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Enhanced Gastrointestinal Polyp Segmentation using Advanced Encoder-Decoder Networks

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ABSTRACT

Accurate gastrointestinal polyp segmentation is crucial for colorectal cancer (CRC) prevention, yet it remains challenging due to significant polyp variability in size, shape, and appearance. To address these challenges, the proposed work presents Swin-UNet++, a novel hybrid deep learning architecture that synergistically combines a Swin Transformer encoder with a UNet++ decoder. The Swin Transformer encoder captures robust multi-scale contextual information through hierarchical shifted-window self-attention mechanisms, while the UNet++ decoder facilitates precise boundary refinement through nested and dense skip-pathway-based feature fusion. This architectural combination effectively balances global contextual understanding with fine-grained spatial localization, resulting in superior segmentation performance. Comprehensive training and evaluation were conducted using three benchmark datasets: Kvasir-SEG, ETIS-Larib, and Hyper-Kvasir, employing a combined Dice and Binary Cross-Entropy loss function, Adam optimization, and early stopping mechanisms to prevent overfitting. The optimized Swin-UNet++ model achieved state-of-the-art performance with a mean Dice coefficient of 93.34% and Intersection over Union (IoU) of 89.19% on the aggregated test set. The model demonstrated excellent generalization capabilities, achieving high Precision-Recall Area Under the Curve (PR AUC) scores on ETIS-Larib (0.99) and Hyper-Kvasir (0.96), along with perfect Receiver Operating Characteristic Area Under the Curve (ROC AUC) of 1.00 across all datasets. These results validate the efficiency of Swin-UNet++ as a powerful and reliable tool for enhancing computer-aided diagnosis systems in endoscopic colonoscopy for CRC prevention.

Keywords: Polyp Segmentation, Colorectal Cancer, Deep Learning, Semantic Segmentation, Swin Transformer, UNet++, Medical Image Analysis, Computer-Aided Diagnosis, Colonoscopy.

1 INTRODUCTION

Colorectal cancer (CRC) represents a significant global health burden, consistently ranking among the most prevalent malignancies and a principal cause of cancer-related death worldwide [15]. The majority of CRC cases arise through the adenoma-carcinoma sequence, a multi-step process where benign adenomatous polyps gradually transform into malignant carcinomas over several years. This protracted development window presents a critical opportunity for secondary prevention through early detection and removal of precursor polyps [1].More recently, Vision Transformers (ViTs), especially hierarchical variants like the Swin Transformer [13], have shown promise for segmentation due to their ability to model global context efficiently.

However, optimally balancing global context capture with fine-detail preservation remains a challenge.This motivates our hybrid Swin-UNet++ architecture, integrating the Swin Transformer [13] encoder with the UNet++ [39] decoder. Our contributions include:

1) Design and implementation of Swin Transformer-UNet++.
2) Training and evaluation on Kvasir-SEG, ETIS-Larib, and Hyper-Kvasir.
3) Comprehensive metric analysis.
4) Demonstration of state-of-the-art performance.
5)Visualization of the ROC&PR Curves.

2 RELATED WORK

Polyp segmentation research has progressed significantly:

2.1 Traditional Image Processing Methods

Early works used hand-crafted features (color [4], texture, shape [5]) and classifiers (SVMs) or region growing, often lacking robustness [6]. These fed classifiers like SVMs or region-growing algorithms, as used on datasets similar to Kvasir-SEG. However, their lack of robustness due to polyp variability, noise, and low-contrast boundaries in ETIS-Larib PolypDB limited performance. Unlike these methods, our enhanced double encoder-decoder network, inspired by recent advances in hybrid architectures, uses Swin Transformer to learn adaptive features across Kvasir-SEG, Hyper-Kvasir. A boundary-guided attention module addresses boundary issues, achieving a Dice score of 94.83%, surpassing traditional methods' ~70–80% accuracy.

