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BONE TUMOR DETECTION USING MACHINE LEARNING

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Abstract

Cancer is a deadly illness, caused by unchecked growth of the cells. Nearly 100 different forms of cancer have been found in the human body, following much study. One of the most commonly spread out of these is bone cancer, which leads to death. Bone cancer diagnosis is very important, and has little expectation. Part of the work is currently conducted using data mining tools and the image processing technologies for the process of medical image analysis. Many academic scholars have become reliable with the data and information obtained from broad datasets and associated websites. The most widely used approaches for identifying and classifying bone cancer are association rule mining, support vector machines, fuzzy theory and probabilistic neural networks, and learning vector quantizations. This paper used superpixel algorithm for segmentation of the bone image. For identification of bone cancer the segmented image is further processed by determining the mean strength of the detected region. Threshold values for classifying medical images for presence or absence of bone cancer are proposed. With less computational time, the results using this method give 97.5 per cent accuracy.

Keywords: *Bone Cancer, SVM, superpixel, segmentation.*

INTRODUCTION

The bone is the body's hollow support skeleton. The outer portion of bones is a hard tissue structure called calcium salt matrix. The hard out layer is made from cortical bones, it covers the trabecular bone inside and outside the periosteal-covered bone. Some bones are hollow and the soft tissue known as bone marrow contains the medullary cavity. Endosperm is a lining of the tissue. At each bone end is a area of bone like cartilage that's thinner than a bone made from the fibrous matrix of a gel-like substance that doesn't contain much calcium. The bulk of the bones are like cartilage. Instead the body puts the calcium on the bone. Some cartilage can remain at the ends of the bone formation to serve as reinforcement between bones. The cartilage connects bones to form a joint, along with ligaments and some other tissue. The bone is very rigid and muscular itself. Bone will carry up to 12,000 livers per centimeter per inch. The strain to crack the thigh bone takes as much as 1200 to 1800 pounds. There are two cells in the bone. The Osteoclast is the new bone cell, and the Osteoclast is the old bone cell. Some bones of the marrow are soft tissues.

The marrow of certain bones is a concoction of fat cells and blood cells. Blood-forming cells contain red blood cells, white blood cells and blood platelets. Certain cells in the marrow include plasma cells, fibroblast cells and reticuloendothelial cells. Cancer, which induces unfettered cell formation, can subdivide the cells and grow wild, develop malevolent tumors, and invade neighboring areas of the body. This tumor can expand and obstruct the digestive, nervous, and circulatory systems, and may release hormones that change the function of the body. Cells which were treated as cancer cells due to DNA damage. When DNA damaged the cell, the damage is maintained in a regular cell, or the cell dies. If the damaged DNA is not repaired,

the damaged DNA will cause unnecessary new cells to die. Cancer cells also travel to other areas of the body and start growing tumors that return to normal tissue. Metastasis is called this phase. After that cancer cells get into the human body's bloodstream or lymph vessels.

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Figure 1: a)Input Normal Image b) Filtered Image

There are various types of cancer detected in the human body. If the tumor affects bone directly then that type of disease is known as bone cancer. The sarcomas are called bone cancers. Sarcomas arise in muscle , bone, fibrous tissue, blood vessels, fat tissue and several other tissues. They can grow in the body anyplace. Bone refashion operation is attributed exclusively to Bone Cancer cells. Standard bone is being tirelessly changed, or conked out and rebuilt. Cancer cells fault equilibrium for cell growth and bone development. If cancer cells are in the bones, then as opposed to normal bone density, the bone structure is bent at a higher rate. The cancer of the bone may either be primary or secondary. Bone cancer occurs primarily in the bone. Whereas secondary bone cancer develops in every portion of the body.

LITREATURE REVIEW

Sinthia P & K. Sujatha[1] suggested a novel approach to bone cancer detection using the K-means algorithm and edge detection process. To detect the edge, this methodology utilized Sobel edge detection. Sobel edge detector only detects pixels on the boundary. The tumor region is identified using K-Means clustering algorithm. The challenging step in K-Means clustering algorithm is determining the number of clusters..

