

Review Of Breast Diagnosis Detection and Classification Based on Machine Learning

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Abstract – The most frequent kind of cancer among females is breast cancer (BC). Imaging techniques including mammography, MRI, and ultrasound are often used for diagnosis and screening. Although mammography and ultrasound imaging have improved greatly over the years, they still have their limitations, particularly in the presence of thick breast parenchyma, when it comes to detecting tumors and distinguishing between malignant and benign ones. When compared to other methods for detecting and diagnosing lesions, MRI has the highest specificity and sensitivity because of the superior picture quality it provides. However, even MRI has limitations, notably for diagnosis, that are only partly alleviated by combining it with mammography. Because of the limitations of these imaging methods, patients sometimes have to undergo painful and expensive optics operations only to be sure of a diagnosis. Numerous computational strategies have been developed to improve the sensitivity of BC diagnosis and screening without compromising specificity. Radionics, in particular, is gaining interest in oncology as a method of improving all three of these facets of cancer treatment. The term "radiomics" refers to the practice of extracting various quantitative aspects from a single or several medical imaging modalities, therefore revealing qualities of pictures that are not immediately evident and substantially increasing the diagnostic and prognostic utility of medical imaging. The purpose of this article is to offer a brief summary of the current state of radionics research for BC. The majority of the data points to the promising potential of radiomics in breast cancer diagnosis, classification of BC subtypes and grades, and prognosis of treatment success and recurrence. Several aspects of breast cancer care, including diagnosis, prognosis, prediction, monitoring, image-based intervention, and evaluation of therapy response, stand to benefit from radiomics in the era of personalized medicine.

Keywords – Breast Diagnosis, Tumor, Cancer, Classification, Segmentation

I. INTRODUCTION

Both "Deep Learning" (DL) and "Neural Networks" (NN) have entered the common lexicon, with widespread application in many fields of study and everyday life. When compared to traditional AI methods, NN-based AI algorithms have shown to be much more effective, particularly for jobs that call for the integration of large amounts of data and nuanced judgment. To create a desired (usually predictive) output given a specified input by learning from examples, without explicit human interaction while selecting the input attributes, DL

algorithms are a subset of ML algorithms (the larger family of AI). Given sufficient training and knowledge, DL may beat human specialists in many cognitive tasks, providing the capacity to examine huge and diverse data. As a result, DL has spurred a revolution in fields as disparate as autonomous driving [1], poker [2], picture recognition [3], voice recognition [4], translation [5,6], and synthesis [7,8]. Such architectures have been extensively trained on web-sourced data since the early 2000s, and DL techniques have shown to be particularly helpful in image-based applications (such as image

identification, segmentation, and classification). The tools' intrinsic generality and portability make the transition to image data from other domains fairly uncomplicated, provided a sufficiently enough database of labeled data for training is available. Considering the above, it is generally agreed that NN-based algorithms are (or will soon be) the gold standard in areas such as drug discovery [7], genomics [8], and image processing [9].

The pathologist is generally entrusted with doing extensive searches through a large number of images, often within the area of Whole Slide Imaging, in order to extract clinically essential information and establish or confirm a diagnosis (WSI). In this respect, the widespread usage of certified whole-slide scanners and digital WSI infrastructure has permitted the effective deployment of automated AI-based solutions [10] in the field of (digital) pathology (to be compared with classical microscopy [11]). It's also worth noting that physicians' mistrust and professional worry have been fueled by the fast development of artificial intelligence systems for assessing and classifying medical imagery. Both the possible role AI could/could play in shaping the future role of professional practice [12], and the degree to which confidence should be placed in a diagnostic system whose underlying workings are (with currently available architectures) unintelligible, are key issues of concern. Despite this, the vast majority of individuals (about 90%) [13–16] see more benefits than drawbacks in using AI technology. Artificial intelligence (AI) is poised to provide additional value to professionals in carrying out work tasks, such as limiting the packed schedule and freeing up the resources that could be dedicated to important aspects such as interprofessional interactions, the patient-physician relationship, and possibly playing a more satisfying role in the improvement of patient safety.

