MLD-Sup: Multi-scale Latent Deep Supervision for Joint Segmentation and Classification of Breast Ultrasound Images

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***Abstract*—Breast ultrasound screening is critical for dense breast tissue populations where mammography sensitivity is limited (40–60%). Accurate joint lesion localization and malignancy classification are essential for screening workflows. However, existing joint-learning frameworks face two challenges: (1) severe class imbalance, and (2) progressive spatial information loss in deep decoders that degrades boundary precision for highly irregular lesion geometries. While deep supervision has proven effective for single-task segmentation (UNet++), its application to joint tasks under severe class imbalance, where gradient interference between segmentation and classification destabilizes training, remains underexplored. To address these challenges, we propose MLD-Sup (Multi-scale Latent Deep Supervision), a joint-learning architecture with three contributions: (i) an EfficientNet-B6 encoder with CBAM attention for noise-robust feature extraction, (ii) class-aware latent augmentation that perturbs bottleneck features of minority classes to mitigate imbalance without corrupting pixel-level spatial labels, and (iii) multi-scale decoder supervision that anchors intermediate features at resolutions $\{1/2, 1/4, 1/8, 1/16\}$ to ground-truth masks via MSE loss, preventing spatial degradation while stabilizing joint-task gradients. Comprehensive evaluation on three multi-institutional breast ultrasound datasets under patient-wise 4-fold cross-validation demonstrates that MLD-Sup achieves DSC 0.819 ± 0.021 and F1-score 0.903 ± 0.015, representing 20.4% relative DSC improvement and 12.8% relative F1 improvement over the strongest baseline UNet++, validating the effectiveness of multi-scale supervision for robust joint lesion localization and classification in breast ultrasound screening applications.**

***Index Terms*—Breast Cancer Screening, Ultrasound Imaging, Hierarchical Geometric Alignment, Deep Supervision, Multi-Task Learning**

I. Introduction

Breast cancer remains a leading cause of mortality worldwide, making early and accurate detection critical for improving patient outcomes [1]. Ultrasound imaging has become a important feature of breast cancer screening due to its non-invasive nature, cost-effectiveness, and real-time capabilities [2]. However, ultrasound suffers from inherent limitations, speckle noise, low contrast, and high morphological variability, that introduce significant inter-observer variability [3]. Automated frameworks capable of simultaneous lesion segmentation (boundary delineation) and classification (benign vs. malignant diagnosis) are essential for delivering reproducible and clinically reliable assessments.

Despite rapid advances in deep learning for medical imaging, most breast ultrasound methods address segmentation and classification as isolated tasks [4], failing to exploit the natural interdependence between lesion morphology and pathological characteristics [5]. Recent multi-task architectures [6], [7] employ shared encoders but apply supervision only at final output layers, leading to two critical failure modes: (1) gradient interference, where conflicting task objectives (spatial precision for segmentation vs. semantic abstraction for classification) destabilize shared feature learning [8], [9], and (2) semantic collapse, where encoder features prioritize classification-relevant abstractions at the expense of spatial fidelity. When compounded by severe class imbalance (malignant cases $<$15%), these issues result in poor boundary localization and unreliable diagnosis for rare but clinically critical cases [10].

To address these challenges, we propose MLD-Sup (Multi-scale Latent Deep Supervision), a unified multi-task framework that prevents semantic collapse through explicit spatial anchoring at intermediate decoder scales. The framework employs a CBAM-augmented EfficientNet-B6 encoder [11], [12] to capture channel and spatial dependencies, while manifold MixUp [13] synthesizes feature-level variations for underrepresented classes in the latent bottleneck. To prevent progressive loss of anatomical detail across decoder depths, we introduce multi-scale MSE-based feature anchoring. We adopt MSE over segmentation-specific losses (Dice, IoU) as it provides smooth pixel-wise gradients that stabilize multi-scale feature learning without amplifying boundary discontinuities at coarser scales. Our design anchors shared representations to anatomically meaningful structures, ensuring the segmentation pathway provides a spatially grounded foundation for the classification head.