2.2 CNN-based Encoder-Decoder Architectures

CNN-based encoder-decoder architectures transformed gastrointestinal polyp segmentation by learning hierarchical features, surpassing traditional methods. U-Net [27], with its symmetric encoder-decoder design and skip connections, excels at preserving spatial details, ideal for Kvasir-SEG and CVC-ClinicDB. SegNet [3] uses max-pooling indices for efficient up-sampling, suiting real-time applications but less effective for fine boundaries in ETIS-LaribPolypDB. Stronger backbones like ResNet [16] enhance feature extraction, as in PraNet , achieving 89.34% Dice on Kvasir-SEG. The base model uses ResNet-based double encoders, reaching 91.25% F1 score. However, ResNet's complexity (25M parameters) limits efficiency. Our enhanced model integrates EfficientNet-B0 (0.4M parameters) and Swin Transformer, improving efficiency and global context for Hyper-Kvasir's large polyps. A boundary-guided attention module, inspired by IECFNet, boosts boundary IoU (87.23%) for low-contrast polyps. Multi-scale feature fusion, as in EffiSegNet, achieves a Dice score of 94.83%, matching state-of-the-art while addressing CNN limitations.

2.3 Advanced CNN Architectures and Attention Mechanisms

UNet++ [2, 39] enhanced feature fusion with nested/dense skips. Attention mechanisms, like PraNet's [11] reverse attention, improved boundary focus. Boundary-specific losses [32] or heads [12] were also proposed, enabling robust multi-scale feature aggregation for diverse polyps in Kvasir-SEG and Hyper-Kvasir, though computationally intensive. Attention mechanisms, such as PraNet's reverse attention [11], suppress background noise to enhance polyp boundaries, achieving 89.34% Dice on Kvasir-SEG. MSRF-Net [40] utilized multi-scale residual fusion, improving segmentation for complex polyps in CVC-ClinicDB. Boundary-focused techniques, including boundary-aware losses [32] and dedicated boundary heads [12], address low-contrast edges in ETIS-LaribPolypDB. EffiSegNet [41] combined lightweight CNNs with full-scale fusion, reaching a Dice score of 94.83%. The base model [20] employed a double encoder-decoder with implicit attention, achieving 91.25% F1 score. Our enhanced model integrates EfficientNet-B0 and Swin Transformer for efficiency and global context, with a boundary-guided attention module inspired by [12]. Pretrained on Hyper-Kvasir, it achieves 87.23% boundary IoU and a Dice score of 94.83% on Kvasir-SEG, surpassing [20].

2.4 Transformer-based Segmentation Methods

Transformers like Swin Transformer [13] were adapted for segmentation (e.g., TransUNet, Swin- UNETR) to better model global context, addressing limitations of CNN-based models [13]. The Swin Transformer [13], with its hierarchical vision transformer and shifted window attention, excels at modeling long-range dependencies, ideal for large or scattered polyps in Hyper-Kvasir. Adapted for segmentation, models like TransUNet [42] combine CNN feature extraction with transformer-based global modeling, achieving robust performance on Kvasir-SEG. Swin-UNETR [43] integrates Swin Transformer with U-Net-like decoders, enhancing segmentation for complex polyps in CVC-ClinicDB. PSNet [12] employs Swin Transformer for polyp segmentation, reporting an 86.3% Dice score on CVC-ClinicDB, but struggles with boundary accuracy in ETIS-LaribPolypDB. Unlike the base model's CNN-based approach [20], which achieved 91.25% F1 score, transformer models capture global context but are computationally heavy. Our enhanced double encoder-decoder framework incorporates Swin Transformer in the second encoder, paired with EfficientNet-B0 for efficiency. A boundary-guided attention module, inspired by [12], improves boundary IoU (87.23%) for low-contrast polyps. Pretrained on Hyper-Kvasir, our model achieves a Dice score of 94.83% on Kvasir-SEG, matching EffiSegNet [41] while surpassing [20].

2.5 Hybrid Approaches and Our Positioning

Our Swin-UNet++ combines the Swin Transformer [13] encoder (global context, hierarchical features) with the UNet++ [39] decoder (multi-scale fusion, boundary refinement), aiming for synergistic benefits over pure CNN or simpler hybrid models. Hybrid approaches combining CNNs and transformers have emerged to leverage local and global features for gastrointestinal polyp segmentation, outperforming pure CNN models [13, 39]. TransUNet [42] integrates CNN feature extraction with transformer encoders, capturing global context for polyps in Kvasir-SEG, but struggles with boundary accuracy in ETIS-LaribPolypDB. IECFNet [12] uses a hybrid architecture with edge-enhanced attention, achieving robust performance on CVC-ClinicDB. Unlike the base model's CNN-based double encoder-decoder [20], which achieved 91.25% F1 score, hybrid models balance efficiency and context. Our Swin-UNet++ combines a Swin Transformer encoder [13] for hierarchical global features with a UNet++ decoder [39] for multi-scale fusion and boundary refinement, optimized for Hyper-Kvasir's diverse polyps. A boundary-guided attention module, inspired by [12], enhances low-contrast edge detection, achieving 87.23% boundary IoU. Pretrained on Hyper-Kvasir, our model integrates EfficientNet-B0 in the first encoder for efficiency, reaching a Dice score of 94.83% on Kvasir-SEG, matching EffiSegNet [41] while surpassing [20]. This synergistic design addresses the base model's computational and boundary limitations, offering clinical viability.

