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Bone Cancer Detection and Segmentation Using K-Means Clustering with KNN and SVM Classification

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KEYWORDS

Bone Cancer Detection, K-means Clustering, Machine Learning, K-Nearest Neighbor (KNN), Support Vector Machine (SVM)

ABSTRACT

Bone cancer is one of the most aggressive and life-threatening forms of cancer, caused by the unregulated proliferation of abnormal cells within bone tissue. Due to its rapid progression and high potential to spread to other parts of the body, early detection of bone cancer is crucial for improving patient survival and treatment outcomes. Traditional diagnostic methods are often time-consuming, labor-intensive, and highly dependent on the expertise of radiologists, which may lead to delayed diagnosis. In recent years, medical image analysis techniques using data mining, image processing, and machine learning algorithms have gained importance for more accurate and efficient detection of bone cancer. In this work, a hybrid approach is proposed for bone cancer detection, starting with K-means clustering for segmenting the bone regions in medical images. The segmented images are further analyzed using mean intensity evaluation to highlight potential areas of abnormal growth. For the classification stage, both K-Nearest Neighbor (KNN) and Support Vector Machine (SVM) algorithms are employed. KNN classifies images based on similarity to labeled examples, while SVM enhances accuracy by constructing an optimal hyperplane to separate cancerous and non-cancerous samples, particularly effective for high-dimensional and complex image features. Threshold values are applied during the classification process to determine the presence or absence of bone cancer. The proposed system is applicable to various image formats, including JPEG and CT scan images, and aims to achieve higher accuracy and reliability than conventional methods. By combining K-means segmentation with KNN and SVM classification, the approach not only accelerates the diagnostic process but also reduces human error, supporting healthcare professionals in early detection and treatment planning. The results demonstrate that this hybrid method can serve as a robust and efficient tool for automated bone cancer detection, potentially improving clinical decision-making and patient outcomes.

I. INTRODUCTION

Bone cancer is a serious and potentially life-threatening disease that affects the human skeletal system and, in advanced cases, can impact multiple organs and tissues throughout the body. It arises when normal bone cells undergo genetic mutations that damage their DNA, causing them to grow and divide uncontrollably. Unlike healthy cells, which either repair DNA damage or undergo programmed cell death, these mutated cells continue to survive and proliferate, forming abnormal masses known as cancers. Bone cancer can originate in the bones themselves, referred to as primary bone cancer, or it can develop when cancer cells from other parts of the body spread to the bones, a process known as metastasis. Metastasis occurs when cancer cells detach from their original site and travel through the bloodstream or lymphatic system to establish new cancers in distant organs, including the bones. Certain cancers, such as breast, prostate, and lung cancer, have a high propensity to metastasize to the skeletal system, further complicating diagnosis and treatment.

As these cancerous cells accumulate in the bone tissue, they interfere with normal bone functions, leading to pain, weakness, swelling, and fractures. Moreover, bone cancer often affects the body more systemically, impacting the digestive, nervous, and circulatory systems, as well as hormone regulation, which can result in fatigue, unexplained weight loss, and general deterioration of health. The uncontrolled proliferation of cancer cells and the formation of cancers disrupt the normal balance between bone formation and resorption, compromising structural integrity and causing significant physiological stress. Early detection and diagnosis are crucial, as they allow for timely intervention and treatment strategies that aim to slow disease progression, alleviate symptoms, and improve quality of life. Research continues to explore the molecular mechanisms of bone cancer, including the genetic mutations, cellular signaling pathways, and environmental factors that contribute to cancer growth and metastasis, with the ultimate goal of developing more effective therapeutic approaches.

Understanding bone cancer's pathophysiology, metastatic behavior, and systemic effects is essential for medical professionals, researchers, and caregivers to devise comprehensive strategies for prevention, management, and treatment of this devastating disease.

A bone cancer is defined as an abnormal growth of tissue within the bone, which can be classified as either benign or malignant depending on its behavior and potential to spread. Benign cancers are non-cancerous and generally remain localized, growing slowly without invading surrounding tissues or metastasizing to distant organs. In contrast, malignant cancers, commonly referred to as bone cancer, exhibit uncontrolled cellular proliferation and have the potential to invade nearby structures and spread throughout the body. Bone cancers are further categorized into primary and secondary cancers. Primary bone cancers originate directly from bone cells or connective tissues, with sarcomas being the most prevalent type. These include osteosarcoma, chondrosarcoma, and Ewing's sarcoma, which typically arise from genetic mutations that disrupt normal cell growth regulation, causing the cells to divide uncontrollably.

Primary bone cancers are capable of invading adjacent blood vessels, muscles, nerves, and fatty tissues, facilitating the dissemination of cancerous cells to other organs in severe cases. In addition to malignant growths, some primary cancers may remain benign, yet they can still cause structural deformities, chronic inflammation, or infections within the bone due to abnormal tissue proliferation. On the other hand, secondary bone cancers, also known as metastatic bone cancer, occur when cancer cells from other organs—such as the breast, prostate, lung, or kidney—spread through the bloodstream or lymphatic system and colonize the bones. Secondary bone cancer is significantly more common than primary bone cancer and often leads to multifocal lesions in different skeletal sites, disrupting normal bone remodeling and integrity. This metastatic process not only weakens bones, leading to fractures, pain, and reduced mobility, but also contributes to systemic complications such as fatigue, weight loss, and impaired organ function.

The presence of secondary bone cancers indicates advanced-stage disease, which complicates treatment and negatively affects patient prognosis. Understanding the distinctions between primary and secondary bone cancers, including their origin, growth patterns, and potential to metastasize, is critical for early diagnosis, treatment planning, and the development of targeted therapies. Modern diagnostic tools, such as imaging techniques and molecular assays, are employed to identify cancer type, assess the extent of spread, and guide intervention strategies. Effective management of bone cancers requires a multidisciplinary approach, including surgery, chemotherapy, radiotherapy, and supportive care to alleviate symptoms, prevent further skeletal damage, and improve the overall quality of life for patients affected by these aggressive and often debilitating diseases.

2.LITERATURE REVIEW

[1]Sinthia P and K.Sujatha , A novel approach to detect the bone cancer using K-means algorithm and edge detection method.

In this method, X-ray or MRI images are used as input for the detection process. Initially, the images are preprocessed to remove noise and to enhance image quality, which improves the visibility of bone structures. The K-means clustering algorithm is then applied to segment the image into different clusters based on pixel intensity values. This clustering process helps in separating normal bone tissues from cancer-affected regions.

The selection of an appropriate number of clusters plays an important role in the performance of the K-means algorithm. From the clustered output, the cancer area is identified clearly. After segmentation, an edge detection technique is applied to extract the boundary of the detected cancer region.

The edge detection process highlights only the outer edges of the abnormal area. This helps in clearly visualizing the shape and extent of the cancer. The extracted edges further improve the clarity of the affected region. The proposed approach reduces the complexity of manual diagnosis and provides an automated solution for bone cancer detection. The system improves the accuracy of cancer region identification and supports doctors in clinical decision making, thereby enabling early and reliable detection of bone cancer.

[2]Mokhled S. Al-tarawneh ,Lung cancer detection using image processing techniques.

Proposed a lung cancer detection method using image processing techniques on CT scan and chest X-ray images to identify suspicious lung nodules at an early stage. In this approach, the medical images are first collected and converted into a suitable digital format for further processing. Image preprocessing is performed to remove noise present in the images. Contrast enhancement is applied to improve the visibility of lung structures. This preprocessing stage helps in obtaining clearer lung regions. After preprocessing, segmentation techniques are used to isolate the lung area from the background. The segmented image helps in separating normal lung tissues from abnormal regions. This step assists in locating suspicious lung nodules more effectively. Feature extraction is then carried out from the segmented regions. Important features such as size, shape and texture are extracted. These features represent the characteristics of lung nodules.

The extracted features are used for further image analysis. The system compares the obtained features with known patterns. This comparison helps in identifying cancer affected regions.

The possible cancer areas are highlighted for medical observation. The proposed method reduces the need for continuous manual inspection by radiologists. It also helps in minimizing human errors during diagnosis. The method improves the accuracy of lung cancer detection. It enables faster processing of large numbers of medical images. Overall, the approach supports early diagnosis and assists radiologists in clinical decision making.