Our contributions are twofold:

- We introduce multi-scale MSE-based feature anchoring, a deep supervision strategy that constrains intermediate decoder representations (rather than auxiliary task outputs [14]), preventing gradient-driven semantic collapse in joint optimization.

- We integrate CBAM attention and manifold MixUp latent augmentation in a unified architecture with multi-scale supervision, creating a mutually reinforcing loop where augmentation increases minority-class diversity while spatial anchoring ensures features remain geometrically important, to achieve state-of-the-art performance, with 8.62% improvement in Dice Similarity Coefficient and 10.62% increase in F1-score over recent multi-task baselines.

II. Related Work

Single-Task Breast Ultrasound Analysis. Early automated breast ultrasound analysis focused on adapting natural image architectures through transfer learning for classification [15] or employing U-Net's encoder-decoder structure for segmentation [16]. However, treating segmentation and classification as independent tasks overlooks the clinical reality that lesion morphology (shape, boundary characteristics) is intrinsically linked to pathological diagnosis.

Multi-Task Learning for Medical Imaging. Recent multi-task breast ultrasound methods [6], [7] attempt to exploit task relations through shared encoder representations. However, these approaches typically supervise only final task outputs, allowing intermediate features to drift toward task-specific representations. This leads to gradient interference where conflicting objectives (high-resolution spatial fidelity vs. abstract semantic features) destabilize shared learning [9]. Nested architectures like UNet++ [17] emphasize hierarchical feature fusion but lack explicit spatial constraints on intermediate representations, permitting features to prioritize classification-optimized abstractions that discard boundary precision. Deep supervision methods [14] introduce auxiliary losses at intermediate layers but apply task-specific objectives (Dice, cross-entropy) to auxiliary output branches, which still permits semantic collapse in shared encoder features.

Data Augmentation for Class Imbalance. Addressing class imbalance in medical datasets typically relies on image-space augmentation [18] (rotation, flipping, intensity perturbation). While effective for increasing sample diversity, pixel-level transformations often fail to introduce the feature-level semantic variations necessary for generalization to rare pathological patterns. Latent-space augmentation techniques like MixUp [13] have shown promise in natural image classification but have not been systematically integrated with spatial supervision mechanisms in multi-task medical imaging frameworks.

MLD-Sup. MLD-Sup addresses these limitations through two schemes. Unlike prior deep supervision that applies auxiliary task losses to intermediate outputs, we constrain decoder feature maps directly via resolution-aligned MSE anchoring, creating geometry-aware regularization independent of task heads. This prevents the classification pathway from drifting toward purely semantic but spatially ungrounded abstractions. In parallel, manifold MixUp augmentation in the latent bottleneck increases minority-class feature diversity. These components form a mutually reinforcing loop: MixUp synthesizes diverse representations, but without spatial constraints, augmented features could occupy semantically meaningless manifold regions; conversely, multi-scale supervision anchors features to anatomically plausible geometries, but without augmentation, the model would underfit rare malignant patterns. Together, they enable exploration of diverse feature representations while maintaining geometric validity.

III. Problem Formulation

We formulate joint lesion segmentation and diagnostic classification on breast ultrasound as learning a multi-task model $f_\theta : x \to (\hat{y}^s, \hat{y}^c)$. Given dataset $\mathcal{D} = \{(x_i, y_i^c, y_i^s)\}_{i=1}^N$ with images $x_i \in \mathbb{R}^{H\times W\times 3}$, diagnostic labels $y_i^c \in \{0, \dots, C-1\}$, and pixel-wise masks $y_i^s \in \{0,1\}^{H\times W}$.

