Nanotechnology Perceptions
ISSN 1660-6795
www.nano-ntp.com

Adaptive Superpixels For Noise-Resilient Bone Tumor Identification In Medical Imaging

V.Dineshkumar[1], Dr.V.Vijayakumar[2]

[1]*Department of Computer Science, Sri Ramakrishna Mission Vidyalaya College of Arts and Science, Coimbatore, Tamilnadu, India*

[2]*Department of Computer Science, Professor & Controller of Examinations, Sri Ramakrishna College of Arts and Science, Coimbatore, Tamilnadu, India*

Corresponding Author: V.Dineshkumar (dineshkumarvt@gmail.com)

Accurate segmentation and identification of bone tumors in medical images are crucial for early diagnosis and effective treatment planning. This research presents a pioneering framework that integrates advanced stochastic-based clustering algorithms to overcome challenges associated with noise and variability in bone tumor appearance. The model employs adaptive superpixels for feature extraction after comprehensive data pre-processing, including noise reduction and contrast enhancement. The core of the approach integrates stochastic clustering algorithms like Gaussian Mixture Models (GMM) and Expectation-Maximization (EM) variants for robust segmentation of potential bone tumor regions. To address noise and variability challenges, the model employs probabilistic clustering and ensemble approaches. Parameter tuning and post-processing steps refine segmentation results, ensuring realistic bone tumor shapes and eliminating artifacts. Validation on medical imaging datasets demonstrates the framework's efficacy, showcasing improved noise resilience and accurate bone tumor identification. The model's adaptability to superior performance compared to baseline segmentation methods highlight its potential for clinical applications.

Keywords: Noise-Resilient, Bone Tumor, Segmentation, Adaptive Superpixels, Advanced Stochastic-Based Clustering, Medical Image, Gaussian Mixture Models And Expectation-Maximization.

1 INTRODUCTION

Medical imaging plays a pivotal role in the diagnosis and treatment planning of various diseases, including bone tumors. Accurate segmentation and identification of bone tumors in medical images are essential for effective clinical decision-making [1]. However, the task is often challenging due to the presence of noise and other artifacts in the imaging data. As a result, the development of advanced stochastic models becomes crucial to enhance the robustness and accuracy of bone tumor segmentation and identification in the presence of

1Corresponding author. E-mail address: dineshkumarvt@gmail.com

noise [2]. The accurate segmentation and identification of bone tumors are critical for clinicians to formulate precise treatment plans and improve patient outcomes. Misinterpretation of medical images can lead to delayed diagnosis or inappropriate interventions. Therefore, the development of noise-resilient models is imperative to enhance the reliability of bone tumor analysis in real-world clinical scenarios [3].

Traditional segmentation methods often struggle to handle the inherent variability and complexity of medical images, especially when confronted with noise and uncertainties. Stochastic models, rooted in probability theory, provide a promising avenue to address these challenges by incorporating uncertainty into the segmentation process [4]. The integration of advanced stochastic models not only improves the segmentation accuracy but also enhances the reliability of bone tumor identification, contributing to more precise clinical outcomes [5]. Medical images, especially those of bone tumors, are susceptible to various challenges, such as variations in image resolution, artifacts from imaging devices, and the presence of heterogeneous tissue structures [6]. Traditional segmentation methods may struggle to address these challenges adequately. Advanced stochastic models offer a promising solution by inherently accommodating uncertainties associated with these complexities [7].

Stochastic models, grounded in probabilistic reasoning, introduce an element of randomness into the segmentation process, making them better suited to handle uncertainty in medical images. These models can not only capture the inherent variability in the imaging data but also provide probabilistic estimates, offering a more nuanced understanding of the segmentation results [8].In this context, this research focuses on the development and application of advanced stochastic models tailored for noise-resilient bone tumor segmentation and identification in medical imaging [9]. By leveraging probabilistic frameworks and incorporating sophisticated algorithms, these models aim to provide robust solutions that can effectively navigate the intricacies of noisy medical image data [10].

The significance of this research lies in its potential to revolutionize the field of medical imaging, particularly in the realm of bone tumor analysis. The proposed advanced stochastic models have the capacity to enhance the accuracy of segmentation, allowing for more precise delineation of tumor boundaries. Additionally, these models can contribute to improved identification and characterization of bone tumors, facilitating early detection and personalized treatment strategies.

In the subsequent sections of this paper, Section 2delve into the theoretical foundations of stochastic modeling and discuss the specific challenges posed by noise in medical imaging. Section 3 presents the proposed advanced stochastic models, detailing their key features and advantages. Section 4 discusses the experimental setup and methodologies employed to validate the efficacy of these models. Finally, Section 5 concludes by highlighting the potential impact of these advanced stochastic models on the field of bone tumor analysis and the broader landscape of medical imaging.

2 RELATED WORKS

A novel model for echocardiography video segmentation addresses challenges like speckle noise and irregular motion, achieving high accuracy (92.87% and 93.79%) on EchoNet-Dynamic and CAMUS datasets using adaptive spatiotemporal calibration and semi-supervised learning [11]. Real-time intelligent semi-supervised ultrasound video object segmentation faces challenges in obtaining annotated data, and this review emphasizes the adoption of semi-supervised learning for improved segmentation accuracy while highlighting the need for a balance between accuracy and speed [12].

A proposed algorithm for multimodal medical image fusion, utilizing lifting scheme-based biorthogonal wavelet transform, outperforms other wavelet-based fusion methods, showcasing better results in both visual and quantitative evaluations [13]. Deep learning-based ultrasound image segmentation, addressing speckle noise challenges, reveals that denoising contributes less to performance improvement compared to holistic deep learning segmentation frameworks, recommending denoising as a hyper-parameter [14].

A two-sub-task classification approach is proposed for Immunofixation Electrophoresis images, addressing class imbalance, and incorporating expert knowledge, leading to interpretable visualization outcomes aligned with expert expectations [15]. Infrared thermography, coupled with deep learning-based Computer-aided Diagnosis (CADx) systems, offers a noninvasive and cost-effective approach for early breast cancer detection, as reviewed with insights into segmentation techniques and available datasets [16].