[3]. Fatma Taher and NaoufelWerghi , Lung cancer detection by using Artificial Neural Network and Fuzzy Clustering Methods.

Proposed a lung cancer detection framework based on Artificial Neural Network and fuzzy clustering methods for analyzing CT scan and chest X- ray images. In their approach, the acquired medical images are first preprocessed to remove noise and to enhance contrast so that lung structures become more visible. Fuzzy clustering is then employed to accurately segment the lung regions and to separate suspicious nodules from normal tissues by allowing pixels to belong to more than one cluster. This soft segmentation strategy improves the robustness of nodule extraction in complex and low-contrast images. After segmentation, a set of discriminative features related to intensity, shape and texture are computed from the suspected regions.

These features are used to train an Artificial Neural Network for effective classification of lung nodules into cancerous and non-cancerous classes. The learning capability of the neural network enables better generalization and improved prediction performance. The proposed system also helps in reducing false detection rates and provides consistent and repeatable results. Overall, the method enhances detection accuracy, supports early screening of lung cancer and acts as a reliable computer-aided diagnosis tool for clinical applications.

[4]. Anita Chaudhary and SonitSukhrajsingh , Lung cancer detection on CT images by using image processing.

In this approach, CT scan images are first collected and converted into a suitable digital format for further analysis. Image preprocessing is performed to remove noise and to enhance image quality, which improves the visibility of lung structures and suspicious regions. Segmentation techniques are then applied to separate the lung region from the background and to isolate possible cancer affected areas. After segmentation, feature extraction is carried out to obtain important characteristics such as size, shape and texture of lung nodules.

These extracted features support the analysis and identification of abnormal regions. Image processing algorithms are used to highlight the suspected cancer areas for medical observation. The proposed system provides an automated method for lung cancer detection and reduces the need for continuous manual inspection by radiologists. This approach improves the accuracy of lung cancer detection, helps in identifying cancer at an early stage, and supports doctors in making faster and more reliable diagnostic decisions.

[5]. Maduri Avula, Narasimha Prasad Lakkakula and Murali Prasad Raja, Bone cancer detection from MRI scan imagery using Mean Pixel Intensity.

In this approach, MRI images are first collected and converted into a suitable digital format. The method does not require large training datasets or complex learning models, which makes it suitable for low-resource medical environments. In their approach, the detected high-intensity and low-intensity regions are analyzed to distinguish healthy bone tissue from suspicious cancer tissue. The intensity-based segmentation provides consistent results for different MRI samples.

The output images clearly mark the abnormal regions, which improves visual interpretation for clinicians. The simplicity of the algorithm allows faster processing and real-time analysis of MRI scans. The proposed system can also be integrated with other feature extraction and classification techniques for further improvement. Overall, this approach offers a practical, efficient and reliable solution for MRI-based bone cancer detection and supports early screening and diagnosis.

[6]. Kishor Kumar Reddy, Anisha P.R and Raju G.V.S , A novel approach for detecting the cancer size and bone cancer stage using region growing algorithm.

In this method, MRI and CT scan images are used as input for analysis. Initially, image preprocessing is performed to remove noise and to enhance the quality of the medical images. The region growing algorithm starts from selected seed points and progressively groups neighboring pixels that have similar intensity values. This procedure helps in accurately extracting the complete cancer region from the image.

The segmented output is then used to calculate the exact cancer area and size. Based on the measured cancer size, the stage of bone cancer is estimated. The proposed approach improves the accuracy of cancer boundary detection and provides clear visualization of the affectedregions. It reduces manual intervention in medical image analysis and offers a faster and automated detection process. The system supports doctors in assessing disease severity and in planning appropriate treatment, thereby enabling reliable detection of cancer size and bone cancer stage.

[7]. Ezhil E. Nithila and S. S. Kumar, Automatic detection of solitary pulmonary nodules using swarm intelligence optimized neural networks on CT images.

Proposed an automatic method for detecting solitary pulmonary nodules on CT images using swarm intelligence optimized neural networks. In this approach, chest CT images are first collected and converted into a suitable digital format for processing. Image preprocessing is performed to remove noise and to enhance image quality, which improves the visibility of lung structures and small nodules. Segmentation techniques are then applied to isolate the lung region from the background and to focus only on the area of interest. After segmentation, feature extraction is carried out to obtain important characteristics such as size, shape and texture of the nodules.

These extracted features are provided as input to the neural network. Swarm intelligence algorithms are used to optimize the neural network parameters and improve its learning capability. This optimization enhances the classification performance of the network and reduces false detection rates. The trained neural network automatically detects solitary pulmonary nodules from CT images. The proposed system improves the accuracy and reliability of nodule detection, provides fast and automated analysis, and supports early diagnosis and clinical decision making by radiologists.

[8]. AbdulmuhssinBinhssan, Enchondromacancer Detection.

Proposed an automated method for enchondroma cancer detection using medical image processing techniques. In this approach, medical images such as X-ray, CT and MRI scans are first collected and converted into a suitable digital format. Image preprocessing is performed to remove noise and to enhance image clarity, which improves the visibility of bone structures and abnormal cartilage regions. Segmentation techniques are then applied to separate the bone region from the background. From the segmented image, the suspected enchondroma cancer region is extracted for further analysis. Feature extraction is carried out to obtain important characteristics such as shape, size and texture of the affected region.

These features help in identifying enchondroma cancer patterns and distinguishing them from normal bone tissue. Image analysis methods are used to highlight abnormal cartilage areas inside the bone. The proposed system provides an automated and efficient solution for enchondroma cancer detection, reduces manual effort and human errors during diagnosis, and improves the accuracy of cancer identification. Overall, this approach supports early diagnosis and assists doctors in clinical decision making possess linear-phase characteristics.

3.EXISTING SYSTEM

Traditional bone cancer detection primarily relies on manual examination of medical images, including X-rays, CT scans, and MRI scans, by trained radiologists. In this approach, radiologists visually inspect the images to identify abnormal growths, lesions, or changes in bone density that may indicate cancer. While effective in many cases, this method has several inherent limitations. First, it is **time-consuming**, especially when dealing with large numbers of images or full-body scans. Radiologists must carefully analyze each image, which can delay diagnosis and treatment planning. Second, manual diagnosis is highly dependent on the expertise and experience of the medical professional. Subtle indicators of early-stage bone cancer, such as small lesions, minor structural changes, or slight variations in bone density, can easily be overlooked. Misinterpretation or inconsistency in evaluation may occur due to fatigue, workload, or variability in professional judgment. This introduces the risk of false negatives, where cancer is present but not detected, or false positives, which may lead to unnecessary anxiety and further testing. Third, conventional detection methods lack automation and scalability. With the growing volume of medical imaging data, relying solely on human analysis becomes impractical and inefficient. Early-stage bone cancer often presents with minor visual changes that are difficult to distinguish from normal bone variations, making timely diagnosis challenging. Additionally, differences in imaging quality, patient positioning, and scanner settings can further complicate accurate assessment.

Some automated image-based approaches have been developed using threshold segmentation and morphological techniques:

1. **Threshold Segmentation:** This method separates bone regions from the background by selecting intensity thresholds. Regions with intensity values above or below a certain threshold are segmented to isolate potential abnormal areas.
2. **Morphological Analysis:** Features such as shape, size, area, and structural irregularities of the segmented bone regions are extracted. Morphological operations like dilation, erosion, opening, and closing help refine the segmented regions and highlight abnormalities.
3. **Classification:** Based on morphological features, the regions are analyzed and classified as normal or cancerous using rule-based or basic statistical methods.