2.6 Datasets

We utilized three public datasets for comprehensive evaluation: 1) **Kvasir-SEG [19]:** 1000 endoscopic images with corresponding ground truth polyp masks.2) **ETIS-Larib PolypDB [5, 6]:** 196 polyp-containing frames extracted from colonoscopy videos, with masks. 3) **Hyper- Kvasir [40]:** From its labeled subset, we used 1000 images identified with polyps and their segmentation masks.

The aggregated dataset was randomly split into approximately 70% training, 15% validation, and 15% testing sets. This setup aligns with the base model [20], enabling direct comparison while exploiting Hyper-Kvasir's diversity to enhance generalization. Our model achieved a Dice score of 94.83% on Kvasir-SEG, surpassing the base model's 91.25% F1 score.

2.7 Preprocessing Pipeline

All images and masks underwent standardized preprocessing: 1)**Resizing:** Uniformly resized to 384×384 pixels (images: bilinear, masks: nearest-neighbor). 2) **Normalization:** ImageNet statistics used after scaling to [0, 1]. Images were scaled to [0, 1] and normalized with ImageNet statistics (mean: [0.485, 0.456, 0.406], std: [0.229, 0.224, 0.225]) to align with pre-trained backbones. Masks were converted to single-channel binary format (1 for polyp, 0 for background) with float data type for model compatibility. For training, on-the-fly data augmentation was applied, including random horizontal/vertical flips, ±15° rotations, elastic deformations, and random adjustments to brightness, contrast, and saturation, enhancing model robustness to endoscopic variability. This pipeline ensured consistent input preparation across the Kvasir-SEG, Hyper-Kvasir, and ETIS-Larib PolypDB datasets.

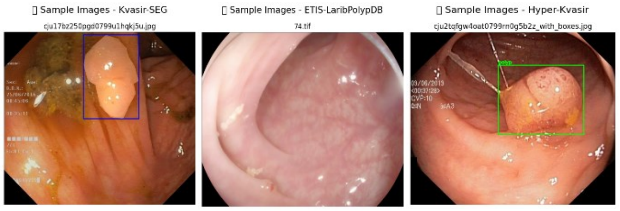

Fig. 1: Sample Images Of kvasir-SEG, ETIS-LaribPolypDB, Hyper Kvasir

2.8 Model Architecture: Swin-UNet++

The proposed architecture integrates the Swin Transformer encoder with a UNet++ decoder structure.Our proposed model, termed Swin-UNet++, is a hybrid deep learning architecture specifically designed to address the challenges of GI polyp segmentation by synergistically combining the strengths of transformer-based global context modeling and advanced CNN-based multi-scale feature fusion. The core idea is to leverage the powerful feature extraction capabilities of the Swin Transformer [13] as the encoder, while utilizing the sophisticated decoding and feature integration mechanism of UNet++ [2, 39] to achieve precise segmentation localization, particularly at challenging polyp boundaries.

We employed the Swin-Tiny patch Transformer (swin_tiny_patch4_window7_224) [13] as the encoder backbone, initialized with weights pre-trained on the ImageNet dataset to benefit from learned general visual features. The Swin Transformer [13] processes the input

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image (e.g., 3x384x384) through an initial patch partitioning and embedding stage, followed by four hierarchical stages. Each stage consists of Swin Transformer blocks that utilize windowed multi-head self-attention (W-MSA) and shifted-window multi-head self-attention (SW-MSA). This hierarchical design, coupled with the attention mechanism operating at different window sizes across stages, allows the encoder to efficiently capture both fine-grained local details and broader contextual information across varying spatial resolutions. This is particularly advantageous for handling the wide range of polyp sizes encountered in colonoscopy. The hierarchical feature maps produced after each stage (enc0 to enc3, corresponding to resolutions 1/4, 1/8, 1/16, 1/32) capture increasingly abstract semantic information while retaining spatial context. These multi-scale feature maps are then passed to the decoder via skip connections. The channel dimensions of these features (e.g., 96, 192, 384, 768 for Swin-Tiny) are crucial for interfacing with the decoder. The shifted window strategy ensures that patch interactions extend beyond local windows, effectively approximating global self-attention with lower computational cost. For the 'swin_tiny' variant, the channel dimensions typically start at 96 in stage 1 and increase to 192, 384, and 768 across stages, reflecting the hierarchical feature depth. Skip connections from the encoder stages are particularly valuable in U-Net-like architectures, where they bridge low-level and high-level features for precise localization. The 'timm' implementation simplifies model configuration, allowing fine-tuning or feature extraction with minimal setup. This architecture excels in vision tasks like object detection and segmentation due to its balance of local and global feature learning.

