

Viral and bacterial pneumonia Detection in x-ray images using artificial neural networks

Detección de Neumonía viral y bacteriana en imágenes de rayos x utilizando redes neuronales artificiales

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Abstract

This paper presents the experiments and results on the viral and bacterial pneumonia identification, which were obtained by means of image processing techniques and artificial neural networks. The objective of this research is to reduce the patient's waiting time to obtain the result of the x-rays diagnosis of a pulmonary disease of pneumonia. At the time of this writing, pneumonia is considered the most common cause of infant mortality in the world, responsible for 15% of all deaths in children under 5 years. To obtain the classifier model we start from the detection in the pulmonary region through digital image processing and obtaining the characteristics in the segmented images, discriminating against those that provide a diagnosis through Gray Level Co-occurrence Matrix (GLCM). Finally, those features are used as the description in the classification of images such as: healthy, viral pneumonia and bacterial pneumonia. We use a total of eight features: autocorrelation, contrast, cluster prominence, variance cluster shade, sum of entropy, difference of entropy and number of pixels. These characteristics were used to model and train an artificial neural network Backpropagation, obtaining results that are presented in their confusion matrix along with the accuracy percentage obtained.

X-Ray, Pneumonia, Backpropagation

Resumen

En el presente artículo se presentan los experimentos y resultados obtenidos en la identificación de neumonía viral y bacteriana mediante técnicas de procesamiento de imágenes y redes neuronales artificiales. El objetivo de esta investigación es reducir el tiempo de espera del paciente para obtener el resultado del diagnóstico de rayos X en la enfermedad pulmonar de neumonía. En la actualidad la neumonía se considera la causa más común de mortalidad infantil en el mundo, responsable del 15% de todas las defunciones en menores de 5 años. Para obtener el modelo clasificador partimos de la detección en la región pulmonar a través de procesamiento digital de imágenes y la obtención de las características en las imágenes segmentadas, discriminando aquellos que nos proporcionen un diagnóstico a través de Gray Level Co-occurrence Matrix (GLCM). Finalmente, dichas características son utilizadas como la descripción en la clasificación de imágenes como son: predictores en la clasificación y diagnóstico de las imágenes: Sin Neumonía (sano), Neumonía Viral y Neumonía Bacteriana. Usamos un total de ocho características: autocorrelación, contraste, cluster prominence, varianza, cluster shade, suma de entropía, diferencia de entropía y número de píxeles. Dichas características fueron utilizadas para modelar y entrenar una red neuronal artificial, obteniendo los resultados que se ven expresados en su matriz de confusión con el porcentaje de clasificación obtenido.

X-Ray, Neumonía, Backpropagation

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1. Introduction

The National Heart, Lung and Blood Institute (Institute, 2018) defines pneumonia as a bacterial, viral or fungal infection of one or both sides of the lungs that causes the alveoli to be filled with microorganisms, inflammatory cells or fluids, which cause an abnormal dysfunction of the lungs. Symptoms may worsen in children under five years of age, which is why it is considered the main cause of infant mortality in the world, responsible for 15% of all deaths in children under 5 years. The World Report on Pneumonia of the World Health Organization (Health, 2016) addressed that the prevention and diagnosis of pneumonia is of fundamental importance for the reduction of infant mortality. Chest X-ray remains the most important diagnostic method that is easily accessible, fast, economical and effective. However, to discriminate between bacterial pneumonia and viral pneumonia, it is difficult to find the diagnosis based on X-rays, which is why the specialist requires more specific tests such as laboratory tests, which implies a greater expenditure of both time and money. Nevertheless, chest images contain abundant noise caused by the thoracic cage, the clavicle, the complex lung structure, the position of the arms at the time of obtaining the radiograph and the subtle texture on the chest radiograph. Segmentation of the region of interest, in this case the lung area, will be a preliminary step to detect the type of pneumonia that the patient presents. The purpose of this document is to establish a tool for analysis of pneumonia infections using algorithms for processing infected and normal X-ray images from the segmentation and extraction of characteristics with the GLCM method; its study is linked to certain works and applications that will be mentioned throughout the document.

2. Related Works

The growth in the field of digital image processing in medical images has given a new dimension to the detection and diagnosis of diseases. Standard chest radiography has been identified as the most complex imaging tool. However, there are different techniques for both segmentation, as well as the classification of lung diseases, which propose to detect lung regions in chest X-ray images contributing to an important component for diagnosis (Sema Candemir, 2014).