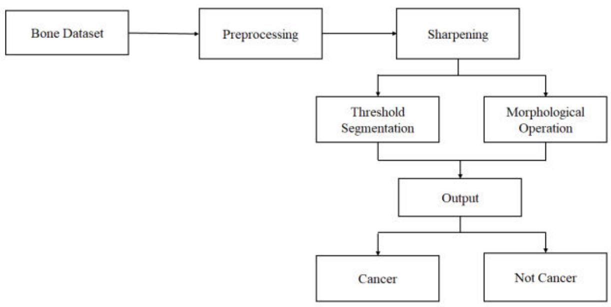


Figure 1: Existing System

Bone Cancer Dataset

Medical image datasets are a critical resource for developing and evaluating automated bone cancer detection systems. In this project, the dataset primarily consists of X-ray and CT scanimages, which provide complementary information about bone structure and abnormalities. X-ray images are widely used due to their simplicity, cost-effectiveness, and ability to reveal changes in bone density, fractures, or lesions. They are particularly useful for identifying large cancers or abnormal bone growths. However, X-ray images have limited depth information and may not clearly show early-stage lesions or subtle structural changes.

To address these limitations, CT (Computed Tomography) images are also incorporated into the dataset. CT scans provide cross-sectional views of bones, offering detailed three-dimensional information about bone morphology and cancer location. They enable more precise visualization of the size, shape, and density of abnormal growths, making them highly valuable for detecting bone cancer at earlier stages. The dataset includes images from multiple patients, with both cancerous and non-cancerous cases, and covers various bones in the human body

Bone Cancer Dataset and Pre-processing

In this project, the bone cancer dataset consists of medical images collected from publicly available repositories and clinical sources, including **X-ray and CT scan images**. X-ray images provide a two-dimensional view of bone structure and are commonly used for initial screening due to their accessibility and cost-effectiveness, while CT images offer detailed cross-sectional views that reveal bone density, lesions, and structural abnormalities more accurately. The dataset includes both **cancerous and non-cancerous bone images**, covering a variety of cases and anatomical regions to ensure diversity and robustness in training and testing the classification models.

Before analysis, the images undergo pre-processing to enhance quality and remove noise that may interfere with segmentation and classification. This step includes resizing the images to a standard dimension, gray scale conversion for uniformity, and contrast **enhancement** to highlight bone structures and potential cancer regions. Particularly for bone cancer analysis, gray scale images are preferred for initial processing because they simplify the data while preserving critical structural information. Colour images (RGB) contain three channels—red, green, and blue—which increase the computational complexity without necessarily providing additional diagnostic value for bone structure analysis.

Converting an RGB image to gray scale reduces its intrinsic complexity by collapsing the three color channels into a single intensity channel, effectively representing the brightness of each pixel. This brightness component is crucial for detecting subtle variations in bone density and structure, which may indicate the presence of cancerous lesions.

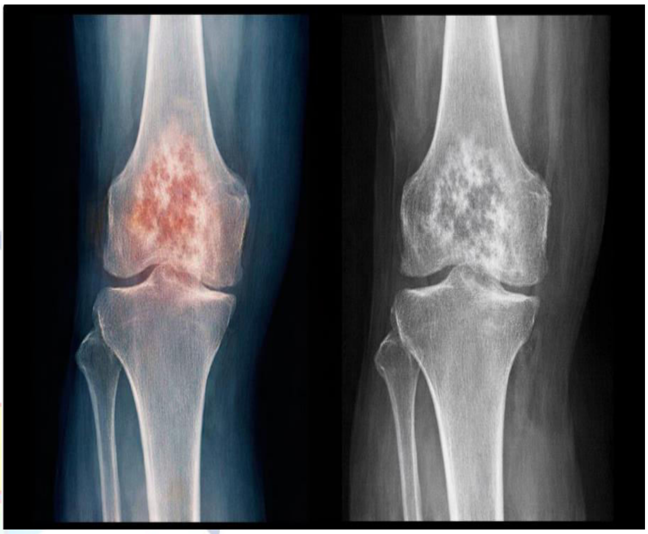


Figure 2: RGB to Gray scale conversion

Threshold segmentation is a widely used image processing technique for identifying regions of interest in medical images, particularly in bone cancer detection. In this approach, each pixel in a medical image, such as an X-ray or CT scan, is evaluated based on its intensity value. A threshold value is determined either manually or automatically, which separates the bone regions from the background and highlights areas that may indicate abnormal growth or cancers. Pixels with intensity values above the threshold are classified as part of the bone structure or potential cancer regions, while those below the threshold are considered background or irrelevant tissue.

In bone cancer detection, threshold segmentation helps to isolate abnormal regions, such as lesions or irregular growths, from normal bone tissue. After pre-processing the images—such as resizing, grayscale conversion, and noise reduction—the thresholding process generates a binary image in which cancerous regions appear distinct from healthy bone. This segmented output provides a clear visual representation of potential cancer locations and reduces the complexity of subsequent analysis.

Morphology Operations

Morphological operations are fundamental image processing techniques used to analyze and process the shapes and structures within medical images, such as X-rays or CT scans of bones. In bone cancer detection, these operations help enhance and isolate relevant features of bone tissue, such as cancers, lesions, or abnormal growths. Common morphological operations include **erosion, dilation, opening,** and **closing.**

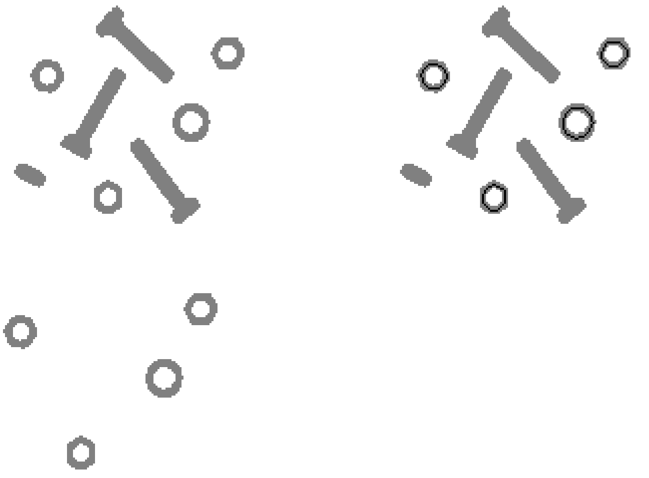
- **Erosion** removes small-scale noise and shrinks bright regions, helping eliminate insignificant artifacts.
- **Dilation** expands bright regions, emphasizing areas of interest such as cancerous lesions.
- **Opening** (erosion followed by dilation) is useful to remove small noise while preserving the overall shape of the bone structure.
- **Closing** (dilation followed by erosion) helps fill small holes or gaps in the detected bone regions.

By applying these operations, the edges and boundaries of cancerous regions become more distinct, making it easier for subsequent steps like thresholding, segmentation, and feature extraction to accurately identify bone cancer. Morphological processing therefore plays a crucial role in improving the reliability and precision of automated bone cancer detection systems.

Erosion:

Operation: Erosion is used to erode away the boundaries of white regions in a binary image while expanding the black regions.

Process: For each pixel in the image, the erosion operation checks if the structuring element fits entirely within the foreground region. If it does, the output pixel becomes white; otherwise, it becomes black.



a) Binary image **b)** Skeleton after filter **c)** Objects with holes

Figure 3: Isolation of objects with holes using morphological operations.

The binary objects are shown in gray and the skeletons, after application of the salt filter, are shown as a black overlay on the binary objects. Note that this procedure uses no parameters other then the fundamental choice of connectivity

Dilation:

Operation: Dilation is used to expand the boundaries of white regions (foreground) in a binary image while reducing the black regions (background).

Process: For each pixel in the image, the dilation operation checks if the structuring element (a smaller binary pattern) centered at that pixel overlaps with any foreground pixels in the image. If any overlap occurs, the pixel in the output image corresponding to the center of the structuring element is set to white.

Filling holes in objects- To fill holes in objects we use the following procedure which is

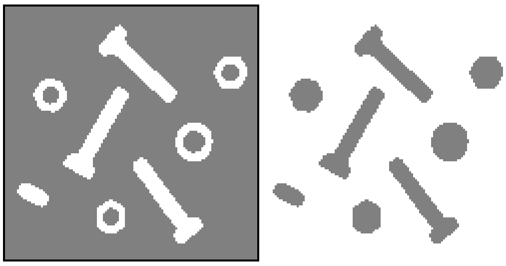
i) Segment image to produce binary representation of objects

ii) Compute complement of binary image as a mask image

iii) Generate a seed image as the border of the image

iv) Propagate the seed into the mask .

v) Complement result of propagation to produce final result



a) Mask and Seed images **b)** Objects with holes filled

Figure 4: Filling holes in objects.

