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Deep learning for enhancing cancer identification and diagnosis

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Abstract. One of the promising and significant fields of technology is the use of automated computer techniques, particularly machine learning, to facilitate and enhance medical analysis and diagnosis. In the area of artificial intelligence (AI), deep learning techniques using artificial neural networks (CNNs) – so-called because they superficially resemble biological neural networks - are computational network models for discovering large, high-dimensional data sets (such as medical datasets) for complex structures and patterns. In this paper, the focus is on summarizing contemporary applications of various deep learning algorithms in the direction of cancer identification and diagnosis, and on re-implementing supervised learning for cancer detection after a new database based on the lung cancer detection project from the book Deep Learning with PyTorch. The automatic detection of lung malignancies from patient CT scans was re-implemented by deep learning. In this paper, the technique is applied to data provided by the Iraqi Oncology Teaching Hospital. The author demonstrates that the application of the new data will also maintain the accuracy of the identification, and thus promises to develop into a more comprehensive and general cancer detection and diagnosis method in the future as the algorithm and technology are further refined.

Keywords: deep learning, cancer identification, PyTorch, LUNA model.

1. Introduction

One of the top causes of death in the world is cancer. Cancer research and treatment are a challenge for both doctors and researchers. In the United States, 609,360 cancer deaths and an estimated 1.9 million new cases of the disease are predicted in 2022 according to the American Cancer Society [1]. Deep learning, as a powerful machine learning algorithm, can undoubtedly contribute to attacking cancer. There are two primary sections of this article. Firstly, in the section on related work, deep learning algorithms applied to various cancers today are investigated and summarized. The second part is a learning network that automatically identifies lung lesions by analyzing the image processing of patient CTs. It is performed through deep learning using a lung cancer dataset which is collected in the autumn of 2019 at the specialist hospital (IQ-OTH/NCCD) for three months. This method allows for the effective identification of malignant nodules in the lung. The significance of the project is to reduce the pressure of manual testing. This approach will undoubtedly detect lung cancer earlier, thus significantly improving the survival of patients and contributing to the detection and diagnosis of lung malignancies, especially in the comprehensive population-wide scenario.

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2. Related work

2.1. An overview of deep learning

A unique method of learning from data through consecutive layers is called deep learning, a subfield of machine learning. The depth of the model is the total number of layers in the data model. Hierarchical representation learning and layered representation learning are other names for this discipline. In recent years, modern deep learning generally has dozens or even hundreds of subsequent representation layers that are all automatically learned from the training data due to improved computational capacity. Other machine learning techniques, on the other hand, frequently concentrate on learning only with one or two layers of data representation and are hence also known as shallow learning [2].

2.2. The field of cancer diagnosis

There are breast, lung, brain, and skin cancer, and in this paper, lung cancer will be discussed. To save as many lives as possible, early cancer detection is of utmost priority. Asymmetry, boundary, color, the seven-point test, diameter (ABCD), Menzies, and pattern analysis are some of the diagnostic techniques used in the field of cancer [3]. Doctors often use them to diagnose cancer, although they are not considered very effective in getting better performance [4]. However, the majority of the time, these forms of tumors are diagnosed manually and through visual inspection. This manual approach to medical image interpretation takes a lot of time and is susceptible to mistakes [5].

2.3. Related deep learning research for cancer

Early in the 1980s, computer-aided diagnosis (CAD) systems were developed to help doctors interpret medical images more quickly and accurately. Feature extraction is a crucial step in earlier picture learning [6]. Different feature extraction methods for different types of cancer have been refined thanks to the efforts of researchers [7]. At present, the main deep learning technologies include convolutional neural networks (CNN), generative adduction models (GANs), cyclic neural networks (RNNs), long- and short-term memory (LTSM), deep autoencoder (dan), stacked autoencoder (SAE), convolutional autoencoder (CAE), restricted Boltzmann machine (RBM), and multi-scale convolutional neural network (M-CNN) and multi-instance learning convolutional neural network (MIL-CNN) [8].