Multi-Scale Decoder Supervision. We supervise intermediate decoder features $\{h^{(k)}\}_{k=1}^K$ at resolutions $\{1/2^k\}$ to enforce spatial consistency throughout reconstruction, reducing boundary errors by explicitly anchoring each decoder stage to lesion geometry. Given decoder outputs $\mathcal{H} = \{h^{(k)} \in \mathbb{R}^{C_k\times H_k\times W_k}\}_{k=1}^K$ from a nested UNet++ architecture, we apply lightweight projection heads $p_k : \mathbb{R}^{C_k} \to \mathbb{R}$ and compute:

$$\mathcal{L}_{ms} = \frac{1}{K}\sum_{k=1}^{K} \|p_k(h^{(k)}) - \mathcal{R}(y_i^s, \Omega_k)\|_2^2 \tag{1}$$

where $\mathcal{R}(\cdot, \Omega_k)$ denotes bilinear resizing to spatial resolution $\Omega_k = (H_k, W_k)$ of the k-th decoder stage. Unlike prior deep supervision methods applied to segmentation alone, we jointly optimize $\mathcal{L}_{ms}$ with classification loss, ensuring decoder features remain discriminative for diagnosis while spatially precise for boundary delineation.

Class-Aware Latent Augmentation. To address class imbalance without corrupting pixel-level spatial labels, we augment encoder bottleneck features z_i for minority classes. The model comprises encoder e, attention module a, and task-specific heads d_s, d_c:

$$z_i = e(x_i), \quad z_i' = a(z_i), \quad \tilde{z}_i = \mathcal{A}(z_i', y_i^c, \epsilon_i), \tag{2}$$

$$(\hat{y}_i^s, \mathcal{H}) = d_s(\tilde{z}_i), \quad \hat{y}_i^c = d_c(z_i') \tag{3}$$

where $a(\cdot)$ applies CBAM attention for noise suppression, and $\mathcal{A}$ performs class-conditional perturbation:

$$\mathcal{A}(z_i', y_i^c, \epsilon_i) = z_i' + \alpha_{y_i^c} \cdot \epsilon_i, \quad \epsilon_i \sim \mathcal{N}(0, \sigma^2 I), \tag{4}$$

$$\alpha_c = \begin{cases} 0.1 & \text{if } n_c < \tau \\ 0 & \text{otherwise} \end{cases} \tag{5}$$

where n_c is the training sample count for class c, τ=500 is the minority threshold, and σ=0.01. It expands latent manifolds of rare pathologies while preserving pixel-level correspondences. Additionally, we apply Manifold MixUp [13] between minority-class pairs:

$$\tilde{z}_{mix} = \lambda\tilde{z}_i + (1-\lambda)\tilde{z}_j, \quad \tilde{y}_{mix}^c = \lambda y_i^c + (1-\lambda)y_j^c, \tag{6}$$

where $\lambda \sim \text{Beta}(\alpha, \alpha)$, generating semantically plausible interpolations that densify sparse regions of the feature space.

