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Abstract

Background: One of the most remarkable applications of deep learning emerges in medical diagnosis. New improvements in this field have shown that with large enough datasets and the right methods, one can achieve results as reliable as diagnoses made by experienced doctors. One of such developments is MURA, which is a dataset of musculoskeletal radiographs consisting of 14863 studies from 12173 patients, resulting in 40561 multi-view radiograph images. Each one of these studies concerns one of the seven standard upper extremity radiographic study types, namely finger, forearm, elbow, hand, shoulder, homeruns, and wrist. Each study was categorized as normal or abnormal by board-certified radiologists in the diagnostic radiology environment between 2001 and 2012. Abnormality detection in muscular radiography is of great clinical application. This gains more importance in cases in which abnormality detection is difficult for physicians. If the proposed model can help us in detection, the process of treatment will precipitate. This model is termed Inception-v3.

Methods: In this study, we evaluated the MURA dataset through Dense NET and inception-v3 methods.

Results: The results indicated that the former had better performance and we added a pre-processing module to it to improve the accuracy of the DenseNet method in detecting the abnormality. In this context, we trained the machine to be sensitive to the presence of external objects to be distinguished from actual abnormality such as bone fraction. We achieved this condition by many various radiographs as machine inputs. By this strategy, both techniques (DenseNet and Inception-v3) showed improvements in accuracy. Thus, we sub-grouped abnormality into with or without the presence of external objects.

Conclusion: Although the average opinion of radiologists still shows better results, in images with delicate fracture detection, such as finger fracture, the proposed model worked more accurately, and it could be a decision support assistant for physicians in the final detection of fracture. The precision of the proposed model will enhance if the image is separated from normal images using Platinum, a new class is made, and pre-processing is done.

Therefore, the model can automatically detect abnormality by identifying that part of the image that is detected to be abnormal. An efficient model can interpret images more efficiently, can reduce errors, and can enhance quality. More studies are needed to evaluate the integration of this model with other models of deep learning in clinical settings.

Keywords: Musculoskeletal Radiographs; Deep Learning; Medical Image Processing; Abnormal Detection

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Fully Automated Computer-Assisted Diagnostic Method for Mitosis Detection on Histology Slide Images of Breast Cancer

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Abstract

Background: Nowadays, advances in the field of medical science, especially the branch of histology, have made it possible to detect cancer, its growth rate, type, and extent of cancer malignancy. According to GLOBOCAN 2012, breast cancer ranks second in terms of prevalence and mortality [1]. The number of mitoses in histology slide images is considered as one of the three significant factors in grading breast cancer. The mitosis count is done manually by pathologists but automating the mitosis count process can decrease its time and costs. Different automatic techniques have been proposed in the literature for breast cancer mitotic counting [2-5].

Objectives: In this paper, we propose an automated method for accurate mitotic cell detection in breast cancer histology slide images.

Methods: To evaluate experiments, we used the Mitos-ICPR 2012 dataset consisting of 50 HPFs with the train-to-test ratio of 70% to 30%, accounting for 35 images for training and 15 images for testing. These 50 HPFs were obtained by analyzing the texture of five different patients. Each slide was stained with standard Hematoxylin and Eosin (H&E) stains and two expert pathologists marked the mitotic cells with labels in 10 selected distinct microscopic HPFs at 40x magnification. The slides were scanned by two slide scanners, including Aperio Scanscope XT and

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Hamamatsu Nano-zoomer. Totally, there were 326 mitotic cells in this dataset [6]. As shown in Figure 1, the proposed fully automated system consisted of the following stages: segmentation and extraction of mitosis candidates using statistical Gaussian Mixture Model (GMM), feature extraction, and classification using SVM classifier (with different kernels) and decision tree classifier. After candidate extraction using GMM, to identify candidates as mitoses or non-mitoses, it was necessary to extract discriminant and reliable features. In the proposed feature extraction stage, we focused on the extraction of textural features including GLCM, CLBP, and statistical moments of filtered images by the Gabor filter in the RGB color

space. Moreover, several shape features were proposed to achieve a better distinction of mitosis from non-mitosis candidates. The proposed shape features were based on calculating the Euclidean distance of boundary pixels from the center of each cell. Two types of textural and shape features were combined with each other to provide the final feature vector with a length of 214.