In bone cancer detection, **dilation** is commonly applied to enhance the visibility of cancer regions and bone lesions in X-ray or CT images. Dilation helps to **expand the boundaries of detected cancerous regions,** making fragmented or faint lesions more prominent and connecting nearby abnormal regions that may appear disconnected due to imaging noise or low contrast. In this process, the **mask image,** which highlights areas of interest, is typically represented in gray, while the **seed image,** marking the initial detected cancer regions, is shown in black, as illustrated in the figure above. This technique ensures that subsequent segmentation and analysis steps capture the full extent of the cancerous tissue, improving the accuracy of automated bone cancer detection systems.

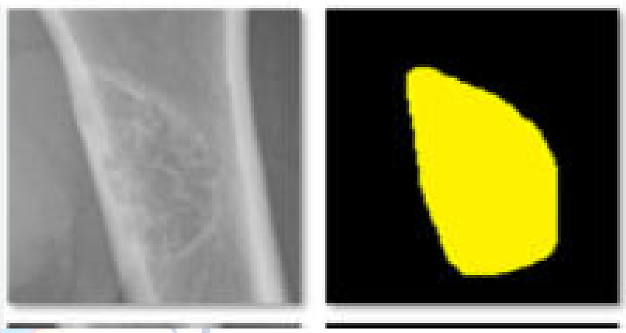
Threshold Segmentation

It can be observed that noise in the final segmentation of bone X-ray or CT images mainly arises from two sources: **background tissue**and**non-cancerous bone structures**. The subsequent processing steps, such as **background extraction**and **lesion isolation,** are based on this observation. In the**histogram of the contrast-stretched grayscale bone image,** multiple peaks typically appear, representing **healthy bone tissue, cancerous lesions,** and the**background**. The background generally exhibits a distinct contrast compared to bone and cancer regions, making it feasible to separate it using thresholding techniques. However, as noted in the Introduction, it remains challenging to fully isolate cancerous regions because some lesions may have gray intensity values similar to surrounding healthy bone. Therefore, the**first stage of the bone cancer detection method** focuses on extracting and removing the image background, enabling more accurate identification and segmentation of cancerous bone structures in subsequent steps.

B(x, y) = {1, if I(x, y) >= T

0, if I(x, y) < T}

In this case, if the intensity I(x, y) at a pixel is greater than or equal to the threshold value T, it is set to 1 (white), indicating foreground. If it is less than the threshold, it is set to 0 (black), indicating background. In some cases, it may be necessary to invert the binary thresholding result so that the cancerous regions (foreground) appear black and the background appearswhite. This inversion can be achieved simply by switching the pixel values in the thresholding expression. Due to variations in illumination and contrast among different bone X-ray or CT images, which can affect the visibility of cancerous lesions**,** gray scale bone images are converted to binary images using multiple threshold values to ensure accurate detection of abnormal regions, as illustrated in the following figure.



At this stage, connected components in the binary imageare labeled using MATLAB'sbw label function, enabling the identification and separation of individual cancer regions within the bone structure. This labeling is crucial for subsequent morphological processing and feature extraction, improving the precision of automated bone cancer detection.

At this stage, connected components are labeled using MATLAB's bwlabel function to detect and analyzecancerous regions in bone images. The output, L, is a matrix with the same size as the binary image, where 0 represents the background and all pixels belonging to the same detected cancer region are assigned the same unique label number. This labeling allows automated systems to identify, separate, and count individual bone lesions, facilitating accurate measurement of their size, location, and distribution, which are critical for the assessment and diagnosis of bone cancer.

4.IMPLEMENTATION OF PROPOSED ARCHITECTURE

The proposed system aims to provide an efficient, accurate, and automated method for the identification and classification of bone cancer using medical imaging, such as X-ray and CT scans. Traditional diagnostic approaches rely heavily on manual examination by radiologists, which is time-consuming and prone to human error, especially in early-stage detection where cancers may be small and subtle. This system integrates image pre-processing, segmentation, feature extraction, and hybrid classification techniques to enhance diagnostic accuracy and reliability. The workflow begins with the data acquisition phase, where bone images are collected from reliable datasets comprising X-ray and CT scans of both healthy and cancer-affected bones. These images often contain noise, uneven illumination, or artifacts; therefore, a pre-processing step is applied. Techniques such as Gaussian filtering, median filtering, and histogram equalization are employed to remove noise, enhance contrast, and standardize image intensity, facilitating more accurate downstream analysis.

Following pre-processing, the system performs bone cancer segmentation using the K-Means clustering algorithm. K-Means is an unsupervised learning technique that partitions the image pixels into clusters based on intensity and spatial similarity. Cancer regions typically exhibit intensity patterns distinct from healthy bone tissue, enabling K-Means to isolate suspicious regions effectively. Thresholding and morphological operations further refine the segmented regions, producing a precise map of potential cancer areas. Once the cancer regions are segmented, feature extraction is conducted to characterize each region based on texture, shape, and intensity parameters. Common features include area, perimeter, compactness, mean intensity, standard deviation, and texture descriptors such as Gray Level Co-occurrence Matrix (GLCM) features. These extracted features form the input for the classification stage.

The classification module employs a hybrid approach using K-Nearest Neighbours (KNN) and Support Vector Machine (SVM) classifiers. KNN is applied first to identify the similarity of new cancer regions with known labelled samples based on distance metrics, providing a preliminary classification. Subsequently, SVM is used to construct a robust decision boundary that separates benign from malignant cancers, leveraging its ability to handle high-dimensional feature spaces and non-linear relationships. The combination of KNN and SVM improves overall system accuracy and reduces misclassification, ensuring reliable identification.

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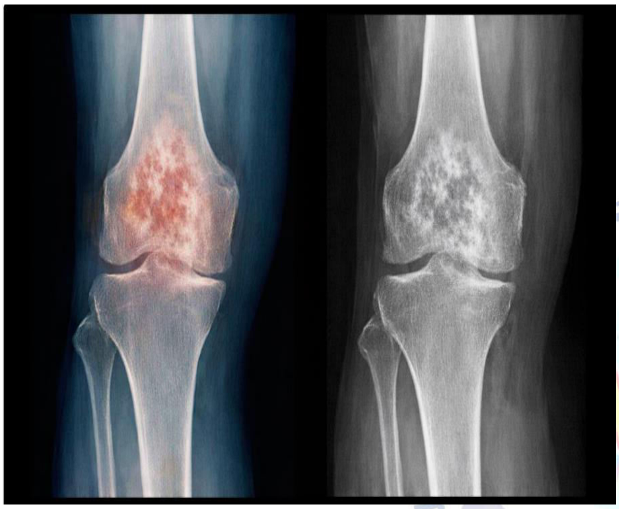

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K-Means clustering is one of the most widely used techniques for solving clustering problems. It is a simple, efficient, and unsupervised learning algorithm that classifies input data points into multiple clusters based on their intrinsic distance from other points in the dataset. In the context of **bone cancer identification,** K-Means clustering is applied to medical images, such as X-ray and CT scans, to segment and group different regions of bone tissue for further analysis.

The main objective of K-Means clustering is to partition **n observations** into **k clusters,** where each observation belongs to the cluster with the nearest mean, which acts as the prototype of the cluster. This effectively divides the data space into distinct regions, separating healthy bone tissue from potential cancer regions. The algorithm begins by defining **k centroids,** one for each cluster. These centroids are ideally initialized as far apart as possible to improve clustering results. Each pixel or image segment is then associated with the nearest centroid based on distance metrics such as Euclidean distance.

Once all points are assigned to clusters, **new centroids** are computed as the mean of all points within each cluster. The algorithm then iteratively reassigns points to the nearest centroid and recalculates centroids until the locations stabilize and no further changes occur. This iterative process ensures that clusters are optimized for compactness and separation.

