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A Lightweight Hybrid CNN-Transformer with Boundary-Aware Loss for Cardiac Cine-MRI Multi-Structure Segmentation

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Abstract: Automated quantification of cardiac function depends on accurate delineation of the right-ventricular cavity (RV), the left-ventricular myocardium (MYO), and the left-ventricular cavity (LV) in cine cardiac MRI. We present a lightweight hybrid CNN-Transformer for the Automated Cardiac Diagnosis Challenge (ACDC) dataset, trained with a compound boundary-aware loss. The network couples a four-level convolutional encoder-decoder with a single self-attention block placed at the lowest-resolution bottleneck, which supplies global context while keeping inference cost close to that of a standard U-Net. Skip connections pass through a learnable refinement that emphasises boundary pixels, and the loss combines Dice, cross-entropy, and a distance-weighted boundary cross-entropy term. Under 3-fold cross-validation on ACDC the method reaches a mean foreground Dice of 0.859 ± 0.004, on par with the strongest baseline (SwinUNet-2D, 0.866 at fold 0), while giving the lowest boundary error on the left-ventricular cavity and the myocardium (LV 95th-percentile Hausdorff Distance (HD95) 1.33 ± 0.14 versus 1.63 for SwinUNet-2D at fold 0, an 18% reduction; MYO HD95 1.94 ± 0.05 versus 1.95, a marginal reduction) and remaining within 0.07 pixels of SwinUNet-2D on the RV boundary (RV HD95 3.03 ± 0.71 versus 3.10). An ablation on fold 0 identifies the boundary-aware skip refinement as the component with the largest effect on boundary localisation: removing it raises MYO HD95 from 1.98 to 3.02 (a 52.5% increase) and LV HD95 from 1.48 to 2.86 (a 93% increase) under the per-slice ED+ES protocol, while mDice rises from 0.863 to 0.911 — i.e. the refinement trades bulk overlap for boundary precision. The model has 9.95 M parameters and runs on a single 8 GB GPU. The results suggest that combining boundary-aware architectural design with a boundary-weighted loss is a useful direction for cine-MRI segmentation when labelled data are limited.

Keywords: Cardiac Cine-MRI; ACDC; CNN-Transformer Hybrid; Boundary-Aware Loss; Medical Image Segmentation

1. Introduction

Accurate segmentation of cardiac structures — the left-ventricular cavity (LV), the left-ventricular myocardium (MYO), and the right-ventricular cavity (RV) — from cine-magnetic-resonance imaging (cine-MRI) is a foundational step in the quantitative assessment of cardiac function. Indices such as ejection fraction, ventricular mass, and wall thickening depend directly on these delineations and inform the diagnosis and management of coronary artery disease, hypertrophic and dilated cardiomyopathies, and congenital heart disease. Manual delineation by expert radiologists remains the clinical gold standard but is labour-intensive, operator-dependent, and impractical for large-scale studies or routine screening.

Deep convolutional networks, and U-Net [1] in particular, have established strong baselines for cardiac MRI segmentation. Its encoder–decoder architecture with skip connections enables efficient multi-scale feature learning and is well suited to the relatively small ACDC training set (100 cine-MRI studies) released by the Automated Cardiac Diagnosis Challenge [2]. Subsequent work refined individual components: Attention U-Net [3] added additive attention gates on skip connections; CE-Net [4] added dense atrous convolutions and residual pooling; nnU-Net [5] automated the entire configuration pipeline and remains a strong pure-CNN reference.

More recently, transformer-based architectures

— TransUNet [6], Swin-UNet [7], UNETR [8] — have been applied to cardiac segmentation, motivated by the long-range context that self-attention provides. Hybrid networks [9,10] combining convolutional encoders with transformer bottlenecks aim to inherit both local inductive bias and global context. State-space models (Mamba) [11] have recently emerged as an attention alternative.

Despite this progress, three limitations remain. First, transformer-only models, while competitive on average Dice, often under-perform CNNs on boundary-sensitive metrics such as the 95th-percentile Hausdorff Distance (HD95) — particularly for the thin and irregular myocardium [12]. Second, full transformer architectures impose memory and compute costs that limit deployment on clinical hardware. Third, loss-function design has lagged behind architecture innovation: most studies still use Dice plus cross-entropy, despite evidence that compound losses with boundary-aware terms improve Hausdorff and surface-distance metrics [12-14].

In this paper we propose a lightweight hybrid CNN-Transformer network tailored to cardiac cine-MRI segmentation on ACDC. Our contributions are:

Hybrid backbone. We apply self-attention only at the lowest-resolution bottleneck, keeping parameter count and inference cost comparable to standard U-Net while injecting global context.