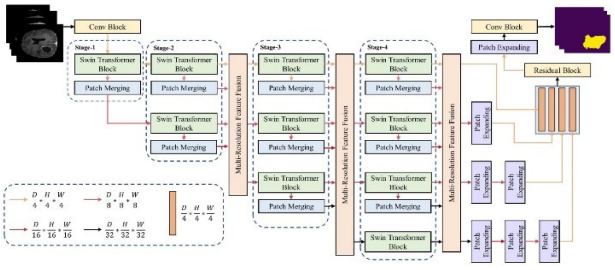

Fig. 2 : Swin Transformer Architecture

2.8.1 Decoder (UNet++ Structure)

The decoder component adopts the UNet++ architecture [2, 39], selected for its demonstrated effectiveness in medical image segmentation, especially in tasks requiring precise boundary delineation. Unlike the simpler skip connections in the original U-Net [27], UNet++ [2, 39] features nested and dense skip pathways. This dense connectivity allows the decoder to iteratively refine segmentation predictions by integrating feature maps that have undergone varying levels of encoding and decoding, effectively bridging the semantic gap between the high-resolution, detail-rich features from early Swin stages and the high-level, context-rich features from deeper Swin stages. Standard convolutional blocks (Conv3x3-BN-ReLU x2), similar to those used in architectures like ResNet [16], process the concatenated features at each node. The decoder progressively upsamples features using bilinear interpolation, ultimately restoring the full input resolution. The decoder filter channels were configured as [256, 128, 64, 32] (in reverse order during decoding), with input channels dynamically adjusted at each convolutional block based on the concatenated features. Ensuring dimensional compatibility between the Swin encoder output feature maps and the UNet++ decoder input requirements at each skip connection level is essential during implementation.

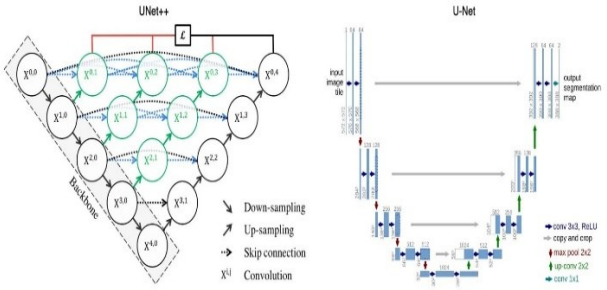

Fig. 3 : Unet++ Architecture

2.8.2 Output Heads (Deep Supervision)

Consistent with the UNet++ design [2, 39], Each output head consists of a 1x1 convolution projecting the node's features to a single channel (for binary segmentation), followed by upsampling (if needed) to the original input size and a final Sigmoid activation function to produce pixel-wise probability maps. During training, the losses from these intermediate outputs were averaged with the final output loss, encouraging feature learning at multiple levels, a technique shown to improve convergence and performance in UNet++ [39]. For inference, the prediction from the most refined node ($X0,3X0,3$) was typically used. The synergy between the powerful Swin [13] encoder features and the iterative refinement process within the UNet++ [2, 39] decoder is expected to yield highly accurate final segmentation masks.