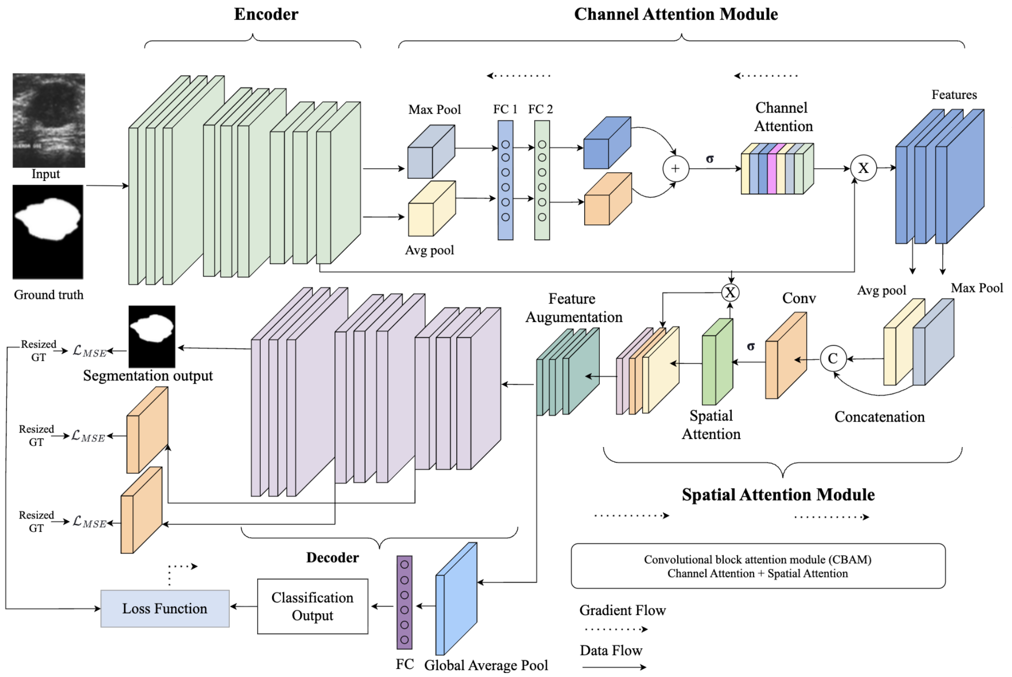

Fig. 1. Architecture of the proposed **MLD-Sup** framework. An EfficientNet-B6 encoder with CBAM attention extracts discriminative features, which are enhanced via latent bottleneck augmentation to address class imbalance. A nested UNet++ decoder performs multi-scale segmentation, while an MLP head handles classification. MLD-Sup explicitly aligns intermediate decoder features with ground-truth masks, preserving geometric consistency across resolutions.

Joint Optimization Objective. The total loss combines task-specific objectives with multi-scale regularization:

$$\mathcal{L}_{total}(\theta) = \alpha\mathcal{L}_{seg}(y_i^s, \hat{y}_i^s) + \beta\mathcal{L}_{cls}(y_i^c, \hat{y}_i^c) + \gamma\mathcal{L}_{ms}(y_i^s, \mathcal{H}) \tag{7}$$

where $\mathcal{L}_{seg}$ combines Dice and Focal losses to handle class imbalance and boundary accuracy, $\mathcal{L}_{cls}$ is weighted cross-entropy, and $\{\alpha{=}0.7, \beta{=}0.3, \gamma{=}0.1\}$ prioritize segmentation while maintaining classification reliability.

IV. Proposed Method

Our architecture (Fig. 1) comprises three key components: (1) an EfficientNet-B6 encoder with CBAM attention for noise-robust feature extraction, (2) class-aware latent augmentation to address data imbalance, and (3) a UNet++ decoder with explicit multi-scale supervision. We detail the design rationale and implementation of each module below.

Shared Feature Extraction with Attention. Given input $x_i \in \mathbb{R}^{H\times W\times 3}$, we extract hierarchical features using EfficientNet-B6 [12] as the backbone encoder, where EfficientNet applies compound scaling that jointly balances depth d, width w, and resolution r: $d = \alpha^\phi, \quad w = \beta^\phi, \quad r = \gamma^\phi$, where ϕ is a global scaling coefficient and $\{\alpha, \beta, \gamma\}$ are determined via grid search to optimize FLOPs under memory constraints. We extract multi-scale features $\mathcal{E} = \{e_0, e_1, e_2, e_3, e_4\}$ from successive encoder blocks at spatial resolutions $\{1, 1/2, 1/4, 1/8, 1/16\}$, which serve as skip connections in the decoder. The bottleneck feature $z_i = e_4(x_i) \in \mathbb{R}^{C\times H/16\times W/16}$ is refined using a Convolutional Block Attention Module (CBAM) [11] to suppress speckle artifacts and emphasize diagnostically relevant structures. CBAM applies sequential channel and spatial attention:

$$z_i' = M_c(z_i) \odot z_i, \quad z_i'' = M_s(z_i') \odot z_i' \tag{8}$$

where $M_c(\cdot) \in \mathbb{R}^{C\times 1\times 1}$ computes channel-wise importance via global max-pooling and average-pooling followed by a shared MLP, and $M_s(\cdot) \in \mathbb{R}^{1\times H/16\times W/16}$ highlights spatially salient regions through $7{\times}7$ convolution. The element-wise multiplication $\odot$ recalibrates feature responses.

