# Comparative Analysis of Deep Learning Techniques for Breast Tumor Segmentation in DW-MRI Images \*

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**Abstract.** Breast cancer remains one of the leading causes of mortality among women, making early detection and accurate diagnosis essential. Magnetic resonance imaging (MRI) plays a key role in this, offering detailed insights into tumor characteristics. However, manual tumor segmentation is labor-intensive and prone to variability, prompting the exploration of automated deep learning techniques. These methods hold promise for improving diagnostic precision, treatment planning, and monitoring therapeutic response.

In this study, the performance of 2D and 3D deep learning techniques for breast tumor segmentation on diffusion-weighted MRI (DW-MRI) is evaluated. Although 3D techniques are widely regarded as superior, this assumption may not hold in the context of DW-MRI due to specific limitations. Breast tissue is highly heterogeneous, complicating segmentation. The 4mm gap between DW-MRI slices hampers volumetric reconstruction, and the high sensitivity of DW imaging to water diffusion leads to poor anatomical continuity between slices, further complicating 3D segmentation.

DW-MRI remains underutilized compared to dynamic contrast-enhanced MRI (DCE-MRI), yet it offers key advantages for patients unable to receive contrast agents, being faster, safer, and more cost-effective. This study focuses on DW-MRI and its associated ADC maps, which provide valuable information about tissue characteristics.

Extensive experiments on a diverse clinical dataset reveal that, contrary to common assumptions, 2D segmentation models outperform 3D approaches in DW-MRI, suggesting a reconsideration of 3D methods in this context.

Keywords: Breast cancer· tumor segmentation· deep learning· U-Net· DW-MRI

## 1 Introduction

Cancer remains one of the leading causes of global mortality [24], with breast cancer being the most commonly diagnosed cancer among women worldwide. Recent estimates indicate approximately 2.3 million new cases of breast cancer are diagnosed annually [30]. Breast cancer refers to the uncontrolled proliferation of malignant cells within the breast tissue, often forming a tumor that can invade surrounding structures and metastasize to distant organs.

Early detection and monitoring are crucial for effective treatment, with Magnetic Resonance Imaging (MRI) playing a key role [8]. Among MRI techniques, Dynamic Contrast-Enhanced MRI (DCE-MRI) is widely used for its ability to enhance blood flow visualization, which is often irregular in malignant tumors [18]. However, despite its diagnostic advantages, DCE-MRI has limitations, including the need for contrast agents that can cause allergic reactions, high costs, and complex post-processing [27]. As a result, Diffusion-Weighted MRI (DW-MRI) has emerged as a viable alternative for breast cancer imaging, especially in patients for whom contrast administration is contraindicated. Unlike DCE-MRI, DW-MRI does not require contrast agents but instead measures water molecule diffusion, making it a safer and more accessible imaging option [2]. In DW-MRI studies, pixel intensity values vary with different b-values. Apparent

Diffusion Coefficient (ADC) maps are a derivate of DW-MRI, which integrate multiple b-values to provide quantitative insights into tissue characteristics by measuring water diffusion [14].

Recent advancements in Deep Learning (DL) have significantly improved medical imaging, particularly in computer vision applications [25]. Convolutional neural networks (CNNs) have become a preferred approach for medical image analysis [17], with semantic segmentation playing a crucial role in pixel-wise classification tasks.

Applying deep learning-based semantic segmentation to ADC maps has the potential to assist radiologists in breast cancer diagnosis, treatment planning, and longitudinal monitoring. However, segmentation approaches vary. While 3D techniques are often considered superior [26] [12], breast tissue heterogeneity poses challenges [20]. Additionally, the 1 cm gap between MRI slices can hinder accurate 3D volume reconstruction, and DW imaging's sensitivity to water movement may not consistently capture anatomical structures across slices [11]. Therefore, it is crucial to evaluate whether the added complexity of 3D deep learning models is justified in the context of DW-MRI, where technical and biological constraints may limit their effectiveness.

The remainder of this paper is structured as follows: Section 2 reviews state-of-theart computer vision techniques in medical imaging; Section 3 details dataset preparation, model architecture, and experimental methodology; Section 4 presents and discusses the results; and Section 5 concludes and presents potential directions for future research.