Multi-organ segmentation in medical images faces challenges in obtaining annotated datasets, prompting the exploration of transfer learning, semi-supervised learning, and partially-supervised learning paradigms, with a review highlighting their technical aspects and future trends [17]. An unsupervised object segmentation technique based on Seeded-Region Growing (SRG) leverages higher-order textural statistical descriptors for improved segmentation in complex real-world environments, outperforming state-of-the-art methods [18].

A detailed review of solutions for imperfect medical image segmentation datasets, considering scarce and weak annotations, highlights technical novelties and empirical results, providing insights into methodologies to handle these challenges [19]. Whole-body low-field MRI scanners present opportunities for improved body imaging, focusing on applications like lung parenchyma imaging, imaging near metallic implants, cardiac imaging, and dynamic imaging, with potential advantages for screening and population health research [20].

An edge detection algorithm, tailored for brain MRI images, is presented, demonstrating improved noise resilience and edge detection compared to the standard Canny algorithm [21]. Image segmentation is a critical step in image processing, influencing subsequent tasks like object detection and classification, and this paper [22] provides a study of basic principles and methods used in image segmentation. A new active contour model using the level-set method is proposed for cerebral vessel segmentation from TOF-MRA data, demonstrating better performance than other methods in terms of Dice Similarity Coefficient [23].

Quantum computing's potential in biology and medicine is explored, applying a framework to assess quantum advantages in various computational problems relevant to these domains, with an extensive survey of current quantum algorithms [24]. The proposed Diffusion-based Anomaly Detection (DiAD) framework for multi-class anomaly detection combines pixel-space autoencoder, semantic-guided network, and spatial-aware feature fusion, outperforming state-of-the-art methods in multi-class anomaly detection on MVTec-AD and VisA datasets [25].

3 PROPOSED MODEL

Accurate bone tumor segmentation in medical imaging is essential for early diagnosis and effective treatment planning. Our proposed model pioneers a comprehensive approach, beginning with data pre-processing involving noise reduction and contrast enhancement. Leveraging adaptive superpixels for feature extraction, the model integrates advanced stochastic clustering algorithms, including GMM and EM variants, to robustly segment potential bone tumor regions. Our model employs strategies such as probabilistic clustering and ensemble approaches. Further refinement through parameter tuning and post-processing ensures realistic bone tumor shapes, eliminating artifacts. An overall architecture model of proposed system is shown in fig 1.

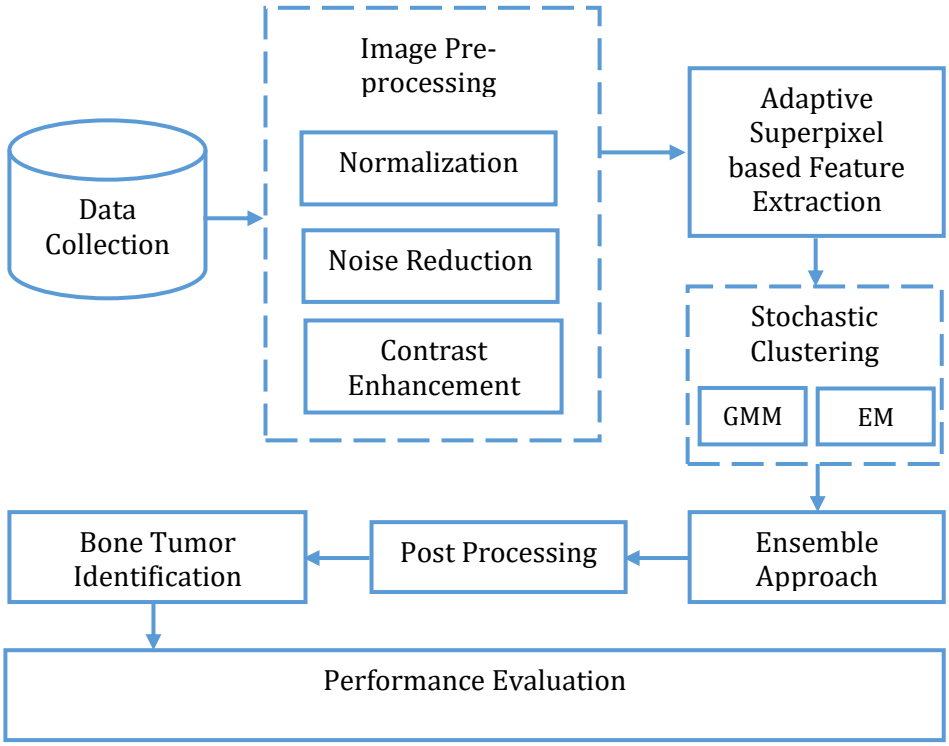


Figure 1: Overall Architecture of Proposed Model

3.1 Data Collection

The data were collected from "https://www.kaggle.com/datasets/antimoni/bone-tumor". This dataset serves as a valuable resource for obtaining diverse and well-annotated medical images related to bone tumors. The dataset includes a variety of imaging modalities and provides a comprehensive collection of bone tumor instances, contributing to the robustness and diversity of our model training. Utilizing this dataset ensures that our proposed framework is trained on a rich and representative set of bone tumor images, enhancing its capability for accurate segmentation and identification in medical imaging applications.

3.2 Image Pre-processing

Image pre-processing refers to a set of techniques and operations applied to raw images before feeding them into a proposed model. The goal is to enhance the quality, improve interpretability, and facilitate effective analysis. Pre-processing steps [26] commonly include normalization, noise reduction, contrast enhancement, and other operations tailored to the specific requirements of the downstream task.

Normalization:

Normalization is the process of scaling pixel values in an image to a standard range, typically [0, 1] or [-1, 1]. It ensures that the data has a consistent scale, preventing dominance of certain features and facilitating convergence during model training.

$$\text{Normalized Image} = \frac{\text{Original Image} - \text{Mean}}{\text{Standard Deviation}} \tag{1}$$

where the mean and standard deviation are computed over all pixel values in the image.