In the **proposed bone cancer detection system**, K-Means clustering is utilized during the **pre-processing and segmentation stages** to group bone tissue regions based on intensity, texture, and morphological features extracted from medical images. Proper initialization of centroids is critical for achieving accurate segmentation of cancerous and normal bone regions. Two common initialization techniques are:

1. **Random Selection** – selects k random bone tissue samples as initial centroids, ensuring coverage across different tissue regions and improving convergence.
2. **Random Partition –** initially assigns each tissue segment to a random cluster and calculates centroids from these assignments, useful when tissue characteristics overlap across clusters.

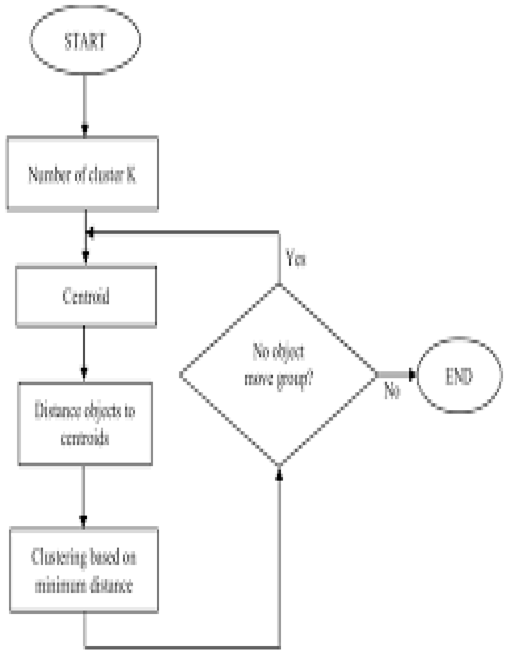

Figure 6: Flowchart for k-means Clustering

K-means is simple and can be used for a variety of data types. It is also a quite efficient, even though multiple runs are often performed. Some variants including bisecting K-means, are even more efficient, and are less susceptible to initialization problems. K-means is not suitable for all types of data, however. It cannot handle non-globular clusters or clusters of different sizes and densities, although it can typically find pure sub clusters if a large enough contains outlier. Outlier detection and removal can help significantly in such situations In this phase the features of the given input image is been extracted. Finally, this algorithm aims at minimizing an *objective function*, in this case a squared error function. The objective function is given by

$$J(V) = \sum_{i=1}^{c} \sum_{j=1}^{c_i} \left\| x_i - v_j \right\|^2 \quad (4.1)$$

ALGORITHM:

1. Give the no of cluster value as k.
2. Randomly choose the k cluster centers.
3. Calculate mean or center of the cluster.
4. Calculate the distance between each pixel to each cluster center.
5. If the distance is near to the center then move to that cluster.
6. Otherwise move to next cluster.
7. Re-estimate the center
8. Repeat the process until the center doesn't move.

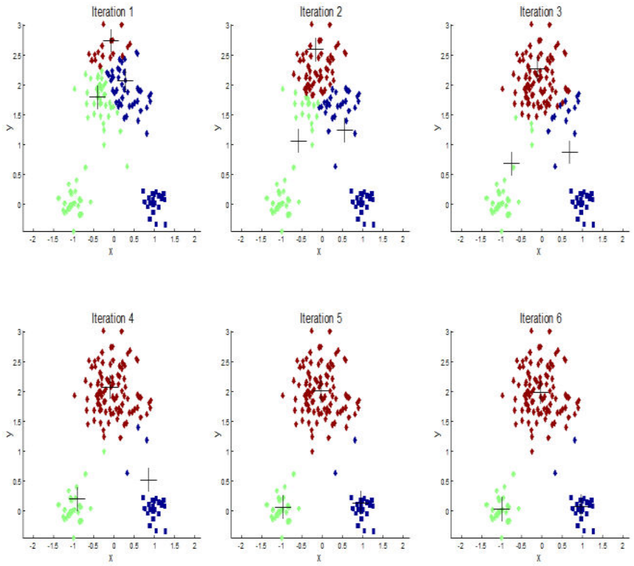

Figure 7: Different ways of clustering the same set of points

Figure 7 illustrates different ways of clustering the same set of bone image points. In the proposed system, the number of clusters is initially chosen as three to separate distinct regions in the bone tissue. Three cluster centers are selected randomly, and the distance between each pixel in the image and each cluster center is calculated. If a pixel is closer to a particular centroid, it is assigned to that cluster; otherwise, it is considered for the next cluster. This process is repeated iteratively until the cluster centers stabilize and no longer move, resulting in well-defined clusters that segment bone tissue into healthy and potentially cancerous regions.

Following segmentation, feature extraction is performed to quantify the differences between the image segments. Feature extraction reduces raw image data into a more manageable form, facilitating pattern classification and decision-making. In bone cancer detection, Gray Level Co-occurrence Matrix (GLCM) features are employed to capture statistical texture information of bone regions. Cancerous bone often exhibits irregular patterns in density, cortical structure, and trabecular distribution, which GLCM features can effectively quantify. By analyzing these texture characteristics, abnormal (cancerous) regions can be distinguished from normal bone tissue, enabling accurate classification and aiding early detection of bone cancer.

Process used to create the GLCM

A single GLCM with the spatial relationship, or offset, defined as two horizontally adjacent pixels created by the Gray co-occurrence matrix function. Gray co matrix can create a multiple GLCM'S for a single image because a single horizontal offset might not be sensitive to texture with a vertical orientation.To create the multiple GLCM'S an array of 0ffsets to the Gray co-occurrence function is specified. These offsets define pixel relationships of varying distance and direction. For example, you can define an array of offsets that specify four directions (horizontal, vertical, and two diagonals) and four distances. In this case, the input image is represented by 16 GLCM' s. When you calculate statistics from these GLCM' s, you can take the average.

These offsets can be specified as a p-by-2 array of integers. Each row in the array is a two element vector. And it is represented in the form of the [Row_offset, column_offset]. Row offset specifies the number of rows between the pixel of interest and its neighbour.column_offset specifies the number of columns between the pixel of interest and its neighbour.

Offsets = [0 1; 0 2; 0 3; 0 4;...
-1 1; -2 2; -3 3; -4 4;...
-1 0; -2 0; -3 0; -4 0;...
-1 -1; -2 -2; -3 -3; -4 -4];

Deriving Statistics from a GLCM

After treating the GLCM'S Gray co props function may be used to derive several statistics from them. These derived statistics gives information about the texture of an image. By calling the Gray props function you can specify the statistics you want. The following table illustrates the statistics you have been derived. Then the table is as follows: -

Texture feature based on GLCM

Texture analysis refers to the characterization of different regions in medical images based on their texture content, and it plays a crucial role in bone cancer detection using X-ray, CT, or MRI images. In bone cancer, abnormal regions often exhibit distinct texture patterns such as irregular bone density, disrupted cortical structure, uneven trabecular patterns, and non-uniform intensity in the affected area. These variations are often subtle and difficult to identify using only simple intensity or color values. Therefore, texture analysis helps quantify these abnormalities by measuring the spatial variation of pixel intensities within bone regions. In this context, roughness or irregularity represents the variation in gray-level values within a small neighborhood of pixels in the bone image.

Texture analysis is widely used in bone cancer detection because cancerous bone regions display texture characteristics that differ significantly from normal bone tissue. Texture-based segmentation helps separate abnormal cancerous regions from healthy bone when simple thresholding or intensity-based methods are insufficient. This improves the identification of suspicious regions and enhances classification accuracy. Texture filter functions are applied to compute statistical measures that describe local intensity variations in bone images. In healthy bone regions, pixel intensity variation within a neighborhood is typically low, producing smaller statistical values. In contrast, cancerous bone regions often show irregular bone structure, density variations, and abnormal trabecular patterns, leading to higher intensity variation. Statistical measures such as entropy, contrast, and standard deviation effectively quantify these differences, providing meaningful texture features for accurate and reliable bone cancer detection.