Results: The visual results of the proposed automated mitosis detection system for a sample histopathology slide image are shown in Figure 2.

Figure 3 shows the performance of the proposed mitosis detection and classification method.

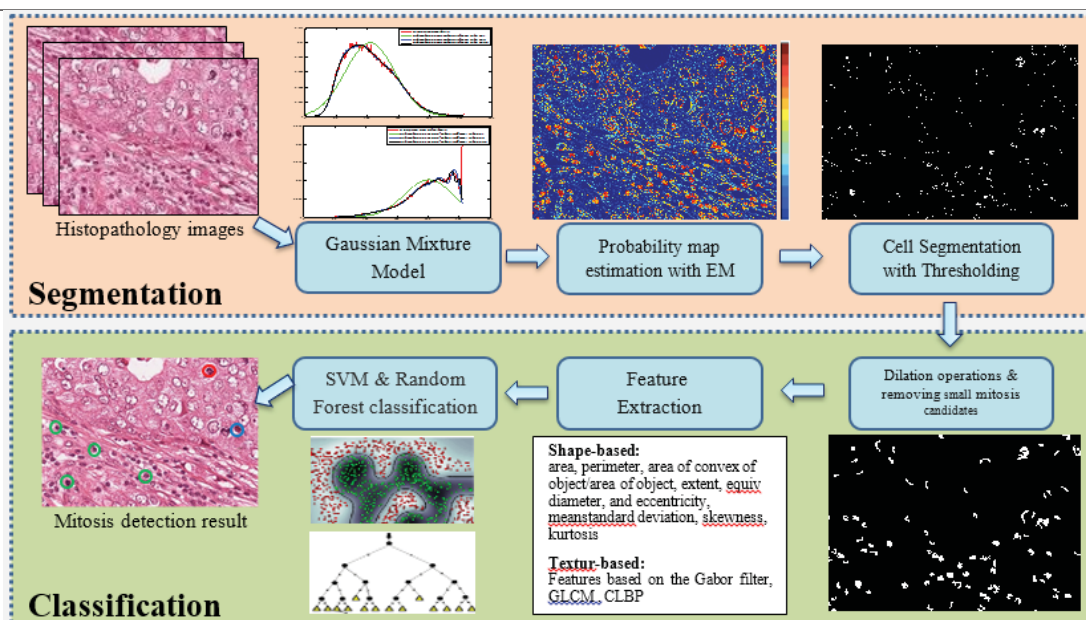


Figure 1. The framework of the proposed fully automated mitosis detection system

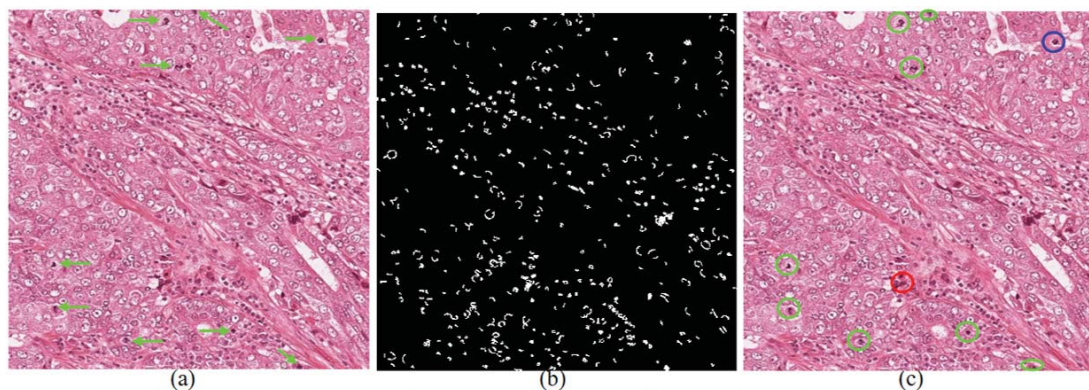


Figure 2. Visual results of the automated mitosis detection system: a, a sample histopathology slide image, b, extracted candidates using the proposed GMM method, c, mitosis detection results: green circles are TPs, the blue circle is FN, and the red circle is FP.

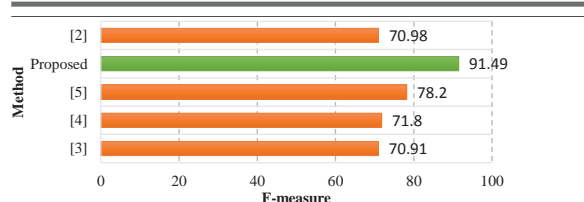


Figure 3. Comparison of the proposed mitosis detection system results with the best results of other methods in Mitos-ICPR2012 contest

Conclusion: The detailed experimental results demonstrated the promising performance of the proposed fully automated method for mitosis detection with F-measure (91.49%).

Keywords: Breast Cancer Grading; Mitosis Detection; Histopathology Image; Gaussian Mixture Model; Feature Extraction

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Automatic Bone Age Determination Using Wrist MRI Based on FIFA Grading System for Athletes: A Deep Learning Approach

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Abstract

Background: Young athletes need to comply with fair play principles including age-specific rules for each category of matches (1). Although birth certificates are considered the main document indicating the age of players, in some regions of the world, the registration of birth is subject to variation, which makes the certificates