To better inform decisions made from complicated, high-volume healthcare data, several DL methods have been created recently [17]. What follows is a discussion of the similarities and differences between typical ML approaches and DL approaches, beginning with a look at the DL

approach's overall architecture. We will describe a variety of DL methods well-suited for computer-assisted detection in breast cancer, as well as a number of important publically accessible information sources of manually labeled pictures of breast cancer that are often used for training DL models. Here, we talk about the results of recent, heightened research efforts in these areas generally and in the field of understanding WSI specifically, including the insights gained, obstacles encountered, and challenges faced.

II. RELATED WORKS IN MEDICAL IMAGING

Radiology, pathology, and dermatology are just a few of the many medical specialties thamedica on imaging to diagnose a wide range of disorders. The use of machine learning in medical image analysis, object recognition, segmentation, and registration has been the subject of a number of recent review publications [18–22]. In [23], the most popular convolutional neural networks (CNNs) utilized in medical imaging, including ResNet and GoogleNet, are discussed. Data limits are only one of the obstacles to the expansion of ML applications in medical pictures, which are discussed by Varoquaux and Cheplygina in 2022. In addition, they provide suggestions for improving ML application research, such as implementing more stringent benchmarks for assessment [23]. Brief but useful, [23] guides you through the process of creating your first DL application in the field of medical imaging. [24] provides another summary of both cutting-edge and mainstream medical imaging techniques. Class imbalance is a typical issue in medical datasets, and the study examines this issue and potential remedies including assessing the dataset using various loss functions. The human eye has difficulty detecting subtle differences in patterns, which is an inherent issue in most medical imaging. Take a look at Figure 1 to observe how visually similar benign and cancerous pictures may be. This problem, brought on by sloppy picture tagging, is studied in [25]. For the PCAM dataset, the authors developed a new method based on co-training with global and local interpretations.

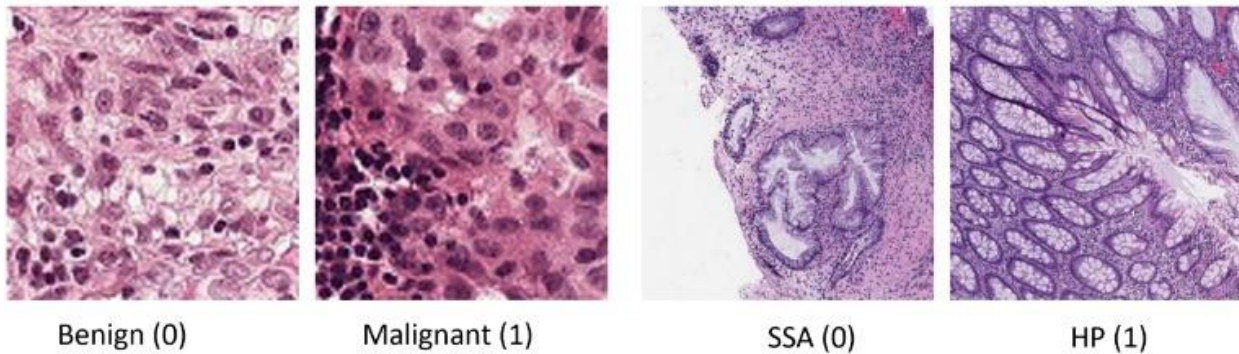


Fig. 1 One example picture from each dataset. Evidence from a PCAM database and images from the MHIST

A. Works Associated with Mathematical Pathology

In this study, we concentrate on histopathology photographs, which are histology images used by pathologists for diagnosis, since they are a good example of the kind of pathology images studied by computational pathologists. Developments in image processing, particularly with the use of CNNs, have spurred the emergence of the field of computational pathology in recent years. Whole slide images (WSI) are the primary data source in computational pathology. These are very high-resolution pictures, with resolutions of up to 10 k x 10 k pixels. Numerous computational pathology facets have been investigated by researchers [26–31]. Due to the difficulties inherent in processing WSI directly, a unique and compressed form of WSI is presented in [32]. This representation, built on top of the cellular data in the WSI, has the potential to boost prediction accuracy by as much as 26%. According to [33], the PCAM dataset is the best for histopathology image classification, and they advise employing color modification methods. Utilizing a collection of CNN models, they determined that the accuracy results produced using a mixture of color changes were superior to those using the original RGB color.

B. The Processing And Analyzing Methods

Using methods like fuzzy logic, evolutionary computing, and artificial neural networks, scientists have attempted several times to improve the diagnostic accuracy of breast cancer detection.

