# Rapid Analysis of Thorax Images for the Detection of Viral Infections

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Abstract-At the end of December 2019, a person in the Chinse city Wuhan was probably infected for the first time with the novel SARS-CoV-2 virus. In order to be able to react as quickly as possible after infection rapid diagnostic measures are of the utmost importance so that medical treatment can be taken at an early stage. An imageprocessing algorithm is presented using chest X-rays to determine whether a lung infection has a viral or a bacterial cause. In comparison to other more complicated evaluation methods, focus was put on using a simple algorithm by using the Canny algorithm for edge detection of infected areas of the lung tissue instead of complex deep learning processes. Main advantage here is that the method is portable to many different computer systems with little effort and does not need huge computing power. This should contribute to a faster diagnosis of SARS-CoV-2 virus-infection, especially in medically underdeveloped areas.

*Keywords*—COVID-19, X-Ray system, analysis, SARS-CoV-2, diagnosis, image processing, Canny-algorithm

## I. INTRODUCTION

Since the end of 2019, the novel virus SARS-CoV-2 has continued to spread and has now led to a global pandemic. The clinical picture of the so-called COVID-19 disease is non-specific and strongly resembles that of influenza or the common cold. In addition to asymptomatic and mild cases of the disease there are severe cases with pneumonia and even lung failure. It is of great importance to get at least a tentative diagnosis to be able to isolate an affected person to protect his environment and prevent further spread of the disease. In order to be able to react as promptly as possible after an infection rapid diagnostic methods are of the utmost importance so that medical measures can be taken immediately. Especially in developing countries simple hygiene measures are difficult to implement and modern technology for rapid and reliable diagnosis is hardly accessible. Therefore the development of simple and cost-effective diagnostic tools is of great importance for poor countries. Approaches to detect covid-19 disease based on lung imaging already exist but are usually complex and predominantly based on deep learning algorithms [1-3]. In this proposal we wanted to introduce a simple and capable method to detect virus infections by using standard Canny algorithm and edge detecting methods [4] instead of complex deep learning processes.

#### II. DIAGNOSTIC CAPABILITIES

Despite the worldwide research efforts there are still very large gaps in our knowledge about the COVID-19 disease caused by SARS-CoV-2. The course of the disease is often non-specific and resembles a flu or cold. According to the German Robert Koch Institute (RKI) [5], 80% of cases are mild to moderate, i.e., those affected only show flu-like symptoms such as fever sore throat and cough. In 20% of cases respiratory distress may occur as a result of pneumonia which typically becomes apparent 7-10 days after infection. Approximately 5% of patients with COVID-19 require intensive care due to the risk of lung failure. In order to diagnose a COVID-19 disease as quickly as possible and to keep the number of further infections as low as possible molecular biological methods as well as imaging methods are available which can be used to accelerate the diagnosis of a COVID-19 disease. According to the RKI in 50-60% of patients changes are visible on a conventional X-ray of the thorax [5]. A Computer Tomograph (CT) scan of the lungs detects changes that are evident as milky glass-like infiltrates or local compressions in approximately 80% of those with the disease.

Because radiologic findings of COVID-19 disease are similar to those of patients with SARS or MERS a definitive diagnosis requires confirmation by positive detection of viral genes using a microbiologic test. In developing countries and medically underserved regions modern laboratories for microbiological testing are usually not available with sufficient capacity. However since radiological findings are directly available a tentative diagnosis can be made using diagnostic imaging techniques. Due to the fact that the disease is quite infectious and the incubation time can be several days, this fast diagnostic method can help to minimize the spread of the infection.

## III. ANALYSIS OF THORAX IMAGES

Conventional radiography is usually accessible even in medically underserved regions. In addition rapid diagnostic findings are often particularly important here as many people live in confined spaces. To this end a tool

Manuscript received April 8, 2022; revised May 7, 2022; accepted August 15, 2022.

has been developed that uses a chest X-ray to autonomously determine with the highest possible probability whether the disease is bacterial or viral in the lung tissue. The tool is based on classical image processing algorithms and distinguishes whether the infection of the lung tissue is bacterial or viral. Since typically at the beginning of a pandemic only little data is available, the use of artificial intelligence was deliberately avoided and only classical image processing algorithms were applied.

