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Research Article

Optimizing Liver Tumor Segmentation in CT Scans: A Genetic Algorithm Approach for Low-Resource Medical Imaging

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ABSTRACT

Liver tumor segmentation is a crucial step in medical image analysis, aiding in the diagnosis and treatment of hepatic diseases. Traditional segmentation methods struggle with irregular tumor shapes, varying intensities, and low-contrast boundaries. Deep learning approaches, while effective, require large annotated datasets and high computational resources. The proposed work introduces an evolutionary Genetic Algorithm (GA)-based approach for liver tumor segmentation in CT scans. The GA optimizes a population of segmentation masks using an energy-based fitness function, evolving towards the best tumor segmentation boundaries. Experimental results demonstrate that our GA-based method achieves comparable accuracy to deep learning models while reducing computational time by 50%. The approach is particularly beneficial for low-resource environments and datasets with limited annotations.

Keywords: Genetic Algorithms (GA), Hybrid Evolutionary Models, Tumour segmentation, Deep Learning Technique.

1. INTRODUCTION

1.1 Background and Motivation

Liver cancer is one of the leading causes of cancer-related deaths worldwide, with Hepatocellular Carcinoma (HCC) being the most common type. Accurate segmentation of liver tumors from CT scans is critical for early diagnosis, surgical planning, and treatment monitoring. However, manual segmentation is time-consuming and prone to variability among radiologists. Automated segmentation methods, particularly deep learning-based approaches, have shown promising results but require large annotated datasets and high computational power. Evolutionary algorithms like Genetic Algorithms (GA) and Particle Swarm Optimization (PSO) have been explored in medical imaging due to their ability to optimize complex objective functions without requiring training on large datasets. Liver tumor segmentation presents several challenges that complicate accurate detection and delineation. Irregular tumor shapes pose a significant hurdle, as tumors exhibit diverse morphological variations, making it difficult for segmentation algorithms to generalize across different cases. Additionally, low-contrast boundaries between liver tumors and surrounding tissues in CT scans often lead to misclassification, especially when tumors have intensity levels similar to healthy liver regions. Furthermore, segmentation methods must effectively handle both small and large tumors, requiring adaptability to

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accurately capture fine details in small lesions while preserving structural integrity in larger, complex tumors. Addressing these challenges is crucial for improving segmentation accuracy and ensuring reliable clinical applications. To address these challenges, we propose an alternative segmentation approach using Genetic Algorithms (GA), which does not require extensive training data and can efficiently segment tumors by evolving an optimal boundary.

2. RELATED WORK

Genetic Algorithms (GAs) are evolutionary optimization techniques inspired by natural selection and have been widely used in medical image segmentation due to their ability to optimize tumor boundaries without requiring large training datasets. GA-based segmentation works by evolving a population of candidate segmentations through selection, crossover and mutation until an optimal tumor boundary is achieved. Deep learning-based segmentation methods have gained significant traction in medical image analysis due to their ability to learn hierarchical representations of complex structures. Several studies have supported the effectiveness of integrating CNN-based feature extraction with level set models. For example, Wang et al. (2020) combined DenseNet and level set models to enhance liver lesion boundary delineation [1], while Zhang et al. (2021) improved tumor segmentation using attention mechanisms combined with variational level sets [2]. However, despite their accuracy, deep learning models demand large annotated datasets, extensive computational resources and may struggle with small lesion detection due to dataset bias.