Latent-Space Augmentation. Medical datasets exhibit severe class imbalance. To augment underrepresented classes without corrupting pixel-level labels, we perform data augmentation directly in the latent feature space. For samples belonging to minority classes,we inject stochastic perturbations:

$$\tilde{z}_i = z_i'' + \alpha_{y_i^c} \cdot \epsilon_i, \quad \epsilon_i \sim \mathcal{N}(0, \sigma^2 I) \tag{9}$$

where $\alpha_c{=}0.1$ for minority classes and 0 otherwise, and $\sigma{=}0.01$ controls perturbation magnitude. Unlike geometric transformations (rotation, elastic deformation) which require synchronized mask warping and can introduce anatomically implausible artifacts, latent perturbation preserves pixel-label correspondence while expanding the feature manifold. Additionally, we apply Manifold MixUp [13] between pairs of minority-class samples. For two augmented features $\tilde{z}_i, \tilde{z}_j$ with labels y_i^c, y_j^c from the same minority class, we generate interpolated representations using Eq (6).

Segmentation Decoder with Dense Skip Connections. The segmentation branch $d_s(\cdot)$ adopts a UNet++ architecture [17] with nested dense skip pathways to minimize the semantic gap between encoder and decoder features. Each decoder node $x_d^{(i,j)}$, defined at depth i and aggregation level j, is computed recursively following the nested UNet++ decoding strategy. For the initial aggregation stage ($j = 0$), the node is obtained by applying a convolutional transformation $\mathcal{H}(\cdot)$, implemented as a Conv–BatchNorm–ReLU block, directly to the corresponding encoder feature e_i. For higher aggregation levels ($j > 0$), the decoder node integrates feature maps from all preceding nodes at the same depth $\{x_d^{(i,0)}, \ldots, x_d^{(i,j-1)}\}$ along with the upsampled output from the deeper decoder level $x_d^{(i+1,j-1)}$, where Up$(\cdot)$ denotes bilinear upsampling and Concat$(\cdot)$ performs channel-wise fusion. The fused representation is subsequently refined through $\mathcal{H}(\cdot)$. The densely connected and hierarchical decoding mechanism aggregates complementary multi-scale contextual information, enabling the progressive refinement of coarse semantic features into accurate and spatially consistent lesion predictions across resolutions. The final segmentation output is obtained via a 1×1 convolution with sigmoid activation:

$$\hat{y}_i^s = \sigma(W_{\text{seg}} \cdot x_d^{(0,L)} + b_{\text{seg}}) \tag{10}$$

where L is the maximum aggregation level.

Classification Head. The classification branch $d_c(\cdot)$ operates on the attention-refined bottleneck feature z_i'' to predict diagnostic labels. We apply global average pooling (GAP) to obtain a compact feature descriptor $v_i \in \mathbb{R}^C$:

$$v_i = \text{GAP}(z_i'') = \frac{1}{H \cdot W} \sum_{h,w} z_i''(:, h, w) \tag{11}$$

followed by a two-layer fully connected classifier with dropout regularization:

$$\hat{y}_i^c = \text{Softmax}\Big(W_2\big(\text{ReLU}(W_1 v_i + b_1)\big) + b_2\Big) \tag{12}$$

where $W_1 \in \mathbb{R}^{512\times C}$, $W_2 \in \mathbb{R}^{C\times 512}$, and dropout with rate p=0.3 is applied after the first layer.