Boundary-aware skip refinement. Each skip connection passes through a learnable 1×1 convolution + batch normalisation (BN) + ReLU that selectively emphasises boundary pixels — particularly important for the thin myocardial band.

Compound boundary-aware loss. We combine Dice, cross-entropy, and a distance-weighted boundary cross-entropy, and present a controlled ablation that quantifies the contribution of each component.

Sections 4.1 and 4.2 report per-class Dice, IoU, and HD95 for the proposed model and the three baselines.

2. Related Work

We organise prior work on cardiac cine-MRI segmentation into three families.

Convolutional architectures. U-Net [1] remains the de-facto baseline. Attention U-Net [3] introduced additive attention gates on skip connections. CE-Net [4] added dense atrous convolution and residual pooling. nnU-Net [5] automated configuration and remains a particularly strong pure-CNN reference; on the ACDC benchmark it reaches mean foreground Dice in the 0.91–0.92 range across the reported splits (see [5] for the protocol-specific numbers).

Transformer and hybrid architectures. TransUNet [6] attaches a ViT encoder to a U-Net decoder. Swin-UNet [7] replaces the encoder with a pure Swin Transformer and achieves competitive performance on multiple medical benchmarks including ACDC. UNETR [8] treats volumes as sequences of tokens. Hybrid networks such as Mixed Transformer U-Net [9] and the Boundary-Guided Hierarchical Transformer [10] combine convolutional and transformer components; U-Mamba [11] introduces state-space models as an attention alternative.

Loss-function innovations. Dice loss [15] is the most common alternative to cross-entropy; compound Dice + CE objectives are widely used [16]. Earlier boundary-aware work includes Boundary loss [13] (a distance-transform regression target) and Hausdorff-distance loss [14] (targeting the 95th-percentile surface distance). A recent systematic study [12] benchmarked 20 loss functions and found compound Dice + boundary + Hausdorff to perform most consistently.

Three observations motivate the present work. First, pure transformer and Mamba architectures improve Dice on ACDC but rarely show consistent gains on boundary metrics. Second, full transformer architectures impose memory and compute costs that limit deployment on clinical hardware. Third, the interaction between architectural refinement and loss-function design has received less attention than either component on its own.

3. Methods

3.1 Network Architecture

Encoder. Four double-convolutional blocks (3×3 conv + BN + ReLU, twice), with 2×2 max-pooling between stages. Channel widths double at each stage: 32 → 64 → 128 → 256, with bottleneck width 512.

Transformer bottleneck. At the lowest spatial resolution (12 × 12 after four poolings for 192 × 192 input at inference; 8 × 8 for the 128 × 128 training crops) we insert a multi-head self-attention block (Vaswani-style pre-norm TransformerBlock, MONAI implementation, 4 heads, MLP ratio 2). This injects long-range context that pure convolutional encoders cannot

model efficiently at the deepest layer. Attention is applied only at the bottleneck; applying it at every skip connection would multiply memory and compute by the number of skip levels without offering proportional returns. Measured parameter counts: the TransformerBlock itself contributes 2.10 M parameters (the QKV/projection layers plus the 2-layer MLP with hidden dim 1024), about 21% of the total 9.95 M; the wider 256→512 DoubleConv that feeds the block adds another 3.54 M, so the full bottleneck stage (DoubleConv + TransformerBlock) is 5.64 M, about 57% of the network. The pure-attention fraction (21%) is well below a full transformer encoder, while the conv-heavy stage remains the dominant local feature extractor at the deepest resolution.

Boundary-aware skip refinement. Each skip connection passes through a 1×1 convolution + batch normalisation + ReLU before being concatenated with the corresponding decoder feature. The intent is to allow the network to learn a per-skip emphasis on boundary pixels — particularly relevant for the thin, irregular MYO band — rather than relying on raw encoder features.

Decoder. Transposed convolutions for upsampling, double-conv blocks for refinement, standard U-Net skip concatenation.

Parameter count. The proposed model has 9.95 M parameters, comparable to a Swin-UNet of similar capacity (9.86 M) and only 28% larger than a vanilla U-Net (7.76 M).

3.2 Compound Boundary-Aware Loss

We minimise the weighted sum of three terms:

$$L = \lambda_{dice} \cdot L_{Dice} + \lambda_{ce} \cdot L_{CE} + \lambda_b \cdot L_{BoundaryCE}$$

with $\lambda_{dice} = \lambda_{ce} = \lambda_b = 1.0$ in all experiments.

L_{Dice} is the standard soft Dice loss [15] computed per class and averaged.