Other techniques apply two steps ranging from image enhancement and image filter, where the intensity and contrast of the X-ray image is adjusted to adapt the subsequent stages of processing, using histogram equalization (SR Abhishek Sharma, 2015). Other studies propose a computer-assisted system to identify bacterial and viral pneumonia, classifying it from an SVM support vector machine (Xianghong Gu, 2017).

For this study the main contributions are:

- Obtaining lung segmentation to develop a diagnosis and detection of pneumonia based on an image segmentation algorithm.
- Extraction of mathematical characteristics in the segmented image from the GLCM method.
- Training the neural network and compare models with different layers and neurons for image classification.

The acquired image is segmented from the combination of certain image processing algorithms that will be mentioned in the next section, followed by the calculation and extraction of features. A trained classifier will classify the chest X-ray image samples as healthy or not healthy. The work will culminate in making a final classification with not healthy images where the diagnosis of viral pneumonia and bacterial pneumonia occurs.

3. Data set

The standard digital image database created, *Chest X-Ray Images* (Features, 2018), is used for training and testing purposes; it is organized in 3 folders (train, test, val) and contains subfolders for each image category (pneumonia/normal) with a total of 84,495 X-ray images (JPEG) and 2 categories (pneumonia/normal). These chest X-ray images were selected from pediatric patients of approximately one and five years of the Guangzhou Women's and Children's Medical Center. All chest radiographs were performed as part of the usual clinical care of the patients. For the purpose of this work they were resized to 512x512 pixels and reduced to 8-bit gray scale levels. The database can be useful for various educational and research purposes, along with other demonstrations.

4. Feature Extraction

Feature extraction is the process of reducing the data size of each image by obtaining the necessary information from the segmented image. From the extracted characteristics it is possible to depend on the segmentation method and the extracted characteristics. In this work, the characteristic matrix is obtained using Gray Level Co-occurrence Matrix (GLCM) (Shijin Kumar P.S, Extraction of Texture Features using GLCM and Shape Features using Connected Regions, 2017). Images with Viral Pneumonia, Bacterial Pneumonia and Healthy have different characteristics. This variation in the values obtained by characteristics is useful for the classification of X-ray images. The values of the characteristics obtained will be delivered in a test and training classifier. From GLCM, it extracts the statistical characteristics of texture, where we will take 8 texture parameters such as: autocorrelation, contrast, cluster prominence, cluster shade, sum of entropy, difference of entropy, variance and number of pixels.

Texture parameters	Formula	Description
Autocorrelation	$\sum_{k=0}^{N-1-n} I(m, n + k)^2 I(m, k)^2$	Comparison of each pair of pixels to find the probability that their intensity is the same given a specific direction and distance.
Cluster Prominence	$\sum \sum (i + j - \mu - \mu)^3 X P(i, j)$	Asymmetry measurement which indicates whether the prominence value of the cluster is high, the image is less symmetrical and when the prominence value of the group is low, there is a peak in the GLCM matrix around the mean values.
Cluster Shade	$\sum \sum (i + j - \mu - \mu)^4 X P(i, j)$	Measurement of matrix asymmetry and is believed to measure the perceptual concepts of uniformity. A new $I + j$ image is created, with a range of integer intensities of 0 and $2(N g - I)$.

Texture parameters	Formula	Description
Variance	$\sum_{i=1}^N \sum_{j=1}^N (i - \mu)^2 p(i, j)$	Measures the dispersion (with respect to the average) of the gray level distribution.
Entropy sum	$- \sum_{i=1}^N \sum_{j=1}^N p x + y(i) \log [P x + y(i)]$	Measures the disorder related to the distribution of the gray levels of the image.
Entropy difference	$- \sum_{i=1}^N \sum_{j=1}^N p x - y(i) \log [P x - y(i)]$	Measures the disorder related to the distribution of the gray level difference of the image.

Table 1 GLCM texture parameter formulas

Where $p(i, j)$ is the probability of occurrence of the element (i, j) in the GLCM, L is the quantization level, and the vector $P_{x+y}(k) = \sum_{i=1}^L \sum_{j=1}^L P(i, j)$ for $k = 2, 3, \dots, 2L$.