However, these feature extraction-based methods have weaknesses [9]. Besides, unsupervised autonomous network learning methods have also been used in the field of cancer to address these issues and enhance performance. For example, unsupervised learning has begun to be used in the detection of cancer and how to analyze cancer types from gene expression data [10]. This method improves the detection and diagnosis of particular diseases by applying different data on the likelihood of cancer kinds to automatically form features as opposed to earlier cancer detection methods. And the method has been used to detect and classify cancer types based on gene expression [11].

This paper's second part offers a fundamental framework for how machine learning functions in medical imaging, along with a practical illustration of pre-processing, image segmentation, and post-processing.

3. An example of a lung cancer test

3.1. Method

Supervised learning, unsupervised learning, self-supervised learning, and reinforcement learning are the four primary disciplines of machine learning. Of these, supervised learning is the most typical kind and, in addition to mainly including classification and regression, also includes other niche variants such as sequence generation, syntax tree prediction, object detection, and image segmentation [12]. The lung cancer identification method used in this paper is also supervised learning, as shown in Figure 1.

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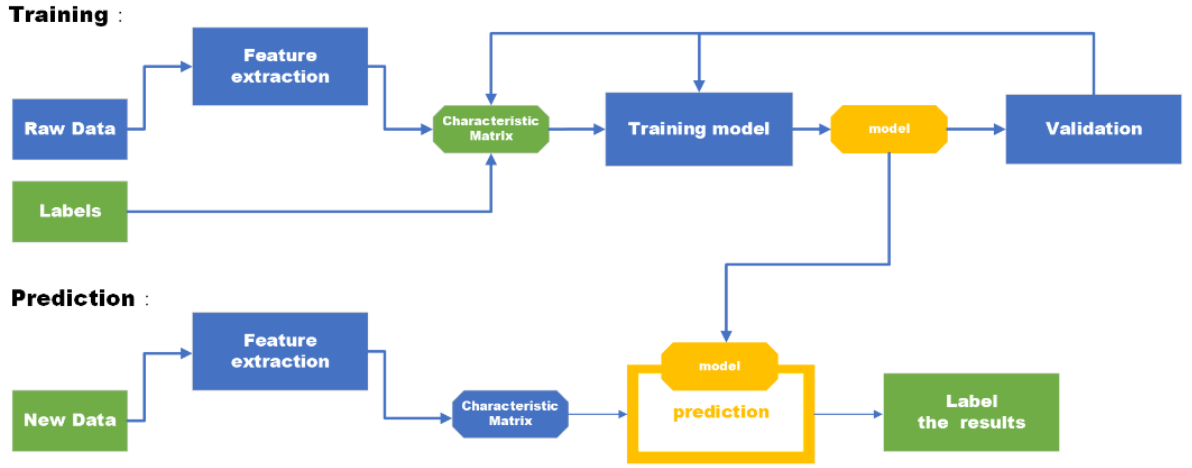

Figure 1. Supervised learning is divided into the training stage and the prediction stage. The purpose of the training stage is to get the training model, while the purpose of the prediction stage is to use the training model to predict the input data.

First, the original and additional CT datasets are loaded, and their data formats are converted. Potential tumor voxels in the lung are then identified by segmentation techniques, while other extraneous anatomical structures are ignored. The voxels are further analyzed and grouped into blocks to find candidate nodules. Pulmonary nodules are nodular shadows of non-normal lung tissue detected by chest CT, distinguished by shadow size as microscopic nodules (less than 5 mm in diameter), small nodules (5-10 mm), and nodules (10-30 mm in diameter). The rough center of each point was found in the heat map. The candidate nodules were then integrated into the actual nodules by 3D convolution. Finally, a joint classification of individual nodules is used to diagnose the patient, and the analysis of the imaging data attempts to determine whether the nodule is benign or malignant [13]. As Figure 2 shows:

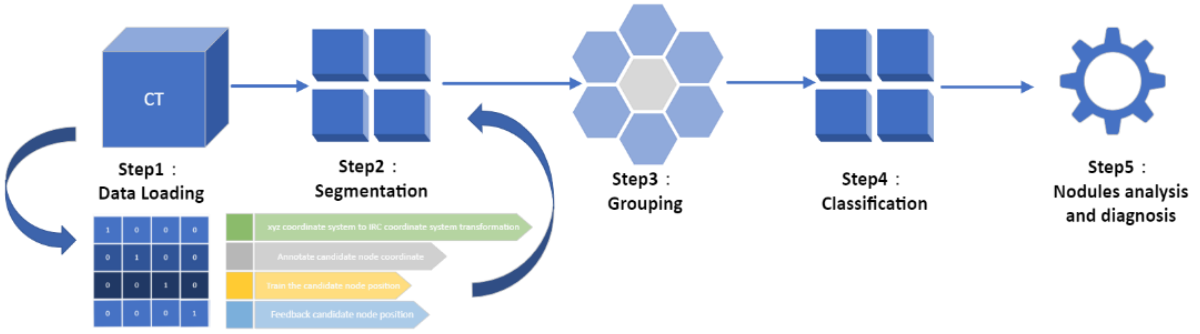

Figure 2. Project implementation method.

3.2. Two core models

3.2.1. The classification model. To further work with the data, a nodal classification model and a training loop were first built. The data was provided for the data loader instances via the Ct and Dataset classes (which load data from disk and provide access to the cropped regions around the points of interest). At the same time, these instances will also provide data for the classification model via training loops and validation loops.

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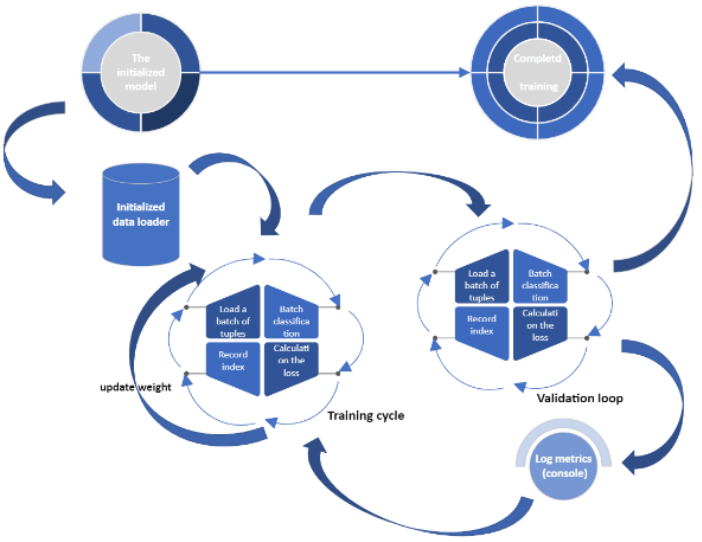

Figure 3. Train and validate scripts.

In the tail of the classification model structure, the first several layers of network input need to be processed. These early layers often had a different structure or organization than the rest of the network because they had to transform the input into the form expected of the master. A simple batch specification layer is used, whose tail contains a convolution layer, which allows large down sampling of the image size.

Figure 4 depicts a CNN, a feed-forward neural network. In this scenario, the signal is handled directly without any loops or cycles. The formula for this is:

$$G(X) = g_N\left(g_{N-1}(\ldots(g_1(X)))\right) \tag{1}$$

where X denotes the input signal, N denotes the number of hidden layers, and gN means the function for layer N. A function g with numerous convolutional kernels (h1,... hk-1, hk) makes up the convolutional layer of a basic CNN model. Each hk represents a linear function in the kth kernel, which is illustrated as follows:

$$h_k(x,y) = \sum_{s=-m}^{m} \sum_{t=-}^{n} \sum_{v=-d}^{w} Vk(s,t,v)X(x-s,y-t,z-v) \tag{2}$$

where (x, y, z) denotes a pixel's location in the input X, m denotes the height, n the width, w the depth of the filter, and Vk the weight of the kth kernel.