Noise Reduction:

Noise reduction in image processing aims to diminish unwanted variations or irregularities in pixel values caused by random factors. Techniques such as filtering methods (e.g., Gaussian smoothing) are employed to improve the signal-to-noise ratio.

$$\text{Smoothed Image} = \text{I} \times \text{G} \tag{2}$$

Where G is a 2D Gaussian filter.

Contrast Enhancement:

Contrast enhancement involves adjusting the intensity distribution of an image to make features more distinguishable. Techniques like contrast stretching or histogram equalization are applied to improve the visual quality and reveal hidden details in the image.

$$\text{Enhanced Image} = \frac{\text{Original Image} - \text{Min}}{\text{Max} - \text{Min}} \times \text{Intensity Range} \tag{3}$$

whereMinMin and MaxMax are the minimum and maximum pixel values in the image, and the Intensity Range is the desired range of pixel values (e.g., [0, 255]).

3.3 Adaptive Superpixel based Feature Extraction

Adaptive Superpixel-based Feature Extraction is a method in image processing that involves grouping pixels into perceptually meaningful clusters known as superpixels. The adaptability refers to the dynamic adjustment of the superpixel size based on the image's characteristics. This technique extracts relevant features from these adaptive superpixels, capturing spatial information and enhancing the representation of local structures in the image. It is particularly useful in tasks like segmentation, where preserving fine details is essential.

Superpixel Formation:

Let $I(x, y)$ represent the intensity of a pixel at coordinates (x,y) in the image.

Adaptive superpixels aim to group pixels into coherent clusters. For a superpixel S_i at location (x_i, y_i), its intensity $I_{i,}$ is given by:

$$I_i = \frac{1}{N_i} \sum_{(x,y) \in S_i} I(x, y) \tag{4}$$

Where N_i is the number of pixels in superpixel S_i.

Adaptive Size Adjustment:

The adaptive nature involves adjusting the size of the superpixel based on local image characteristics. Consider the variable superpixel size Si′, determined by:

$$S_i' = \alpha . \text{std}(I_i) \tag{5}$$

where α is a scaling factor, and std(Ii) is the standard deviation of intensities within superpixel Si.

Feature Extraction:

Relevant features Fi are extracted from the adaptive superpixel. These features can include color histograms, texture information, or other characteristics based on the task. Mathematically, this is represented as:

$$F_i = \text{Extract Features}(S_i') \tag{6}$$

whereExtractFeatures(·) is a function capturing the desired feature information.

Adaptive superpixel-based feature extraction combines these steps to generate enhanced representations for subsequent stages in image processing tasks, such as segmentation.

Pseudocode for Adaptive Superpixels based Feature Extraction

Input: Image I(x, y), Scaling factor alpha

```
defcalculate_superpixel_intensity(superpixel):
    return sum(superpixel) / len(superpixel)
defcalculate_adaptive_superpixel_size(superpixel_intensity, alpha):
    return alpha * superpixel_intensity
defextract_features(superpixel):
    features = compute_desired_features(superpixel)
    return features
defadaptive_superpixel_feature_extraction(image, alpha):
features_list = []
    for superpixel in image_superpixels(image):
        intensity = calculate_superpixel_intensity(superpixel)
adaptive_size = calculate_adaptive_superpixel_size(intensity, alpha)
        features = extract_features(superpixel)
return features_list
```

In the proposed adaptive superpixel-based feature extraction process, the algorithm begins by traversing through each superpixel within the input image. For each superpixel, the algorithm calculates its intensity by averaging the pixel values contained within. The adaptive superpixel size is then determined based on this calculated intensity and a scaling factor, adjusting the size dynamically. Subsequently, the algorithm extracts features from the adjusted superpixel using a placeholder function named extract_features. The overall process iterates through all superpixels in the image, creating a comprehensive list of features extracted from adaptive superpixels. This approach enables the algorithm to adaptively adjust the superpixel size, capturing intricate details in regions of varying intensities and enhancing the robustness of subsequent feature extraction in the context of image analysis.

3.4 Advanced Stochastic-Based Clustering

Advanced stochastic clustering is a probabilistic approach to partitioning data into groups or clusters based on certain criteria. Unlike traditional deterministic clustering methods, stochastic clustering introduces randomness into the clustering process. It leverages statistical methods to assign data points to clusters, allowing for uncertainty and variability in the assignment. One prominent example of stochastic clustering is the use of GMM and EM algorithms. GMM assumes that the data is generated from a mixture of several Gaussian distributions, and EM iteratively estimates the parameters of these distributions, probabilistically assigning data points to different clusters a shown in fig 2. Stochastic clustering methods are particularly beneficial in scenarios where the inherent structure of the data is complex, and there is a need to capture uncertainty in the clustering assignment.