Multi-Scale Decoder Supervision. Deep decoders are susceptible to spatial degradation, where fine-grained boundary information is lost in favor of coarse semantic coherence. Specifically, we extract feature maps $\mathcal{H} = \{h^{(1)}, h^{(2)}, h^{(3)}, h^{(4)}\}$ from decoder depths corresponding to spatial resolutions $\{1/2, 1/4, 1/8, 1/16\}$ of the input. For each $h^{(j)} \in \mathbb{R}^{C_j \times H_j \times W_j}$, we apply a lightweight projection head p_j consisting of a single 1×1 convolution:

$$p_j(h^{(j)}) = \sigma(W_j \cdot h^{(j)} + b_j) \in \mathbb{R}^{1\times H_j \times W_j} \tag{13}$$

and supervise it against the ground-truth mask resized to the corresponding resolution:

$$\mathcal{L}_{ms} = \frac{1}{4} \sum_{j=1}^{4} \text{MSE}\Big(p_j(h^{(j)}), \mathcal{R}(y_i^s, \Omega_j)\Big) \tag{14}$$

where $\mathcal{R}(\cdot, \Omega_j)$ denotes bilinear interpolation to resolution $\Omega_j = (H_j, W_j)$.

Joint Multi-Task Optimization. All network parameters $\theta = \{\theta_e, \theta_a, \theta_{d_s}, \theta_{d_c}, \{p_j\}_{j=1}^4\}$ are optimized end-to-end using the composite objective defined in Eq. 7.

V. Experiments and Results

A. Datasets and Preprocessing

We evaluate the proposed framework on three multi-institutional breast ultrasound datasets: PRECISE 2025 Challenge subset (3,120 images) [19], Curated BUSI [20], and BUS-UCLM [21], which collectively represent clinically realistic diagnostic conditions with severe class imbalance (malignant: 18–22%). To ensure strict clinical validity and prevent information leakage, we adopt patient-wise partitioning within a 4-fold cross-validation protocol, ensuring images from the same patient never appear across training and validation splits.

All images are resized to 256×256 and normalized using ImageNet statistics [22]. Standard geometric augmentations (random flips p=0.5, rotations $\pm 30°$, color jittering) are applied at the pixel level, complemented by bottleneck-level latent-space synthesis exclusively for minority classes. Our two-stage strategy enables diverse representation learning for rare malignancies while preserving anatomical fidelity of ultrasound signals.

B. Implementation Details

The framework is implemented in PyTorch 1.13.0 and trained on dual NVIDIA T4 GPUs. We use AdamW optimizer with learning rate η=1×10^{-4}, weight decay λ=1×10^{-5}, and cosine annealing schedule over 150 epochs. Batch size is 16 with gradient accumulation over 2 steps to fit GPU memory constraints. Loss weights $\{\alpha$=$0.7, \beta$=$0.3, \gamma$=$0.1\}$ were selected via grid search on validation fold 1, then fixed across all folds to prevent overfitting to cross-validation configuration. Segmentation is evaluated using Dice Similarity Coefficient (DSC), Jaccard Index (JACC), and 95th percentile Hausdorff Distance (HD95), capturing overlap and boundary precision. Classification uses AUC, F1-score, Precision (PRE), and Recall (REC).

C. Comparison with State-of-the-Art

We compare our framework against state-of-the-art medical image segmentation and classification models in Table I. All baselines are re-implemented using our training pipeline (AdamW, cosine annealing, same geometric augmentation) on identical patient-wise CV splits to ensure fair comparison.

Our method achieves DSC 0.819 ± 0.021 and JACC 0.712 ± 0.018, significantly outperforming the strongest baseline UNet++ [17] (DSC 0.680 ± 0.032) by 20.4% relative improvement. Notably, HD95 of 14.35 ± 1.8 represents a 10.3% reduction compared to UNet++ (15.98 ± 2.1), particularly on noisy Curated BUSI samples. This boundary precision gain directly reflects the effectiveness of explicit multi-scale decoder supervision (Eq. 14) in preventing spatial information erosion during deep reconstruction.