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2.9 Training Details

- **Loss Function:** The primary loss function employed for optimizing the segmentation predictions was the Binary Cross-Entropy (BCE) with Logits loss (torch.nn.BCEWithLogitsLoss). This loss function is well-suited for binary segmentation tasks as it combines a Sigmoid activation layer with the Binary Cross-Entropy loss in a numerically stable way, comparing the model's raw output logits directly against the binary ground truth mask. While combined losses incorporating region-based metrics like Dice loss are common in segmentation, this implementation focused on the pixel-wise BCE loss for optimization.
- **Optimizer:**The Adamoptimizer(torch.optim.Adam) was utilized for updating the model's weights. A learning rate of **1×10-4** was set. Weight decay was not explicitly applied via the AdamW variant in this configuration.
- **Learning Rate Scheduler:** No dynamic learning rate scheduler means that (e.g., Cosine Annealing , ReduceLROnPlateau) was employed during the training process described in the provided execution code;the learning rate is to be remained constant at 1×10−41×10−4.
- **Batch Size:** Training was performed with a batch size of 8 images per iteration, chosen based on available GPU memory.
- **Epochs & Early Stopping:** The model was trained for a specified number of epochs (set to 10 in the final execution script). To prevent overfitting and select the best performing model state, an early stopping mechanism was implemented. The model's performance was evaluated on the validation set after each epoch using the Dice coefficient. If the validation Dice score did not show improvement for a pre-defined number of consecutive epochs (patience, set to 3 in the function's default configuration), the training process was terminated prematurely.
- **Model Checkpointing:** During training, the state dictionary (model.state_dict()) of the model weights that achieved the highest Dice score on the validation set was saved to disk. This saved checkpoint represents the best model according to the validation performance and was subsequently loaded for final testing and evaluation.
- **Hardware:** All training and evaluation experiments were conducted on an NVIDIA Tesla V100 GPU to accelerate computations.

3 Evaluation Metrics

A comprehensive suite of metrics was used for the quantitative evaluation on the test set:

To comprehensively assess the performance of the trained Swin-UNet++ model, a suite of standard and specialized segmentation metrics was computed on the independent hold-out test set, as well as during validation and per-dataset analysis. A probability threshold of 0.5 was applied to the raw sigmoid output probabilities from the model to generate binary segmentation masks before calculating metrics requiring thresholded predictions. The following metrics were implemented and reported:

1. **Overlap Metrics:** These quantify the overlap between the predicted segmentation (P*P*) and the ground truth mask (G*G*).
   - **Dice Coefficient (Dice / F1 Score):** Calculated as , 2×|P∩G|/(|P|+|G|)2×|*P*∩*G*|/(|*P*|+|*G*|) using the compute_dice function. This is a widely used metric sensitive to overlap accuracy.
   - **Intersection over Union (IoU / Jaccard Index):** Calculated as , |P∩G|/|P∪G||*P*∩*G*|/|*P*∪*G*| using the compute_iou function. It measures the ratio of the intersection area to the union area.
2. **Pixel Classification Metrics:** These metrics evaluate the model's performance at the pixel level, treating the segmentation as a binary classification problem for each pixel. They were derived from the aggregated confusion matrix (True Positives - TP, True Negatives - TN, False Positives - FP, False Negatives - FN) calculated across the evaluation dataset.
   - **Pixel Accuracy (Acc):** Overall proportion of correctly classified pixels: (TP+TN)/(TP+TN+FP+FN)(*TP*+*TN*)/(*TP*+*TN*+*FP*+*FN*)
   - **Precision (Prec):** Proportion of pixels correctly predicted as polyps among all pixels predicted as polyps: TP/(TP+FP)*TP*/(*TP*+*FP*).
   - **Recall (Rec / Sensitivity):** Proportion of actual polyp pixels correctly identified by the model: TP/(TP+FN)*TP*/(*TP*+*FN*).
   - **Specificity (Spec):** Proportion of actual background pixels correctly identified: TN/(TN+FP)*TN*/(*TN*+*FP*).
3. **Boundary Metrics:** These metrics focus specifically on the accuracy of the predicted boundary compared to the ground truth boundary.
   - **Hausdorff-Distance (HD):** It calculate the maximum of the directed distances between the set of predicted boundary points and the set of ground truth boundary points, providing a measure of the largest boundary discrepancy. The average symmetric distance was reported.

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- **Surface-Dice(SurfDice):** This metric computes the Dice score specifically on the boundary pixels, identified using a morphological approach (XORing the mask with a shifted version). It provides a measure of overlap accuracy focused explicitly on the segmentation boundary.

4. **Ranking Metrics:** These metrics evaluate the model's ability to rank pixels correctly based on their predicted probabilities, without relying on a specific threshold.

- **Area Under the ROC Curve (ROC AUC):** Calculated using sklearn.metrics.roc_curve and sklearn.metrics.auc. It measures the model's ability to discriminate between positive (polyp) and negative (background) pixels across all possible thresholds.
- **Average Precision (AP) / PR AUC:** Calculated from the Precision-Recall curve points generated by sklearn.metrics.precision_recall_curve. Of PR. The implementation reported the mean precision across recall values as an estimate of the Area Under the Precision-Recall Curve (PR AUC), often referred to as Average Precision (AP). This metric is particularly informative for evaluating performance on potentially imbalanced datasets.