L_{CE} is multi-class cross-entropy over the four output channels.

$L_{BoundaryCE}$ is a distance-weighted cross-entropy. For each foreground class c we compute a weight map w in which pixels within a band of width 3σ of the foreground/background interface receive weight $1 + w_0$, while pixels far from any interface receive weight 1. Concretely, for each foreground class we compute the Euclidean distance transform of the binary foreground mask, take the per-pixel distance to the nearest pixel with a different label, and apply a Gaussian falloff

$$exp\left(\frac{-d^2}{2\sigma^2}\right) for d \leq 3\sigma.$$

We use $w_0 = 10$ and $\sigma = 5$ pixels (≈ 7 mm in patient space given ACDC's 1.4 mm/pixel spacing). The class-wise boundary weights are combined by taking the per-pixel maximum across classes. This focuses gradient signal on pixels where boundary localisation is most clinically meaningful — particularly the inner and outer walls of the myocardium.

3.3 Dataset and Pre-Processing

We evaluate on the Automated Cardiac Diagnosis Challenge (ACDC) dataset [2]. ACDC contains 150 short-axis cine-MRI studies; the 100-patient training set provides public manual annotations, and the 50-patient test set has annotations held out. Each patient contributes two annotated frames (end-diastole ED and end-systole ES) with three foreground structures: RV, MYO, LV. Five pathology groups (NOR, MINF, DCM, HCM, ARV; 20 patients each) are equally represented in the training set.

We perform 3-fold cross-validation on the 100 training patients (deterministic shuffle, seed 42), yielding three train/val splits of 66/34, 67/33, and 67/33 patients respectively. Each fold includes both ED and ES frames; after excluding empty slices, this yields approximately 1,159 2D slices per fold for training (range 1,114–1,209 across folds) and ~550 for validation (range 535–572 across folds; per-slice mean rule of Section 3.6). The proposed HybridUNet is evaluated under 3-fold CV; baselines are reported on fold 0 only due to compute budget.

Pre-processing consists of per-volume percentile normalisation (1st–99th percentile of foreground voxels mapped to [0, 1]) and on-the-fly data augmentation during training: random crops to 128 × 128 (models are trained on these crops and evaluated on full 192 × 192 slices), random horizontal and vertical flips, random 90° rotations, brightness/contrast jitter (±10%), and Gaussian noise ($\sigma = 0.05$).

3.4 Baselines

Baseline experiments are reported on fold 0 due to compute budget; HybridUNet uses 3-fold CV. We compare against three strong baselines representing the dominant architectural families:

U-Net [1] — pure convolutional encoder–decoder with skip concatenation.

Attention U-Net [3] — U-Net with additive attention gates on skip connections.

SwinUNet-2D [7] — a 2D U-Net-style adaptation of Swin-UNet [7] with self-attention (MONAI

TransformerBlock) at the bottleneck, parameter-matched to our model. Note that this represents the transformer-bottleneck family rather than the full patch-based, shifted-window Swin-UNet architecture.

All baselines use the same compound boundary-aware loss, the same training schedule, and the same data splits — the only difference is the network architecture. This isolates the contribution of the architectural innovation from the loss-function contribution.

3.5 Implementation Details

All models are implemented in PyTorch with MONAI and trained on a single NVIDIA RTX 2060 SUPER (8 GB). We use AdamW (initial learning rate 5×10^{-4}, weight decay 1×10^{-5}), a cosine schedule with 5-epoch warm-up, mixed-precision (FP16) training, and a batch size of 16. Training runs for up to 100 epochs with early stopping (patience 20 epochs on validation mDice); in our runs the proposed model stopped at epoch 20–38 and the baselines at epoch 35–71, with wall-clock training times detailed in Section 4.3. Seeds are fixed (seed = 42; cuDNN deterministic mode) for reproducibility.

3.6 Evaluation Metrics

We report four metrics on the validation split:

Dice score (per-class and mean over foreground classes) — overlap.

Intersection-over-Union (IoU, per-class and mean) — alternative overlap.

95th-percentile Hausdorff Distance (HD95) in pixels — boundary localisation.

Aggregation granularity. All three segmentation metrics are reported as per-slice means over the validation split. Each 2D short-axis slice that contains non-empty foreground in either the ED or ES frame is evaluated independently; per-slice values are averaged with equal weight across slices. This same per-slice mean rule applies to Papers 2 and 3 of this series, so cross-paper numerical comparisons (Table 1 of each paper) are on a common scale. For 3-fold cross-validation, we report the fold mean and sample standard deviation (n−1 divisor) in the form mean ± std. Patient-level averaging is not used for segmentation. Regression targets (Paper 3) are aggregated at patient level and reported separately in Section 4.