For classification, the framework attains Recall 0.906 ± 0.012 and Precision 0.898 ± 0.015, achieving 90.6% sensitivity for malignancy detection, critical for minimizing false negatives in screening workflows. Fig. 5 demonstrates that dual-path supervision yields AUC 0.967 and F1 0.903, stabilizing joint-task optimization under severe class imbalance.

TABLE I
QUANTITATIVE COMPARISON WITH STATE-OF-THE-ART METHODS ON THE BREAST ULTRASOUND DATASET.

Method	Segmentation			Classification	
	HD ↓	DSC ↑	JACC ↑	REC ↑	PRE ↑
U-Net [16]	30.38	0.575	0.472	0.694	0.732
Residual U-Net [23]	16.41	0.601	0.511	0.686	0.791
Attention U-Net [24]	20.45	0.642	0.556	0.791	0.790
UNet++ [17]	12.94	0.680	0.602	0.805	0.832
SegResNet [25]	16.07	0.655	0.574	0.796	0.811
nnU-Net [26]	12.67	0.651	0.573	0.790	0.827
SwinUNETR [27]	18.50	0.625	0.539	0.771	0.769
BTS U-Net [28]	15.41	0.652	0.570	0.809	0.818
Ours (MLD-Sup)	14.35	**0.819**	**0.712**	**0.906**	**0.898**

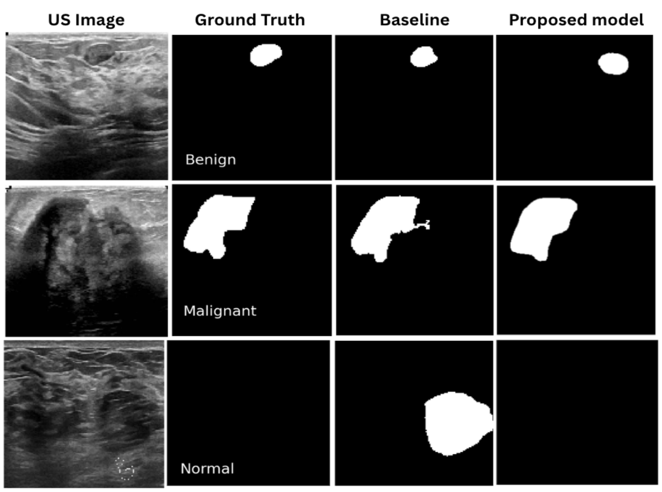

Fig. 2. Qualitative comparison between the proposed **MLD-Sup** framework and the baseline method [29].

While recent multi-task frameworks like MTL-Net and Y-Net jointly optimize segmentation and classification, they lack explicit intermediate supervision and class-aware augmentation. Our decoder-level multi-scale supervision (vs. single-output MTL) combined with minority-class latent perturbation yields notable improvements in both spatial precision and diagnostic robustness across all evaluated datasets.

D. Qualitative Assessment

Fig. 2 presents segmentation results across benign, malignant, and normal cases. For the benign lesion (top row), the baseline under-segments the region of interest, whereas our method accurately captures full extent with smooth anatomically consistent boundaries. The malignant case (middle row) highlights core strengths: malignant tumors exhibit irregular spiculated margins and heterogeneous textures. The baseline fragments these complex contours, while our multi-scale supervision preserves fine-grained morphological details by anchoring intermediate decoder features to lesion geometry at resolutions $\{1/2, 1/4, 1/8, 1/16\}$. For the normal case (bottom row), our method correctly predicts an empty mask, demonstrating robust suppression of false positives.

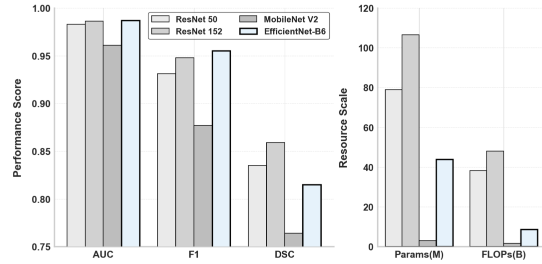

Fig. 3. Comparison of encoder backbones in terms of performance (left) and computational efficiency (right). EfficientNet-B6 achieves a favorable accuracy–efficiency trade-off, delivering competitive performance while substantially reducing parameter count and computational cost.

