

Breast Cancer Detection using Convolutional Neural Network

L. Vinoth Kumar

Department of Electronics and

Communication Engineering

Velammal College of Engineering and

Technology

Madurai, India

logvinoth@gmail.com

B. Mukesh

Department of Electronics and

Communication Engineering

Velammal College of Engineering and

Technology

Madurai, India

mukesh19ece50@gmail.com

G. Nalin kumar

Department of Electronics and

Communication Engineering

Velammal College of Engineering

and Technology

Madurai, India

nalinkumar012629@gmail.com

A.Suriya

Department of Electronics and

Communication Engineering

Velammal College of Engineering and

Technology

Madurai, India

Suriyacri903@gmail.com

Abstract

Breast cancer remains one of the primary causes of death in women, and extensive efforts have been made to prevent it through screening programs. With the substantial increase in mammogram screenings, computer-assisted diagnosis has become essential. Although computer-assisted detection techniques have been developed to improve diagnosis without requiring multiple readings, they have not shown a significant improvement in performance measures. Hence, deep learning-based automatic image processing techniques are a promising solution for aiding breast cancer diagnosis.

Introduction

Breast cancer is a type of cancer that arises in or around the breast tissue, typically starting as an abnormal lump or a calcium deposit due to abnormal

cell growth. Although most breast lumps are benign, some can be either pre-cancerous or cancerous. Breast cancer can be localized, appearing only in the breast, or metastatic, spreading to other parts of the body. A physical examination by a doctor is usually the first step in evaluating a breast lump. Further tests, such as mammography, breast ultrasound, breast MRI, PET/CT, or scintimammography, may be ordered to determine the nature of the lump. If the lump is benign, the doctor may still want to monitor it for any changes. If the results are unclear, a biopsy may be performed using ultrasound, x-ray, or magnetic resonance imaging guidance. The choice of treatment depends on various factors such as tumor size, spread, type, receptor status, growth rate, and patient health. Treatment options include surgery, radiation therapy, chemotherapy, hormone therapy, or a combination of these approaches.

Benign Breast Disease

The presence of benign breast disease can increase the likelihood of developing breast lumps.

While discovering a lump can be frightening, it's important to note that not all changes in breast tissue are cancerous. However, some forms of benign breast disease can increase the risk of breast cancer. Therefore, it's crucial to inform your healthcare provider of any breast lumps or changes you experience. In most cases, noncancerous lumps resolve on their own without requiring treatment.

In breast histopathology images, the number of cells undergoing mitosis is one of the three components used to grade breast cancer tissue slides, along with tubule formation and nuclear pleomorphism. Counting and detecting mitotic cells automatically is a challenging task due to the biological variability of these cells. The significance of determining the mitotic count lies in its ability to assess the tumor's aggressiveness. Mitotic cells have the ability to replicate their chromosomes and divide them into two identical sets, resulting in the formation of two new cells.

Here are four phases of mitosis:

Mitosis is a complex process that involves several phases, such as prophase and metaphase, where chromosomes are aligned and separated to ensure each new nucleus has a copy of each chromosome. Histopathology slides are an essential tool for pathology studies, but manual observation can be time-consuming. To address this, a proposed solution is an automatic mitosis detection system (AMDS) designed specifically for breast cancer histopathological slides.

The AMDS employs 2D anisotropic diffusion filters in the pre-processing step, maximum likelihood estimation for segmentation, and non-linear support vector machine classifiers for pixel-wise and object-wise classification. The proposed method outperforms other systems in the Mitos-ICPR2012 contest in breast cancer histopathological images,

according to object and region-based evaluation measures, with an f-measure metric of 70.94% for Aperio XT scanner images and 70.11% for Hamamatsu images. The results demonstrate the effectiveness of the proposed AMDS in automated mitosis detection.

I. EXISTING METHODOLOGY

Medical image segmentation is a widely studied research area, and various algorithms and methodologies have been proposed. One such method is the brain tumor segmentation method introduced by Bandhyopadhyaya, which uses the K-means clustering technique. This method involves three steps, including segmentation based on the K-means algorithm, coarse-grain localization guided by local standard deviation, and fine-grain localization guided by local standard deviation. The method extracts the brain tumor region from MRI images by segmenting them into two parts, one containing normal brain cells, such as grey matter (GM), white matter (WM), and cerebrospinal fluid (CSF), and the other containing tumor cells. However, this segmentation technique has limitations, such as being restricted to adjacent imaging layers. Additionally, the image fusion method used in this technique provides good results in fusing multiple images, but it may ignore finer anatomical details, such as twists and turns in the tumor boundary or overlapping regions of gray and white matter in the brain.