For more information consult (P. Mohanaiah, 2013).

5. Methodology

This section details the proposed techniques for the detection of pneumonia which includes three stages: pulmonary segmentation, feature extraction and classification. The representation of the flow chart of our system is presented in Figure 1 and the mentioned steps are explained in detail.

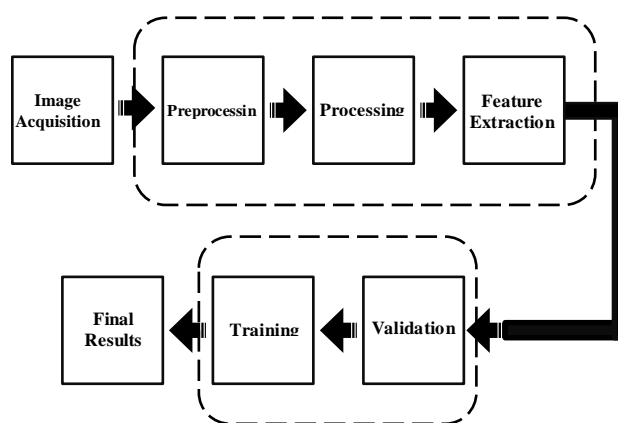


Figure 1 General Diagram

A. Pulmonary Segmentation

From the general diagram, we start in two blocks for the implementation and development of the project. The first stage corresponds to the methodology of digital image processing, as seen in Figure 2.

The image is acquired, a pre-processing and processing are carried out and at the end we obtain the segmented image, each of the mentioned processes will be described later.

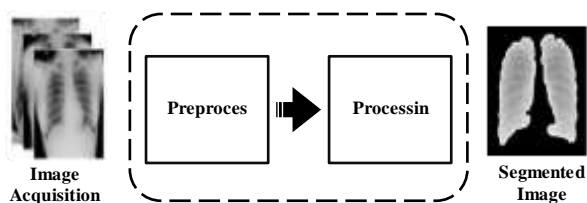


Figure 2 Diagram for image processing

The Matlab software was used to develop the algorithm. The contrast improvement method (The MathWorks, 2019) is used to optimize the performance of lung segmentation. We use a normalization method, which creates a certain independence of the image's properties, later a histogram equalization algorithm is used (Histeq, 2019), opting for Enhace contrast using histogram equalization (Histeq), where the lung area stands out best. The Otsu method (Otsu, 2019), unlike the pixel intensities of each region, separates the foreground image objects and the background image objects, illuminating the specific area. The input is a grayscale or color image and results in a binary image (in black and white) that indicates the segmented part. The preparation of the mask includes morphological measures, as well as the method of erosion, inversion, edge cleaning, removal of small objects and dilation. Figure 3 shows the methodological proposal for this section.

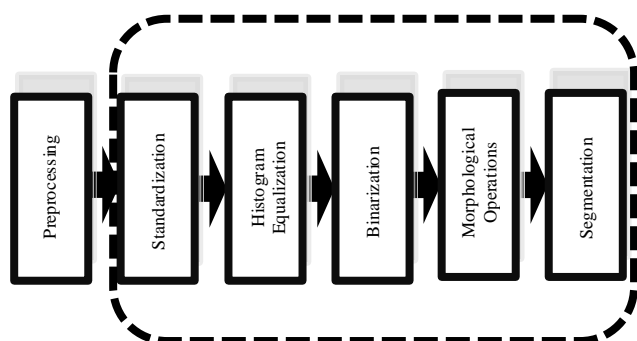


Figure 3 Methodological proposal

The segmented lung image is obtained by multiplying the mask by the original image, as shown in Figure 4, then delivered to the feature extraction stage.

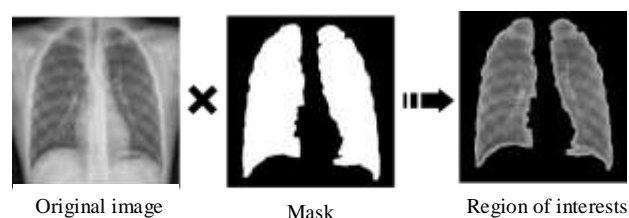


Figure 4 Lung segmentation

B. Feature Extraction using GLCM

The second stage corresponds to the extraction of the characteristics in the segmented image, in the third stage a training and validation is carried out from various tests to finally contribute to the expected result, as shown in Figure 5.