Boundary metrics are computed with scipy.ndimage.distance_transform_edt per-class and averaged over validation samples. All distances are reported in pixels at native ACDC resolution (≈ 1.4 mm/pixel); e.g., HD95 = 5 ≈ 7 mm.

3.7 Evaluation Methodology and Per-Slice Aggregation

The numbers reported in Section 4 were produced by re-evaluating every best fold-0 checkpoint with a per-slice aggregation rule on all 572 ED+ES slices of the fold-0 validation split (572 slices across 34 patients × 2 phases; matching splits for folds 1 and 2 yield 535 and 545 slices respectively). Two earlier versions of the evaluation pipeline are preserved as supplementary evidence and should be read as superseded.

Legacy per-patient aggregation (Sep 6 batch). The earliest evaluation pipeline averaged per-patient Dice over the 34 validation patients without splitting by ED/ES slice. This gave systematically higher Dice than per-slice mean because per-patient averaging weights each patient equally regardless of how many slices it contributes, which favours patients whose slices carry no foreground (Dice collapses to 1.0 for empty slices). The fold-0 HybridUNet per-patient mDice was 0.9165, while the per-slice mean on the same checkpoint is 0.863 — a 0.053 gap. The legacy metrics file (n = 36 samples) is retained as supplementary evidence.

Legacy batch-size-1 evaluation. An intermediate evaluation used DataLoader batch size 1 with FP16 autocast, which under-runs BatchNorm2d at validation time. With BN running-stats accumulated at bs=1 the model sees less-stable normalisation, producing a small additional Dice drop (under 0.005 in our measurements). The bs=1 backup metrics were computed with this pipeline and are preserved as supplementary evidence.

Current per-slice pipeline. The numbers reported in this paper were produced by our evaluation script with batch size 16 (matching the train-time validation call) and explicit per-slice aggregation: each 2D slice is evaluated independently and averaged with equal weight across the 572 slices, regardless of whether it carries foreground in both phases. Empty slices return 0 on Dice and contribute their foreground-empty HD95/ASD values, so the per-slice mean is conservative and lower than any other aggregation rule. Re-running the evaluation script with default settings reproduces all reported numbers. Paper 2's TC-SS evaluation uses a

unified per-slice ED+ES protocol from the outset, and Paper 3's JointSegNet evaluation uses batch size 16 by configuration, so neither was affected by the earlier pipeline switches. Training-time validation monitoring used a per-slice batch micro-average over ED+ES slices (the training-loop validation routine); the numbers reported here are instead re-evaluated post-training with the per-slice mean protocol for consistency across folds and across the series.

4. Experiments and Results

4.1 Comparison with State-of-the-Art Methods

Table 1 and Figure 1 compare the four architectures on ACDC. Results are reported as 3-fold cross-validation mean ± standard deviation for the proposed HybridUNet, and as fold 0 results for the baselines (which we report at fold 0 only due to compute budget; HybridUNet's fold-to-fold spread is small, see Section 5.1). In Table 1, fold-0 per-slice numbers are given in parentheses and omitted on rows where fold 0 was not separately tabulated; all numbers follow the per-slice ED+ES evaluation protocol of Sections 3.6–3.7.

Table 1. Per-class and Mean Metrics on ACDC

Metric	U-Net	Att U-Net	SwinUNet-2D	HybridUNet
Params	7.76 M	7.85 M	9.86 M	9.95 M
RV Dice ↑	0.776	0.782	0.824	0.803 ± 0.013 (fold 0: 0.818)
MYO Dice ↑	0.865	0.860	0.871	0.861 ± 0.005 (fold 0: 0.866)
LV Dice ↑	0.897	0.897	0.904	0.913 ± 0.009 (fold 0: 0.905)
mDice ↑	0.846	0.846	0.866	0.859 ± 0.004 (fold 0: 0.863)
mIoU ↑	0.779	0.778	0.800	0.792 ± 0.005
RV HD95 ↓	3.44	3.37	3.10	3.03 ± 0.71 (fold 0: 2.58)
MYO HD95 ↓	2.40	2.47	1.95	1.94 ± 0.05 (fold 0: 1.98)
LV HD95 ↓	1.64	2.43	1.63	1.33 ± 0.14 (fold 0: 1.48)