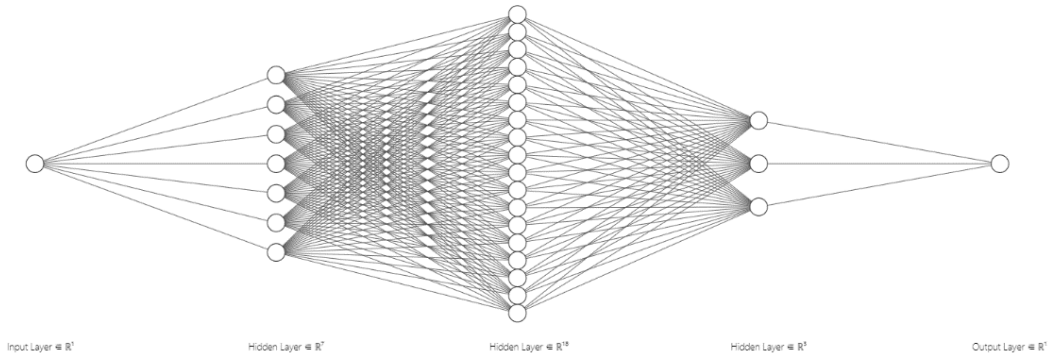

Figure 4. General convolutional neural networks.

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3.2.2. The segmentation model. Having successfully built a classification model, the data is now still unavailable. However, a method is still needed to tell the classifier where to look. The original CT scans that were acquired need to be taken in an attempt to find all possible nodules. And to find the possible nodules, those voxels in them that look like part of a nodule need to be flagged. This process is called segmentation. The architecture of the second segmentation model allows for pixel-by-pixel labeling or segmentation to be performed. Here an already existing segmented U-NET model is added to the segmented model. U-Net was created by O.Ronneberger for the segmentation of biological images. They contain two distinct pathways in the design. Since it preserves the context of the image, the initial contraction path is referred to as an encoder. The majority of this stack consists of convolution and pooling layers. The second approach, also referred to as a decoder and using transposed convolutions to provide exact localization, is the symmetric expanding path. There are no thick layers and only convolutional layers in this end-to-end FCN network. Therefore, images of any size may be accepted.

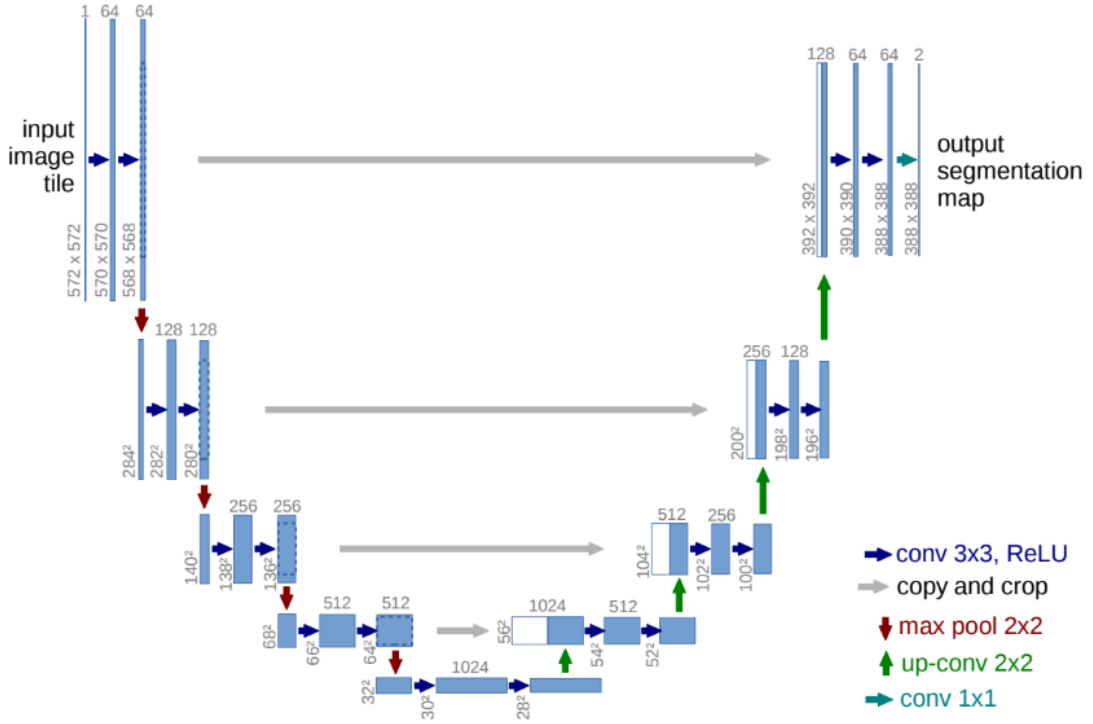

Figure 5. U-net architecture (example for 32x32 pixels in the lowest resolution). Each blue box corresponds to a multi-channel feature map. The number of channels is denoted on top of the box. The x-y-size is provided at the lower left edge of the box. White boxes represent copied feature maps. The arrows denote the different operations [14].