Kishor Kumar Reddy [2] proposed a novel approach to detect tumor size and the stage of bone cancer using region-widening algorithm. By using region-widening algorithm this methodology segmented the region of interest. Tumor size is determined by the amount of pixels in the portion of the tumor removed. Depending on the level of cancer average pixel value is determined. Selection of seed point is based on the picture, and correct selection is difficult.

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The automated identification of single lung nodules using the CT photographic swarm intelligence engineered neural networks has been proposed by EzhilE.Nithila and S.S.kumar[5]. The Gaussian filter was used in this technique to eliminate the noise and contour to segment the

image. Owing to the low line, the leakage issue occurs. From the segmented image the nodule is found. To order to restore the lung nodule, nodule boundaries are corrected. Various characteristics are removed to correctly identify the tumor. The extracted feature is used to train data and classify the tumor in the back-up neural network.

The Lung Cancer Identification System for using image processing techniques was introduced by Mokhled S. Al-Tarawneh[6]. Gabor filter was used to define the image using this technique. The best results are obtained from Gabor filter. Two segmentation methods are used to segment the file. The two algorithms are the threshold solution and the marker-controlled segmentation. In accordance with thresholds, the technology of marker guided segmentation gives a stronger performance. The picture characteristics are derived using the cancer detection technique of binarization and masking.

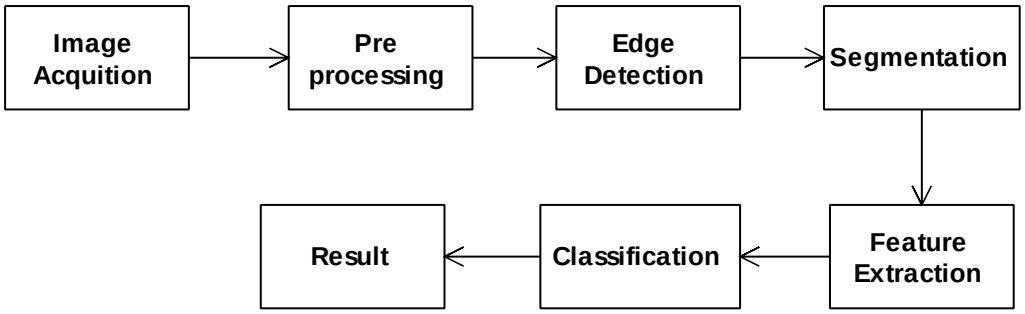
The approach to diagnose lung cancer using an artificial neural network and fuzzy division approaches was introduced by FatmaTaher and NaoufelWerghi[7]. The technique employed two Hopfield neural network segmentation methods and one c-striking approach that separated the image into one segment. In the early stages of cancer detection, a computer-aided diagnosis program is established. 1000 sample images are checked for all segmentation techniques in this article. Compared with the blurred cluster method, HNN showed a better grouping.

The method for detecting lung cancer in CT images has been developed with imaging processing. Anita chaudhary[8]. Gabor filters are used in this approach to minimize noise. Segmentation occurs by two threshold segmentation methods and watershed segmentation with marker controls. The features of the tumor are removed. The three characteristics extracted in this paper are area, perimeter and roundness.

Md.-Md. The technique for detecting lung cancer from CT image using the imaging and neural networks has been proposed by BadrulAlam Miah and Mohamma Abu Yousuf [9]. Several preprocessing methods are employed to improve the image in this methodology. After preprocessing the image fragment, the segmentation procedure is carried out. Features are extracted and used to train and classify cancer on the neural network.

A method for diagnosing the use of CT-scan imagery based on cellular training automatons was proposed by NooshinHadavi and Md. Jan Nordin[9]. Gabor filter was used to eliminate the noise in the input picture using this tool. A region-widening image segment algorithm is used. Different features are derived from the segmented image and used by the new cells to classify cancer.