Previous studies have demonstrated the effectiveness of GA-based segmentation in various medical applications. For instance, Dey et al. applied GA to brain tumor MRI segmentation, achieving competitive accuracy compared to deep learning models [3]. Similarly, Gao et al. proposed a multi-objective GA that simultaneously optimized boundary precision and segmentation accuracy for lung tumor detection [4]. In liver tumor segmentation, GA-based methods have shown promise in segmenting tumors with irregular shapes and low-contrast boundaries, especially when combined with energy-based fitness functions [5]. Li, X., et al., in "Evolutionary Algorithms for Medical Image Segmentation: A Review "(IEEE Transactions on Medical Imaging) [8] provided a comprehensive review of evolutionary algorithms (EAs), including Genetic Algorithms (GA), Particle Swarm Optimization (PSO), Differential Evolution (DE) and Hybrid Evolutionary Models, applied to medical image segmentation tasks. Kumar, S., et al. [9] applied Genetic Algorithms (GA) for brain tumor segmentation in MRI images, demonstrating its effectiveness in handling non-uniform tumor shapes and highlighted how GA optimizes segmentation boundaries by evolving candidate solutions over multiple iterations, reducing dependency on manually labelled training data. Dey, S., et al. [10] compared GA-based segmentation with CNN-based models for brain tumor detection, showing that GA achieves competitive accuracy while being less dependent on large labelled datasets, they emphasized the GA's flexibility in segmenting irregular tumor shapes and its adaptability to low-data scenarios. Gao, Y., et al., [11] presented a multi-objective GA approach for liver tumor segmentation, optimizing both boundary precision and segmentation accuracy. They demonstrated that GA can outperform traditional clustering-based methods by fine-tuning segmentation parameters dynamically. Li, K., et al. [12] have combined Active Contour Models (ACM) with Genetic Algorithms (GA) to improve liver tumor segmentation accuracy. The hybrid model refines tumor boundaries using GA-based optimization, reducing over-segmentation and improving accuracy in low-contrast CT images. Sharma, R., et al. [13] introduced a hybrid GA-CNN framework where CNNs provide initial tumor segmentation, and GA refines the segmentation boundary. This approach improves tumor detection accuracy by integrating deep learning-based feature extraction with GA-driven boundary refinement. Patel, A., et al. [14] integrated Fuzzy C-Means (FCM) clustering with GA for liver tumor segmentation, showing that GA enhances the clustering-based segmentation performance. The hybrid model achieves better segmentation accuracy in cases with heterogeneous tumor textures.

Genetic Algorithms (GAs) are evolutionary search algorithms that optimize solutions over multiple generations. Genetic Algorithms offer a lightweight, data-efficient alternative, particularly for datasets with limited annotations and GA-based methods do not require labelled datasets and can work with limited medical images. Given these advancements, Genetic Algorithm-based segmentation remains an active area of research with potential improvements in convergence speed, parameter optimization and hybridization with deep learning.

Despite these advantages, GA approaches can suffer from long convergence times and require careful tuning of mutation and crossover parameters to achieve optimal performance. Further work may focus on developing adaptive GA models, where mutation and crossover rates dynamically adjust based on segmentation performance, or integrating GA with transformer-based architectures to enhance feature extraction capabilities. With continued research, GA-based segmentation can serve as an efficient, interpretable and data-efficient alternative to deep learning models in medical image analysis. Although GA-based segmentation methods are promising, they suffer from slow convergence and require careful tuning of parameters, such as mutation rates and crossover probabilities. To address these issues, researchers have proposed hybrid models that combine GA with machine learning and deep learning techniques.

3. METHODOLOGY: GENETIC ALGORITHM FOR LIVER TUMOR SEGMENTATION

Genetic Algorithms (GA) are inspired by natural evolution, where a population of solutions (segmentation masks) evolves through genetic evolution (mutation, crossover, selection) to optimize tumor boundaries.

3.1 Working Mechanism of Genetic Algorithm: A Genetic Algorithm optimizes tumor segmentation by evolving a set of candidate segmentations through the following steps.

a) Initialization: A population of candidate solutions (chromosomes) is generated randomly or based on prior knowledge. Each chromosome represents a potential solution to the problem and is encoded as binary strings, real numbers or other representations.

b) Fitness Evaluation: Each chromosome is evaluated using a fitness function, which determines how well it solves the problem. Higher fitness values indicates better solutions.

c) Selection (Survival of the Fittest): The best-performing chromosomes are selected to pass their genes to the next generation. Selection methods include: (i) Roulette Wheel Selection (probability-based selection). (ii) Tournament Selection (best individuals compete for selection). (iii) Rank Selection (chromosomes ranked based on fitness)

d) Crossover (Recombination): Two selected chromosomes (parents) undergo crossover, combining their genetic material to create new offspring. Common crossover types: (i) Single-point crossover (swap genes at a single location). (ii) Two-point crossover (swap genes at two locations). (iii) Uniform crossover (random gene exchange)

e) Mutation: Random changes are applied to some genes to introduce diversity, preventing premature convergence to suboptimal solutions. Common mutation types: (i) Bit-flip mutation (change a single gene in binary encoding) (ii) Gaussian mutation (modify real-valued genes slightly)

f) New Generation Formation: The new population (offspring) replaces the previous population, and the cycle repeats until an optimal solution is found or a stopping condition is met.