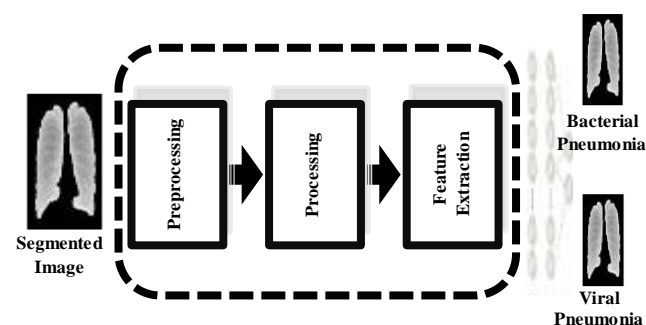


Figure 5 Diagram of the method of image classification

Gray Level Co-occurrence Matrix (GLCM) is calculated by counting the number of times that adjacent pixels have the same orientation (Shijin Kumar P.S, Extraction of Texture Features using GLCM and Shape Features using Connected Regions, 2017).

There are a total of 20 GLCM functions for each segmented region. The average value is calculated from eight basic features: autocorrelation, contrast, prominence cluster, cluster shade, entropy sum, entropy difference, variance and number of pixels. The data that gave us the best results were those shown in Table 2, where the result with the greatest difference was the one considered.

Features	Healthy/Not Healthy
Autocorrelation	5541.45
Contrast	4267.8
Cluster Prominence	629858000
Cluster Shade	1104369
Variance	91345.1
Entropy sum	23203.5
Entropy difference	4267.8

Table 2 Data used for feature extraction

With the features that make up elements for the discrimination of results, an 8x30 training matrix is created for general training and 8x15 for general validation (Healthy/Not healthy). And 8x20 for specific training and 8x10 for specific validation (viral pneumonia/bacterial pneumonia). Figure 6 shows the creation of the input matrix.

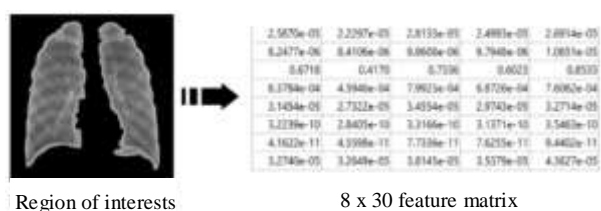


Figure 6 Steps to create the characteristics matrix

C. Classification with Backpropagation

The neural network has two operation techniques: training and validation (Rahmati, 2014). The training set consists of 30 images: 10 healthy images and 20 not healthy images, giving a 30x8 matrix for training the neural network. The validation set consists of a total of 15 images: 5 healthy images and 10 not healthy images. All data corresponds to the information that flows through the network in the learning phase. The learning algorithm used is Backpropagation, which was already mentioned above as a supervised learning algorithm. This learning algorithm applies to multilayer advance networks that consist of processing elements (neurons) with continuous differentiable activation functions (tan-sigmoid and log-sigmoid). Matlab offers specialized libraries to work with neural networks through its tools and functions for managing large data sets. Figure 7 shows the distribution of the classification.

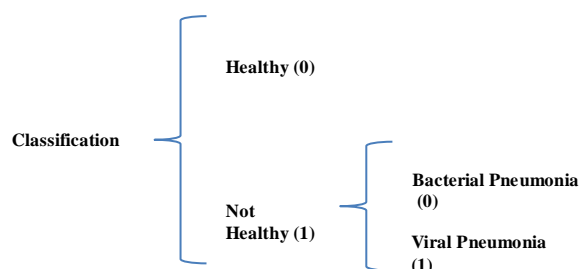


Figure 7 General diagram of the distribution for classification

The trained set of the Healthy images are labeled as class 0 and the Not-Healthy images are labeled as class 1.

In turn, the not healthy images are divided into the subclasses Viral Pneumonia class (1) and Bacterial Pneumonia class (0).

6. Results

The purpose of the segmentation stage was to isolate the anatomical regions of interest from the medical image; for this purpose contrast enhancement techniques and morphological methods were used to reduce noise such as shadows on clavicles and spine. The learning phase was carried out following the Backpropagation technique using a subset of the Chest X-Ray Images (84,495 images). The subset of data (45 images in total) was divided into 30 (66.7%) training elements and 15 (33.3%) validation elements. All images were resized to a size of 512x512 pixels.