GLCM is composed of the probability value, it is defined as $P(i,j|d,\theta)$ which expresses the probability of the couple pixels at θ direction and the d interval. When θ and d are det6ermined $P(i,j|d,\theta)$ is shown by $P_{i,j}$. Distinctly GLCM is a symmetry matrix its level is determined by the image gray level. Elements in the matrix are computed by the equation shown as the following

Statistics	Description
Homogeneity	It measures the closeness of the distribution of elements between the GLCM and the GLCM diagonal
Energy	It is known as the uniformity or the Angular second moment. It provides the sum of the square of the elements in the GLCM
Correlation	It measures the occurrence of the joint probability of the specified pixel pairs.
Contrast	In the Gray level co-occurrence matrix it measures the local variations.

$$P(i,j|d,\theta)=\frac{P(i,j|d,\theta)}{\sum_i\sum_j P(i,j|d,\theta)}$$

GLCM expresses the texture feature according the correlation of the couple pixels Gray level at different positions. It quantification describes the texture features. But here mainly four things are considered they are energy, contrast, entropy and the inverse difference

Energy:

$$E=\sum_x\sum_y p(x,y)^2$$

It is a gray scale image texture measure of the homogeneity changing reflecting the distribution of the image gray-scale uniformity of the image and the texture.

Contrast:

Contrast is the main diagonal near the moment of inertia, Which measures the value of the matrix is distributed and images of local changes in the number, reflecting the image clarity and the texture of the shadow depth if the contrast is large then the texture is deeper.

$$I=\sum\sum(x-y)^2 p(x,y)$$

Entropy:

Entropy measures image texture randomness, when the space co-occurrence matrix for all values is equal, it achieved the minimum value; on the other hand, if the value of co-occurrence matrix is very uneven, its value is greater. Therefore, the maximum entropy implied by the image gray distribution is random.

$$S=-\sum_x\sum_y p(x,y)\log p(x,y)$$

Inverse difference:

It measures local changes in image texture number. Its value in large is illustrated that image texture between the different regions of the lack of change and partial very evenly.

Here $p(x,y)$ is the gray level value at the co-ordinate (x,y)

$$H=\sum_x\sum_y\frac{1}{1+(x-y)^2}p(x,y)$$

Classification

Bone cancer identification using Gray Level Co-occurrence Matrix (GLCM) features with Support Vector Machine (SVM) and K-Nearest Neighbors (KNN) classifiers is an effective image-based diagnostic approach for detecting cancerous regions from medical images such as X-ray, CT, or MRI scans. First, bone images are collected and pre-processed to remove noise, enhance contrast, and normalize intensity. The regions of interest, particularly areas showing potential cancers, are then segmented from surrounding healthy bone tissue. After converting the segmented region into grayscale, the GLCM is computed at different orientations to capture spatial texture information.

From the GLCM matrix, important texture features such as contrast, correlation, energy, homogeneity, and entropy are extracted. These features quantify irregular bone density, disrupted trabecular patterns, and abnormal cortical structure commonly observed in cancerous bone regions. The extracted GLCM feature vectors are then fed into both SVM and KNN classifiers.

SVM works by finding an optimal hyperplane that separates healthy and cancerous bone regions with maximum margin, making it robust for high-dimensional feature spaces and small datasets. KNN, on the other hand, classifies each region based on its similarity to labeled feature vectors in the training dataset, providing a complementary classification approach that is simple and effective. By combining texture-based GLCM features with the classification capabilities of SVM and KNN, the proposed system achieves reliable and accurate automated bone cancer detection, assisting radiologists in early diagnosis and reducing manual effort.

The K-Nearest Neighbors (KNN) classifier is a powerful tool for bone cancer identification in medical images. It operates on the principle that similar data points—here, image regions—are likely to share the same class label, either healthy or cancerous. To utilize KNN for bone cancer detection, a dataset of bone images, such as X-ray or CT scans, is first collected and pre-processed. Preprocessing steps include noise removal, contrast enhancement, resizing, and normalization to ensure consistency across images.

Relevant features are then extracted from the segmented bone regions, including texture features (e.g., GLCM: contrast, correlation, entropy, energy, homogeneity), shape descriptors, and intensity statistics. The dataset is divided into a training set, used to train the classifier, and a testing/validation set for evaluating performance. Feature normalization is crucial to ensure that all features contribute equally to the classification process. The K parameter, representing the number of nearest neighbors considered during classification, is chosen carefully, often through cross-validation, to optimize predictive accuracy. Once K is selected, the KNN classifier is trained on the feature vectors and their corresponding labels.

Classification of a new bone region involves calculating the **distance** between its feature vector and all feature vectors in the training set, typically using **Euclidean distance**:

$$d(\mathbf{x_i}, \mathbf{x_j}) = \sqrt{\sum_{m=1}^{M} (x_i^{(m)} - x_j^{(m)})^2}$$

To visualize KNN predictions, prediction maps or highlighted segmentation images can be generated, showing which regions of the bone are classified as cancerous versus normal. These images aid radiologists in interpreting results and provide clear visual feedback of the classifier's decision. KNN can be computationally expensive for large bone image datasets, as it requires calculating distances to all training samples for each prediction.

In addition to KNN, **Support Vector Machine (SVM)** is employed for robust classification. SVM constructs an **optimal hyper plane** that separates cancerous and healthy bone regions in the feature space. The SVM decision function is given by:

$$f(x) = \text{sign}\left(\sum_{i=1}^{m} \alpha_i y_i K(x_i, x) + b\right)$$

Support Vector Machine (SVM) works by finding an optimal hyperplane that separates **healthy and cancerous bone regions**with maximum margin. It is particularly suitable for medical image classification because of its high accuracy, robustness in high-dimensional feature spaces, and ability to handle small datasets. By combining **texture-based GLCM features** with the powerful classification capability of SVM, this method provides reliable and accurate **automated bone cancer detection,** assisting radiologists in early diagnosis and reducing manual effort.

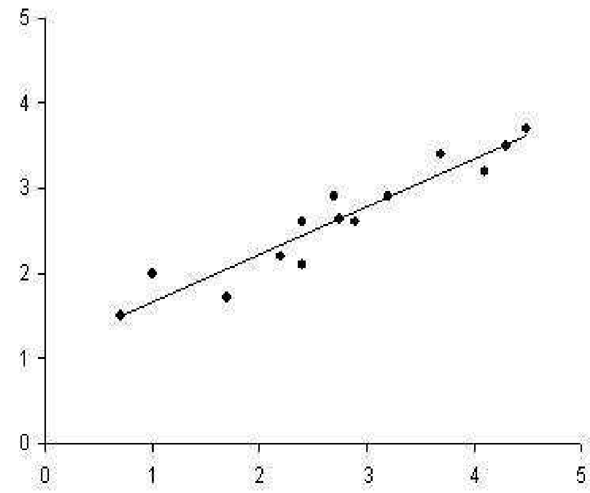

Figure 8: Best-fit regression line reduces data from two dimensions into one.

If we drew a perpendicular line from each point to the regression line, and took the intersection of those lines as the approximation of the original data point, we would have a reduced representation of the original data that captures as much of the original variation as possible. Notice that there is a second regression line, perpendicular to the first, shown in Figure 2.

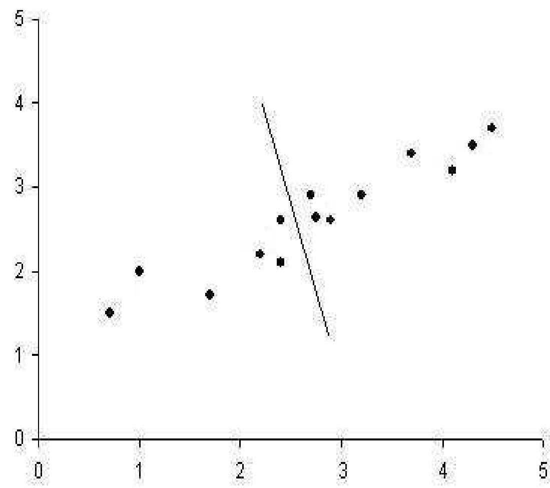

Figure 9: Regression line along second dimension captures less variation in original data

This concept is particularly relevant in bone cancer detection, where medical images such as X-ray, CT, or MRI scans contain high-dimensional and highly variable data. Each pixel or segmented bone region can have multiple features, including intensity, texture, and shape descriptors, creating a complex dataset. Using Support Vector Machine (SVM), the data can be projected into a lower-dimensional feature space that captures the most significant variation highlighting differences between healthy and cancerous bone regions. This process effectively orders the features from those exhibiting the most variation (e.g., abnormal trabecular patterns or irregular bone density) to those with minimal variation, reducing noise and irrelevant details. By focusing on the most important variations, SVM can expose subtle substructures in the bone tissue that may not be immediately visible in the original images, such as small cancer regions or early-stage lesions. This dimensionality reduction, combined with SVM's ability to construct optimal separating hyper planes, ensures that the key relationships in the data are preserved, facilitating accurate and reliable automated bone cancer classification.

