

IDENTIFYING BONE TUMOR USING X-RAY IMAGES

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Abstract- The development of technology has made it simple to employ image processing in a variety of sectors, including computer science, data science, and medicine. Extraction of information from medical images is the major goal of medical image processing. Five steps make up the methodology that numerous academics have suggested: preprocessing, edge detection, segmentation, feature extraction, and classification. The project's goal is to use X-ray images to identify tumour in their earliest stages and increase the quality and accuracy of X-ray images. The detection of fractures and the diagnosis of diseases have both made extensive use of bone X-ray pictures. For the segmentation of the spine area, the approach makes use of adaptive thresholding, morphology, and region growth. For the detection of bone lesions, a method based on the watershed model is used, and a support vector machine classifier is used for feature classification and to diagnose the affected lesions.

Keywords: X-ray images, pre-processing, U-net model, Watershed algorithm, SVM classifier.

INTRODUCTION

One of the least expensive primary screening methods for the detection of bone cancer is X-ray image analysis. A primary bone tumour typically manifests with unexpected symptoms such as a bone fracture, swelling around a bone, a new bone growth, or swelling in the soft tissues surrounding a bone, according to the medical literature [16]. An X-ray image of a cancer-affected bone frequently looks different from the healthy bones and flesh nearby. The cancer-affected area's bone cells absorb X-rays at a different rate than healthy bone cells do. A "ragged" surface (permeative bone deterioration), a tumour (geographic bone destruction), or holes (moth-eaten pattern of bone loss) are the resultant images of cancer-affected bones.

Different methods for detecting bone tumours have been developed by researchers in recent years. For the purpose of identifying the tumour zone in X-ray pictures, traditional image-analysis methods like thresholding, region expanding, classifiers, and Markov random field model have been applied. For the purpose of segmenting bone tumours, Frangi et al. performed multi-scale analysis of MRI perfusion images. In order to differentiate between viable and non-viable tumours, they suggested a two-stage cascaded classifier for hierarchical categorization of healthy and tumour tissues. Ping et al. have suggested a method for identifying and classifying bone tumours from clinical X-ray pictures that is based on intensity analysis and graph description. The procedure examines a graph representation to identify the potential tumour site. In accordance with the number of pixels recovered from the study of brightness values, it may also classify benign and malignant tumours. For the segmentation of the spine area, the approach makes use of adaptive thresholding, morphology, and region growth. A support vector machine (SVM) classifier is utilized for feature classification and to identify the afflicted lesions, and a watershed model-based technique is used for the detection of lytic bone lesions.

This study put forth a computer-aided diagnosis technique that can analyze bone X-ray pictures automatically and pinpoint the area that has cancer. Based on the disease's stage and grade, our approach may be utilised to pinpoint the destruction pattern and determine how serious the condition is.

The intensity, shape, and texture characteristics of an image are used to differentiate it in the classic image segmentation method. However, there are several instances where some of the methods used to identify the image's constituents would not work, making it challenging to draw conclusions from one issue to the next. Additionally, conventional picture segmentation takes a long time to process, which lowers the accuracy of image measurements. Researchers have recently shifted from using conventional methods of picture segmentation to more sophisticated techniques such as edge-based detection, thresholding, region expansion, and deformable models [2]. These techniques make it possible to divide pictures into several segments depending on distinct characteristics like intensity value, color, texture, and others. Based on the aspects of the picture that are largely consistent in each zone, segmentation attempts to divide the image into regions. Typically, segmentation is done to retrieve crucial data from medical images. Bone structure Medical

image processing has significantly advanced in the areas of medical diagnosis that can be utilized by medical workers in examining the anatomical structures of the picture and deciding the appropriate course of treatment to be delivered to the patient.

OBJECTIVES:

1. pre-process the image
2. detect edges of the objects in an image
3. improve quality of an x-ray
4. build a model to segment the image
5. identify the tumor in x-ray bone.

IMPLEMENTATION

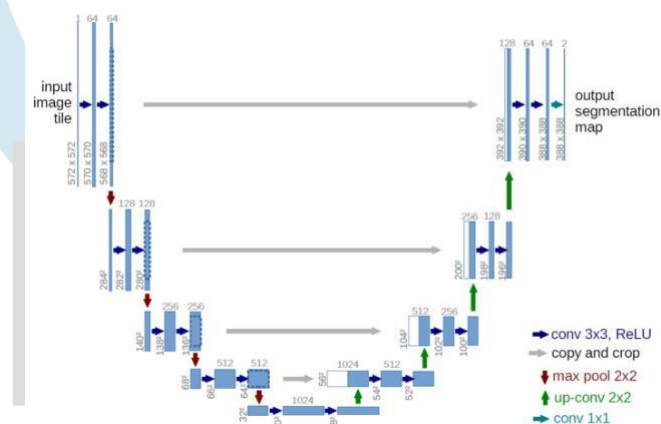
DATA COLLECTION

The suggested approach has been examined using data sets of long-bone X-ray pictures with malignancy. The majority of the images were gathered from various publicly accessible datasets and websites, including the TCIA dataset (<https://wiki.cancerimagingarchive.net/display/Public/Wiki>), Radiology Assistant's website (www.radiologyassistant.nl), Radiopedia's website (<http://radiopaedia.org>), and Bone and Spine's website (<http://boneandspine.com/bone-tumours-images-and-xray>).