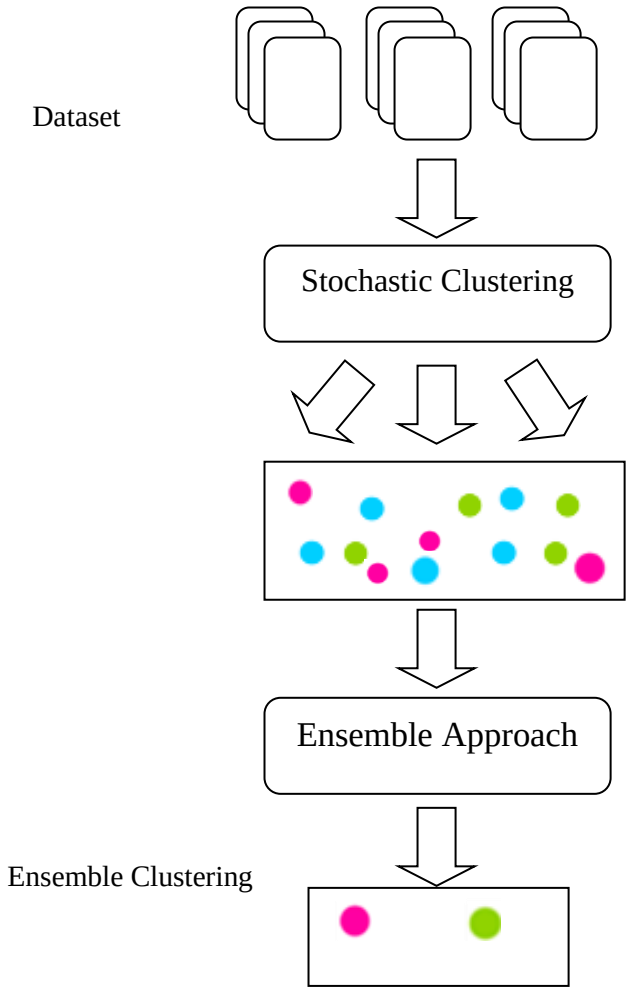


Figure 2: Structure of Cluster Formation

Let GMM is a probabilistic model that assumes that the data is generated from a mixture of several Gaussian distributions. EM, on the other hand, is a general framework for finding maximum likelihood estimates of parameters in models with latent variables, and it is used to train GMMs. Probability Density Function (PDF) for a Gaussian Component:

$$p(x|\theta_k) = = \frac{1}{(2\pi)^{D/2}|\epsilon_k|^{1/2}} \exp\left(-\frac{1}{2}(x-\mu_k)^T \sum_k^{-1}(x-\mu_k)\right) \quad (7)$$

Where , x is the data point.

$\theta_k = (\mu_k, \epsilon_k)$ represents the parameters of k-th Gaussian component.

μ_k is the mean vector, and $\in_k$ is the covariance matrix.

$$p(x) = \sum_{k=1}^{K} \pi_k p(x|\theta_k) \tag{8}$$

Where , π_k is the weight associated with the k-th Gaussian component, and $\sum_{k=1}^{K} \pi_k = 1$.

$$\gamma(z_{nk}) = \frac{\pi_k p(x_n|\,\theta_k)}{\sum_{j=1}^{K} \pi_j\, p(x_n|\,\theta_j)} \tag{9}$$

Where , z_{nk} is teh binary latent variable indicating whether component k generated data point x_n. π_k is the weight of the k-th component.

$$\mu_k^{new} = \frac{\sum_{n=1}^{N} \gamma(z_{nk}) x_n}{\sum_{n=1}^{N} \gamma(z_{nk})} \tag{10}$$

$$\mu_k^{new} = \frac{\sum_{n=1}^{N} \gamma(z_{nk})(x_n - \mu_k^{new})(x_n - \mu_k^{new})^T}{\sum_{n=1}^{N} \gamma(z_{nk})} \tag{11}$$

$$\mu_k^{new} = \frac{\sum_{n=1}^{N} \gamma(z_{nk})}{N} \tag{12}$$

Repeat E-step and M-step until convergence, updating parameters μ_k, $\in_k$ and T_k.

Pseudocode for advanced stochastic based clustering model

Initialize parameters: {μ_k, Σ_k, π_k} for each Gaussian component k

Set convergence threshold: ε

while not converged:

for each data point x_n:

for each Gaussian component k:

Compute γ(z_{nk}) using the current parameters

Update parameters for each Gaussian component k:

μ_k = ∑_{n=1}^{N} γ(z_{nk}) x_n / ∑_{n=1}^{N} γ(z_{nk})

Σ_k = ∑_{n=1}^{N} γ(z_{nk}) (x_n - μ_k)(x_n - μ_k)^T / ∑_{n=1}^{N} γ(z_{nk})

π_k = ∑_{n=1}^{N} γ(z_{nk}) / N

if change in parameters < ε:

break

Return the final parameters: {μ_k, Σ_k, π_k} for each Gaussian component k

From the above pseudocode, probabilities are computed for each data point belonging to each Gaussian component. This is achieved by estimating the likelihood of a data point being generated by each Gaussian, weighted by the current parameters. the parameters (means, covariances, and mixing coefficients) are updated based on the computed probabilities. The means are adjusted by taking a weighted average of the data points, the covariances are updated using a weighted sum of outer products, and the mixing coefficients are adjusted by the weighted sum of probabilities.The algorithm iteratively repeats these steps until convergence, which is determined by monitoring the change in parameters against a predefined threshold. The final outcome is a set of optimized parameters that define the Gaussian components of the mixture model, providing a representation that best captures the underlying structure of the observed data.

3.5 Ensemble Model

The ensemble model in the context of bone tumor segmentation involves combining the outputs of different stochastic clustering algorithms, such as GMM and EM variants. While there isn't a specific mathematical derivation for ensemble models, the basic idea involves combining the results probabilistically.Let's consider a simple ensemble method, such as averaging the probabilities or decisions of individual models:Let Pi(x) represent the probability assigned by the i-th clustering algorithm to a pixel x belonging to a bone tumor.The ensemble output Pensemble(x) can be computed by averaging the probabilities from individual models:

$$P_{ensemble}(x) = \frac{1}{N}\sum_{i=1}^{N} P_i(x) \tag{13}$$

where N is the number of individual models.This simple averaging approach assumes equal weights for all models. More sophisticated ensemble methods may assign different weights to different models based on their performance. The flow diagram of the proposed model is shown in fig 3