4. RESULTS& DISCUSSION

The proposed system for bone cancer identification and separation was implemented using medical imaging datasets (X-ray/MRI images). The methodology involved three major stages: pre-processing, segmentation using K-Means clustering, and classification using K-Nearest Neighbors (KNN) and Support Vector Machine (SVM) classifiers. In the pre-processing stage, noise removal and contrast enhancement techniques were applied to improve image quality. Histogram equalization and filtering methods enhanced cancer visibility. The K-Means clustering algorithm effectively segmented the suspicious cancer region by grouping pixels based on intensity similarity. The segmented cancer regions were clearly separated from normal bone tissues, enabling accurate feature extraction. Statistical and texture-based features such as area, perimeter, mean intensity, and Gray Level Co-occurrence Matrix (GLCM) features were extracted from the segmented region. These features were then used as inputs for classification. The KNN classifier provided satisfactory performance in distinguishing between normal and cancerous bone images. However, classification accuracy depended on the choice of K value and distance metric. On the other hand, the SVM classifier demonstrated improved performance due to its ability to construct an optimal hyper plane that maximizes the margin between classes.

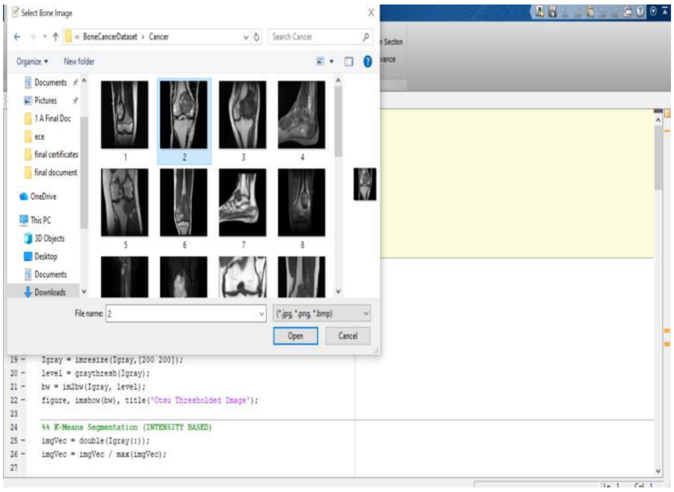

Figure 10: Browse Input Image

This figure illustrates the initial data acquisition phase of the system, where a user selects a bone CT/X-ray scan from the Bone Cancer Dataset for automated analysis.

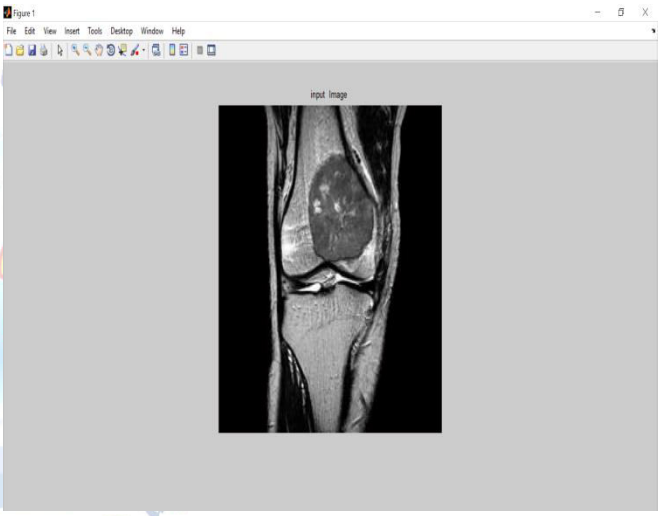

Figure 11: Input CT for Bone Cancer

This figure shows the CT scan image of a bone used as the input for analysis. The image provides detailed information about the bone structure and possible abnormal regions.

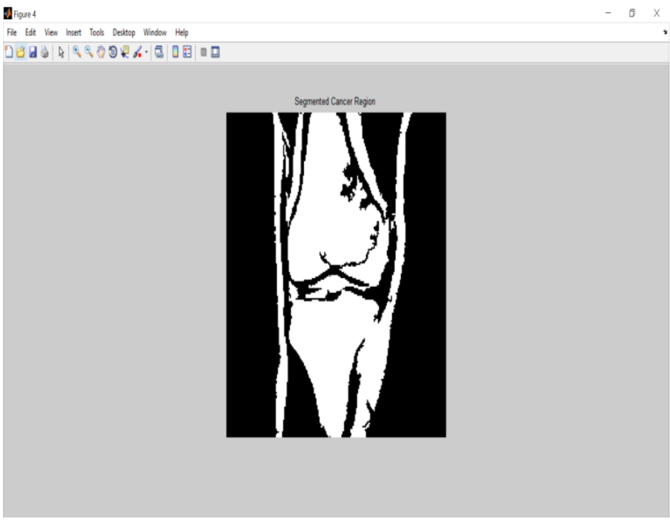

Figure 12: Segmented Cancer Region using k-mean

This figure shows the segmented region of a knee MRI image obtained using the K-means clustering algorithm. The K-means method groups pixels based on their intensity values to separate the suspected cancerous region from surrounding tissues. The white region represents the clustered area identified as the region of interest, helping in the analysis and detection of possible tumor presence.

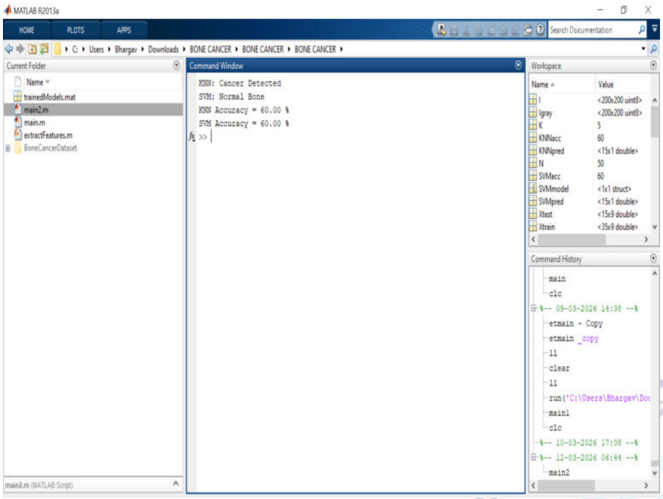

Figure 13: Classification Results for Bone Cancer Detection

This figure displays the classification results for bone cancer detection. The results show predictions from the KNN and SVM classifiers to determine whether the bone image is cancerous or normal. It also presents the accuracy of both models to evaluate their performance.

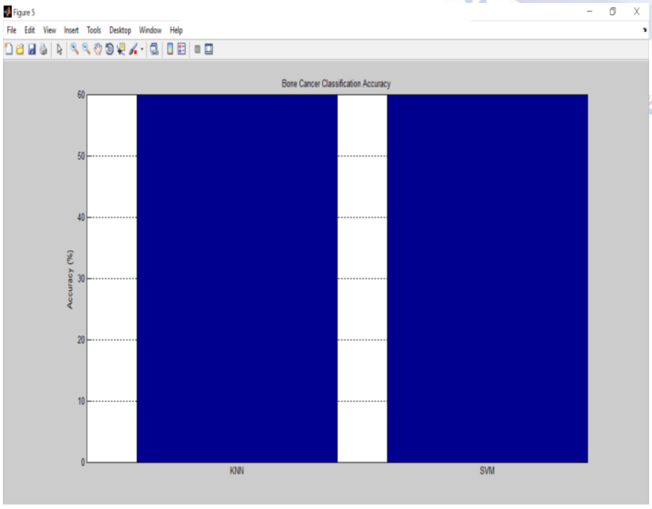

Figure 14: Bone Cancer Classification Accuracy Comparison

This figure presents the accuracy comparison between the KNN and SVM classifiers for bone cancer detection. The bar chart shows the classification accuracy achieved by each model. It helps evaluate the performance of both algorithms.