These photos' accompanying clinical observations and remarks serve as the basis for each individual image. The webpage provides access to the whole database for all the photographs used in this work. It comprises 150 long-bone X-ray pictures, 50 of which are of healthy individuals and 100 of which are of cancer patients. We assessed the classifier's average accuracy using a fivefold cross-validation technique. We used stratified sampling during the data selection procedure to keep a similar ratio of healthy and ill photos in each batch that was chosen.

Built an U-NET MODEL:

U-net architecture is mainly used in biomedical image segmentation. The semantic segmentation architecture is called U-Net. It comprises an expanded path and a contracting path. The contracting route adheres to the standard convolutional network design.



The architecture demonstrates the passage of an input picture.model, which is immediately followed by a fewReLU activation function in convolutional layers We may observe the decrease in picture size from 572X572 to 568X568 is reached after 570X570. The cause of this decrease is a result of their use of unpadding convolutions, defined as "valid" convolutions, which reduces the total dimensionality of the process. In addition to the convolution blocks, we can also see an encoder block on the left and a decoder block on the right.

The max-pooling layers of strides 2 assist the encoder block in maintaining a steady reduction in picture size. The encoder architecture also includes recurrent convolutional layers with a growing number of filters. When we get to the decoder part, we see that the convolutional layers' number of filters begins to go down and that the subsequent layers gradually upsample until we get to the top. We also observe the application of skip connections, which link the decoder blocks' layers with earlier outputs. For the loss from the earlier layers to reflect more strongly on the total values, this skip link is a crucial idea. Additionally, they have been demonstrated scientifically to deliver superior outcomes and hasten model convergence. The last convolution layer is followed by a few convolutional layers in the final convolution block. A filter of 2 with the proper function is present in this layer to display the output. Depending on the intended outcome of the project you're working on, you can alter this last layer.

When learning from a small number of labeled pictures that are suitable for image segmentation in biology or medicine, the "U-Net" may conduct image segmentation without the need for additional runs.

PREPROCESSING:

Our examination begins by separating the bone location from the muscles and tissues that surround it. Pixels of different intensities can be seen in X-ray images of bones that have been impacted by malignancy. The suggested solution uses a technique based on entropy-standard deviation discrimination to segment the impacted area.

Using the function `COLOR_BGR2GRAY`, we can change our original image's BGR color space to gray. We now just need to use the `imshow` function of the CV2 module to display the photos.

Step 1: Import OpenCV.

Step 2: Read the original image using `imread()`.

Step 3: Convert to grayscale using `cv2.cvtColor()` function.



EDGE DETECTION:

Finding the edges of objects in a picture is done using the edge detection image processing approach. It operates by looking for changes in brightness.

A pixel can have any intensity value between 0 and 255 in a grayscale picture. In a zone of heterogeneous intensity, the intensity distribution will be random, while in a region of homogeneous intensity, it will be uniform. The pre-processed picture of the bone surface is used in the suggested approach to identify the area with a heterogeneous intensity distribution.

parameters:

To find the boundaries in an object within the image, we need consider some parameters. Based on those parameters we can draw the edges of an object.

Draw contours

Length

Bounding

connected components for labeling contour perimeter

SEGMENTATION:

Segmentation is the process of dividing a picture into areas based on the features that are essentially consistent throughout each area.

Algorithm for Watershed

In order to prevent over segmentation, watershed segmentation is often accomplished via region growth based on a set of markers.

Both contour detection and region-based segmentation employ the watershed segmentation method. Using morphological operations like opening and shutting, one may determine the exact backdrop.

Utilizing the distance transform to locate the specified foreground Therefore, the region that is in the front or background is the unknown area.

Parameters:

Finding background area

Finding Foreground area
 Shape
 Contour area
 Perimeter
 Marker labelling.



