

## BONE TUMOR DETECTION USING IMAGE PROCESSING

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**Abstract**— The detection of bone cancer remains a significant medical challenge because it frequently results in serious health complications up to patient death. Medical professionals use X-rays alongside MRIs and CT scans to diagnose bone cancer during contemporary diagnostics. Manual interpretation of these images requires skilled personnel since it demands substantial work time. An automated system needs development to detect accurately between cancerous and non-cancerous bone tissue since efficient distinction between both types is an undeniable necessity.

The main indicator which differentiates cancerous bones from normal ones is the texture within infected areas. Other datasets which present identical morphological properties between cancerous and normal bones prove difficult to classify accurately. First the authors find the most efficient detection algorithm that addresses this challenge.

Two different features are developed with one incorporating the addition of Histogram of Oriented Gradients (HOG) and the other without this feature. The performance comparison of these feature sets relies on two electronic classifiers that include Support Vector Machine (SVM) as well as Random Forest. High accuracy results can be obtained using HOG features since the SVM model trained with these features delivered 0.92 F1-score to surpass the Random Forest model at 0.77 F1-score.

### 1. INTRODUCTION

A human body contains 206 bones organized as a structural framework that enables mobility together with stability. The health of bones depends heavily on the presence of ligaments together with fibrous tissues and their spongy bone marrow content. Normal cell transformations lead to tumor development in the bones according to Blackledge et al. (2014) [1]. A characteristic symptom of bone cancer appears as tumor formation that

enlarges gradually until it reaches neighboring parts of the body. Bone tissue suffers severe damage as well as bones become weaker through this specific action. The statistics in 2018 showed that 3,500 Americans were diagnosed with bone cancer and the disease claimed 47% of their lives. X-ray imaging stands as a vital tool for detecting malignancies because it serves as one of several diagnostic tests used in bone cancer detection. The assimilation rate of malignant bone tissue differs from normal tissue which produces irregular and broken X-ray images (Oishila et al., 2018) [2].

The evaluation of bone cancer development relies on stage and grade assessment while the speed of tumor expansion including its destructive traits towards bone tissue (geographic bone destruction) serves as a vital diagnostic element. Medical diagnosis of cancers often requires extensive time from physicians and it remains prone to misdiagnosis. The survival rate for cancer patients becomes higher when cancer is detected at an early stage. The proposed system uses Support Vector Machines together with image processing methods to identify and classify bone tumors. Various studies attempted to generate systems which aid medical workers in their duties through automated diagnosis solutions coupled with techniques to decrease diagnostic time and reduce errors. Research literature demonstrates how existing systems employ the combination of Support Vector Machines with digital image processing methods involving preprocessing and edge detection and feature extraction to achieve these results (Chen et al., 2007) [3].

Yadav and Rathor (2020) [4] developed an automatic bone condition diagnosis system through a deep neural network to identify healthy bone and fractures from one another. The big dataset underwent image augmentation as a performance improvement measure before training the model. Researchers employed k-fold cross-validation tactics as a way to address potential image duplicity concerns that arose during image augmentation. Study research conducted by Asuntha and Srinivasan (2017)

[5] established that GLCM features alone cannot definitely confirm cancerous bones. The research demonstrated how the combination between entropy and skewness information became essential for cancerous region detection because cancerous regions exhibited decreased entropy values than non-cancerous regions. HOG features represent a useful technique to detect cancerous regions because they analyze pixel direction alongside pixel shape to achieve high accuracy. Bandyopadhyay et al. (2018) [2] used multiple techniques and texture features to identify cancerous and normal bone structures. Long bone samples were studied in this research while it emphasized the significance of reaching accuracy levels greater than 85%.

This manuscript provides the following primary contributions: Identification of the best feature set by experimental testing, which enhances the precision of distinguishing between cancerous and normal bones even when there is a small dataset. Comparison of SVM and Random Forest models, with SVM being the better algorithm for bone condition diagnosis.

Increased sensitivity of the developed method to cancerous bone tissue, indicating its viability for real-time use in offering second opinions to medical doctors.

The organization of the paper is: Section 2 offers a summary of the current literature, Section 3 expounds on the suggested methodology, Section 4 describes the obtained results, Section 5 gives an analysis of the results, and Section 6 concludes the research.