Most clinical trials now include digital tools for confirmation and emphasis on decision-making.

To make proper diagnoses, it is required to collect more data utilizing computational methods. In the realm of image processing, edge detection and

pattern recognition are crucial techniques, particularly for locating and retrieving objects of interest. The primary objective of these techniques is to locate the picture anchors in a digital photograph [34].

Extraction of white breast tissue and unicellular detection [35], and topological visualization of human breast proliferation using MRI [36] are only a few of the many research that has been conducted on this topic. Fractionation is a well-known challenging yet essential phase in medical imaging data classification and analysis.

If you want to get rid of a certain thing (a tumor in your breast, for example), you'll need to split the MRI pictures in half [37]. Tumor cells in the breast are the topic of local study, whereas normal cells represent the control group [38]. It was suggested in [39] that we employ fuzzy clustering techniques (FCM) for picture segmentation. Using a hybrid strategy, [40] suggests splitting breast cancers into two groups.

In order to solve issues with image analysis, a number of transformations are available (such as the Canny, Pruitt, Log, Roberts, and Pruitt [41, 42], and the shift transformation [43]).

Tumor detection and assessment approaches of today may be split down into two categories: spatial and contour. Spatial methods [44–47] define sets of visually similar pixel clusters. These methods streamline several parts of low-level processing, making the radiologist's job easier (e.g., graph analysis, classification, and threshold selection).

It is well-established that the hazards associated with tumors may be mitigated via early identification and subsequent treatment [48]. Knowing this tumor is an oncological tumor helps physicians decide how to treat it, which in turn helps patients regain their health [47, 48].

Research from [49] suggests that classifying tumors may be challenging. This is mostly because of the low contrast and ambiguity of tumor borders on ultrasound pictures, which makes it difficult to identify single ducts with a poorly defined bulk, certain grouped features of tumors, etc.

A novel computational foundation for object detection and segmentation in ultrasound scans (breast cancers) is provided in [50]. In [51], a strategy is suggested for detecting a local item (breast tumor) by segmenting mammography pictures (using basic methods of image processing) that provide reliable results in real time.

These techniques (wavelet transform and the K-clustering approach) are used in practice to segment a mammographic tumor [51]. The contrasted picture is then processed using the K-mean technique, and the tumor region is identified using a threshold.

In [52], a double-cutoff strategy was used to improve mammography picture segmentation. To aid in the diagnosis of breast cancer in

mammograms of varying quality, a border was superimposed on the final segmented picture.

Using a deep neural network for breast tumor detection on mammograms can help physicians make more precise diagnoses. Objects of interest may be classified as abnormal or normal using deep learning (e.g., neural networks) to solve a diagnosis issue [53, 54].

III. LITERATURE ANALYSIS

The existing BC classification, classified into two groups: ML-based and Deep Learning (DL) based techniques. The focus of this research is only deep learning-based schemes used for cancer diagnosis. The state-of-the-art CNN based schemes was critically analyzed (Nahid et al., 2018), (Das et al., 2018), (Mehra et al., 2018), (Deniz et al., 2018) and (Jiang et al., 2019). Table 1 shows the critical analysis of CNN-based schemes for BCD.

Table 1. State of arts of machine learning on breast cancer diagnosis

Author	Year	Techniques	Dataset	Limitations
Nahid et al.	2018	CNN, LSTM, and combination of CNN and LSTM	BreakHis	Overfitting, gradient vanishing and exploding problems.
Das et al.	2018	CNN with multiple Instance Learning (MIP)	BreakHis	Overfitting, and depth wise feature scaling.
Mehra et al.	2018	Resnet-50, VGG-16 and VGG-19 models	BreakHis	Gradient vanishing, feature map redundancy, and Single dimension scaling.
Deniz et al.	2018	Transfer Learning, Alexnet, VGG-16 and SVM	BreakHis	Gradient vanishing, kernel function dependency.
Jiang et al.	2019	Squeeze and Excited ResNet	BreakHis	Feature map redundancy, single dimension scaling, and network saturation.

IV. BREAST HISTOLOGY REQUIREMENTS

The complete study of medical pictures requires the ability to draw conclusions and diagnose conditions, which requires the integration of data from several sources. In the dissertation, many strategies for automatically analyzing photographs of the target objects (breast cancers) are discussed.

