Segmentation and classification of medical images

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1. Abstract

In this case study is presented a method of segmentation and classification of medical images, specially X-rays of healthy and diseased lungs. In the segmentation process it was used different kinds of methods such as: thresholding, contour detection, morphological operations such as opening, erosion for isolating the lungs section from the rest of the image and for better visualisation. Likewise, masks are used for identifying the bounding box. The code was implemented using Python with the OpenCV and Numpy libraries for more efficient processing.

For the classification part, the standard deviation is used to calculate the contrast and the size of the segmented white pixel arias. The images are classified as healthy, sick or undefined depending on the results obtained.

2. Introduction

Pneumonia is an inflammation of lung tissue caused by bacteria, viruses or other microorganisms. The cause of the infection, the patient's age and general health can determine how severe it can affect them and whether one or both lungs will be affected. Some symptoms of this disease are: productive cough, fever and chills, chest pain and difficulty breathing, fatigue.

SARS-CoV-2 causes COVID-19 and produces respiratory infections ranging in severity from moderate to severe and can even lead to death. Common symptoms include: fever, dry cough, fatigue, sore throat, loss of sense of taste and smell.

These two diseases are increasingly common, especially in the cold season, and manifest themselves very similar. Identifying and treating them early can make all the difference, especially in cases patients also suffer from chronic conditions.

Early detection of cases in their early stages could help save many lives and analysing images can take a long time. Image processing helps radiologists.

3. Methods

a. Data set

For making this project we needed more data sets: healthy lungs [1], with covid [2] and with pneumonia [3]. This data set is divided in three categories for identifying and differentiating the healthy lungs from the ones affected by a disease. The data set has a large number of images.

b. Preprocessing

In order for the algorithm to be efficient and run faster, all the images from the data set were resized, so all of them were the same size 244x244 pixels. We used a separate function that takes the images from the folder, processes them, and after the execution, we have them in a new folder, so they don't get mixed with the original data. Next, we made a function to visualise the histogram of the original image to constrain differences of the grey levels of different kinds of lungs. This aspect will help us later for the classification part.

c. Segmentation

The process of lung segmentation includes using different functions from the OpenCV library. First of all, we used adaptive thresholding for binarization, obtaining just black and white images. This method assumes replacing every pixel in the original image with a black pixel if its intensity is lower than the thresholding value, or with a white pixel if its intensity is higher. Because it is an adaptive method, the thresholding value is calculated on smaller parts from the image, this way we obtain different values for different regions. This way, the results are better because the images are illuminated differently. We also tried with a fixed value for the entire data set , but it was found that the adaptive method performs better.
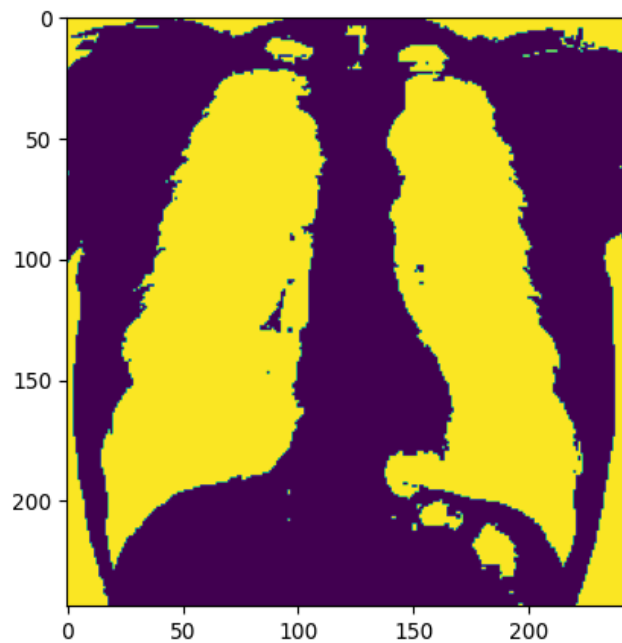
Following up, we used a few functions for dilatation, erosion and opening for reducing the noise from the image.
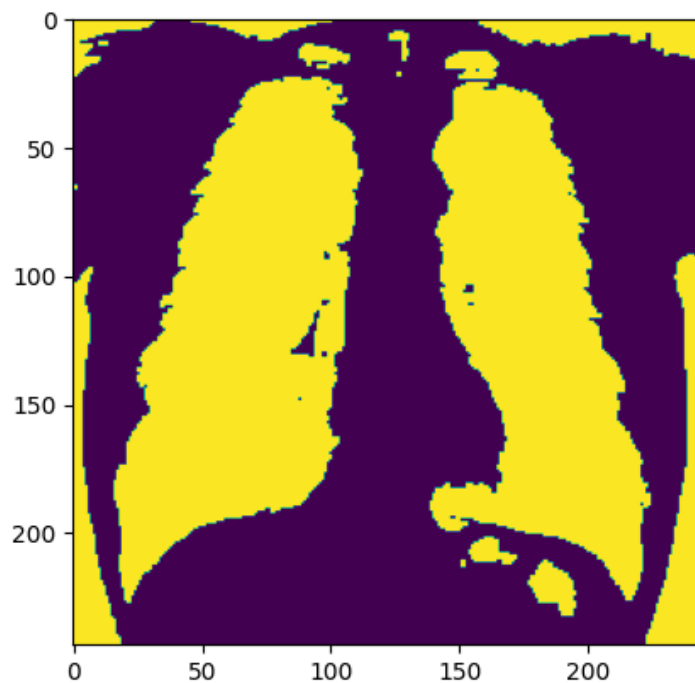