Feature Selection for Analysis:

We have employed a few feature characteristics to categorize the bone cancer's stage, grade, and pattern of destruction. According to medical literature, the progression of the illness in the bones determines the stage of bone cancer, whereas the severity of the disease is indicated by the cancer's grade. High-grade cancer has fast development that causes bone loss, whereas low-grade cancer has cells that are just slightly aberrant. Therefore, the size of the afflicted region and the gap (discontinuity) in the bone barrier are crucial in determining the stage and grade of malignancy. Bone-destruction patterns are categorized depending on how the surface of the bone changes in texture and form. A ragged bone surface can be seen in an X-ray picture of a bone afflicted by cancer.

During the edge identification procedure, this irregularity in the texture of the bone surface manifests as fictitious edges. Edges on the surface of the bone thus reflect a change in bone texture. The alteration in bone contour curvature suggests an irregularity in the long bone's form and aids in the classification of various bone-decay patterns. We used the following feature parameters for our investigation based on these scenarios:

- impacted area's width (w).
- contour gap
- Concavity change rate (CI)

Feature Extraction

The shape of the bone and its surface roughness are both impacted by the progression of bone cancer. To find the aspects that should be considered while making decisions, the malformation of the bone's shape and the altered texture are analyzed..

Here, we are taking into account a few factors.

Bone Contour analysis:

Multiple linked components on the left and right sides of the bone's contour or on the bone's surface are signs of a bone defect. Connected component analysis (CCA) is what we do. of the bone contour's single-pixel picture Our examination of training-set photos reveals that although cancer-affected bones have several linked components, a healthy long bone has very few edges on the bone surface.

Runs-Test for Bone Texture Analysis:

Because the bone surface damaged by cancer has an uneven texture and lacks a clear pattern, structural and geometrical texture analysis methodologies may not be particularly helpful in this case. The pixels' intensity distributions are seen to be homogenous in the healthy bone area and diverse in the cancer-affected regions. As a result, they may be distinguished based on a metric that captures the randomization of pixel intensities. The runs-test [19] is used in this instance to find the degree of unpredictability in the intensity values in cancer-affected areas.

Localization of cancer affected region

To determine the stage and severity of the disease, the cancer-affected area must be localized. Locating the cancer-affected area in the bone X-ray picture is made easier with the aid of CCA and the previously stated bone texture analysis. The segmentation of the ROI necessitates the determination of a contour that closely encloses both islands of healthy area surrounded by cancer-affected areas and pixel clusters of cancer-affected regions. We have used the ortho-

convex polygon's property in this study and suggested a strategy to create a 4-staircase ortho-convex cover that encloses the cancer-affected area on the bone surface.

CLASSIFICATION:

With datasets of healthy and cancer-affected X-ray images, we trained the binary SVM, and we utilized the test dataset for diagnosis. The binary SVM model uses two feature parameters: the quantity of linked components (s) present on the surface of the bone image and the proportion of ROI pixels with a heterogeneous intensity distribution (h). The distribution of training pictures in the feature space is seen in Figure 9. A bone X-ray picture from our medical database is represented by each (s,h) pair in the feature space.

The points marked with the red circle represent correctly classified test images.

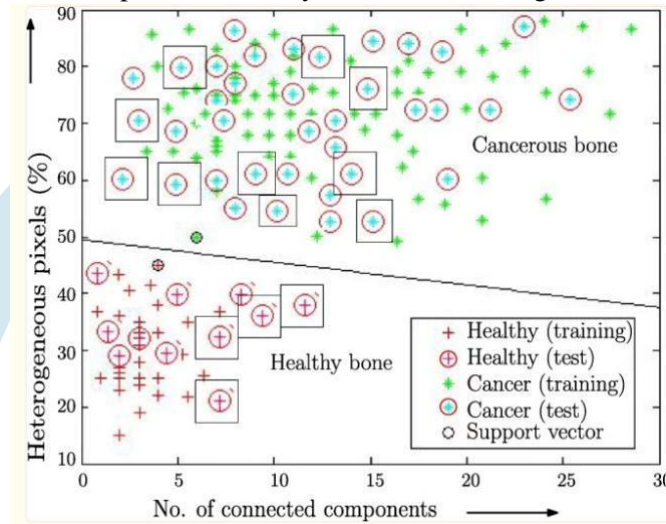


fig: SVM (binary) for bone cancer diagnosis (points in rectangle represent misclassification)

CONCLUSION

The main advantage of our approach is that we segment X-ray images using a convolutional neural network as a pixel classifier. Each pixel is examined by the network to determine if it falls into the "bone" or "non-bone" category. By doing this, we intend to separate the bone tissue from the surrounding tissue. Our methodology is totally automated in comparison to other X-ray image segmentation methods due to the use of CNN. We chose a CNN configuration and contrasted its outcomes with those of three additional networks that utilized the identical design but varied variables. We can see the tumour in a bone x-ray at the conclusion of the study.

Future Scope:

A future study may help increase the x-ray pictures' precision and quality. This will be valuable for cheap and early tumour detection.