An alternative approach for medical image segmentation is the PET-SFCM clustering algorithm proposed for Positron Emission Tomography (PET) scan image datasets. This algorithm incorporates spatial neighborhood information with the traditional Fuzzy C-means algorithm by updating the objective function of each cluster. By taking the spatial relationship of neighboring pixels into account, the algorithm is able to aid in image

segmentation. The memberships of the neighbor-centered pixels are specified to obtain cluster distribution statistics, which are used to calculate a weighting function that is applied to the membership function. While the algorithm was tested on a dataset of patients with Alzheimer's disease, the researchers did not report their quality assessment without human involvement or calculate an objective-based quality assessment. Another study proposed a deep learning-based framework for the segmentation of brain tumors in Magnetic Resonance Imaging (MRI) scans. They used a Fully Convolutional Network (FCN) that maps the input image to an output segmentation map with pixel-level accuracy. Their proposed method achieved state-of-the-art results on two publicly available benchmark datasets and demonstrated robustness to variations in data acquisition protocols. However, their method requires a large amount of annotated data for training and may not perform well on small datasets. They also noted that the model's interpretability and transparency can be challenging due to the complex architecture of deep neural networks. Additionally, some researchers proposed graph-based methods for image segmentation, such as Graph Cuts and Normalized Cuts. Graph Cuts minimize the energy function by partitioning a graph into two sets of pixels, foreground and background. Normalized Cuts maximize the ratio of between-cluster similarity to within-cluster similarity by partitioning the graph into segments. Both algorithms have shown good performance in image segmentation, but they require defining the graph and its parameters, which can be a challenging task. Moreover, they may not perform well in images with complex structures or large variations in intensity.

Additionally, some researchers have proposed hybrid algorithms, such as the integration between K-means and Fuzzy C-means. They chose the

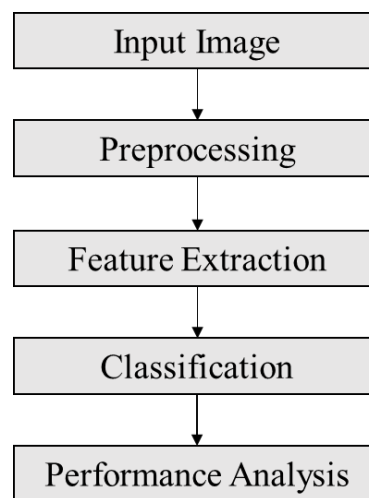
number of clusters, fuzziness, distance, and stopping criterion, and then initialized the memberships randomly or obtained them from K-means. In iterations, centers and memberships were recalculated until the objective function was reached. Their method can deal with overlapping grayscale intensities, but it cannot clearly define borders between tissues successfully. Although it minimizes the within-class sum square errors, its performance degrades when applied to noise-corrupted images. The researchers solved this problem by introducing a preprocessing step before applying the integration. They compared their result with KM, FCM, and the integration FKM in case of under-segmentation and over-segmentation, proving that FKM gives the minimum under or over-segmentation. However, they did not demonstrate the time of each algorithm or in the integration method.

II. PROPOSED METHODOLOGY

That sounds like a comprehensive method for analyzing spiral drawing data. The use of texture-based features through the GLCM algorithm is a useful approach to extract relevant information from the image. It is also good to see that the classifier's performance is evaluated using multiple metrics to provide a more complete picture of the algorithm's performance. The performance analysis can help to identify potential areas of improvement for the method. Overall, this approach seems like a promising method for analyzing spiral drawing data. Input image is the image which contains the RGB color channels. The input image is known as the dataset image. The input image is always taken from the dataset image, so that the intensity and the pixel value of all the images are nearly equal to one another. The input image which is from the dataset will give the better result than the other images

which is taken from the other web pages. The accuracy of the process is increased due to the selection of the dataset image. In the realm of computer graphics and digital imaging, scaling refers to altering the size of a digital image. In the field of video technology, increasing the size of digital material is referred to as up-scaling or resolution enhancement. When scaling a vector graphic image, the graphic primitives that compose the image can be resized through geometric transformations without losing image quality. Conversely, when scaling a raster graphics image, a new image with a higher or lower pixel count must be produced. The Gray-Level Co-occurrence Matrix (GLCM) is a well-known statistical technique utilized for feature extraction. The GLCM tabulates the frequency at which different combinations of pixel gray levels appear in an image. Its objective is to allocate an unknown sample image to one of a predetermined set of known texture classes. Textural features can take the form of scalar numbers, discrete histograms, or empirical distributions. They describe textural characteristics of images, such as spatial structure, contrast, roughness, orientation, and so forth, and exhibit a certain correlation with the desired output. In machine learning, multiclass or multinomial classification refers to the task of categorizing instances into more than two classes (classifying instances into one of two classes is known as binary classification). While certain classification algorithms are naturally able to use more than two classes, others are fundamentally binary algorithms. Nevertheless, they can be transformed into multinomial classifiers using various techniques. In information retrieval, precision denotes the measure of result relevancy, while recall measures the number of genuinely relevant results retrieved. A high area under the curve corresponds to high recall and high precision. High precision relates to a low false positive rate,