After this, a mask for contour is created, applied on the binarized image. This step is necessary for a better delimitation of the interes region from the rest of the objects from the image.
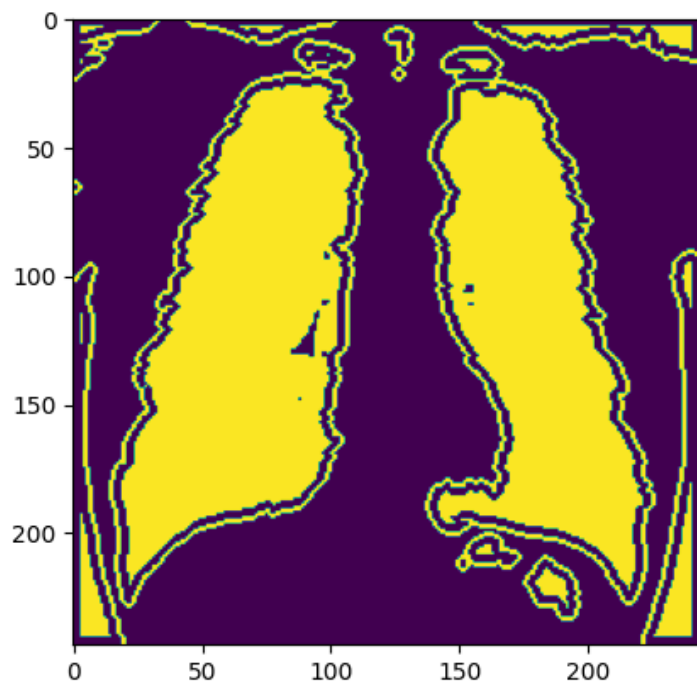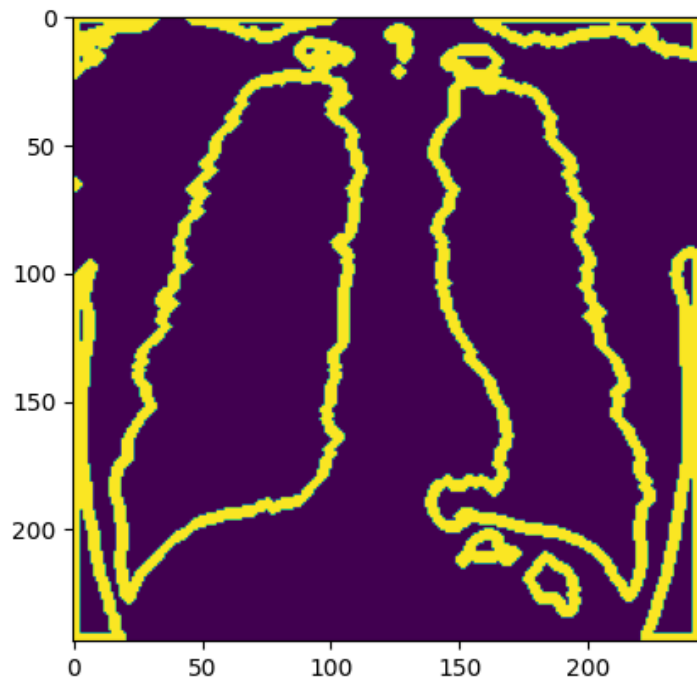
In the following step we removed regions from the images which were too close to the edges: we divided the image in two regions equal through the OY axe, left and right. Every region is labelled with the help of a bounding box. If a label is found halfway distance on each of those