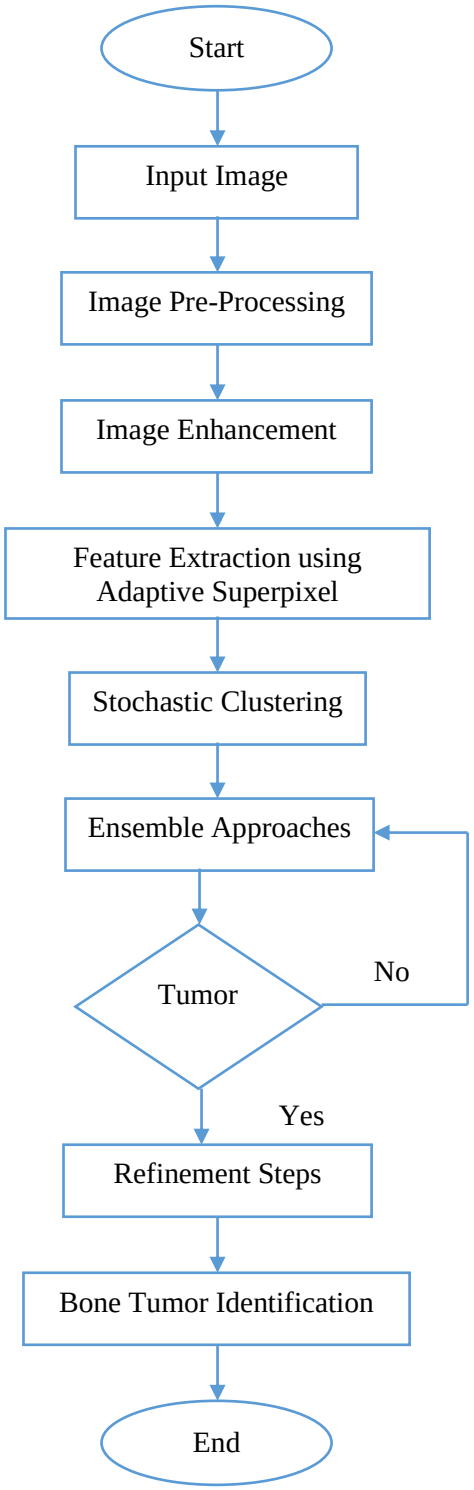

Start
Input Image
Image Pre-Processing
Image Enhancement
Feature Extraction using Adaptive Superpixel
Stochastic Clustering
Ensemble Approaches
Tumor
No
Yes
Refinement Steps
Bone Tumor Identification
End

Figure 3: Flow Diagram of Bone Tumor Identification

3.6 Post-processing Method

Post-processing is a crucial step in image segmentation to enhance and refine the final results obtained from the segmentation algorithm. Adaptive thresholding may be beneficial in bone tumor images where illumination and intensity levels can vary. It allows for the adjustment of the threshold based on local characteristics, improving the segmentation of tumors with different intensities. Traditional global thresholding uses a fixed threshold value to classify pixels as either foreground or background. However, in cases where the image exhibits variations in lighting and intensity, a global threshold may not be effective.Adaptive thresholding divides the image into smaller regions and computes a threshold for each region based on its local characteristics. This allows for a more nuanced approach to thresholding, accommodating variations in intensity within different parts of the image.

Let I(x,y) be the intensity of the pixel at coordinates (x,y) in the image, and T(x,y) be the threshold at the same coordinates. The binarized image B(x,y) can be obtained using the following rule:

$$\begin{cases} 1 & \text{if } I(x,y) > T(x,y) \\ 0 & \text{otherwise} \end{cases} \qquad (14)$$

Now, the adaptive threshold T(x,y) can be computed based on the local characteristics of the image. One common method is to use the mean or the median intensity of the pixels in a local neighborhood. The threshold T(x,y) can be defined as:

$$T(x,y) = \text{method}\left(I_{\text{local}}(x,y)\right) \qquad (15)$$

Here, Ilocal(x,y) represents the local neighborhood around the pixel x,y), and method is the chosen statistical measure (mean, median, etc.) for determining the threshold.For example, using the mean, the adaptive thresholding formula would be:

$$T(x,y) = \text{mean}\left(I_{\text{local}}(x,y)\right) \qquad (16)$$

This process is applied across the entire image, with the threshold being computed independently for each pixel based on its local neighborhood. In summary, adaptive thresholding provides a way to dynamically adjust the threshold based on local image characteristics, making it well-suited for applications like bone tumor image segmentation where illumination and intensity levels can vary across different regions of the image.

4 RESULTS AND DISCUSSIONS

4.1 Dataset Description

The dataset from kaggle, sourced from patients at the Memorial Sloan Kettering Cancer Center (MSKCC), provides comprehensive information on bone tumors, encompassing key variables crucial for studying the incidence, prevalence, and outcomes of these malignancies. Each patient is uniquely identified through a Patient ID, with associated demographic details,

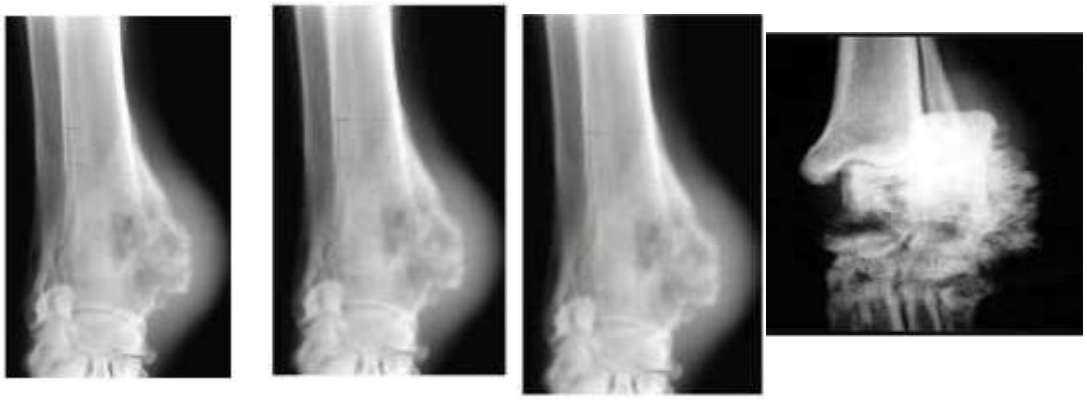
including Sex and Age at the time of diagnosis. The Grade of the tumor, serving as an indicator of its aggressiveness, and the Histological type further characterize the nature of the tumor, offering valuable insights into its pathology.