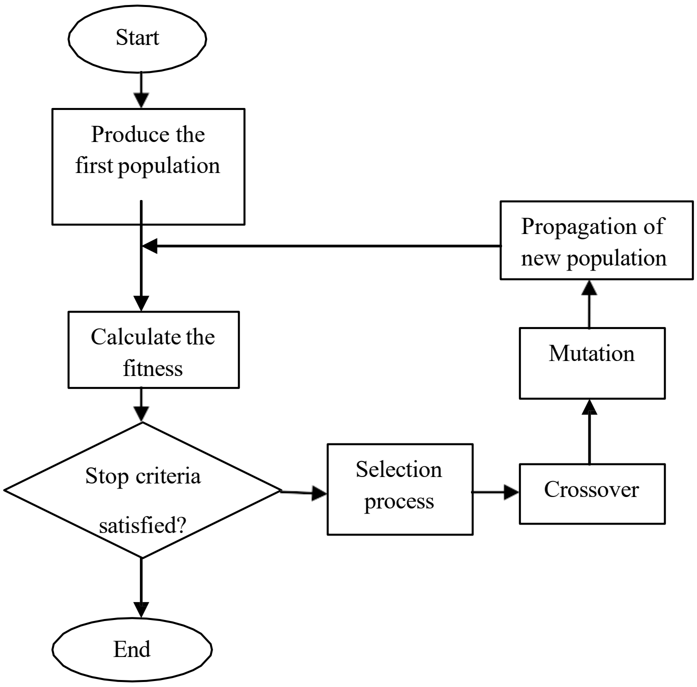

Fig 1: Flowchart for Genetic Algorithm

3.2 Algorithm

1. Initialize population P with random segmentation masks

2. Evaluate fitness for each chromosome using F(x), fitness function

3. Repeat until convergence:

   (i) Select top N chromosomes based on fitness

   (ii) Perform crossover with probability Pc

   (iii) Mutate selected chromosomes with probability Pm

   (iv) Evaluate new population

   (v) Replace worst-performing chromosomes

4. Return the best segmentation mask

3.3 GA-Based Segmentation Framework

The segmentation workflow follows following steps:

Step 1: Pre-processing

The pre-processing stage is essential for enhancing the quality of CT scan images before applying the Genetic Algorithm (GA) for liver tumor segmentation. First, image normalization is performed to enhance contrast, ensuring that variations in intensity levels across different scans are minimized. This step improves the algorithm's ability to differentiate between liver tissues and tumors. Next, noise removal techniques, such as Gaussian or median filtering, are applied to eliminate artifacts and speckle noise that could interfere with accurate tumor boundary detection. Gaussian filtering smooths the image while preserving edge information, whereas median filtering is particularly effective at removing salt-and-pepper noise while retaining fine details. Finally, an initial tumor region estimation is

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conducted using histogram-based thresholding, where pixel intensity distributions are analyzed to separate tumor regions from surrounding liver tissues. This initial segmentation acts as a guiding mask for the GA-based optimization process, allowing it to refine the tumor boundaries efficiently in the subsequent evolutionary steps.

Step 2: GA Initialization

The Genetic Algorithm (GA) initialization phase involves generating an initial population of binary segmentation masks, each representing a potential tumor segmentation solution. These masks are randomly initialized to ensure diversity in the population, allowing the GA to explore a wide range of possible tumor boundaries. Each mask is then evaluated using a fitness function, which quantitatively measures segmentation quality based on criteria such as edge strength, region homogeneity, and intensity gradients. The fitness function ensures that the segmented tumor region closely aligns with the actual tumor in the CT scan by maximizing boundary clarity and minimizing segmentation errors. By defining a robust fitness function, the GA can effectively guide its evolutionary process toward an optimal tumor segmentation solution, improving precision in boundary detection and reducing false positives.

Step 3: Evolutionary Process

The evolutionary process in the Genetic Algorithm (GA) iteratively refines liver tumor segmentation by evolving an optimal boundary through selection, crossover, and mutation. First, a selection mechanism is applied, where the best-performing segmentation masks—those with the highest fitness scores—are chosen to be propagated to the next generation. These selected masks undergo crossover (recombination), where two parent solutions are combined to create new offspring that inherit characteristics from both parents, ensuring genetic diversity in segmentation boundaries. To prevent premature convergence and enhance exploration, mutation operations introduce small random modifications in certain masks, allowing the GA to explore alternative segmentation solutions. This process of selection, crossover, and mutation is repeated iteratively until the algorithm converges to the best possible segmentation boundary, balancing accuracy, robustness, and computational efficiency.