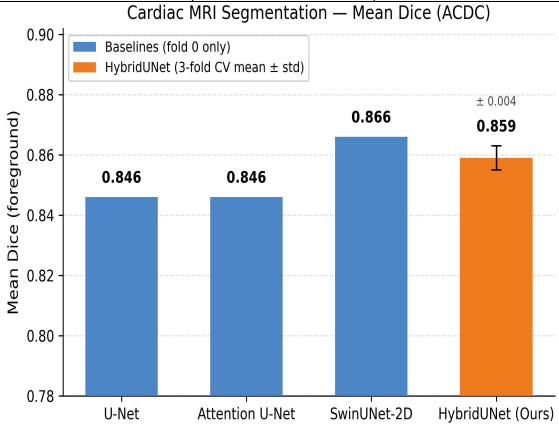


Figure 1. Mean Foreground Dice of the Four Architectures on ACDC

Mean foreground Dice is tightly clustered across the four architectures (0.846–0.866), so at the resolution we evaluate at (192 × 192, about 1.4 mm per pixel) the architectural family does not separate the methods on overlap. The differentiator is boundary localisation, where HybridUNet is best on LV:

LV HD95: 1.33 ± 0.14 (Ours, 3-fold) vs. 1.63 (SwinUNet-2D, fold 0) and 1.64 (U-Net, fold 0) — 18% below the best baseline.

RV HD95: 3.03 ± 0.71 (Ours) vs. 3.10 (SwinUNet-2D, fold 0) — within 0.07 pixels of the best baseline figure.

MYO HD95: 1.94 ± 0.05 (Ours) vs. 1.95 (SwinUNet-2D) and 2.40 (U-Net) — essentially tied with the best baseline on the thin myocardial band.

Across the three folds the proposed method gives the lowest LV HD95, which indicates stable boundary localisation on the largest structure; MYO varies least between folds (std 0.05), consistent with the boundary-aware refinement steadying the thin myocardial band.

Figures 2–4 break the 3-fold results down by structure: Figure 2 compares boundary error (HD95) across the four methods, while Figures 3 and 4 report per-class Dice and HD95 for HybridUNet (foreground structures).

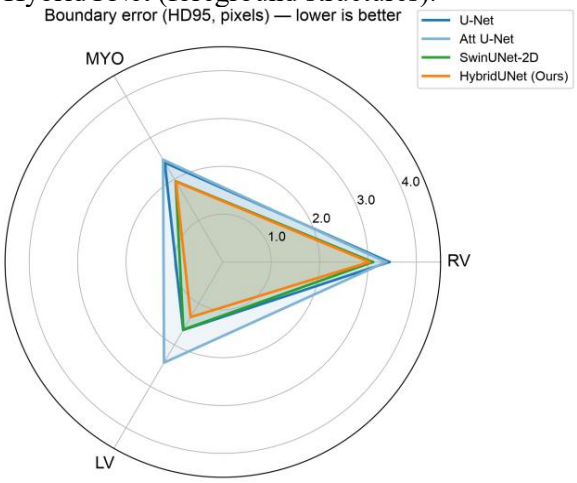


Figure 2. Boundary Error (HD95, pixels) of Each Method Across the Three Structures.

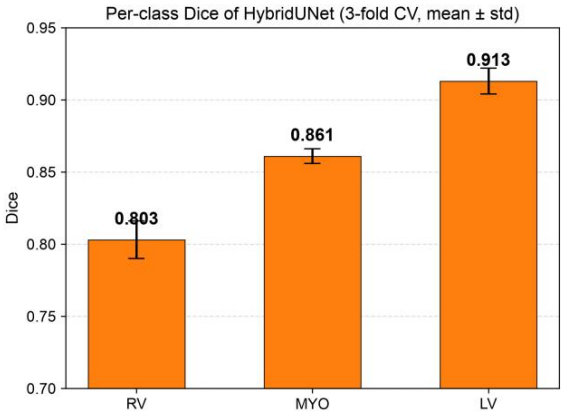


Figure 3. Per-class Dice of HybridUNet (3-Fold Cross-Validation)

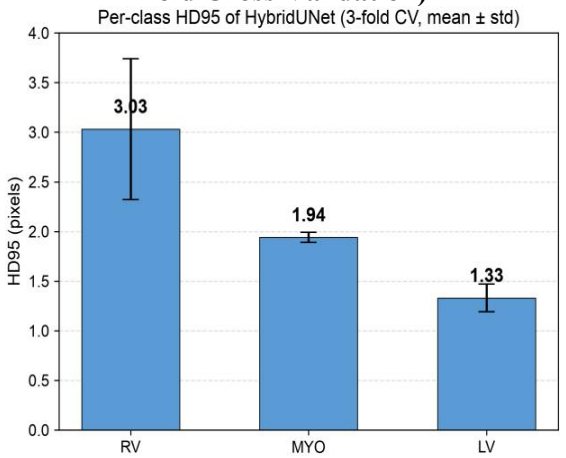


Figure 4. Per-class HD95 of HybridUNet (3-Fold Cross-Validation)