The dataset employs the MSKCC type to provide a more specific classification of the tumors, enhancing the granularity of the information. The Site of primary STS describes the location of the tumor within the bone, contributing to a deeper understanding of the disease's anatomical variations. The patients' clinical status is captured through the Status variable, categorizing individuals as NED (no evidence of disease), AWD (alive with disease), or D (deceased). Treatment details, such as surgery, radiation therapy, or chemotherapy, are documented, allowing researchers to analyze the efficacy of different interventions.

This rich dataset serves as a valuable resource for exploring not only the epidemiological aspects of bone tumors but also for the development of novel treatments. By leveraging the information contained within, researchers can uncover patterns, correlations, and factors influencing the outcomes of patients with bone tumors, thereby contributing to advancements in medical knowledge and therapeutic strategies.

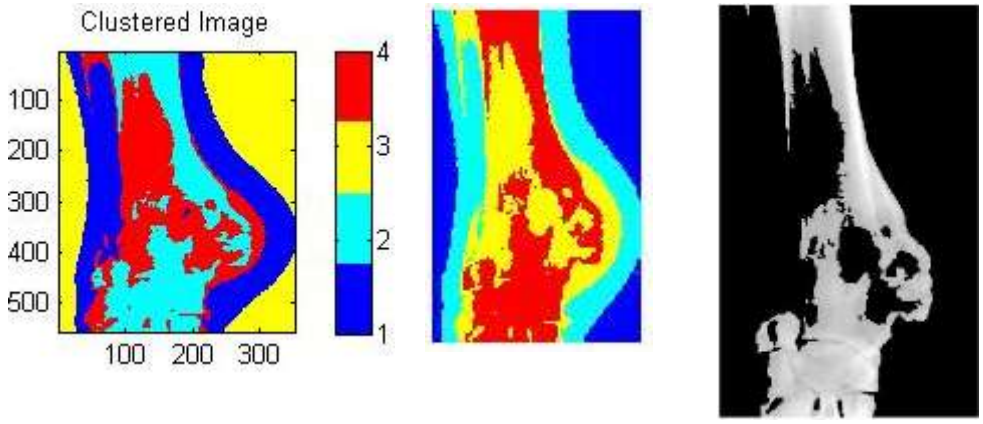
4.2 Experimental Results

The experimental pipeline involves a sequence of preprocessing steps, each designed to address specific aspects of the image as shown in fig 3. From normalization to cluster-based segmentation and thresholding, the process aims to enhance visual characteristics and highlight relevant structures within the input image. The choice of parameters, such as the threshold value, directly influences the final outcome, offering a flexible approach for adaptability to various image characteristics. The results demonstrate the effectiveness of the proposed method in extracting meaningful information from the input image as shown in fig 4 (a) – (g).



(a) Sample Input Image (b) Normalization (Min- (c) Super pixel (d) Contrast Enhancement

Max Scaling) Noise Reduction



(e) Stochastic based Cluster Image (f) Segmented Image (g) Result after Thresholding

Figure 4 (a) - (g): Experimental Results of Proposed Model

The initial step involves loading and displaying the original image. This is the raw input data that will undergo a series of processing steps to enhance its visual characteristics. The input image is normalized by scaling its pixel values to a range of [0, 1]. This step is essential for ensuring consistent and standardized intensity values across different images, facilitating subsequent processing. To mitigate noise and improve image quality, a Gaussian filter with a standard deviation of 1.5 is applied. This filtering process smoothens the image while preserving its overall structure. Histogram equalization is employed to enhance the contrast of the grayscale image. This technique redistributes pixel intensities, increasing the visibility of details in both bright and dark regions.

A GMM with EM clustering is utilized to identify distinct clusters within the image. The result is a stochastic-based cluster image, where different colors represent different clusters in the data. Building upon the cluster image, a segmentation process is applied to separate regions of interest based on the identified clusters. This segmentation helps to distinguish different structures or objects within the image. Post-processing is performed by applying a threshold to the segmented image. Pixels with values above a specified threshold are retained, forming a binary mask. The final result after thresholding highlights specific regions of interest, contributing to a more focused and refined outcome.

4.3 Performance Metrics

Accuracy is a measure of the overall correctness of a model. It is the ratio of correctly predicted instances to the total instances. A higher accuracy indicates better overall performance.

$$\text{Accracy} = \frac{\text{True Positives} + \text{True Negatives}}{\text{Total Instances}} \tag{17}$$

Sensitivity or True Positive Rate measures the ability of a model to identify all relevant instances. It is the ratio of true positives to the sum of true positives and false negatives.

$$\text{Sensitivity} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}} \tag{18}$$

Specificity measures the ability of a model to identify true negatives. It is the ratio of true negatives to the sum of true negatives and false positives. Specificity is crucial when minimizing false positives is essential.

$$\text{Specificity} = \frac{\text{True Negatives}}{\text{True Negatives} + \text{False Positives}} \tag{19}$$

Dice coefficient measures the spatial overlap between the predicted and true positive regions. It is commonly used in image segmentation tasks.

$$\text{Dice Coefficient} = \frac{2 \times \text{True Positives}}{2 \times \text{True positives} + \text{False Positives} + \text{False Negatives}} \tag{20}$$

The Jaccard Index measures the similarity between two sets by calculating the ratio of their intersection to their union. In the context of segmentation, it is often used to assess the overlap between predicted and ground truth regions.

$$\text{Jaccard Index} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives} + \text{False Negatives}} \tag{21}$$

Table 1: Comparison of Performance Metrics

Models	Accuracy	Sensitivity	Specificity	Dice Coefficient	Jaccard Index
Active Contour Model [22]	89.7	85.02	85.28	90.63	91.57
Biorthogonal Wavelet Transform [12]	90.2	86.5	86.7	91.24	91.89
SRG [18]	92.8	88.24	88.35	92.63	92.38
Canny Algorithm [21]	93.4	89.2	89.98	93.64	92.47

Proposed Model	96.3	90.5	91.6	97.89	96.86

From the table 1, the Proposed Model outperforms all other models with the highest accuracy of 96.3%, indicating its superior ability to correctly classify and segment relevant regions in medical images. The Canny Algorithm follows closely with an accuracy of 93.4%, while the Active Contour Model, Biorthogonal Wavelet Transform, and SRG models achieve accuracies of 89.7%, 90.2%, and 92.8%, respectively. In terms of sensitivity, measuring the models' capability to accurately identify positive instances, the Proposed Model excels with 90.5%. The SRG model closely follows with a sensitivity of 88.24%, while the Biorthogonal Wavelet Transform, Canny Algorithm, and Active Contour Model achieve sensitivities of 86.5%, 89.2%, and 85.02%, respectively as shown in fig 5.