The final result for the segmentation part is seen in Figure 8.

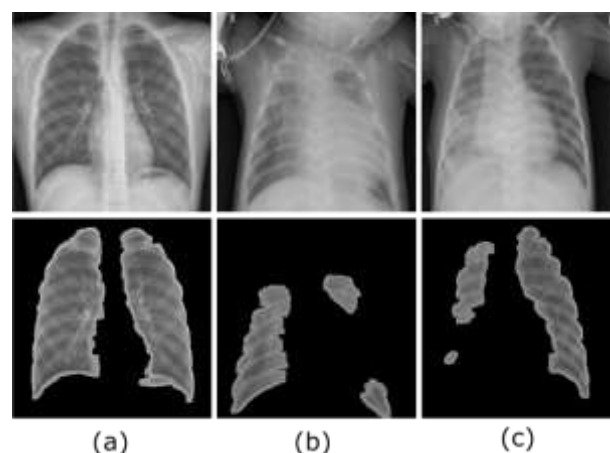


Figure 8 Segmented image of a healthy lung (a), lung with viral pneumonia (b) and lung with bacterial pneumonia (c)

Not all images of Chest X-Ray Images worked and gave us the ideal result. 75 samples were contemplated by selecting 45 which did not lose fundamental information when processed. In the failed cases we lost a part of the lung or the entire pulmonary region, or the opposite happened, where more information was leaked, for example clavicles, shoulders etc. As shown in Figure 9.

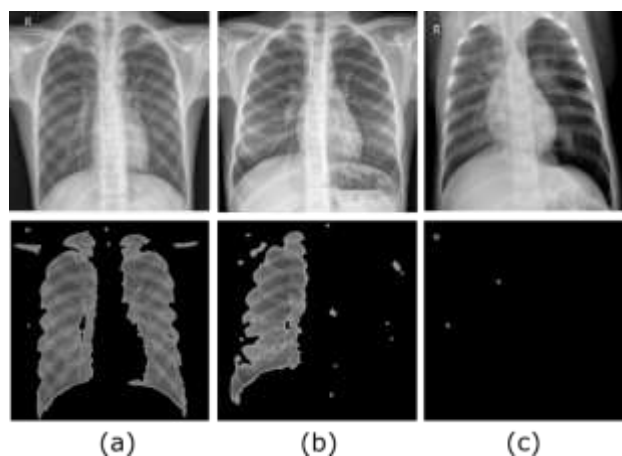


Figure 9 Image of lungs and clavicles (a), image with a single segmented lung (b) image with no segmentation

The RNA architecture based on the Backpropagation training technique is divided into two tests: the first to classify between healthy and not healthy lungs, the second is to classify not healthy lungs in bacterial pneumonia and viral pneumonia.

A. Classification Healthy/Not healthy

Before starting the training of the neural network for the first classification, our parameters were established as: 10,000 times, performance objective of 0.01 and a learning rate of 0.1. The architecture consisted of 8 inputs, 1 output layer and a varied number of hidden layers and the neurons that made them up. Table 3 shows some of the best models and results obtained in the training and validation stages, taking into account the number of layers and neurons, as well as their classification, both correct and incorrect.

Tests No.	Layers and Values	Correct Classification	Incorrect Classification
1	[16,32]	66.66%	33.33%
2	[16,32,64]	80%	20%
3	[20,32,64]	80%	20%
4	[16,32,64]	86.66%	13.33%
5	[5,20,25]	80%	20%
6	[5,15,20]	80%	20%
7	[5,10,15]	86.66%	13.33%

Table 3 Healthy / Not healthy RNA Test

Model 4 and 7 of Table 3 of RNA designed in Matlab, gave us the best classification result for HEALTHY/NOT HEALTHY image recognition. The first model is composed of 8 inputs, three hidden layers with [16 32 64] neurons and one output layer.

The second best model made use of fewer neurons in its hidden layer, which decreases the time in the processing and resources of the PC, is made up of 8 inputs, three hidden layers with [5 10 15] neurons and one output; so far it is taken as the best model, since it obtains good results using fewer resources.