## 2 Background

Convolutional neural networks (CNNs) have revolutionized computer vision in recent years, with [16] establishing their superiority over traditional hand-crafted feature methods in image classification tasks. In biomedical image segmentation, the U-Net architecture [22] has become a foundational model, widely adopted for pixel-wise semantic segmentation due to its encoder–decoder structure and skip connections. These foundational models inform our approach; to contextualize our contribution, we review recent advances in both 2D and 3D segmentation methods specifically applied to breast cancer imaging.

We first review 2D segmentation approaches, which remain widely used due to their reduced computational complexity and compatibility with slice-based annotations. In 2D segmentation, [3] applied DeepLab and Mask R-CNN to segment malignant and benign cancer regions. [15] employed a U-Net to segment regions of interest in ultrasound images of breast cancer patients. Using ResNet50 within the DeepLab framework, [23] achieved strong segmentation metrics, though their study focused on the wellestablished dynamic contrast-enhanced MRI (DCE-MRI). [4] introduced Connected-UNets, a U-Net modification designed to enhance contextual information within the encoder-decoder architecture for breast cancer segmentation. Additionally, [5] leveraged fuzzy logic for pre-processing, significantly improving tumor segmentation across multiple CNN models. A different approach was taken by [7], who utilized Mask R-CNN for breast cancer detection, classification, and segmentation in thermal images.

We then discuss 3D approaches, which aim to capture volumetric context but pose greater challenges in clinical settings. In 3D segmentation, [21] trained multiple CNN models for the 3D semantic segmentation of breast cancer. [29] adopted a different strategy, using a U-Net for multi-class segmentation to reconstruct breast tissue. Meanwhile, [9] performed 3D multi-class semantic segmentation on ultrasound images, aiming to

enhance interpretability. Additionally, [13] conducted an extensive study using multiple patient datasets and 3D architectures, determining that a 3D U-Net with dynamic contrast-enhanced input yielded the best results.

### 3 Materials and Methods

A robust dataset is essential to ensure a fair and meaningful comparison between 2D and 3D segmentation models, particularly when dealing with clinical data variability. The dataset chosen is ACRIN 6698 [1], a multi-center study designed to evaluate the effectiveness of quantitative Diffusion-Weighted Imaging in assessing breast cancer response to neoadjuvant chemotherapy (NAC). ACRIN 6698 provides, among other data, diffusion-weighted magnetic resonance images of 406 breast cancer patients. Additionally, it includes ADC maps derived from these DW-MRIs. Furthermore, despite manual annotation of different classes being a highly time-consuming process, ACRIN 6698 also features expert-labeled segmentation masks for both the DW-MRIs and ADC maps.

The raw dataset requires preprocessing to be suitable for convolutional neural network training, as the original format lacks consistency in volume structure and intensity distribution. Therefore, a pre-processing pipeline is implemented to prepare the data. First, the ADC maps for each patient study are paired with their corresponding segmentation masks. Next, 3D volumes are constructed from the 2D slices of both ADC maps and masks followed by intensity normalization using contrast stretching, which enhances the visibility of tumor regions by adjusting dynamic range. Finally, a zoom operation is performed on all volumes to focus on the region of interest, ensuring a standardized shape of  $16 \times 64 \times 64$  (16 slices of  $64 \times 64$  per study).

As discussed in the background section, U-Net has become a standard in biomedical semantic segmentation. This research evaluates and compares the performance of 2D and 3D U-Net models. Our model architecture follows the original U-Net design, using an encoder path that captures contextual information through convolutional and pooling layers and a decoder path that enables precise localization using transposed convolutions. Skip connections link corresponding encoder and decoder layers to preserve spatial information lost during downsampling [22].

A 5-fold cross-validation strategy is adopted to ensure statistical robustness. The 2D model is trained for 50 epochs, while the 3D model undergoes 70 epochs due to its higher parameter complexity. For each fold, the dataset is split into 60% for training, 20% for validation, and 20% for testing. The 3D U-Net model is trained using the preprocessed 3D volumes, while the 2D U-Net model is trained using the same volumes, split into individual  $64 \times 64$  2D slices.

Since the primary objective of this research is to evaluate both models' performance in tumor segmentation, several metrics are employed: Dice-Sørensen coefficient, accuracy, recall, specificity, precision, and Jaccard Index (IoU). These metrics were selected based on their widespread adoption in medical image segmentation studies and their ability to capture different aspects of model performance [28] [19].