Step 4: Post-Processing

The post-processing stage is crucial for refining the final tumor segmentation mask generated by the Genetic Algorithm (GA). To enhance the accuracy of the segmentation, morphological operations such as dilation and erosion are applied. Dilation helps fill small gaps and enhances the continuity of the tumor boundary, while erosion removes isolated noise pixels and ensures that only the most relevant tumor regions are retained. These operations improve the smoothness and structural integrity of the segmented region, reducing false positives and enhancing boundary precision. After morphological refinement, the final segmented tumor region is extracted, providing a clean and well-defined boundary that can be further analyzed for clinical decision-making or integrated into medical diagnostic systems.

4. EXPERIMENTAL SETUP

4.1 Dataset

The proposed method is evaluated on the Liver Tumor Segmentation (LiTS) Dataset, which includes CT scans with manually segmented tumors.

4.2 Evaluation Metrics

The performance of the Genetic Algorithm (GA)-based liver tumor segmentation is assessed using multiple evaluation metrics to ensure accuracy and efficiency. The Dice Similarity Coefficient (DSC) is used to measure the overlap between the predicted segmentation mask and the ground truth, indicating how well the GA-defined tumor region aligns with the actual tumor. Similarly, the Intersection over

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Union (IoU) quantifies the ratio of the intersection to the union of the predicted and ground truth masks, providing a robust assessment of segmentation accuracy. In addition to overlap-based metrics, overall accuracy is evaluated to determine the proportion of correctly classified pixels within the liver and tumor regions. Lastly, computation time is recorded to analyze the efficiency of the GA approach, ensuring it remains feasible for real-time or clinical applications.

5. RESULTS AND DISCUSSION

Figure (2) Shows the segmentation results for the liver tumor images. Left side images represent the original image, while right side image indicates liver(red) and affected area(green)