## LITERATURE REVIEW

Researchers at Avula et al. (2014) [6] developed a method which used mean pixel intensity analysis to determine bone malignancies in MRI images. They used the average pixel intensity to separate cancerous tissues from healthy tissues while demonstrating the strength of this easily implemented approach. Ranjitha et al. (2019) [7] conducted research using MRI images to identify malignant from benign tumors [7]. Their approach involved extracting texture features followed by using the K-means clustering algorithms for detecting tumor areas. The researchers determined tumor malignancy based on the calculated mean pixel value threshold matched against tumor area pixel totals. The pixel intensity-based quantitative process presents a strong foundation that leads this methodological framework.

The research provides essential methods for bone malignancy analysis while demonstrating medical imaging benefits. The research team of Jose et al. (2014) [8]

presented a different brain tumor sectoring method that combined fuzzy C-means and K-means clustering methodologies. This clustering method proves its ability to define tumors in brain images through flexible boundary definitions.

These researchers demonstrated a universal technique for MRI and CT image segmentation which showcases how segmentation methods adapt to various types of medical imaging tools (Patel and Doshi 2014).

The research by Reddy et al. (2015) [9] presented an innovative assessment technique combining region growing methods for measuring bone malignancy size and stage development. During segmentation the region of interest received division according to area growth parameters which calculated the tumor size through pixel count analysis. The mechanism to determine malignancy stage depended on pixel intensity but selecting proper seed points during the process proved difficult. The wide assortment of techniques demonstrates how medical image computing continuously evolves as healthcare providers develop multiple strategies to segment tumors for diagnosis purposes.

The research by Reddy et al. [9] in 2016 relied on MRI images to both detect and stage bone cancer. They applied denoising methods to reduce image noise before creating pixel-based clusters. Mean pixel intensity measurement along with other factors served as key components in determining the cancer stage. Kaushik and Sharma (2016) [10] established a volume calculation system through volumetric analysis suitable for malignant region analysis. The K-means clustering algorithm along with Sobel edge detection methods created bone malignancy detection according to Sinthia and Sujatha (2016) [11]. The system implemented by Sinthia and Sujatha detected tumors through edge pixels analysis using K-means to cluster areas containing tumors. Various medical imaging approaches demonstrate how different detection methods contribute to the development of bone cancer diagnosis methods. Researchers from Asuntha et al. (2017) [12] introduced complex MRI cancer detection methods that involved

Gabor filtering to cleanse images from noise. Through their work the researchers executed superpixel and multilevel segmentation to detect edges before using morphological operations to enhance tumor identification. The developed features helped researchers identify bone cancer in medical images. Shafat et al. (2017) [14] conducted research about destructive stem and progenitor cells in bone marrow to give knowledge about modern medical strategies against bone cancer.

The early identification of bone cancer serves to enhance survival rates according to Asuntha and Srinivasan (2018) [5]. A strong diagnostic system to detect cancer at its initiation points was developed by using image processing methods that boosted the diagnostic speed. Nisthula and Yadhu (2013) [15] developed image enhancement techniques to accentuate cancerous tissue edges followed by using edge detection methods to identify cancerous bone tissue. Torki (2019) [16] designed a bone disease recognition framework to forecast the beginnings of malignant disease through testing with a MATLAB-based validation system. Researchers from Vandana et al. (2020) [17] investigated graph cut-based clustering algorithms for performing bone tissue classification between cancerous and healthy conditions. A multiclass irregular texture analysis approach enabled them to classify bone structures among typical ones and benign along with malignant types. Shrivastava et al. (2020) [18] performed an extensive study which investigated different approaches to categorize bone tissues through DICOM format CT scans. Their research emphasizes the elevated significance of artificial intelligence (AI) in medical imaging which performs well when detecting tumors along with fractures and ulcers. Notable medical research progress occurs because healthcare professionals employ AI methods for accurate anomaly detection and diagnostic tasks.

The analysis of bone cancer requires feature extraction which AI has greatly enhanced as an essential identification step. Bone density and color evaluation with texture examination leads to classification through machine learning approaches which discern healthy from cancerous bones. Researchers evaluated the ROI detection abilities of segmentation methods Canny, Prewitt and Sobel within this research. The investigation produced two features sets for evaluation: HOG together with Entropy, Energy, Gini Index, Skewness, Contrast, Correlation, and Homogeneity Product of  $E(X)$  and  $D(X)$  while the other feature set omitted HOG. The evaluation used these extracted features to build predictive models that allowed researchers to examine Random Forest against Support Vector Machine (SVM). The research demonstrated that SVM achieved better performance rates with HOG included among other features because the model successfully recognized delicate bone structure features for cancer detection purposes.