whereas high recall relates to a low false negative rate. A classifier with high scores for both shows that it produces accurate results (high precision) and returns the majority of all positive results (high recall). A system with high recall but low precision retrieves numerous results, but the majority of its predicted labels are incorrect when compared to the training labels. A system with high precision but low recall is the opposite, returning few results, but most of its predicted labels are correct when compared to the training labels. An ideal system with high precision and high recall returns many results, with all results labeled correctly. Multiclass classification should not be mistaken for multi-label classification, in which multiple labels are predicted for each instance. The harmonic mean of precision and recall, the traditional F-measure or balanced F-score, is a measure that combines precision and recall. This measure is roughly the average of the two when they are similar, and is the harmonic mean more generally, which coincides with the square of the geometric mean divided by the arithmetic mean in the case of two numbers. However, the F-score can be criticized for its bias as an evaluation metric in certain scenarios.



III. RESULTS AND DISCUSSION

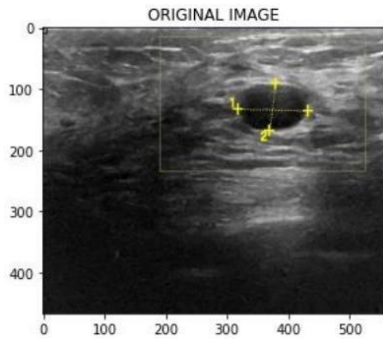


Fig.1

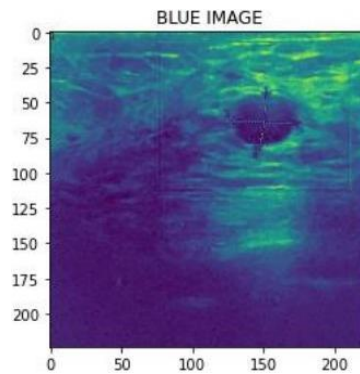


Fig.2

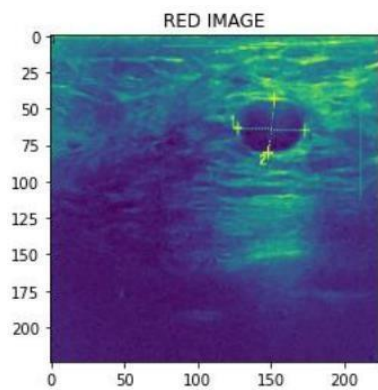
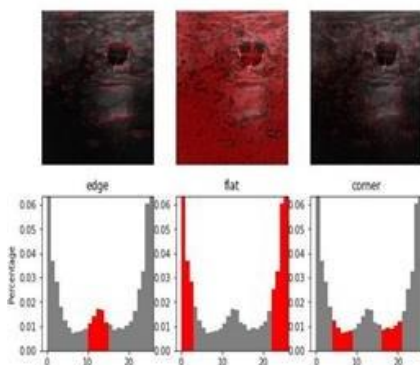
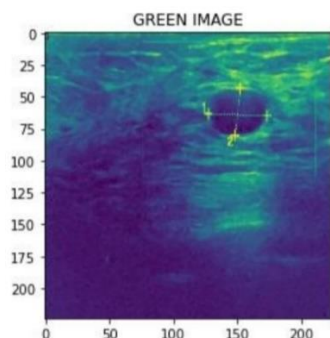


Fig.3



We utilized three different CNN techniques to identify breast cancer in mammograms. Due to the limited number of labeled mammographic images, training a CNN from scratch is not practical. Therefore, we employed transfer learning in CNN, which proved to be a promising approach for breast cancer detection. Our findings indicate that the pre-trained CNN model can automatically extract features from mammographic images, enabling a good NN-classifier to be trained with these features without manually crafting them. Combining pre-trained CNN yielded an average accuracy of approximately 99.3% for distinguishing between abnormal and normal cases in the dataset. Furthermore, our results revealed that the hybrid classification accuracy of the fine-tuning model was 99.4% higher than that of the CNN model.



IV. CONCLUSION

It sounds like you used transfer learning to utilize pre-trained CNN models for detecting breast cancer from mammograms. By doing this, you were able to automatically extract features from mammographic images and train a good NN-classifier using these features without the need for hand-crafted features. Your results show that the pre-trained CNN models were effective in achieving an average accuracy of about 99.3% for classifying abnormal vs. normal cases in the dataset. Additionally, your hybrid classification approach using fine-tuning achieved even higher accuracy at 99.4%. Overall, this suggests that transfer learning with pre-trained CNN models can be an effective solution for breast cancer detection from mammograms.

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