedings of the International Joint Conference on Neural Networks, Budapest, Hungary, 14–19 July 2019; pp. 1–8.

[66] Lecun, Y.; Bottou, L.; Bengio, Y.; Haffner, P. Gradient-based learning applied to document recognition. Proc. IEEE 1998, 86, 2278–2324.

[67] Kainz, P.; Pfeiffer, M.; Urschler, M. Segmentation and classification of colon glands with deep convolutional neural networks and total variation regularization. PeerJ 2017, 2017.

[68] Krizhevsky, A.; Sutskever, I.; Hinton, G.E. ImageNet Classification with Deep Convolutional Neural Networks. In Advances in Neural Information Processing Systems 25; Curran Associates, Inc.: Red Hook, NY, USA, 2012; pp. 1097–1105.

[69] Stanitsas, P.; Cherian, A.; Li, X.; Truskinovsky, A.; Morellas, V.; Papanikolopoulos, N. Evaluation of feature descriptors for cancerous tissue recognition. In Proceedings of the 23rd International Conference on Pattern Recognition, Cancun, Mexico, 4–8 December 2016; pp. 1490–1495.

[70] Spanhol, F.A.; Oliveira, L.S.; Petitjean, C.; Heutte, L. Breast cancer histopathological image classification using Convolutional Neural Networks. In Proceedings of the International Joint Conference on Neural Networks, Vancouver, BC, Canada, 24–29 July 2016; pp. 2560–2567.

[71] Sharma, H.; Zerbe, N.; Klempert, I.; Hellwich, O.; Hufnagl, P. Deep convolutional neural networks for automatic classification of gastric carcinoma using whole slide images in digital histopathology. Comput. Med. Imaging Graph. 2017, 61, 2–13.

[72] Budak, Ü.; Cömert, Z.; Rashid, Z.N.; ¸Sengür, A.; Çıbuk, M. Computer-aided diagnosis system combining FCN and Bi-LSTM model for efficient breast cancer detection from histopathological images. Appl. Soft Comput. 2019, 85, 105765.

[73] Szegedy, C.; Liu, W.; Jia, Y.; Sermanet, P.; Reed, S.E.; Anguelov, D.; Erhan, D.; Vanhoucke, V.; Rabinovich, A. Going deeper with convolutions. In Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition, CVPR, Boston, MA, USA, 7–12 June 2015; pp. 1–9.

[74] Szegedy, C.; Vanhoucke, V.; Ioffe, S.; Shlens, J.; Wojna, Z. Rethinking the Inception Architecture for Computer Vision. arXiv 2015.

[75] Szegedy, C.; Ioffe, S.; Vanhoucke, V.; Alemi, A.A. Inception-v4, Inception-ResNet and the Impact of Residual Connections on Learning. In Proceedings of the Thirty-First AAAI Conference on Artificial Intelligence, San Francisco, CA, USA, 4–9 February 2017; pp. 4278–4284.

[76] Li, W.; Manivannan, S.; Akbar, S.; Zhang, J.; Trucco, E.; McKenna, S.J. Gland segmentation in colon histology images using handcrafted features and convolutional neural networks. In Proceedings of the IEEE 13th International Symposium on Biomedical Imaging, Prague, Czech Republic, 13–16 April 2016; pp. 1405–1408.

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731

[77] Yan, R.; Ren, F.; Wang, Z.; Wang, L.; Zhang, T.; Liu, Y.; Rao, X.; Zheng, C.; Zhang, F. Breast cancer histopathological image classification using a hybrid deep neural network. Methods 2019, 173, 52–60.

[78] Malon, C.; Brachtel, E.; Cosatto, E.; Graf, H.P.; Kurata, A.; Kuroda, M.; Meyer, J.S.; Saito, A.; Wu, S.; Yagi, Y. Mitotic figure recognition: Agreement among pathologists and computerized detector. Anal. Cell. Pathol. 2012, 35, 97–100.

ISSN (Print): 2204-0595
ISSN (Online): 2203-1731