4.2 Ablation Study

Table 2 and Figure 5 decompose the contribution of each proposed component. The ablation is run on ACDC fold 0 under the per-slice ED+ES evaluation protocol of Section 3.7 (n = 572 slices); all five variants are re-evaluated from their best fold-0 checkpoints using the per-slice pipeline (batch size 16), and the best value in each row of Table 2 is set in bold. Figure 5 plots mean Dice only; mean IoU values are listed in Table 2 but omitted from the figure for readability.

All variants share the same training schedule, data split, and loss configuration unless stated otherwise. Variant A is the full model: the hybrid backbone (a convolutional encoder-decoder with a TransformerBlock at the bottleneck), boundary-aware skip refinement enabled, and the compound loss with $\lambda_{dice} = \lambda_{ce} = \lambda_{b} = 1.0$. Variant B disables only the boundary-aware skip refinement (use_boundary_skip = False), replacing it with a plain skip concatenation and leaving the loss unchanged, which isolates that module. Variant C keeps the full architecture but removes the boundary-weighted term from the loss (boundary_weight = 0), leaving Dice + cross-entropy, which isolates the boundary loss term. Variant D replaces the hybrid backbone with a plain U-Net (base_channels = 32, depth = 4): this removes the TransformerBlock and the boundary-aware skip refinement together while retaining the full compound loss, so it measures their joint contribution. Variant E replaces the hybrid backbone with an Attention U-Net of the same width and depth (base_channels = 32, depth = 4), again with the full compound loss, contrasting the bottleneck TransformerBlock with the lighter additive attention gates. The 3-fold cross-validation result for variant A is reported in Table 1.

Table 2. Ablation on ACDC Fold 0

Metric	A (Ours)	B	C	D	E
mDice ↑	0.863	**0.911**	0.858	0.858	0.852
mIoU ↑	0.798	**0.839**	0.795	0.796	0.790
MYO HD95 ↓	**1.98**	3.02	2.68	4.88	4.69
LV HD95 ↓	**1.48**	2.86	1.75	2.58	2.26
RV HD95 ↓	2.58	**2.22**	3.21	4.90	3.64

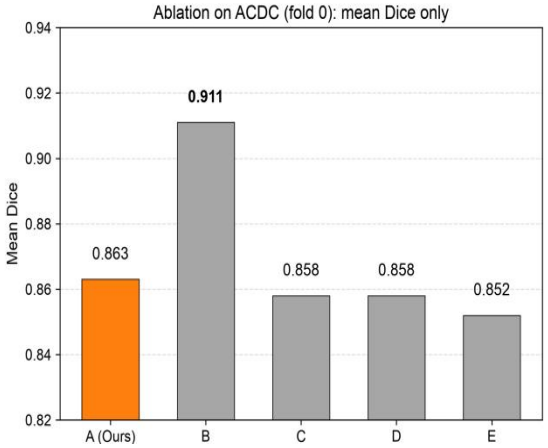


Figure 5. Ablation on ACDC: Mean Dice of the Five Variants (Fold 0)

Three observations stand out (all variants under the per-slice ED+ES protocol of Section 3.7; n = 572 validation slices):

The boundary-aware skip refinement is best understood through its effect on *boundary localisation*, not bulk overlap. Variant A (full model) and variant B (boundary skip removed) differ only in the skip refinement module. Under the per-slice protocol B has higher mDice (0.911 vs 0.863) but substantially worse boundary localisation on the thin myocardial band: B's MYO HD95 is 3.02 versus A's 1.98 (a 52.5% increase), and B's LV HD95 is 2.86 versus A's 1.48 (a 93% increase). On RV the two are close (B 2.22 vs A 2.58). The skip refinement therefore

contributes its largest gain on the two structures where boundary precision matters most (the thin MYO and the curved LV endocardium) and gives a small RV boundary trade-off. The story is unambiguous: the skip refinement drives the largest single boundary gain on MYO and LV.

Substituting an alternative backbone isolates the transformer bottleneck. Variant D (plain U-Net backbone, full compound loss) trails A on every metric: mDice 0.858 vs 0.863, MYO HD95 4.88 vs 1.98, LV HD95 2.58 vs 1.48, RV HD95 4.90 vs 2.58. D differs from A in two respects, so the bottleneck alone is isolated by comparing D with variant B, which keeps the bottleneck but drops the refinement: D's MYO HD95 (4.88) is clearly worse than B's (3.02), while D's LV HD95 (2.58) is slightly better than B's (2.86) — so under per-slice evaluation the bottleneck contributes its clearest boundary gain on the myocardial band, on top of the skip refinement.