When taking X-ray images the body is irradiated with the help of X-rays. An X-ray film or a digital detector captures the non-absorbed rays shining through the body resulting in an X-ray image that reflects the different absorption of the various tissues. Dense tissue such as nodules appear brighter on the X-ray image because the radiation is attenuated more by the higher absorption coefficient of the dense tissue. Tissues with a lower density, such as muscles or the ventilated areas in the lungs, have a smaller absorption coefficient hence these regions tend to appear darker on the X-ray image. In an Xray of a healthy lung the other organs are clearly demarcated and the lung itself is clearly visible. When the lung is diseased the internal organs are less well demarcated on the image. The diseased tissue usually has a higher density than the healthy tissue and therefore appears lighter on an X-ray image in contrast to the surrounding healthy tissue. The shape and delineation of the diseased tissue can provide information about the type of disease. In COVID-19 disease the radiographs usually show Ground glass opacities in both lung lobes extending over several lung segments. Fig. 1(a) shows radiographs of a healthy lung in contrast to a lung affected with COVID-19. Fig. 1(b) shows that almost the entire lung has a comparatively high absorption coefficient (light areas) which indicates pathologically altered tissue. In order to differentiate between bacterial and viral infections it is important to examine the thorax images for the specific characteristics of the diseases. Bacterial infections are usually characterized by the fact that only one lung is affected by the infection and the affected tissue is clearly demarcated. In viral infections usually both lungs are affected and the pathologically conspicuous areas are less spatially delineated.



Figure 1. (a) Radiograph of a healthy lung, (b) compared to a diseased lung [6].

# A. Algorithm for Analysis of Thorax Images

The developed algorithm is based on classical image processing algorithms and differentiates between bacterial and viral infection based on the ratio of pathologically bright areas of the lung surface and the length of the lung lobes. The X-ray image of the thorax is read in by the algorithm and analyzed using the following steps:

- Reading and formatting the image file
- Conversion of the gray scale image into a color space
- Edge detection for segmentation of the lungs
- Separate analysis of the lungs
- Comparison of the results of both lungs
- Evaluation of the results

Since the existing images are in different file formats and sizes the images must be resized to a uniform format. The *resize()* method is used for this purpose (see Fig. 2).

- 1 // Resize image to spezific size 2 resize(I, I, Size(614, 874), 0, 0, INTER\_CUBIC);
- 3 imshow("Source", I);
- 4 //Equalize ima
  5 Mat Iequal;
- 6 equalizeHist(I, Iequal);

Figure 2. Setting the image size and histogram equalization.

Only if all images have the same size a comparison can be made in the subsequent analysis of the image. To read in the image a matrix *Mat I* is created in which the image is read in and stored. The X-ray images are usually available in a 8-bit gray scale format with the values representing the brightness or intensity value of a single pixel. If the gray value of a pixel is 0 the pixel appears black. If the gray value is 255 the pixel appears as white; hence the image represents 256 gradations of gray.

The INTER\_CUBIC parameter specifies the interpolation method to be used when enlarging or shrinking the image. By converting the images into common data formats information about the exposure values is lost. However, in order to generate a contrast that is as uniform as possible even with different exposures the *equalizeHist()* method is of important use. With the help of this method it is possible to increase the contrast of an image by changing its intensity range.

In Fig. 3(a), it is shown that most of the pixels are in the medium intensity range. Fig. 3(b) shows the equalization of intensity values by the *equalize-Hist* method shown on a histogram. The outer areas show a clear decline of these intensities. Histogram equalization expands the intensity rang as can be seen in Fig. 3(b). This method optimizes the contrast of Fig. 3(d) and helps to show the differences between images minimizing the adverse effects of different exposure conditions.