#### 4 Results and Discussion

Table 1 summarizes the performance metrics for both models across the test folds, providing a comparative view of their segmentation capabilities. For each fold of both

models, accuracy, recall, Dice score, IoU, specificity, and precision scores are presented. Mean values across all folds are also reported to highlight overall model performance and consistency.

	Model	Accuracy	Recall	DICE	IoU	Specificity	Precision
2	D Fold 1	0.987	0.612	0.611	0.444	0.994	0.615
2	D Fold 2	0.987	0.587	0.603	0.433	0.994	0.623
2	D Fold 3	0.987	0.633	0.615	0.447	0.993	0.606
2	D Fold 4	0.986	0.672	0.597	0.428	0.991	0.539
2	D Fold 5	0.987	0.668	0.621	0.453	0.992	0.588
	$2\mathrm{D}$	0.987	0.635	0.609	0.441	0.993	0.594
3	D Fold 1	0.974	0.711	0.472	0.309	0.979	0.355
3	D Fold 2	0.982	0.626	0.504	0.337	0.987	0.423
3	D Fold 3	0.975	0.692	0.447	0.288	0.979	0.332
3	D Fold 4	0.979	0.638	0.415	0.262	0.983	0.308
3	D Fold 5	0.981	0.648	0.476	0.314	0.985	0.377
	3D	0.978	0.663	0.463	0.302	0.983	0.359

Table 1: Performance of the models in breast cancer tumor semantic segmentation.

To determine whether the observed performance differences are statistically meaningful, we apply the Student's t-test to each evaluation metric. The recall is the only metric where no statistically significant difference was found between the 2D (0.635  $\pm$  0.045) and 3D (0.663  $\pm$  0.046) models. All remaining metrics show statistically significant differences, consistently favoring the 2D model over its 3D counterpart across key segmentation indicators. The 2D model achieved an accuracy of 0.987  $\pm$  0.001, compared to 0.978  $\pm$  0.004 for the 3D model (0.92% improvement). The Dice score increased from 0.463  $\pm$  0.042 (3D) to 0.609  $\pm$  0.012 (2D), marking a 31.53% improvement. Similarly, the IoU improved by 46.03%, rising from 0.302  $\pm$  0.035 to 0.441  $\pm$  0.013. The specificity of the 2D model reached 0.993  $\pm$  0.002, outperforming the 3D model's 0.983  $\pm$  0.005 (1.02% improvement). Finally, precision saw the most significant gain, jumping from 0.359  $\pm$  0.055 (3D) to 0.594  $\pm$  0.042 (2D), a 65.46% improvement.

These results challenge the common assumption that 3D models are inherently superior for volumetric segmentation, particularly in clinical contexts where data limitations and acquisition constraints are present. Overall, the findings demonstrate a consistent advantage of 2D segmentation over 3D in the context of breast cancer ADC map analysis.While 3D models have shown success in similar segmentation tasks, several factors may explain our findings [6]. Since expert annotations were performed on individual 2D slices, there is no inherent inter-slice consistency in the ground truth, which may negatively affect the learning of volumetric features. Furthermore, ADC maps often depict lesions with irregular, heterogeneous, or complex shapes that vary significantly across slices, making it challenging for 3D U-Nets to learn consistent volumetric features [10].Moreover, 3D models require learning from sparser volumetric data with increased dimensional complexity, which amplifies the risk of overfitting and misalignment with the sparse annotations.

# 5 Conclusions and Future Work

This study demonstrates that, for breast cancer segmentation using ADC maps, a 2D U-Net model significantly outperforms its 3D counterpart across key evaluation metrics. The lower precision and Dice score of the 3D model suggest that it struggles to reliably identify tumor regions, likely due to inconsistencies in volumetric data and annotations. These results underscore the challenges of reconstructing 3D masks from 2D annotations and the complexities introduced by the varied shapes within ADC maps. These findings challenge the prevailing assumption that 3D deep learning models are universally superior for medical image segmentation and emphasize the importance of adapting model architectures to the characteristics of the imaging modality.

Despite outperforming the 3D model, the 2D approach still yields lower segmentation performance than DCE-MRI-based models, likely due to the intrinsic limitations of DW-MRI and ADC contrast. Future research could explore the integration of DW-MRI and ADC maps as multi-channel inputs, or leverage transfer learning with pre-trained encoders to boost the 2D model's generalization capabilities. In parallel, future work should address the limitations of 3D annotations, either by acquiring fully volumetric expert labels or by developing post-processing strategies to improve inter-slice consistency in the ground truth.

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