In [55], the authors developed a technique for automating the detection and segmentation of interest structures in digital histopathology pictures.

The suggested technique integrates picture data across three different spatial scales:

Basic data derived from pixel values: In this phase, a Bayesian classifier is used to generate the probability that each pixel corresponds to an item of interest.

Related pixel data at a higher level for object detection: There are two methods available for the extraction of summary data:

a. Employing a level-set algorithm: a contour develops in the likelihood scenes created by the Bayesian classifier to detect object boundaries.

b. Using a template-matching technique, whereby shape models are used to recognize nuclei and glands in low-level probability scenarios.

Third, histological structure relationships as a source of domain-specific information: domain-specific knowledge is used to impose structural restrictions that are used to confirm if the discovered items are, in fact, members of the structures of interest.

Recent studies have shown that accurate glandular extraction using a nuclear segmentation algorithm may be used for the automated grading of breast cancer, and prostate cancer, and being able to tell the difference between normal and malignant breast tissue in a histology sample.

A new method for extracting breast ROIs was suggested in [56]. By using a neural network and data from nearby pixels, this method attempts to reduce the number of false positives (FP). The model has two phases as well:

First, a trained model is developed in the training phase, which involves the extraction of a large variety of batches from both the region of interest (ROI) and the background.

Second, the testing phase requires scanning the picture with a fixed-size window in order to distinguish the ROI from the background.

The model then employs a distance transform to isolate the ROI and exclude irrelevant data. Finally, an on-data set consisting of 250 ultrasound pictures was used in the authors' studies (100 malignant and 150 benign).

In [57], a collection of computational techniques for locating and segmenting masses in mammograms from the perspectives of MLO and CC are introduced. To start, an artifact-removal algorithm is implemented. Finally, the scientists used a genetic algorithm, wavelet transform, and multiple thresholding to identify and separate breast cancer masses in mammograms. It is important to note that mammograms are selected at random using the Digital Database for Screening Mammography (DDSM), as shown in Figure 2.

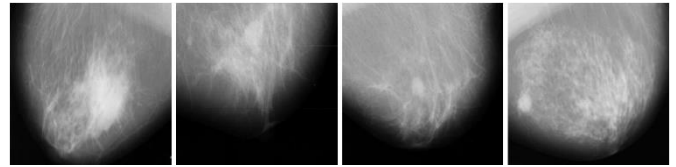


Fig. 2 An example of Mammography images of breast cancer (benign and malignant)

Cancerous tissues in a mammogram may be detected with the use of a simple method presented in [58]. As a further step after identification, mammography tumor regions are segregated. It relies on elementary image processing methods like averaging and thresholding. Max-Mean and Least-Variance methods were developed specifically for tumor identification.

The breast-mass contour characteristics that are retrieved are used in the study suggested in [59]. (determined by automated segmentation methods). These techniques are used to diagnose mammography masses and place them into distinct categories (malignant or benign). Mass contours were calculated in two different ways. One way involves expanding a restricted area, while the other uses dynamic programming. In addition, a set of 6 features created for characterizing mass margins was extracted using reduced versions of contours (modeled as ellipses). One set is made up of educated guesswork (informed by knowledge of edge signatures), and another is a quantitative evaluation of the first. A measurement of conjecture (using relative gradient orientation as a yardstick).

The aforementioned characteristics, as well as other combinations thereof, were then used by three well-known classifiers to make predictions for 349 mass-diagnosis cases. Support vector machines, Fisher's linear discriminants, and Bayesian classifiers are the classifiers available. Finally, the systems were compared in order to assess how well they diagnosed breast lumps.

In order to detect, categorize, and segment the malignant zone in mammograms, the authors of [60] created a computer-assisted approach based on deep learning. A preprocessing approach is also proposed to eliminate the muscle area, artifacts, and noise. Not to add, there is a substantial potential for a false-positive result when preserving muscle areas. The pre-processed picture is then transformed into 512 512 patches to increase system efficiency and deal with the high resource demand. Two public breast cancer datasets may be found online. both the Digital Database for Screening Mammography's

Curated Breast Imaging Subset and the Mammographic Image Analysis Society's (MIAS) digital mammogram dataset (CBIS-DDSM). In addition, two state-of-the-art deep learning-based instance segmentation frameworks are DeepLab and Mask RCNN.