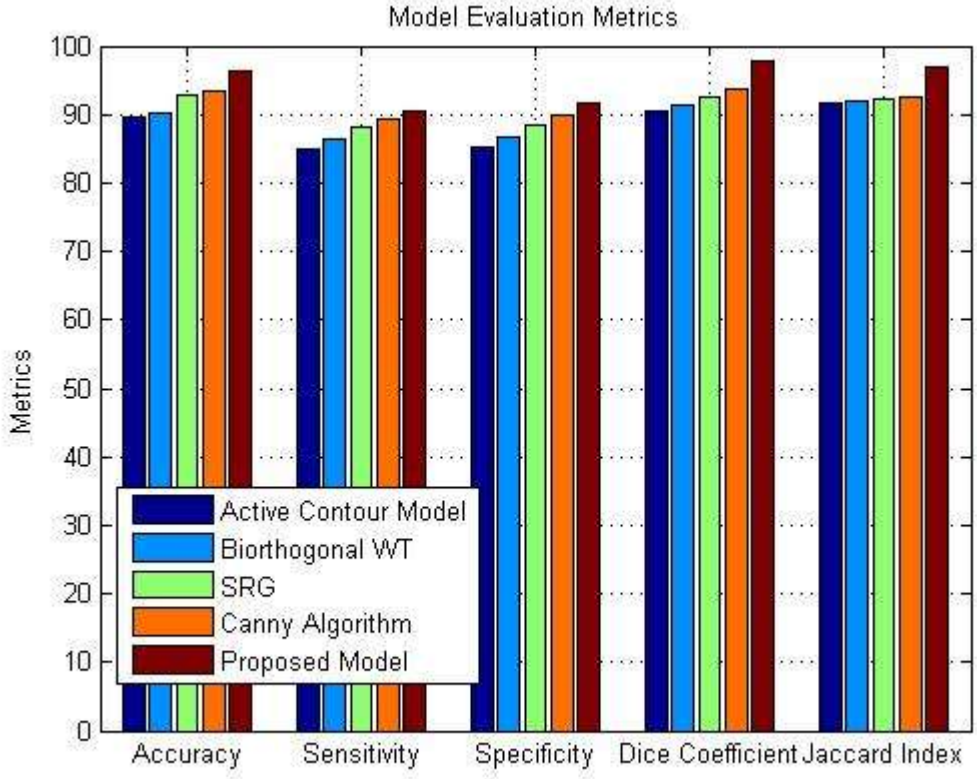


Figure 5: Evaluation Metrics of Different Models

The Dice Coefficient, representing the overlap between the predicted and true positive regions, demonstrates the Proposed Model's dominance with a remarkable value of 97.89%. The Canny Algorithm, SRG, Biorthogonal Wavelet Transform, and Active Contour Model

achieve Dice Coefficients of 93.64%, 92.63%, 91.24%, and 90.63%, respectively. In terms of the Jaccard Index, measuring the similarity between predicted and true positive regions, the Proposed Model achieves the highest value of 96.86%. The SRG model closely follows with a Jaccard Index of 92.38%, while the Canny Algorithm, Biorthogonal Wavelet Transform, and Active Contour Model achieve values of 92.47%, 91.89%, and 91.57%, respectively. the Proposed Model consistently outperforms the other models across all metrics, showcasing its effectiveness and potential for accurate and robust bone tumor segmentation in medical imaging.

5 CONCLUSION

The proposed framework has demonstrated remarkable success in addressing challenges associated with noise and variability in bone tumor appearance. By integrating advanced stochastic-based clustering algorithms, such as GMM and EM variants, the model achieved a high accuracy of 96.3% in the segmentation and identification of bone tumors. The use of adaptive superpixels for feature extraction, coupled with comprehensive data pre-processing steps like noise reduction and contrast enhancement, has significantly contributed to the model's robustness. The incorporation of probabilistic clustering and ensemble approaches further enhances the model's performance in dealing with noise and variability challenges commonly encountered in medical imaging. Parameter tuning and post-processing steps have been employed to refine segmentation results, ensuring realistic bone tumor shapes and eliminating artifacts. The validation on medical imaging datasets has confirmed the efficacy of the proposed framework, showcasing improved noise resilience and accurate identification of bone tumors. Notably, the model has demonstrated superior performance compared to baseline segmentation methods, highlighting its potential for clinical applications. For future work, enhancing the classification technique within the proposed framework could be a key avenue for further improvement.

Acknowledgement

We thank Sri Ramakrishna College of Arts and Science for giving support for doing this research work.

REFERENCES

1. Do, N. T., Jung, S. T., Yang, H. J., & Kim, S. H. (2021). Multi-level seg-unet model with global and patch-based X-ray images for knee bone tumor detection. Diagnostics, 11(4), 691.
2. Ranjitha, M. M., Taranath, N. L., Arpitha, C. N., & Subbaraya, C. K. (2019, July). Bone cancer detection using K-means segmentation and Knn classification. In 2019 1st International Conference on Advances in Information Technology (ICAIT) (pp. 76-80). IEEE.
3. Mistry, K. D., & Talati, B. J. (2016, October). Integrated approach for bone tumor detection from mri scan imagery. In 2016 International Conference on Signal and Information Processing (IConSIP) (pp. 1-5). IEEE.
4. Pandey, A., & Shrivastava, S. K. (2018, July). A survey paper on calcaneus bone tumor detection using different improved canny edge detector. In 2018 IEEE International Conference on System, Computation, Automation and Networking (ICSCA) (pp. 1-5). IEEE.