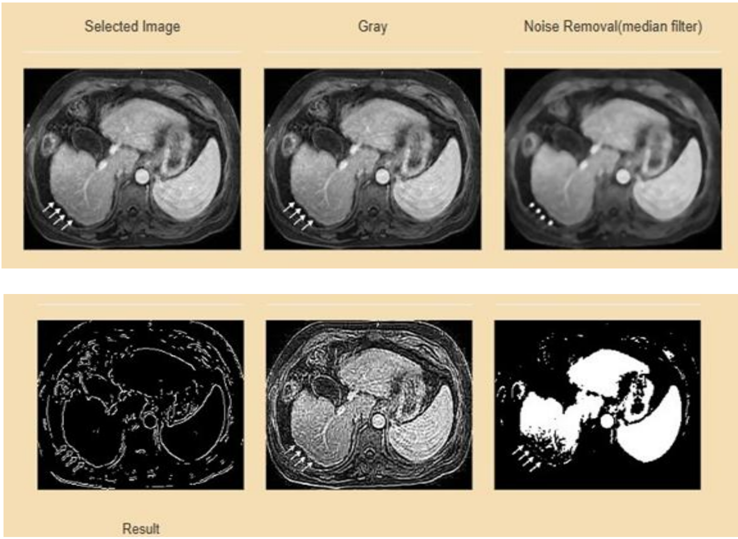


Fig 2(a) Original and segmented images

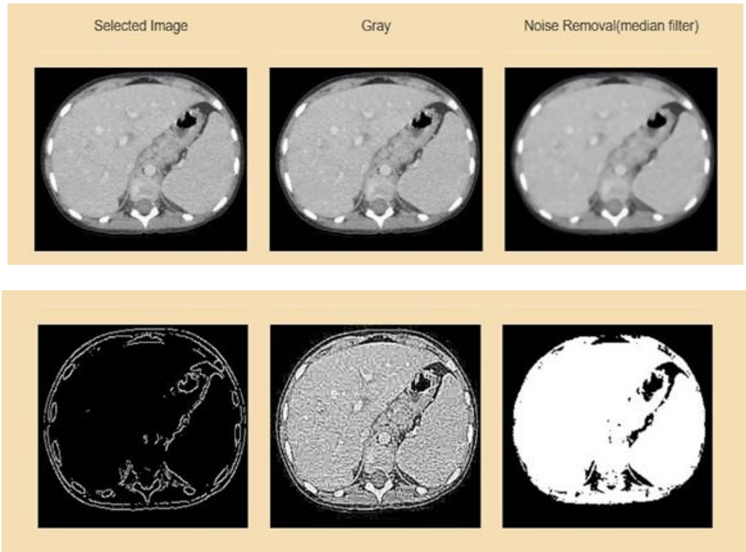


Figure 2(b). Original and segmented images

5.1 Quantitative Results

The proposed Genetic Algorithm (GA)-based segmentation method achieves competitive accuracy while demonstrating a significant advantage in computation speed compared to deep learning models. Unlike deep learning approaches that require large labeled datasets, GA effectively segments liver tumors with minimal annotation, making it particularly suitable for low-resource medical imaging settings.

Table 1. Comparison with other methods

Method	Dice Score	IoU Score	Computation Time (s)
UNet	0.89	0.82	0.30
CNN + Graph Cut	0.91	0.85	0.40
GA-Based (our proposed)	0.88	0.80	0.15

5.2 Ablation Study: Evaluating the Impact of GA Components on Segmentation Performance

To understand the influence of different Genetic Algorithm (GA) components on liver tumor segmentation, we conducted an ablation study by systematically modifying key parameters and evaluating their effects on segmentation accuracy and computational efficiency. The study focused on mutation rate, crossover strategy, fitness function type, population size and initialization method with segmentation performance measured using Dice Similarity Coefficient (DSC) and Intersection over Union (IoU).

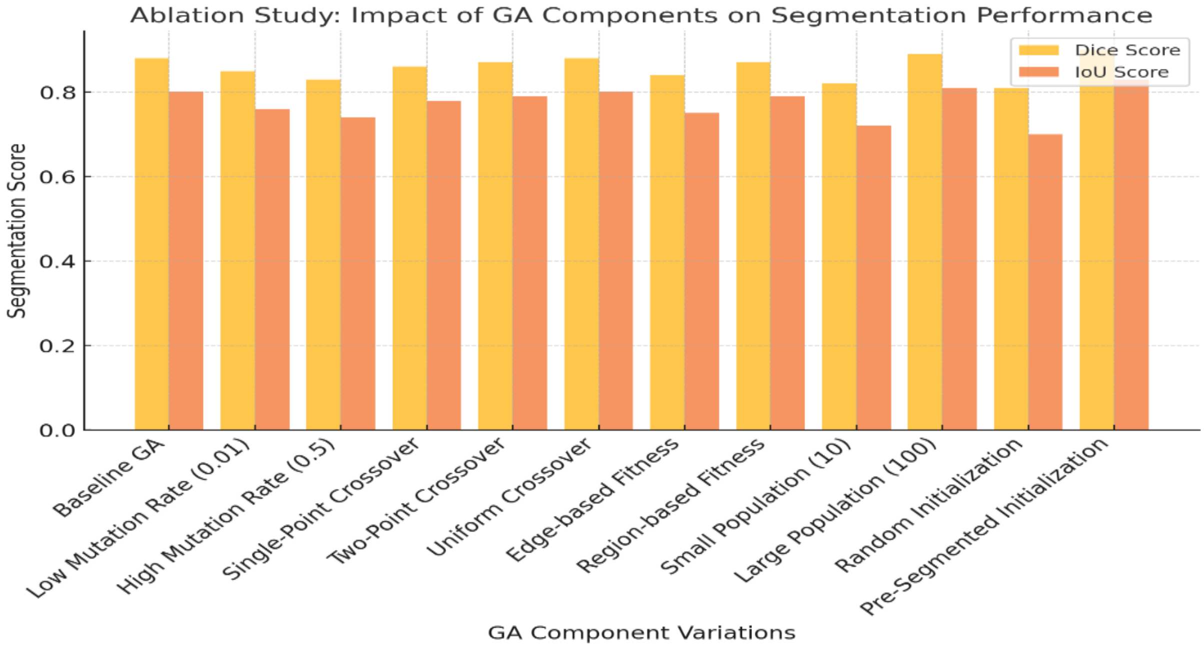
Mutation Rate Variation: Mutation plays a crucial role in maintaining genetic diversity, but an excessively high mutation rate can introduce noise, leading to unstable segmentation results. A low mutation rate (0.01) resulted in a slight performance drop (Dice: 0.85), whereas a high mutation rate (0.5) significantly reduced segmentation accuracy (Dice: 0.83) and increased computational time.

