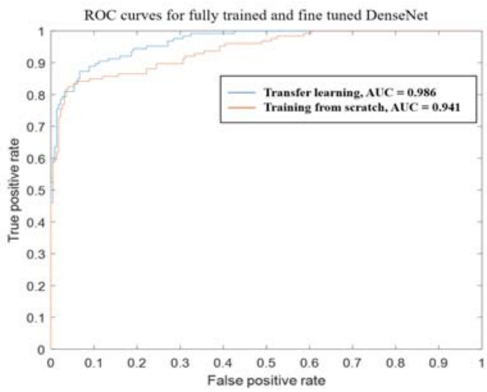

Figure 1. ROC curves for fully trained and fine tuned DenseNet

Conclusion: The results showed the superiority of the transfer learning approach in tumor classification. Higher statistical metrics with lower training time makes this approach more compatible with SWE images.

• 10.5812/IRANJRADIOL.99148

Segmentation of Diabetic Retinopathy Lesions in Retinal Fundus Images Using Multi-View Convolutional Neural Networks

Hassan Khastavaneh[1, *]; Hossein Ebrahimpour-Komleh[1]

[1]*Department of Computer and Electrical Engineering, University of Kashan, Kashan, Iran*

**Corresponding author: Department of Computer and Electrical Engineering, University of Kashan, Kashan, Iran. Email: khastavaneh@hotmail.com*

Abstract

Background: Diabetic retinopathy is one of the leading causes of blindness worldwide. Furthermore, it is considered the most important complication of diabetes mellitus, which creates various lesions in the retina at its different stages. Moreover, these lesions appear in different forms of hemorrhages, exudates, and microaneurysms. The count and type of these lesions can determine the severity and progression of the disease. Early detection of these lesions can lead to better treatment and blindness prevention. The accurate segmentation of these lesions is required to detect them and specify their counts and types. Since the manual segmentation of retinal lesions is tedious and time-consuming, automated segmentation is preferred. Furthermore, in screening programs where a large population needs to be considered, automated segmentation is inevitable. Therefore, automatic segmentation of retinal lesions is the first stage of any typical computer-aided diagnosis system for early diagnosis of the disease. Automated segmentation of retinal lesions is a challenging task due to the shape diversity and inhomogeneity existing in these lesions. Hence, more advanced segmentation techniques capable of modeling lesion complexities are required to tackle difficulties regarding the automated segmentation of diabetic retinopathy lesions in retinal fundus images.

Objectives: In this study, we proposed an automated pixel-based method for the segmentation of different types of lesions on the retinal fundus images.

Methods: This method utilized convolutional neural network with a particular architecture to describe and label the pixels of fundus images as either normal or lesion. The proposed method had four phases of pre-processing, view generation, segmentation, and post-processing. The pre-processing stage attempted to enhance input images for better segmentation. In the view generation phase, multiple views that described a pixel form different perspectives were extracted for all pixels on images. The segmentation phase, which indeed was a convolutional neural network capable of handling multi-view data, received multiple views corresponding to each pixel and decided if it belonged to a normal or a lesion area. The segmentation network with its unique architecture could handle diversities and complexities existing in the retinal lesions, leading to accurate segmentation. Finally, the post-processing phase refined the segmentation results by reducing false positives. In addition to segmentation, the proposed method detected lesion types in the segmentation process.

Results: The proposed method was implemented and its performance was evaluated using standard performance measures including accuracy, sensitivity, specificity, dice similarity coefficient, and Jaccard coefficient. The segmentation network was trained with 54 images and tested with 27 images. The experimental results were very promising and comparable to the state-of-the-art methods of fundus lesion segmentation.

Conclusion: A method based on convolutional neural networks for the segmentation of retinal lesions on fundus images was proposed. Alongside the promising experimental results, the method could jointly produce different lesion masks for different lesion types as a significant functionality.

• 10.5812/IRANJRADIOL.99144

Abnormality Detection in Musculoskeletal Radiographs by DenseNet and Inception-v3

Zahra Rezaei[1, *]; Behnaz Eslami[2]; Hossein Ebrahimpour Komleh[1]; Kaveh Daneshmand Jahromi[3]

[1]Department of Computer and Electrical Engineering University of Kashan, Kashan, Iran

[2]Department of Computer Engineering, Science and Research Branch, Islamic Azad University, Tehran, Iran

[3]Industrial Management Institute (IMI), Tehran, Iran

*Corresponding author: Department of Computer and Electrical Engineering University of Kashan, Kashan, Iran. Email: z.rezaei2010@gmail.com

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

• 10.5812/IRANJRADIOL.99149

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

Fattane Pourakpour[1, *]; Hassan Ghassemian[2]; Ramin Nateghi[3]

[1]National Brain Mapping Laboratory, Tehran, Iran

[2]Image Processing and Information Analysis Lab, Faculty of Electrical and Computer Engineering, Tarbiat Modares University, Tehran, Iran

[3]Department of Electrical and Electronics Engineering, Shiraz University of Technology, Shiraz, Iran

*Corresponding author: National Brain Mapping Laboratory, Tehran, Iran. Email: fattane.pourakpour@gmail.com

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