regions, then it will be taken into count. In general, the lungs occupy a large space in the image and they are positioned in parallel, vertically.
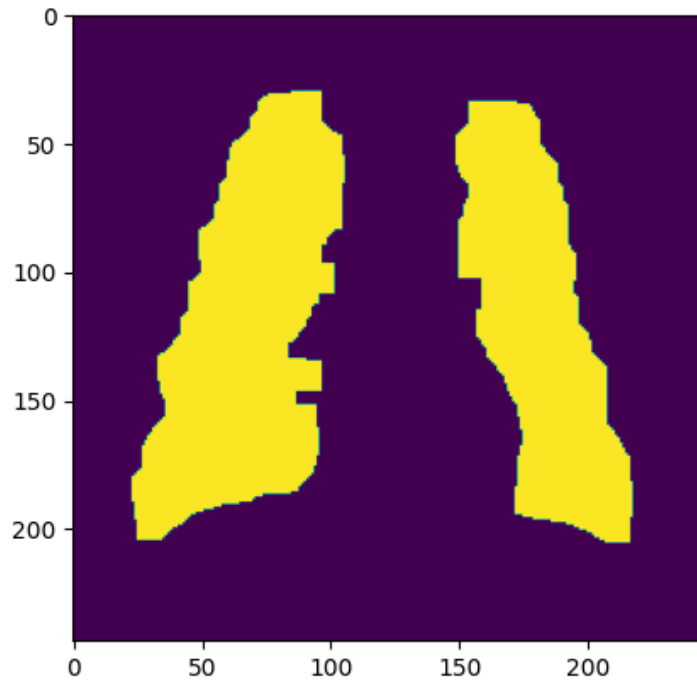
Because the lungs were segmented from the rest of the image, inside of them remained a few patches (remains from bones or pieces that were lost in thresholding) which must be completed so that the lungs are as whole as possible with the help of morphological operations also mentioned above.
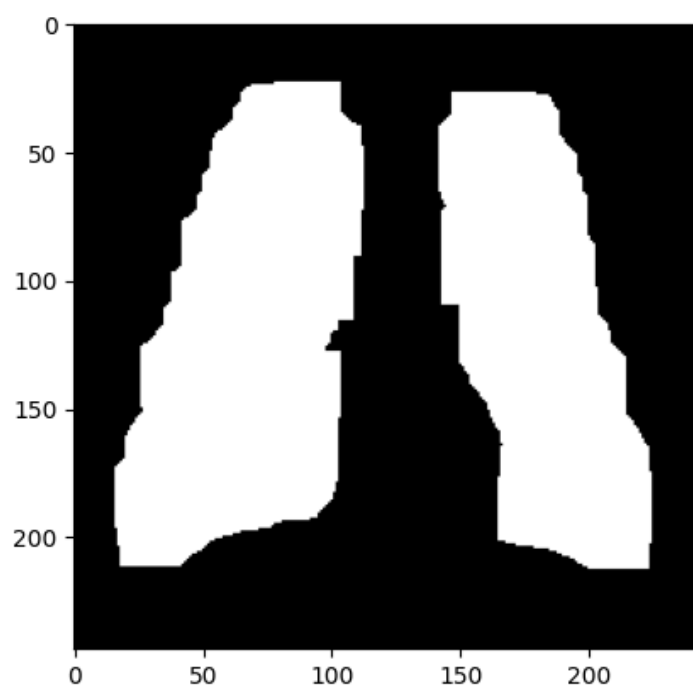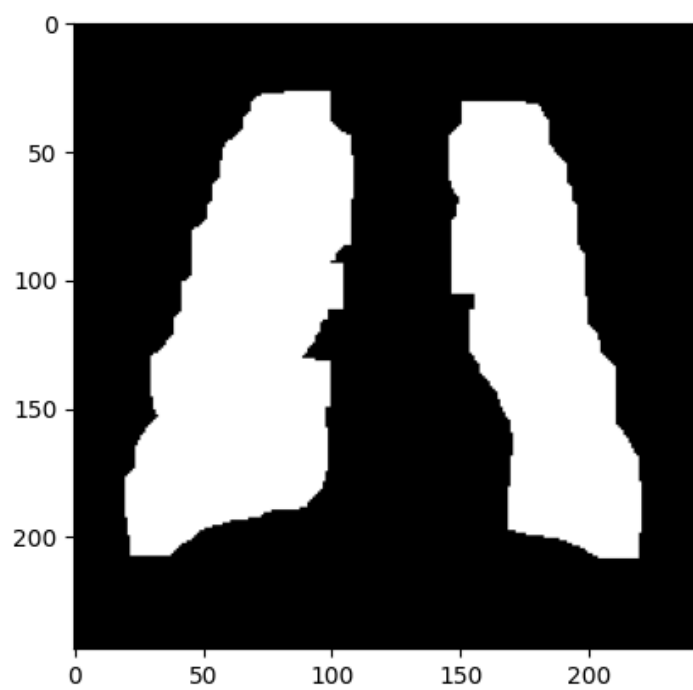
d. Classification

First of all, we analysed the histograms of several images from both categories and we came to the conclusion that the healthy lungs has slightly higher contrast than the others because the lungs are more "whole" and have a more intense grey level compared to the others. Next, we analysed the size of the lungs and found that after the segmentation process, the healthy lungs are bigger and have many more white pixels. So, using these three criteria, we made a classification between healthy/nromal lungs and lungs affected by pneumonia or COVID-19.

e. Results and conclusions

After all processing and classification analysis the results are satisfactory for the processes through which the images were put and the datasets available. In the future, we also will try to introduce a trained learning model for better and efficient prediction.

4. References

1. https://data.mendeley.com/datasets/dvntn9yhd2/1
2. https://github.com/ieee8023/covid-chestxray-dataset/tree/master/images
3. https://www.sciencedirect.com/science/article/pii/S001048252200258X#bib51
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