The confusion matrix of each of the models can be seen in Figure 10, where we will only show the prediction of the Second model (test number 7), which obtains 3 True Positives (TP) and 2 False Negative (FN), for the other test we obtained 0 False Positive (FP) and 10 True Negative (TN).

3 20.0%	0 0.0%	100% 0.0%
2 13.3%	10 66.7%	83.3% 16.7%
60.0% 40.0%	100% 0.0%	86.7% 13.3%

Figure 10 Confusion matrix of the general classification

B. Classification Bacterial Pneumonia / Viral Pneumonia

Table 4 shows some of the tests performed for the classification of not healthy images (Bacterial Pneumonia/Viral Pneumonia), with parameters of 10,000 times, learning rate of 0.1 and a performance objective of 0.01 for each of the tests, these being the same parameters that were stipulated in the beginning.

Tests No.	Layers and Values	Correct Classification	Incorrect Classification
1	[16,32]	50 %	50 %
2	[16,32,64]	80%	20%
3	[20,32,64]	70%	30%
4	[20,35,64]	70%	30%
5	[16,32,64]	90%	10%
6	[10,20,25]	60%	40%
7	[5,15,20]	70%	30%
8	[5,10,20]	70%	30%

Table 4 Bacterial / Viral Pneumonia RNA Test

Of the tests carried out, test 2 and 5 of Table 4 of RNA designed in Matlab gave us a better classification result for image recognition Bacterial Pneumonia/Viral Pneumonia. The tests contain 8 inputs, three hidden layers with [16 32 64] neurons and one output layer.

Figure 11 shows the structure of our RNA

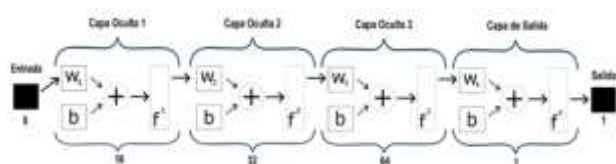


Figure 11 RNA architecture for the NOT HEALTHY classification

We will only expose the model that obtained the best performance (test 5): its confusion matrix (Figure 13) shows results in positive predictions of 5 TP and 0 FN, for negative predictions 1 FP and 4 TN, obtaining only a bad prediction in the Classification of Viral Pneumonia, which discriminated it as Bacterial Pneumonia, this classification had a percentage of 90% of success.

5 50.0%	1 10.0%	83.3% 16.7%
0 0.0%	4 40.0%	100% 0.0%
100% 0.0%	88.0% 20.0%	90.0% 10.0%

Figure 12 Confusion matrix of the specific classification

A supervised training was carried out where the known set of input-output data was used to adjust the weights of our network. As in the previous model, the performance objective was set at 0.01 for greater accuracy and a total number of 10,000 times. Under these parameters, it was avoided to reach overtraining, that is, a state in which the network adapts so perfectly to the training set that it is unable to generalize and correctly classify new images.

Conclusions

In this paper, the implementation of a diagnosis system of viral and bacterial pneumonia through X-ray images, using digital image processing was proposed, some of our images did not give the expected results, so the decision was made to manually select those images that allowed us to filter the pulmonary region of interest. However, it is proposed an improvement in the image processing algorithm that is deeper than generalize any image that enters and can process it in the broadest way.

For texture extraction, texture analysis using the Gray-Level Cooccurrence Matrix (GLCM) was used, which, through statistical methods, examines the texture that considers the spatial relationship of the pixels in the co-occurrence matrix of the level of gray. Data were chosen that pronounced a considerable difference between the HEALTHY and NOT HEALTHY data. It was the best solution to achieve significant changes in our training network compared to the results obtained in validation.

The methodological tests carried out at work have shown that, through the results expressed in the suggested articles, we achieved good results; the tests corresponding to processing have details for the Chest X-Ray Images file. Therefore the search for the improvement of the algorithm is proposed, as well as cross-validation and use of deep learning with deep convolutions neural networks to compare their results with the proposed method.

The model will help to provide solutions in the area of Health Sciences and patients with a pneumonia pattern with their respective radiography. The type of pneumonia they are presenting will be detected at the time and will also save time in diagnosis as well and it will imply an additional expense. Regarding the specialist, now they will have a tool that will help them, when giving such diagnoses.

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