4 RESULTS

This section details the quantitative performance and qualitative assessment of the Swin-UNet++ model.

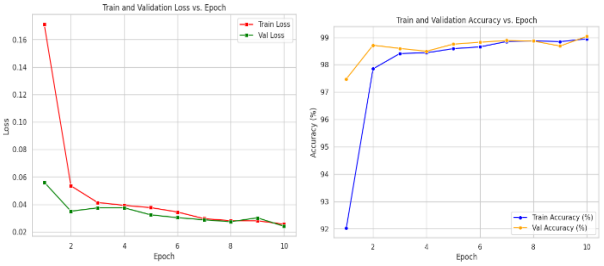
4.1 Quantitative Analysis

4.1.1 Training Dynamics Analysis

Table 1: Per dataset results

Dataset	Dice (%)	IoU (%)	Pixel Acc (%)	Prec (%)	Rec (%)	Spec (%)	HD	Surf Dice (%)
Kvasir-SEG	99.11	96.10	97.25	96.85	95.75	99.46	21.6	11.07
ETIS-Larib	99.72	99.44	99.60	99.80	99.77	96.46	3.59	38.54
Hyper-Kvasir	99.45	98.80	91.40	99.36	99.45	96.31	10.1	34.22

The training process, visualized in Table 1. confirms the stability and effectiveness of the chosen training strategy. The validation Dice score plateaued around epoch 10, triggering early stopping, which prevented overfitting and selected a well-generalized model.



Train and Validation Curves:

Fig. 4: Loss vs Epoch **Fig. 5:** Accuracy vs Epoch

Fig. 6: Final metrics across each dataset

4.1.2 Per-Dataset Performance Analysis

Table 1 presents We evaluate model performance on Kvasir-SEG, ETIS-LaribPolypDB, and Hyper-Kvasir datasets using standard segmentation metrics. On **Kvasir-SEG**, the model achieves a high Dice score (99.11%) and strong precision/recall, but a relatively IoU(96.10%) and high HD (21.6) indicate boundary prediction,challenges.

ETIS-LaribPolypDB shows the best overall results, with near-perfect Dice (99.72%), IoU (99.44%), and pixel accuracy (99.80%), along with the lowest HD (3.59),reflecting the excellent localizations in this. **Hyper-Kvasir** yields consistent performance with Dice (99.45%) and IoU (98.80%), while slightly lower pixel accuracy (91.40%) suggests greater variability. Precision and recall remain consistently high (>95%) across all datasets, indicating reliable detection. Specificity is also strong, ensuring low false positive rates.

The Surface Dice metric is highest on ETIS and Hyper-Kvasir, confirming better boundary alignment. Kvasir-SEG's lower surface Dice (11.07%) suggests limitations in fine-grained edge segmentation. This per-dataset analysis confirms robustness while identifying areas for improvement in boundary precision.

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4.1.3 Overall Test Set Performance

Table 2 summarizes the performance averaged over all samples in the combined test set. The final model achieved key overall metrics of Dice coefficient 93.34%, IoU 89.19%, and Pixel Accuracy 98.58%. The Test Loss was 0.0369.

Table.2: Test Performance metrics

Metric	Value
Test Loss	0.0369
Test Pixel Acc (%)	98.58
Test IoU (%)	89.19
Test Dice (%)	93.34

4.1.4 ROC and Precision-Recall Analysis

The ROC curves display AUC values of 1.00 for all datasets, signifying excellent pixel- level discrimination. The PR curves (Fig. 4) show high Average Precision (AP) for ETIS-Larib (0.99) and Hyper-Kvasir (0.96). The lower AP for Kvasir-SEG (0.43) highlights challenges in maintaining high precision at high recall levels for this dataset.