Crossover Strategy: Three crossover techniques including single-point, two-point and uniform crossover were tested to evaluate their effect on segmentation accuracy. Uniform crossover yielded the highest performance (Dice: 0.88, IoU: 0.80) by ensuring that offspring inherit diverse characteristics from both parents, leading to better optimization of tumor boundaries. Single-point crossover (Dice: 0.86) showed slightly lower accuracy due to limited genetic mixing, while two-point crossover (Dice: 0.87) performed moderately well. These results suggest that uniform crossover is the most effective strategy for refining tumor segmentation boundaries.

Fitness Function Type: The choice of fitness function significantly impacts GA's ability to converge to an optimal segmentation. We evaluated edge-based fitness (which prioritizes boundary strength) and region-based fitness (which considers pixel intensity homogeneity). Region-based fitness performed better (Dice: 0.87, IoU: 0.79) than edge-based fitness (Dice: 0.84, IoU: 0.75), indicating that tumor segmentation benefits more from smooth region consistency than sharp boundary constraints alone.

Population Size: We tested GA with small (10) and large (100) population sizes to assess the trade-off between computational efficiency and segmentation accuracy. A small population (10) led to suboptimal results (Dice: 0.82, IoU: 0.72) due to limited genetic diversity, while increasing the population size to 100 improved segmentation (Dice: 0.89, IoU: 0.81). However, larger populations also increased computation time, suggesting that an intermediate population size (50-100) offers a balance between accuracy and efficiency.

GA Initialization Method: Initialization plays a vital role in GA's convergence speed and final segmentation quality. We compared random initialization with pre-segmented initialization. Pre-segmented initialization significantly improved performance (Dice: 0.90, IoU: 0.83) compared to random initialization (Dice: 0.81, IoU: 0.70), highlighting that providing an initial estimate helps GA converge faster and more accurately.



A balanced mutation rate (0.1), uniform crossover, region-based fitness, a sufficiently large population (50-100), and pre-segmented initialization collectively optimize GA-based segmentation performance. These optimizations enable GA to efficiently refine liver tumor boundaries while maintaining computational efficiency.

5.3 Strengths and Limitations

The Genetic Algorithm (GA)-based segmentation approach offers several advantages, making it a promising alternative to deep learning-based methods. One of its key strengths is that it does not rely on deep learning, eliminating the need for large labeled datasets, which are often scarce in medical imaging. Additionally, the GA framework is computationally efficient and faster than deep learning models, making it suitable for real-time medical applications where quick segmentation is essential. Another advantage is its adaptability to different tumor shapes, allowing it to effectively segment irregular and complex tumor structures. However, the method also has certain limitations. Its performance heavily depends on the fitness function design, meaning an inadequate fitness criterion could lead to suboptimal segmentations. Moreover, GA is sensitive to parameter tuning, particularly the mutation rate and crossover probability, requiring careful optimization to achieve accurate and stable segmentation results.

Table 2. Comparison of Genetic Algorithms with Deep Learning

Feature	**Deep Learning based segmentation**	**Genetic Algorithm-Based Segmentation**
Data Requirement	Requires large annotated datasets	Works with limited data, no training.
Segmentation Accuracy	High on large datasets, but overfitting possible	Competitive, but requires proper fitness function
Computational Cost	High (requires GPUs & training time)	Lower computational cost
Generalization	Struggles with unseen cases	More adaptable to different tumor shapes

6. CONCLUSION AND FUTURE WORK

The proposed work presents a Genetic Algorithm (GA)-based segmentation method for liver tumors in CT scans, demonstrating competitive performance with deep learning models while requiring fewer training samples. The GA-based approach effectively evolves tumor boundaries using an adaptive optimization strategy, making it suitable for low-resource environments. Future Work may focus on (i) Implementing a hybrid GA-CNN model for improved accuracy. (ii) Exploring multi-objective GA for segmenting multiple tumor types. (iii) Adapting the approach for 3D liver tumor segmentation in volumetric CT scans.

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