### 3. Materials and Methods

#### 3.1 Preprocessing

To enhance the quality of the X-ray images, several preprocessing techniques are applied. Since X-ray images often contain noise, a  $3 \times 3$  median filter is used to reduce this noise. After that, the image undergoes a blurring process followed by a sharpening step to enhance the features of the image.

#### 3.1.1 Image Segmentation

Once preprocessing is complete, the next step involves object detection through segmentation. The reliability of the segmentation method is evaluated based on its precision rate, confirming its effectiveness in isolating relevant objects. During segmentation, pixel sets are generated to extract essential information about the identified objects. For image segmentation, the Canny edge detection algorithm is chosen due to its superior ability to capture sharp edges, which are crucial for identifying Regions of Interest (ROIs). The effectiveness of the Canny algorithm is further demonstrated by its excellent performance with small datasets and its ability to scale as the dataset size grows, making it a reliable choice compared to other algorithms such as Sobel and Prewitt.

#### 3.1.2 Feature Extraction

Following the segmentation process, the next step involves feature extraction, which is based on the texture descriptor. Inspired by Haralick et al.'s [25] method, the Gray-Level Cooccurrence Matrix (GLCM) is used to calculate essential texture features. These include contrast, correlation, energy, and homogeneity, which are derived from the pixel values in the segmented image.

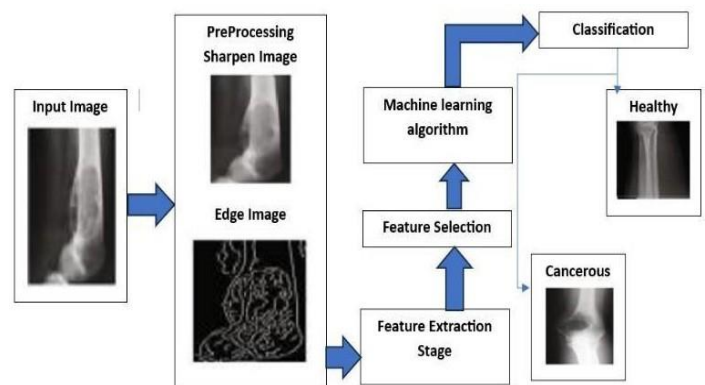


Fig.1: System Flow Diagram

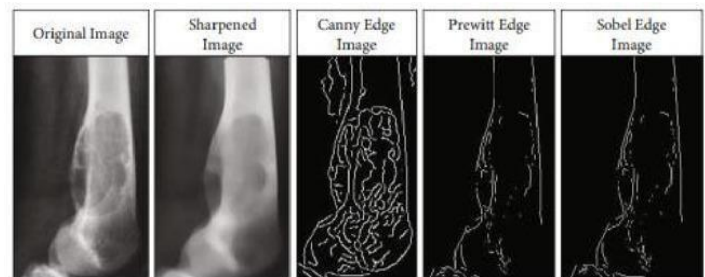


Fig.2: Different Types of Processed Images

### 3.2 SVM Model

Support Vector Machines (SVM) are used effectively for classifying and detecting bone cancer. In this study, a linear SVM model is applied for binary classification, distinguishing between cancerous and healthy bone samples. Let  $x$  represent the input vector, and  $y$  represent the class label, which can either be cancerous or healthy. The training dataset contains instances of both cancerous and healthy bones, denoted as  $f(p_i, q_i), i=1, 2, 3, \dots, n$ . The SVM algorithm constructs a decision function  $F(x)$  to classify the input data. A hyperplane is used to separate the data into two classes, expressed by  $u \cdot p + b = 0$ , where  $u$  is a vector in  $\mathbb{R}^d$  and  $b$  is a real number. The goal of the classification process is to maximize the margin between the two hyperplanes, with the condition  $|u \cdot p - b| \geq 1$ . The linear kernel function is used, with a soft margin parameter  $C=1$ , to achieve the optimal classification.

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#### 3.2.1 SVM Model Training

The SVM model is trained using two different feature sets. In the first experiment, the feature set includes {HOG, Entropy, Energy, Gini Index, Skewness, Contrast, Correlation, Homogeneity Product of  $E(X)$  and  $D(X)$ }, while in the second experiment, the feature set consists of {Entropy, Energy, Gini Index, Skewness, Contrast, Correlation, Homogeneity Product of  $E(X)$  and  $D(X)$ }. Both experiments use a linear kernel and an initial learning rate of 0.001.