PROPOSED METHODOLOGY



I. Acquisition Of Image

The first stage in any vision system is the acquisition of images. The images are considered the best because of their high resolution, such as CT scans, the MRI and X-ray. It is commonly used in scientific applications due to its capacity to create images of the human body that are not invasively high.

II. Preprocessing

Preprocessing an image increases the precision of an optical inspection significantly. Preprocessing is the first step towards improving image quality. The filtering technique is used to start the image processing stage. Image filtering is useful to smoothen, sharpen and remove noise for many purposes. Filtering eliminates noise or other small image fluctuations. Such noises then have to be denoted. Gabor filter is used for noise removal and for the deficiency of the pictures in this methodology. The key advantage of this filter is, as compared with other filters, it achieves excellent noise reduction with less blurring. The gray conversion will be the next step after filtering. This is the process by which pixels with RGB level are converted to gray. The picture of color has more meaning in the process. Therefore, it is appropriate to convert the gray picture. The main aim of this conversion is to remove the information on the color and saturation by retaining the light.

III. Super-Pixel Segmentation

Superpixels have a simple primitive from which local image characteristics can be determined. They record image redundancy and reduce the complexity of future image processing tasks significantly. The applications, such as profile estimation, image division, skeletisation, body model measurement and object localization, have shown their effectiveness. To be useful, superpixelsis fast, easy to use and produce high-quality segments. It begins with sampling K cluster centers that are often scattered and moved to seed sites which value the lower gradient position in a3 [3] very nearby. very 3 [3] It is also done so that they are not added and the odds are lowered To select a pixel. Gradients of the image are determined asThe comparison vector is the regular L2, where it is equivalent to the pixel (x , y). Every color and every colorData on intensity are considered.

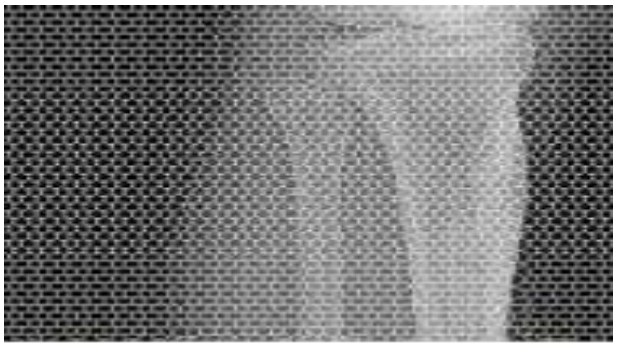


Figure 2: SuperpixelSegmenation

The next center cluster whose search area overlaps with the image is connected to each pixel in the image.In any case, the pixels are connected to the nearest cluster core because of the usual Xy laboratory feature.The brand-new core is weighed for all pixels.At the end of this process, some stray labels will exist, which means a number of pixels within a larger area.However, the same mark is not connected with it. Such re-labelling of the disjoint section with the labels of the largest adjacent cluster improves the property in the last stage of the algorithm.

I. Feature Extraction

The extraction function of the captured images can be carried out using the number of

techniques available. In this article, we will use a machine learning algorithm to make the device more robust. There are many algorithms in the machine learning algorithm which are graded on the basis of their results. Specifically, supervised learning of the Random Forest and the nearest neighbor algorithm is useful, as these algorithms produce a function that maps inputs to the desired outputs.