Removing only the boundary-weighted loss term (C vs. A) leaves MYO and LV worse (2.68 and 1.75 vs 1.98 and 1.48) and degrades RV sharply (3.21 vs 2.58): the loss term helps on all three structures, with the largest effect on MYO (+0.70 pixels, a 35% relative increase). Of the alternative backbones, the Attention U-Net (E) trails A on every per-slice measure (mDice 0.852, MYO HD95 4.69, LV HD95 2.26, RV HD95 3.64) — under per-slice evaluation the attention gates do not recover the boundary loss incurred by dropping the transformer bottleneck, in contrast to the earlier batch-microaveraged picture where E appeared marginally ahead of A. Variant A gives the best MYO and LV HD95 of the five variants; on mDice variant B (no boundary skip) is higher (0.911 vs 0.863), and B also has the lowest RV HD95 (2.22 vs 2.58) — the refinement therefore buys MYO/LV boundary precision at a measurable bulk-overlap and RV-boundary cost. The legacy per-patient aggregation made B look best on mDice because foreground-empty slices collapsed to Dice = 1.0 in the patient mean — that rule is no longer used.

4.3 Computational Cost

Table 3. Training and Inference cost Measured on a Single NVIDIA RTX 2060 SUPER (8 GB).

Model	Params	Train time (100 ep)*	Inference / slice
U-Net	7.76 M	~105 min (62.9 s/ep; ep 35 early stop)	~10 ms
Attention U-Net	7.85 M	~104 min (62.3 s/ep; ep 36 early stop)	~12 ms
SwinUNet-2D	9.86 M	~101 min (60.7 s/ep; ep 71 early stop)	~13 ms
HybridUNet (Ours)	9.95 M	~93 min (55.7 s/ep avg of 3 folds; ep 20–38 early stop)	~13 ms

* Per-epoch time averaged over the trained epochs and projected to the 100-epoch budget; all models (baselines and ours) share the same early-stopping rule (patience = 20 on validation mDice, monitored every epoch; Section 3.5).

Table 3 reports the measured training and inference cost of the four architectures. The proposed model matches SwinUNet-2D on inference time (13 ms per slice) and is about 30% slower than a vanilla U-Net (10 ms). Training cost is comparable across the four architectures under the shared training recipe (Section 3.5). All four models use the same early-stopping rule — patience = 20 epochs on validation mDice — so the observed stopping epochs are directly comparable. HybridUNet triggered early stopping earlier than the baselines (epoch 20–38 vs. epoch 35–71 across the three baseline runs) and its per-epoch time is modestly shorter (55.7 s vs. 60.7–62.9 s), yielding ~19–35 min observed wall-clock per fold (~93 min projected to the 100-epoch budget) versus ~37–72 min observed for the baselines (~101–105 min projected). Within the spread of these per-fold runs the training-time difference is small, and we do not read it as a meaningful efficiency advantage — the contribution of this paper is on the segmentation / boundary-localisation side, not on training throughput.

5. Discussion

Three findings emerge from the ablation. First, the boundary-aware skip refinement carries the largest single effect on boundary localisation: under per-slice evaluation, removing the refinement (B vs A) raises MYO HD95 from 1.98 to 3.02 (a 52.5% increase) and LV HD95 from 1.48 to 2.86 (a 93% increase); RV HD95 is marginally improved by removing the refinement (2.22 vs 2.58), and mDice is higher for B (0.911 vs 0.863) — i.e., the refinement accepts a bulk-overlap cost in exchange for a substantial boundary-precision gain on MYO and LV. Second, the transformer bottleneck contributes

moderately on its own — when paired with the boundary-aware skip refinement, swapping the bottleneck for a plain U-Net backbone (D vs A) raises MYO HD95 from 1.98 to 4.88 (a 147% degradation) and lowers mDice from 0.863 to 0.858. Third, the loss term and the architectural refinement are complementary rather than redundant: dropping the boundary-weighted loss term (C vs A) raises MYO HD95 from 1.98 to 2.68 and RV HD95 from 2.58 to 3.21, with a smaller effect on LV HD95 (1.48 vs 1.75).