unreliable. Therefore, FIFA has tried to use imaging methods without ionizing radiation to find out the bone age as the basis for fair play confirmation. FIFA has developed a grading system consisting of I - VI levels, which can be used in teenage athletes (2). The grading system is currently used as the standard bone age determination method in football players (3,4). All national and club matches are obliged to follow screening procedures strictly like anti-doping procedures.

Objectives: The purpose of this study was to evaluate the performance of a deep learning-based automatic system that provides FIFA grades upon receiving DICOM images of the MRI study to facilitate and speed up the bone age determination.

Methods: The FIFA bone age determination system consists of six grades starting from a totally unfused epiphyseal plate (Grade I) to a completely fused plate (Grade VI) where variable progressive degrees of fusion are considered the basis for Grade II to V. The protocol includes nine slices in the coronal plane with 3 mm gaps between the slices. The recommended MR sequence is T1. Since the middle image in the nine-picture dataset is considered the most informative slice containing the largest image of the distal radius, the study was done using this single slice as the basic source of grading. Then, another volumetric set of slices 4, 5, and 6 was used as the second group. A convolutional neural network was designed in four convolutional layers including pooling, ReLU, and fully connected layers (Figure 1).

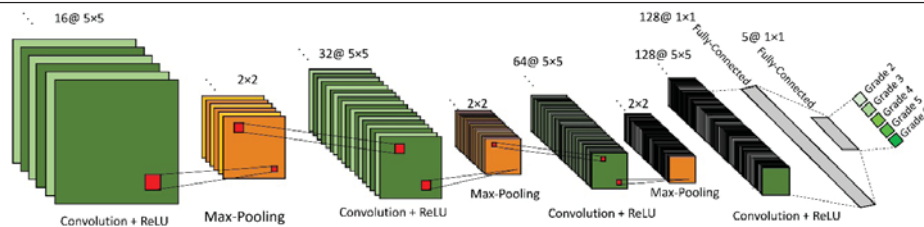


Figure 1. The architecture of the proposed convolutional neural network for bone age determination using wrist MRI