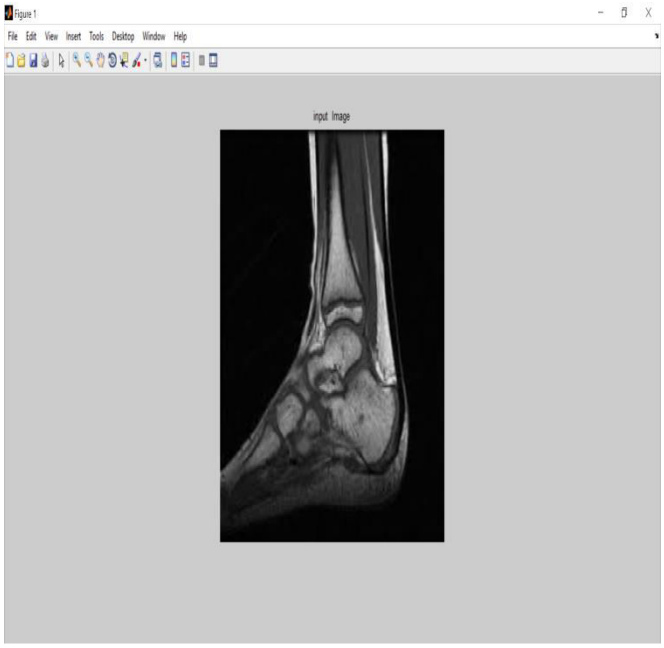

Figure 15: Input CT scan for Bone

This figure shows the CT scan image of a bone used as the input for analysis. The image provides detailed information about the bone structure and possible abnormal regions.

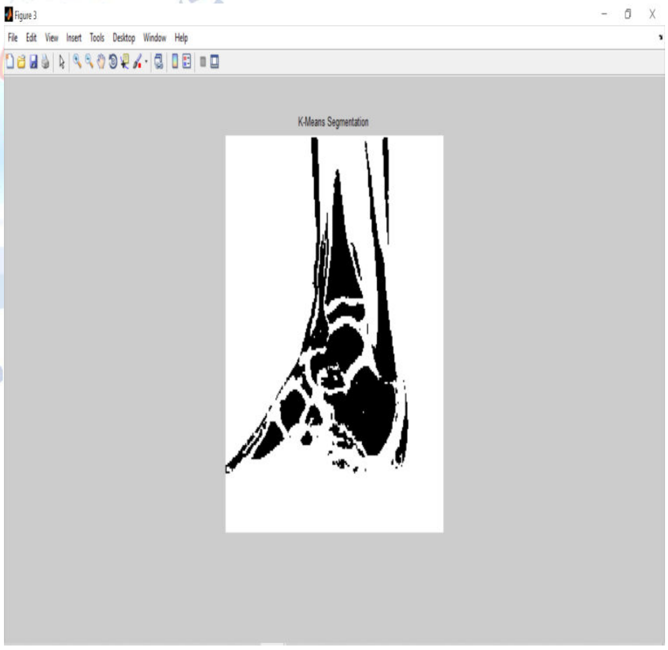

Figure 16: Segmented Cancer Region using k-mean

This figure shows the segmented region of a knee MRI image obtained using the K-means clustering algorithm. The K-means method groups pixels based on their intensity values to separate the suspected cancerous region from surrounding tissues. The white region represents the clustered area identified as the region of interest, helping in the analysis and detection of possible tumor presence.

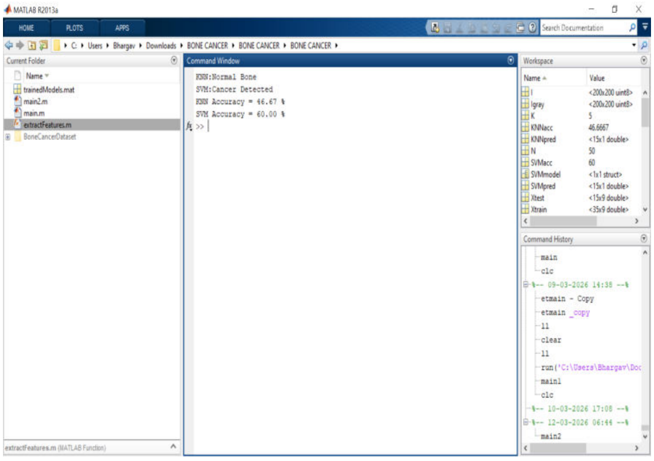

Figure 17: Classification Results for Bone Cancer Detection

This figure displays the classification results for bone cancer detection. The results show predictions from the KNN and SVM classifiers to determine whether the bone image is cancerous or normal. It also presents the accuracy of both models to evaluate their performance.

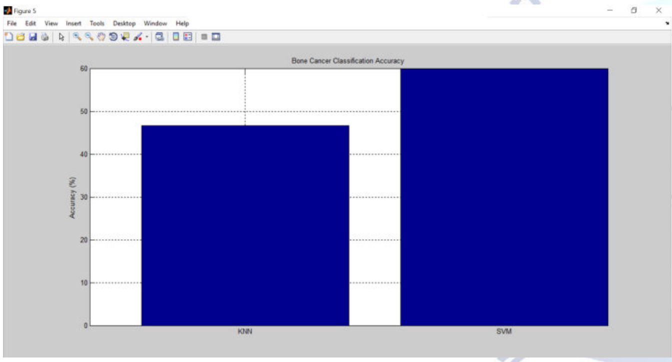

Figure 18: Bone Cancer Classification Accuracy Comparison

This figure presents the accuracy comparison between the KNN and SVM classifiers for bone cancer detection. The bar chart shows the classification accuracy achieved by each model. It helps evaluate the performance of both algorithms

5. CONCLUSIONS

Bone cancer is one of the most life-threatening diseases, and its early detection is crucial to reduce mortality rates. Since symptoms are often not noticeable in the initial stages, an accurate and automated diagnostic system plays a vital role in assisting medical professionals. In this work, Computed Tomography (CT) scan images were utilized to analyze and detect bone cancer at different stages of growth. The proposed methodology included preprocessing techniques such as noise removal, automatic contrast enhancement, and edge detection to improve image clarity. K-Means clustering was effectively applied for segmentation of the bone region and isolation of suspicious tumor areas. Texture feature extraction was performed using the Gray Level Co-occurrence Matrix (GLCM), which provided meaningful statistical parameters for classification. Initially, the K-Nearest Neighbor (KNN) classifier was employed for tumor detection and achieved a high accuracy , demonstrating its effectiveness in identifying cancerous and non-cancerous bone images. However, to further enhance prediction performance and improve generalization capability, a Support Vector Machine (SVM) classifier was incorporated into the system. Experimental analysis showed that SVM provided better decision boundaries, improved sensitivity and specificity, and more robust performance when handling complex and high-dimensional feature spaces. Compared to KNN, SVM reduced misclassification rates and delivered more stable predictions across different CT image datasets.

Future scope

The proposed work can be further enhanced by incorporating advanced machine learning techniques such as Edge Segmentation–based XGBoost for improved bone cancer classification. In future developments, the system can be extended to classify different types of bone cancers, such as osteosarcoma, chondrosarcoma, and metastatic bone tumors, using multi-class learning approaches. Additional discriminative features, including shape descriptors, intensity variations, and advanced texture parameters from segmented cancerous nodules, can be extracted to improve prediction accuracy. Edge-based segmentation techniques can enhance boundary detection of tumor regions, leading to more precise feature representation. By integrating XGBoost, which provides high performance and better handling of complex feature interactions, the system can achieve improved robustness, scalability, and diagnostic reliability.

Conflict of interest statement

Authors declare that they do not have any conflict of interest.

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