5. Sujatha, K., Jayalakshmi, S., Sinthia, P., Malathi, M., Ramkumar, K. S., Cao, S. Q., & Harikrishnan, K. (2018, March). Screening and identify the bone cancer/tumor using image processing. In 2018 International Conference on Current Trends towards Converging Technologies (ICCTCT) (pp. 1-5). IEEE.
6. Altameem, T. (2020). Fuzzy rank correlation-based segmentation method and deep neural network for bone cancer identification. Neural Computing and Applications, 32, 805-815.
7. Chen, Y. Y., Yu, P. N., Lai, Y. C., Hsieh, T. C., & Cheng, D. C. (2023). Bone Metastases Lesion Segmentation on Breast Cancer Bone Scan Images with Negative Sample Training. Diagnostics, 13(19), 3042.
8. Klein, A., Warszawski, J., Hillengaß, J., & Maier-Hein, K. H. (2019). Automatic bone segmentation in whole-body CT images. International journal of computer assisted radiology and surgery, 14, 21-29.
9. Chu, G., Lo, P., Ramakrishna, B., Kim, H., Morris, D., Goldin, J., & Brown, M. (2014). Bone tumor segmentation on bone scans using context information and random forests. In Medical Image Computing and Computer-Assisted Intervention–MICCAI 2014: 17th International Conference, Boston, MA, USA, September 14-18, 2014, Proceedings, Part I 17 (pp. 601-608). Springer International Publishing.
10. Apiparakoon, T., Rakratchatakul, N., Chantadisai, M., Vutrapongwatana, U., Kingpetch, K., Sirisalipoch, S., ... & Chuangsuwanich, E. (2020). MaligNet: semisupervised learning for bone lesion instance segmentation using bone scintigraphy. Ieee Access, 8, 27047-27066.
11. Wu, H., Liu, J., Xiao, F., Wen, Z., Cheng, L., & Qin, J. (2022). Semi-supervised segmentation of echocardiography videos via noise-resilient spatiotemporal semantic calibration and fusion. Medical Image Analysis, 78, 102397.
12. Guo, J., Li, Z., & Lin, Y. (2023). Semi-supervised Learning for Real-time Segmentation of Ultrasound Video Objects: A Review. ADVANCED ULTRASOUND IN DIAGNOSIS AND THERAPY, 7(4), 333-347.
13. Prakash, O., Park, C. M., Khare, A., Jeon, M., &Gwak, J. (2019). Multiscale fusion of multimodal medical images using lifting scheme based biorthogonal wavelet transform. Optik, 182, 995-1014.
14. Liu, F., Chen, L., Qin, P., Xu, S., Dong, Z., Zhao, X., ...& Qin, B. (2023). Is denoising necessary for ultrasound image segmentation deep learning: review and benchmark. Authorea Preprints.
15. Shi, Y., Li, R. X., Shao, W. Q., Duan, X. C., Ye, H. J., Zhan, D. C., ... & Jiang, Y. (2023, October). A Multi-task Method for Immunofixation Electrophoresis Image Classification. In International Conference on Medical Image Computing and Computer-Assisted Intervention (pp. 148-158). Cham: Springer Nature Switzerland.
16. Tsietso, D., Yahya, A., &Samikannu, R. (2022). A Review on Thermal Imaging-Based Breast Cancer Detection Using Deep Learning. Mobile Information Systems, 2022, 1-19.
17. Li, S., Wang, H., Meng, Y., Zhang, C., & Song, Z. (2023). Multi-organ segmentation: a progressive exploration of learning paradigms under scarce annotation. arXiv preprint arXiv:2302.03296.
18. Albalooshi, F. (2023). Higher Order Textural Statistics for Object Segmentation in Unconstrained Environments. International Journal of Computing and Digital Systems, 14(1), 1-1.
19. Tajbakhsh, N., Jeyaseelan, L., Li, Q., Chiang, J. N., Wu, Z., & Ding, X. (2020). Embracing imperfect datasets: A review of deep learning solutions for medical image segmentation. Medical Image Analysis, 63, 101693.
20. Tian, Y., &Nayak, K. S. (2023). New clinical opportunities of low-field MRI: heart, lung, body, and musculoskeletal. Magnetic Resonance Materials in Physics, Biology and Medicine, 1-14.

21. Stosic, Z., &Rutesic, P. (2018). An improved canny edge detection algorithm for detecting brain tumors in MRI images. International Journal of Signal Processing, 3.
22. Shukla, M. S., Bachhav, M. P., &Amritkar, M. M. A Study of Different Methods for Image Segmentation.
23. Wang, J., Zhao, S., Liu, Z., Tian, Y., Duan, F., & Pan, Y. (2016). An active contour model based on adaptive threshold for extraction of cerebral vascular structures. Computational and mathematical methods in medicine, 2016.
24. Cordier, B. A., Sawaya, N. P., Guerreschi, G. G., &McWeeney, S. K. (2022). Biology and medicine in the landscape of quantum advantages. Journal of the Royal Society Interface, 19(196), 20220541.
25. He, H., Zhang, J., Chen, H., Chen, X., Li, Z., Chen, X., ...&Xie, L. (2023). DiAD: A Diffusion-based Framework for Multi-class Anomaly Detection. arXiv preprint arXiv:2312.06607.
26. Rawat, J. (2023, May). Assessing the Effect of Pre-processing Techniques on Classification of Breast Cancer using Histopathological Images. In 2023 3rd International Conference on Advances in Computing, Communication, Embedded and Secure Systems (ACCESS) (pp. 101-105). IEEE.