The hyperplane for the proposed model is plotted using the feature set {Entropy, Energy, Gini Index, Skewness, Contrast, Correlation, Homogeneity Product of  $E(X)$  and  $D(X)$ }. The SVM model efficiently distinguishes between cancerous and healthy bone samples, producing eight support vectors.

### 3.3 Random Forest

Random forests are a type of ensemble learning algorithm that uses multiple decision trees to classify and provide predictions. The model aggregates results from multiple trees by sampling random subsets of the training data (100 times). For each iteration  $b=1, \dots, 100$ , let  $R_b(x)$  denote the class prediction from the  $b$ -th decision tree. The

final prediction  $R_{100}(x)$  is obtained by a majority vote from the predictions  $R_b(x)$  across all iterations.

## 4. Result

### Experimental Evaluation

In this study, we conducted two experiments: one utilizing HOG feature sets and another without HOG features, employing two machine learning models—Random Forest and SVM. The performance of these models was evaluated using 5-fold crossvalidation.

#### 4.1 Data Set

The bone X-ray image datasets used in this study were sourced from publicly available databases, including the Indian Institute of Engineering Science and Technology, Shibpur (IEST), and The Cancer Imaging Archive (TCIA).

##### 4.1.1 Performance Evaluation

The proposed method was implemented using MATLAB 16(a) on a Microsoft Windows 8 system with 16 GB of RAM. The training set comprised 65 images, and the testing set contained 40 images. To reduce noise in the images, a  $3 \times 3$  median filter was applied. Image segmentation was performed using the Canny edge detection method. Features were extracted from both cancerous and healthy bone images, and SVM was utilized for training and classification. Skewness, which measures the symmetry of pixel distribution, showed lower values in cancerous bones, indicating an asymmetrical distribution of pixels. The skewness values for both the training and test images are displayed in Figures 5 and 6.

##### 4.1.2 Performance Evaluation with HOG Features

The Histogram of Oriented Gradients (HOG) feature plays a vital role in training and classification, capturing the shape and direction of pixels through gradient and orientation extraction. The image was divided into smaller regions, and histograms were computed for each region. The window size for the HOG feature was set to 3, with 6 histogram bins, and the image was resized to  $25 \times 25$  pixels. Gradient calculations in both the  $x$  and  $y$  directions indicated changes in intensity. The test results with HOG features are shown in Figure 7, which reveals 1 false negative and 2 false positives out of 20 cancerous and healthy bone images. In contrast, when HOG features were not applied, as shown in Figure 8, 2 false negatives and 3 false positives were observed. The confusion matrices for both the test data with and without HOG



features are presented, and a comparative analysis based on accuracy, precision, recall, and F1 score suggests the significance of HOG features in the accurate identification and classification of cancerous and healthy bones. This finding aligns with similar studies that have used GLCM-based texture features for tumor classification.

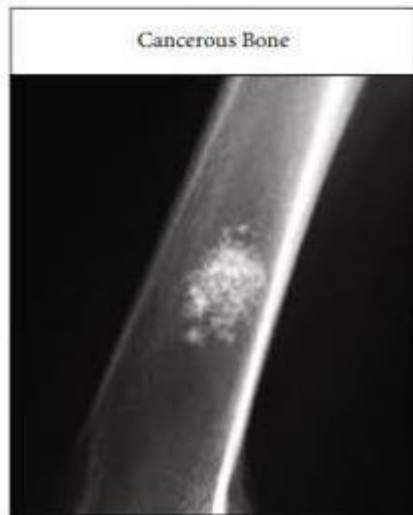


Fig.3: Image with Tumorous Bone

#### 4.2 Performance Evaluation Using 5-Fold Cross-Validation

The dataset used for this study contained 105 images, with 65 representing bone cancer and 40 depicting healthy bone. To ensure unbiased performance evaluation, 5-fold cross-validation was applied. Figures 9 and 10 show the confusion matrices for the Random Forest and SVM models, respectively. The training and validation loss curves for the proposed model are illustrated in Figure 3. Due to the small size of the dataset, the loss curve does not stabilize, with the maximum loss remaining below 1. Further reduction in the loss can be achieved by training for additional epochs on a larger dataset.

### 5. Discussion

#### Bone Cancer Classification and Texture Analysis

The occurrence of bone cancer has been increasing, often attributed to various factors, including fluid accumulation, fat cells, and hematopoietic cells. Research shows that distinguishing between these components is crucial for accurate diagnosis. Texture analysis has emerged as an effective tool for this purpose, with texture being represented by pixel intensity. Cancerous and healthy bone tissues exhibit differing pixel intensities, making texture-based features critical for image classification (Reischauer et al., 2018) [26].