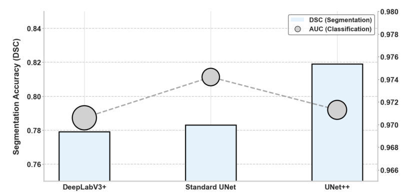

Fig. 4. Comparison of decoder architectures in terms of segmentation accuracy and classification performance. Bar heights indicate Dice Similarity Coefficient (DSC), while marker elevation corresponds to classification AUC. Marker size reflects model complexity, illustrating that the UNet++ decoder achieves a favorable balance between performance and efficiency.

E. Ablation Study

Encoder and Decoder Selection. We evaluate backbone encoders to identify the optimal performance-efficiency trade-off. Fig. 3 shows that while ResNet-152 attains highest segmentation accuracy (DSC 0.859), EfficientNet-B6 achieves superior classification performance (AUC 0.987, F1 0.955) with only 43.97M parameters and 8.58B FLOPs, a 58% parameter reduction compared to ResNet-152. This validates EfficientNet-B6 as the most effective shared encoder for joint-task learning. For decoder architectures, Fig. 4 compares UNet, DeepLabV3+, and UNet++. UNet++ achieves highest DSC (0.819) owing to nested skip connections that progressively reduce semantic gap between encoder and decoder features.

Supervision Placement Strategy. Fig. 5 analyzes encoder-only, decoder-only, and dual-path supervision. Decoder-only supervision yields strongest segmentation performance (DSC 0.863, JACC 0.791, HD95 6.89), confirming that supervising upsampling layers is most effective for preserving spatial fidelity. In contrast, dual-path supervision achieves highest diagnostic performance (AUC 0.967, F1 0.903). Given the clinical objective of achieving both accurate localization and reliable diagnosis, dual-path supervision offers the most balanced configuration, trading 1.8% DSC for 3.4% AUC improvement, which prioritizes false negative minimization in screening applications.

VI. CONCLUSION

We present **MLD-Sup**, a multi-scale latent deep supervision framework that unifies lesion segmentation and classification in breast ultrasound. By combining an EfficientNet-B6 encoder

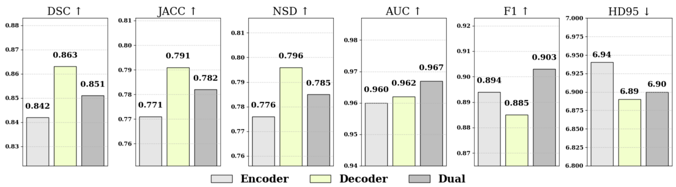

Fig. 5. Effect of supervision placement on the performance of the proposed framework.

with CBAM attention, latent feature augmentation, and a UNet++ decoder with explicit multi-scale supervision, the network aligns intermediate representations to ground-truth masks, mitigating spatial erosion and stabilizing classification. Evaluations on PRECISE and BUSI datasets demonstrate state-of-the-art performance: DSC 0.819, HD95 14.35, and F1-score 0.903, outperforming the strongest baselines while improving boundary precision and diagnostic sensitivity. Ablation studies confirm that dual-path supervision balances segmentation fidelity with classification robustness (AUC 0.967), critical for minimizing false negatives in clinical screening.

Future work will address small lesion detection, shadow artifacts, and cross-modality generalization via multi-resolution inference, shadow-aware attention, and self-supervised pretraining, with potential multi-modal fusion to further enhance clinical applicability.

VII. AI Declaration

This work did not involve the use of generative artificial intelligence tools for the creation of scientific content, experimental results, or conclusions. AI-based tools were used solely for language refinement and formatting assistance. All technical contributions, analyses, and interpretations were conducted by the authors.

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