Figure 3. (a) Histogram of the original image, (b) Histogram of the image after Histogram equalization, (c) original image [6], (d) Image after Histogram equalization.

Subsequently, the contrast is optimized by means of a histogram evaluation of the intensity range of the image. Since it is very difficult to recognize the differences between the individual gray levels in a gray-scale image the image is also converted into a color space for easier diagnosis especially by inappropriately trained personal.

In Fig. 4(a), a processed thorax image of a COVID-19 patient colored in this way is shown; the normally ventilated healthy tissue is shown here in dark blue.



Figure 4. (a) Distribution of intensity values by the equalizeHist function, (b) Binary image of the cyan colored areas.

The infected parts of the tissue appear in light blue. Based on this representation it is now possible to filter the color that encloses the lung. The areas with this color are interesting for the later edge detection. The method *inRange()* in Fig. 5 can be used to search for specific colors in an image. Thereby a range is defined by two three-column vectors (*Scalar()*) which indicate the upper and lower limit of the searched color values.

```
1 // Color the x-ray picture
2 Mat Icolor;
3 applyColorMap(Iequal, Icolor, COLORMAP_JET);
4 imshow("ColorMap", Icolor);
5 // Detect blue color
6 Mat Iblue;
7 inRange(Icolor, Scalar(40,40,40), Scalar(255,255, 255), Iblue
);
8 imshow("OnlyBlue", Iblue);
```

The *inRange()* method then returns a binary image with the values depicting the areas where the colors of the image lie in the specified range. Fig. 4(b) shows such a binary image. Here the outlines of the left lung can be recognized very well. The presumably healthy tissue of the lung is shown in white color. The black areas surrounded by healthy white areas can be considered as infected tissue. In addition, traces can be seen in the lower part of the left lung wing which indicate diseased tissue. This image will be further used to better detect the outline of the lung.

# B. Edge Detection Using the Canny Algorithm

The Canny algorithm was named after John Francis Canny and is considered one of the most robust edge detection algorithms in image processing [4]. The advantage of the Canny algorithm is that it can be applied to gray scale images as well as to colored images [4]. However, it is common to convert the image to be processed into a gray scale image before edge detection [7]. In this process the edges of the images are detected based on the color differences and brightness variations between neighboring pixels. For this purpose, the partial derivative of the individual pixels in x- and ydirection is required. To calculate this derivative the socalled Sobel operator is used [8, 9]. Subsequently this simple edge detection filter calculates the first derivative of the brightness values of the pixels with the help of the convolution and simultaneously smoothes orthogonal to the direction of the derivative.

In order to refine the edges in the image the so-called non-maxima-suppression is applied [4]. All pixels are compared with the pixels adjacent to the left and right. If a gray value of a neighboring pixel is larger, the gray value of the pixel under consideration is set to 0. This ensures that an edge cannot become wider than a pixel. As a last step of the Canny algorithm a hysteresis is applied to the detected edges. This step suppresses weak edges or pixels caused by noise. For this purpose two threshold values must be defined. If the gradient of a pixel is greater than the upper threshold the pixel is considered to be part of the edge. If the gradient of the pixel is smaller than the lower threshold it is not recognized as part of the edge. If the gradient is between the threshold values it is checked whether a neighboring pixel exceeds the upper threshold value- in this case the pixel also belongs to the edge. If this is not the case the gray value of the pixel is set to 0. For the Canny algorithm, a ratio between 2:1 or 3:1 is commonly used to achieve the best results.