The distribution of pixels in healthy bone tissue is distinct from that in cancer-affected regions. Previous research, such as the study by Reddy et al. (2016) [27], utilized mean pixel values for segmenting cancerous bone but did not focus on classification. This method involved extracting the region of interest (ROI) from MRI images of bones affected by cancer, followed by analyzing the affected area based on pixel counts. Subsequently, the mean intensity values were used to predict the cancer stage. A different approach by Asuntha et al. (2017) [12] incorporated GLCM-based texture features, although it lacked the ability to classify bone types. Realizing the limitations of GLCM alone, the current study introduces additional features such as HOG (Histogram of Oriented Gradients) to enhance the identification and classification of cancerous bones.

HOG plays a significant role by capturing pixel direction and shape within local regions, thus assisting in the identification of cancerous areas. Bandyopadhyay et al. (2018) [2] combined multiple techniques and texture features to classify cancerous and healthy bones, primarily focusing on long bones, achieving 85% accuracy. However, their model's performance can be improved, and this study extends beyond long bones, encompassing a more diverse range of bone types.

#### 5.1 Comparative Analysis and Performance Metrics

This study thoroughly compared machine learning algorithms, specifically Support Vector Machine (SVM) and Random Forest, using a 5-fold cross-validation approach with selected features (see Table 4). The features remained consistent throughout the training. The results, displayed in Table 4, show that SVM outperformed Random Forest across all evaluation metrics. As a result, SVM was chosen for the task of diagnosing cancerous and healthy bones.

A visual representation of the cancerous regions detected using HOG features further demonstrates the effectiveness of this approach. To assess the performance of the proposed method, a comparison with a previous study [2] is provided in Table 5. The proposed method shows superior performance in key metrics, including accuracy, precision, recall, and F1 score. This enhanced performance is attributed to HOG's ability to capture pixel direction and shape within specified window sizes and histogram bins. The ROI is identified using a bounding box, which captures the scattered nature of cancerous pixel regions in bone images (Oishila et al., 2018) [2].

## 5.2 Comparative Analysis and Improvement Over Previous Work

The proposed method has been rigorously compared with a previous study by Oishila et al. (2018) [2], which relied on texture features like entropy and standard deviation. Unlike their approach, which faced challenges with various bone types, the new method uses HOG features in combination with entropy and standard deviation, enabling better differentiation between cancerous and healthy bones across a wide range of bone structures.

The proposed method excels across all performance metrics. Notably, the F1 score of the proposed model (0.94) surpasses that of Oishila et al. (2018) [2], which achieved an F1 score of 0.88 for cancerous bone classification. Table 5 provides a detailed comparison, highlighting the superior performance of the proposed approach.

Figure 14 visually compares the results of the proposed method with those from previous research. The SVM model, using the HOG feature set, consistently outperforms Oishila et al.'s (2018) approach. Despite slightly lower precision and F1 scores in the new method, the inclusion of 5-fold cross-validation significantly improves accuracy and recall compared to previous work [2].

## 6. Conclusion

In conclusion, the proposed method combines feature extraction and classification models to effectively distinguish between cancerous and healthy bones. The methodology begins with a preprocessing step that uses a 3x3 median filter to reduce noise, followed by object extraction via the Canny edge detection algorithm. The key difference between cancerous and healthy bones lies in the unique texture of the cancerous areas, which are marked by a more scattered distribution of pixels compared to healthy bone tissue.

Although GLCM-based texture features are commonly used, the experiment demonstrated their limitations. Additional texture features, such as entropy and skewness, proved to be vital in predicting cancerous regions. Particularly, the HOG feature, which captures pixel shape and direction, added significant value to the model. The results show that combining HOG with GLCM features yielded an impressive F1-score of 92.68%, outperforming the 87.80% F1-score achieved without the HOG feature.

The proposed method achieved an accuracy of 92.30% when using HOG features, surpassing the 85% accuracy achieved by Oishila et al. (2018) [2] in their cancerous bone classification model. The system's performance can be further enhanced by incorporating additional texture features. In summary, the proposed approach demonstrates high precision in detecting both cancerous and healthy bone images, showing particular sensitivity to cancerous bone regions. This indicates its potential for real-time application, providing valuable second opinions to healthcare professionals. Future work will focus on developing larger datasets for more comprehensive model evaluation and investigating optimization techniques, such as monarch butterfly optimization, earthworm optimization, elephant herding optimization, moth search, slime mold algorithm, and Harris hawks optimization, to improve performance further.

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