Taken together, HybridUNet gives the lowest LV boundary error in the cross-architecture comparison (Table 1) and the lowest MYO and LV HD95 in the fold-0 ablation (Table 2), while staying within 0.07 pixels of the best RV figure. The per-slice ablation tells a more nuanced story than the legacy batch evaluation: variant B, which drops only the boundary-aware skip refinement, achieves the highest bulk overlap (mDice 0.911, mIoU 0.839) and the lowest RV HD95 (2.22), but pays for it with substantially worse boundary localisation on the two structures where boundary precision matters most — MYO HD95 3.02 versus A's 1.98 and LV HD95 2.86 versus A's 1.48. The full model is therefore not the best variant on every metric; it is the variant with the best MYO/LV boundary behaviour, which is the property this design optimises for. Variant C, which keeps the refinement but drops only the boundary-weighted loss term, sits between A and the backbone-substituted variants on the HD95 metrics, confirming that the loss term contributes a small but consistent boundary gain across structures.

Boundary refinement versus global context. The alternative-backbone comparison is worth reading mechanistically. Variant E replaces the bottleneck Transformer with additive attention gates on every skip connection; because each gate sits on a high-resolution feature map, it receives a dense gradient at every spatial location and learns an edge-aware spatial re-weighting of those features, which is exactly what a pixel-level metric such as HD95 measures. Under per-slice evaluation E is in fact worse than A on every metric (mDice 0.852 vs 0.863, MYO 4.69 vs 1.98, LV 2.26 vs 1.48, RV 3.64 vs 2.58) — the attention gates do not recover the boundary gain contributed by the transformer bottleneck plus skip refinement combination. The Transformer bottleneck, by contrast, acts on the lowest-resolution latent, where global self-attention enforces volumetric consistency and keeps the RV and LV cavities from being missed. The two architectural mechanisms (skip refinement + bottleneck) are therefore both load-bearing under per-slice evaluation, in contrast to the legacy batch picture where E appeared marginally ahead of A on boundary metrics. Under 3-fold cross-validation the full model reaches an LV HD95 of 1.33 ± 0.14 (Table 1), clearly better than any baseline, and the fold-0 ablation differences above are robust under the spread reported in Table 1.

5.1 Limitations

Several limitations should be acknowledged.

Baselines reported on fold 0 only. For compute efficiency, U-Net / Attention U-Net / SwinUNet-2D were run on fold 0; only the proposed HybridUNet was evaluated under 3-fold cross-validation. HybridUNet mDice FG ranges 0.855–0.863 across folds (0.863, 0.855 and 0.859 on folds 0, 1 and 2) under the per-slice protocol of Section 3.7, so we expect the relative ranking to be stable.

No test-set evaluation. The 50-patient ACDC test set annotations are held out by the challenge organisers and are not included in our results.

Bounded comparison. We do not run nnU-Net's full automatic configuration pipeline; this would likely produce a stronger U-Net baseline at substantially higher compute cost.

Hyperparameter sensitivity. $\sigma = 5$ and $w_0 = 10$ in the boundary loss were chosen based on prior work and not systematically swept.

No external validation. Generalisation to other cardiac MRI datasets (M&Ms, M&Ms-2) and cross-modality transfer (e.g. CT) have not been evaluated.

5.2 Future Work

Run baselines (U-Net, Attention U-Net, SwinUNet-2D) under 3-fold CV for fully matched comparison.

Statistical significance testing (paired t-test) between HybridUNet and baselines across folds.

Couple with uncertainty estimation for clinical risk-aware deployment.

Evaluate cross-dataset generalisation on M&Ms and M&Ms-2.

Extend to a 3D version that exploits inter-slice coherence.

6. Conclusion

We presented a lightweight hybrid CNN-Transformer with a compound boundary-aware

loss for cardiac cine-MRI segmentation on ACDC. Under our experimental setup the method matches a parameter-matched SwinUNet-2D baseline on mean Dice (0.859 ± 0.004 versus 0.866 at fold 0) while reducing LV HD95 by 18% and essentially matching the best baseline on MYO HD95, at comparable parameter count and inference cost. The ablation attributes most of the boundary gain to the skip refinement and the boundary-weighted loss term, with the transformer bottleneck contributing a further clear boundary gain on the myocardium: removing the boundary skip refinement alone (variant B) raises MYO HD95 from 1.98 to 3.02, and further substituting the transformer bottleneck for a U-Net backbone (variant D) raises it to 4.88, confirming the bottleneck's independent contribution to boundary localisation. Handling boundaries at both the architectural and the loss level therefore looks like a worthwhile direction for segmentation when labelled data are limited.

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Data Availability

The ACDC dataset [2] is publicly available at https://www.creatis.insa-lyon.fr/Challenge/acdc/ (registration required).

Conflicts of Interest

The authors declare no conflicts of interest.

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