3.3. Points worth noting

The additional dataset (IQ-OTH/NCCD) [15] includes CT scans of lung cancer patients at various stages, as well as healthy subjects. At the center, radiologists and oncologists identified IQ-OTH/NCCD slices. 1190 pictures taken from slices of 110 CT scans make up the dataset. These instances were divided into three groups: benign, malignant, and normal cases. Of them, 40 instances have been determined to be malignant, 15 cases to be benign, and 55 cases to be normal cases.

4. Experiment result

As the CTs used this time came from a fixed set of 110 patients examined over time, the detection results were partially enhanced relative to the original experimental results, but there were still false positive

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results. Of the 100 CTs used for the detection set, 47% of malignant nodules were detected, of which about 85.1% were correctly labeled [9], and a comparison of the two results is shown in Figure 6. This is already an impressive improvement over the previous accuracy of 70%. And of the seven images where the test was incorrect, five of them were from patients with benign tumors and two from normal people. This suggests that if training can be done using previous image data from individual patients, it will greatly improve the recognition of malignant tumors.

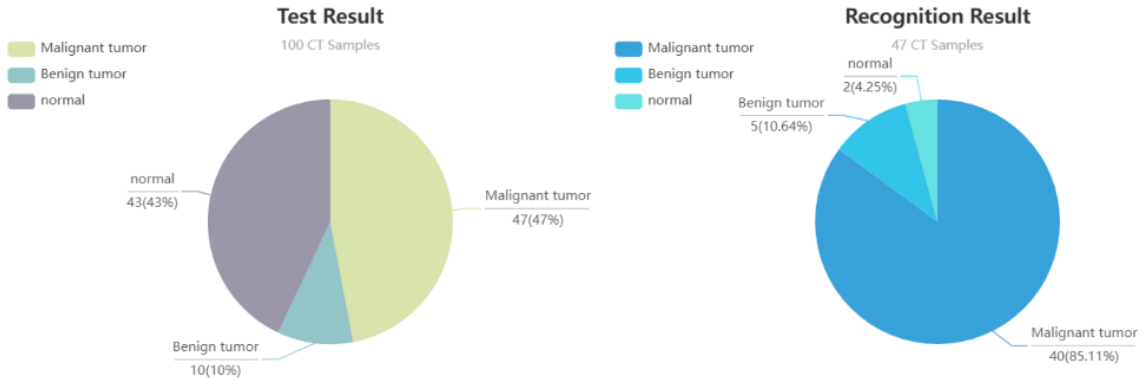

Figure 6. Result of Test.

5. Discussion

The results illustrate that the model still has difficulty in identifying between malignant and benign tumors. However, it also reveals that the ability to identify malignant tumors could be greatly improved if training could be carried out using previous image data from individual patients. In the future, it would be possible to keep everyone in the habit of regular medical check-ups and to synchronize everyone's medical data with various deep learning network models, after which doctors would judge the filtered data and add the results to the training of the models. This model is undoubtedly a virtuous circle and would apply to training various other related neural networks. But the fact is that when faced with large amounts of population data, the storage of existing training data, not to mention the time required to train the models, becomes a new problem. So the question of how to make the models more generalizable and efficient remains a problem to be solved. The first step in turning intriguing research into useful products is training models. It still has a long way to go from clinical validation to regulatory approval. But countless researchers have made a very promising start hoping that, by sharing this work, the progress in this area can be accelerated.

6. Conclusion

Deep learning will surely aid in the identification and treatment of cancer. A number of new algorithms and approaches are being developed to recognize and diagnose different types of cancer. The results of the tests done in this paper show that the accuracy of the experiments is still meaningful and has improved compared to the original experimental results by using the new dataset, which proves that the model is generalizable and somewhat enlightening.

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