In [61], the authors suggest a method for automated quantitative picture analysis (BCH images). Using a top-bottom hat transform, we can isolate nuclei from their backgrounds and improve the overall picture quality. Wavelet decomposition and multi-scale region-growing (WDMR) are then performed to define ROIs and pinpoint the exact location. Next, a double-strategy splitting model (DSSM) is utilized to divide overlapping cells for increased robustness and accuracy. The DSSM includes corner recognition in Curvature Scale Space (CSS) and adaptive mathematical morphology. For cell nuclei categorization, we extract 138 color- and shape-based textural characteristics. Subsequently, a chain-like agent genetic algorithm (CAGA) is combined with a support vector machine (SVM) to provide a superior feature set. Finally, the proposal, which includes almost 3600 cells, has been evaluated using 68 photos of BCH.

Fast-scanning deep convolutional neural networks (FCNNs) are proposed for use in pixel-wise area segmentation [62]. Without compromising on speed, the FCNN eliminates the unnecessary calculations included in the standard CNN. Our results show that segmenting a 1000 x 1000-pixel picture takes just 2.3 seconds.

The review article proposes a trainable segmentation method and a better threshold-based model for deriving ROI. The pectoral muscle and border area of the breast were segmented using a novel hybrid method. Machine learning (ML) and thresholding methods formed the foundation of the company. The breast area was then singled out by band removal in the wavelet transform for breast boundary estimate. Using a novel thresholding method, we were able to locate the original breast border. The overestimated limit was fixed by removing little things. Morphological procedures and masking were used to carry out this technique. The discipline of medical imaging has made major advancements in the segmentation process. The developments centered on making ML techniques that are both fast and precise. The importance of ML techniques in developing effective and more precise

segmentation algorithms has been emphasized in the research literature. An ML method was developed in the study to identify the location of the pectoral muscles and the corresponding ROI. The method combined neural network classifiers with the Histogram of the Oriented Gradient (HOG) feature [63]. To ensure that the segmentation method works, it has been tested on three different sets of mammograms: 100, 200, and 100 pictures. All of the pictures were from the Breast Cancer Digital Repository (BCDR), the breast, and the mammographic image analysis society (mini-MIAS).

Finally, researchers in [64] propose an optimal region growth-based automated method for identifying breast masses. Furthermore, a swarm optimization method is used to provide optimal seed locations and thresholds (Dragon Fly Optimization, or DFO). Pictures are segmented using GLCM and GLRLM to extract texture properties. The textural features are then sent into a backpropagation-trained Feed Forward Neural Network (FFNN) classifier. Remember that the FFNN can tell whether an image shows cancer or not. Finally, the effectiveness of the proposed detection method was evaluated using images from the DDSM database [64, 65].

V. CONCLUSION

The emerging field of research called "radiomics" [66][67] focuses on the extraction of meaning qualities from clinical images. For example, radionics is being used alongside other imaging modalities, diagnostic features, and machine-learning approaches in breast cancer research to predict not only the presence and location of malignant lesions but also prognostic factors like the response to NAC treatment and the risk of tumor progression. The main drawback of radionics is the significant training in computer methods required before they can be applied in a clinical environment. The time required for model construction, training, and execution is influenced by several factors, including but not limited to the size and structure of the dataset, the available computational resources, and the complexity of the model. Processes in traditional radionics that rely on manually constructed qualities need less computing power than DCNN-based radiomics [68]. In addition, the computing requirements of Neural Network-based deep learning systems are higher than those of more

traditional machine learning architectures like KNN and SVM. However, the accuracy of tissue classifications achieved using KNN or SVM is lower than that of classifications obtained using NN [69]. As the size of a dataset grows, so does the amount of time needed to calculate anything. So, various techniques use picture reduction or preemptive resolution degradation to focus on specific areas of interest (ROIs) in the input pictures [70]. For medical image classification, option (a) is preferred because it enables the training of algorithms to recognize lesions in specific areas of clinical interest without having to throw away potentially relevant data (regions outside of the targeted regions) [71]. However, decreased sensitivity may result from lower picture resolutions in the second option [72]. It's possible that the time needed to evaluate a picture may be considerably reduced if researchers in the fields of radiomics and deep learning adopted the practice of using parallel computing approaches on Graphics processing units (GPU) [73].

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