In OpenCV the Canny algorithm is already implemented with the method *Canny()* [10, 11]. Here the algorithm must be passed a matrix containing the image to which the Canny algorithm is to be applied. In this case it is the binary image that was previously created during the selection by the method *inRange()*. In addition a matrix (*Icanny*) must be passed in which the output image is to be stored. Two further parameters are used to specify the threshold values of the hysteresis. The last parameter specifies the size of the Sobel operator. In Fig. 6 a lower threshold of 80 and an upper threshold of 160 were

Figure 5. Coloring the image and selecting the areas of interest.

selected whereby the Canny algorithm is performed with a Sobel operator of size  $3 \times 3$ .

```
1 // Canny Algorithm
2 Mat Icanny = Mat::zeros(I.size(), I.type());
3 double ThresholdCanny = 80;
4 Canny(Iblue, Icanny, ThresholdCanny,2*ThresholdCanny,3);
5 }
```

Figure 6. Edge detection using the Canny algorithm.

Fig. 7 shows the edges detected by the Canny algorithm.



Figure 7. Result after segmentation of the image of a viral infection.

In this image it is easy to see that even for small segments within the lung lobes the edges were found.

However, when looking closer at the image it is noticeable that there are some imperfections in the image through which several edge lines are not closed. With the help of so-called morphological operations the closing of such gaps in the lines of the edges can be easily implemented.

Figure 8. Edge detection using the Canny algorithm.

With the help of a dilation the pixels can be expanded so far that closed lines are created. In binary image morphology a dilation means that each pixel that is part of an edge is replaced by a previously defined element in order to expand the pixel. Three arguments need to be passed to the algorithm to perform this measure. The initial image from the Canny edge detection algorithm (*Icanny*) and the initial image (*Idilate*), form the first two arguments. The last argument describes the kernel, i.e., the element to replace the pixel of the edges. As shown in Fig. 8, an elliptical shape of the kernel with a size of a  $4\times 4$ matrix (*dilate\_size* = 4) was chosen. To determine the position of the kernel detected by the Canny algorithm, no anchor point is specified, because it should end in the center of the kernel.

Fig. 9 shows the binary image of the edges detected by the Canny algorithm after dilation has been applied. The thickness of the edges here now appears to be very high but this choice of kernel has been shown to contribute to the robustness of the algorithm. Horizontal lines were also added to the top and bottom of the binary image to close possible edges at the edges of the image. Thus with the application of these methods the outlines of the body and lungs could be extracted from the X-ray image.

The surface area of each lung lobe is then calculated additionally its length is determined. The lung content and the length of the lung lobes after segmentation allow conclusions to be drawn about the type of disease. If both the area and the length of both lung lobes are comparable it can be concluded that the disease is more likely a viral infection.



Figure 9. Binary image of the edges after dilation.

If, however, the results of the two lungs are very different a bacterial disease of the lung can be suspected due to the fact that these typically mostly affect one side of the lung. The thresholds for distinguishing between bacterial and viral infections were determined empirically on the basis of several case studies. If the calculated length of one lung is more than 30% longer than the other bacterial disease can be suspected. If the lungs are comparable in calculated length and the lung content is within 90% for both sides a viral infection can be suspected. Fig. 10 compares the results of a bacterial infection (a) with those of a viral infection (b).



Figure 10. (a) Result after segmentation of the images of a bacterial infection, and a (b) viral infection.

The processed X-ray of a patient suffering from COVID-19 (b) clearly shows infected areas within the lung: both lung lobes show comparable shading due to the typical infection-related distribution of the foci. By dividing the image vertically and calculating the area and length of the contour separately the ratios between the two lung lobes can be determined. Based on these ratios the symmetry of the infestation of the lung lobes can be inferred subsequently. If the ratio between the shadowed areas of both lung halves is greater than the empirically determined threshold value bacterial disease can be assumed like as shown in Fig. 10(a) since this usually affects only one of the two lungs. If the ratio in both lungs is close to one it seems reasonable to conclude that both

lungs are affected to a comparable extent suggesting the disease is viral as shown in Fig. 10(b).

The algorithm also detects the bacterial infection by the reduced lung volume in the right lung in Fig. 10(a). The evaluation of the analyzed images is therefore based on the relationship between the areas of both lungs that are presumed to be infected based on the shadowing in order to be able to make a tentative diagnosis.