$$Contrast = \sum_{n=0}^{N\ g^{-1}} n^{2} \quad \sum_{i=1}^{N\ g} \quad \sum_{j=0}^{N\ g} \{(i,j)\} \qquad (2)$$

$$Correlation = \frac{\sum_i \quad \sum_j (i,j)p(i,j) - \mu_x \mu_y}{\sigma_x \sigma_y} \qquad (3)$$

$$Energy = \sum_i \sum_j p(i,j)^2 \qquad (4)$$

$$Dissimilarity = \sum_i \sum_j |i-j| * p(i,j) \qquad (5)$$

$$Entropy = \sum_i \sum_j p(i,j)\log(p(i,j)) \qquad (6)$$

$$Homogeneity = \sum_i \quad \sum_j \quad \frac{1}{1+(i-j)^2} p(i,j) \qquad (7)$$

$$Variance = \sum_i \sum_j (i-\mu)^2\, p(i,j) \qquad (8)$$

$$Difference\ Variance = Variance\ of\ \ p_{\ x-y} \qquad (9)$$

$$Cluster\ Shade = \sum_i \sum_j \left(i + j - \mu_x - \mu_y\right)^3 p(i,j) \qquad (10)$$

I. CLASSIFICATION

Vector support machines are supervised learning models that evaluate data and patterns that can be used for classification. The basic SVM uses a number of input data and predicts which of the two groups is the input to construct a non-probabilistic binary linear classification. From a set of training examples, each classified as belonging to one of the two categories, the SVM training algorithm constructs a model that assigns new examples to one category or another. In the proposed process, we use a linear classifier

RESULT AND DISCUSSION

Radiopedia.org has taken data sets that have been used. We have chosen T1W, T2W, STIR, PD, improved tumor contrast images in light range. Our techniques can be applied to higher intense tumor images, instead of other tissue or regions of the bone. The reason behind the selection of these images is because The experimental results of a set of MR images containing two kinds of tumors, Enchondroma, Giant cells

We have analyzed 2000 MR images for our work and collected 507 MR data samples. They are processed separately by manual analysis in tumor and non-tumor archives. The remainder

have been discarded mostly because of poor river segmentation. Data 318 in 507 samples MR images are those without tumors and 189 MR The tumor images are the images.
System accuracy can be defined mathematically as follows:

$$\text{System Accuracy} = \frac{TP + TN}{(TP + TN + FP + FN)} \times 100$$

If the count of True Positives (TP) and True Negatives (TN) are high then the system depicts high accuracy.
When the system correctly classify tumor as tumor then it's sensitivity and true positive rate is calculated as follows:-

$$\text{Sensitivity} = \frac{TP}{(TP + FN)} \times 100$$

$$\text{Specificity} = \frac{TN}{(TN + FP)} \times 100$$

After system development we have checked the proposed system on i3 processor with 6 gb ram machine. We have tested three set of dataset for accuracy measurement 60 images, 80 images and 150 image. Initially system works well so we have tried large dataset to train system. During training phase we have used 845 images for training. After testing on different sets of data we can clearly say with super pixel algorithm accuracy has increase.

Table 1: Accuracy Table

Accuracy		
Data subset	**with superpixel**	**without superpixel**
T1(60 image)	97%	96%
T2 (80 image)	98.50%	97%
T3 (150 image)	98%	94%

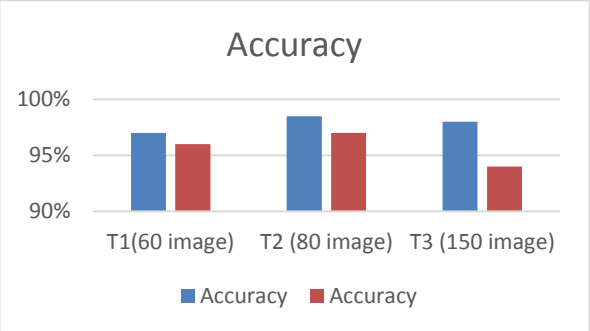


Figure 3: Accuracy Graph

CONCLUSION

Bone cancer is one form of harmful illness, so cancer must be identified in the early stages. But the most difficult task is detecting bone cancer. A lot of techniques are used to detect bone cancer from the literature review but they have some limitations. Our proposed method in the multiple stage as preprocessing, edge detection, morphological function, segmentation, then extraction of features and finally classification. The suggested system successfully identifies cancer of the bone from CT scanning images. By the conclusion of the system , the system is fulfilling the optimal goal.

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