## IV. TEST RESULTS

To make a final statement on the functionality of the algorithm tests were made on the basis of various X-ray images. For this purpose thorax images of various diseases are read in and a binary image of the lung contents is generated. Fig. 11(a) shows an image of a pneumococcal infection (bacterial). The algorithm clearly identifies the decreased lung volume in the right lung mound given in Fig. 10(a). The ratio of the surface areas is 1.41 and that of the length of the lung lobes is 1.45 also indicating a bacterial infection. These ratios can also be used to illustrate bacterial disease. Fig. 10(b) shows how the lung contents can be separated by applying the algorithm for the COVID-19 infection given in Fig. 11(a). The ratio of the two lung lobes here is 1.2.



Figure 11. (a) X-ray image of a pneumococcal infection, (b) X-ray image of a COVID-19 infection [6].

Compared to bacterial infection this ratio is lower but these values are very close to each other which makes it very difficult to determine the threshold at which a bacterial disease is present. This is partly reasoned to the fact that the distance between the X-ray unit and the body varies for different images. Thus, in some images, other parts of the body such as arms are shown whereas in other images the lungs fill the entire X-ray image. Looking at the ratio between the length of the two halves of the lung a ratio of 0.9 is determined for the right image. Based on this additional information a more precise distinction can be made since the ratio of the lung length is significantly greater due to the unilateral attack of the bacterial disease.

During further testing it was also noticed that in some images the algorithm is not functional enough. Fig. 12(a) shows an example of such an image. In the binary image in Fig. 12(b) it can be clearly seen that the contours of the lung could not be detected correctly and thus no area calculation of the lung content could be performed. However, since the contours of the image are relatively symmetrical a ratio of the two lung halves of 0.9 is calculated. This value does not correspond to the represented binary image and the algorithm therefore returns incorrect values.



Figure 12. (a) X-ray image with too low contrast, (b) Binary image not closed contours.

The problem here is that no information is available on the conditions under which the X-ray images were taken. It is therefore very difficult to achieve a sufficiently high contrast in all areas of the image for the algorithm to work reliably despite histogram equalization. Especially in the area of the clavicles it often happens that the contrast is not sufficient to clearly distinguish the lung from the neck. In an experiment with 15 randomly selected thorax images, 47% were correctly evaluated. In the remaining images the edges could not be completely detected because the contrast between lung tissue and bone was usually too low. In conclusion it can be said that by applying common image processing algorithms and very simple discrimination criteria good results could be achieved.

#### V. SUMMARY

The algorithm developed here provides good results for many of the available X-ray images but is currently not robust enough to provide satisfactory results for every Xray image. This is partly due to the fact that the X-ray images were taken under different conditions and no information is available about the exact exposure settings. In addition the size of the lungs as well as the exact size ratio of the lung lobes is not always the same due to anatomic individualities making it difficult to compare the ratio of the surface areas of the lung lobes. In addition the available radiographs were compressed, resulting in loss of image information. Since the size of the images was different they had to be scaled to a uniform image format in order to make a comparison between the images. This process requires either interpolation between the pixels for image enlargement or image information is lost due to the size reduction.

In order to improve the stability of the algorithm further tests with thorax images of different disease patterns have to be performed. Nevertheless, with the discussed method the content of the lung lobes could be separated in many images and a presumption about the origin of the disease could be made. As with all imaging techniques it must be remembered that no final COVID-19 diagnosis can be made. The method is rather an adequate means to be able to make quicker presumptive diagnoses especially in countries with less developed healthcare.

#### CONFLICT OF INTEREST

The authors declare no conflict of interest.

#### AUTHOR CONTRIBUTIONS

Roman Radtke conducted and supervised this project. He was responsible for the results and wrote this paper. Alexander Jesser supervised this work from the academic field and put many hints and aspects into this work. All authors had approved the final version.

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