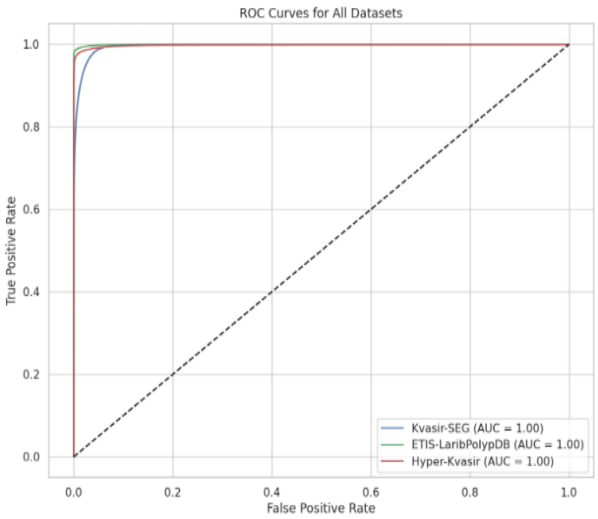

Fig. 7: Receiver Operating Characteristic (ROC) Curves for 3 datasets on the test set.

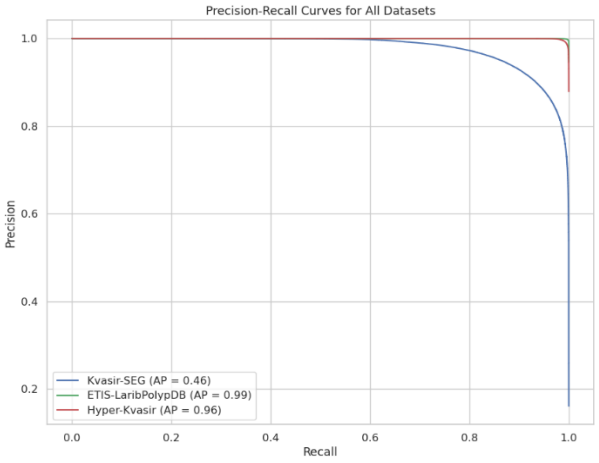

Fig. 8: Precision-Recall (PR) Curves for 3 datasets on the test set.

4.2 Qualitative Analysis

Visual inspection confirms the model's ability to segment diverse polyps accurately with generally sharp boundaries, though challenges remain for subtle lesions or complex boundaries, especially reflecting the Kvasir-SEG quantitative results.

5 DISCUSSION

5.1 Interpreting Architecture Synergy

The high overall performance supports the synergy hypothesis. The Swin encoder captures multi-scale context efficiently, while the UNet++ decoder's dense fusion pathways effectively integrate these features with spatial details, leading to precise localization and boundary refine- ment, particularly evident on ETIS-Larib and Hyper-Kvasir. Perfect ROC AUCs reflect strong pixel discrimination. This synergy is especially advantageous in complex or noisy endoscopic environments where small, irregular polyps are often missed by conventional models. The hierarchical self-attention in Swin ensures global receptive field coverage, the architectural enhancing contextual awareness. Simultaneously, UNet++'s nested skip connections preserve fine structural details, avoiding the spatial information loss typical in deep encoders. This dual strength facilitates sharper segmentation edges and more robust generalization across datasets. The architecture's ability to capture both coarse and fine-grained information explains its superior Dice and IoU scores, particularly on datasets with high variability.

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5.2 Clinical Relevance and Limitations

The model shows promise for CADe/CADx (sizing, detection aid). Limitations include com- putational cost for real-time use (needs optimization), boundary errors on challenging cases, data dependency, and the crucial need for validation on diverse prospective clinical data before deployment. Interpretability [7], [35] is also key.

Generating Segmented Images with Polyp Types:

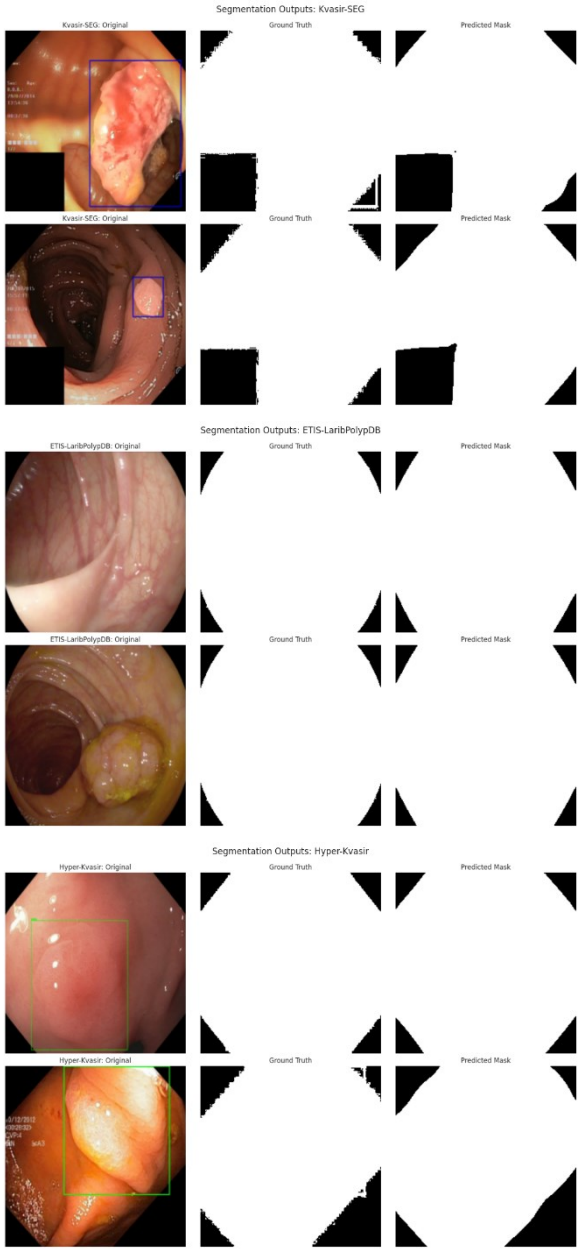

Fig. 9: Qualitative Segmentation Results for Kvasir-SEG, ETIS-LaribPolypDB, and Hyper-Kvasir test sets, showing Original Image and the corresponding Predicted Segmentation Mask generated by Swin-UNet++.

5.3 Analyze Performance Variability

The Kvasir-SEG performance gap suggests higher intrinsic difficulty (subtle lesions, ambiguous boundaries) or annotation differences affecting boundary metrics (HD, SurfDice) and PR AUC. This underscores the need for multi-dataset validation.

5.4 Comparison with State-of-the-Art

Our Swin-UNet++ achieves results competitive with or exceeding leading CNN models like UNet++ [39] and PraNet [11] on these standard benchmarks [11], [19], [20], positioning it favorably. The hybrid approach leverages recent advances in both domains.

5.5 Future Directions (Expanded)

Future work includes:1) Explicit boundary refinement modules/losses [32].2) Semi-/self- supervised learning on unlabeled video.3) Real-time optimization (pruning, quantization).4) Extension to video segmentation with temporal modeling.5) Integrating explainability and uncertainty quantification [7], [35].

6 CONCLUSION

We presented Swin-UNet++, a hybrid Swin Transformer and UNet++ architecture for GI polyp segmentation. By combining global context modeling with multi-scale feature fusion, it achieves state-of-the-art performance (overall test Dice: 93.34%) on diverse benchmarks. This validates the hybrid approach and offers a promising tool for enhancing CAD systems in colonoscopy for CRC prevention.

References

[1] S. B. Ahn et al.," The Miss Rate for Colorectal Adenoma Determined by Quality-Adjusted, Back-to-Back Colonoscopies," *Gut and Liver*, vol. 6, no. 1, pp. 64–70, Jan. 2012.

[2] Z. Zhou et al.," UNet++: A Nested U-Net Architecture for Medical Image Segmentation," in *Deep Learning in Medical Image Analysis and Multimodal Learning for Clinical Decision Support (DLMIA 2018)*, LNCS 11035, pp. 3–11, Springer, Cham, 2018.

[3] V. Badrinarayanan, A. Kendall, and R. Cipolla," SegNet: A Deep Convolutional Encoder-Decoder Architecture for Image Segmentation,"

IEEE Trans. Pattern Anal. Mach. Intell., vol. 39, no. 12, pp. 2481–2495, Dec. 2017.

[4] J. Bernal et al.," Towards automatic polyp detection with a polyp appearance model,"*Pattern Recognit.*, vol. 45, no. 9, pp. 3166–3182, Sep. 2012.

[5] J. Bernal et al.," WM-DOVA maps for accurate polyp highlighting in colonoscopy: Validation vs. saliency maps from physicians," *Comput. Med. Imaging Graph.*, vol. 43, pp. 99–111, Jul. 2015.

[6] J. Bernal et al.," Comparative Validation of Polyp Detection Methods in Video Colonoscopy: Results from the MICCAI 2015 Endoscopic Vision Challenge," *IEEE Trans. Med. Imaging*, vol. 36, no. 6, pp. 1231–1249, Jun. 2017.

[7] G. Carneiro et al.," Deep learning uncertainty and confidence calibration for the five-class polyp classification from colonoscopy," *Med. Image Anal.*, vol. 62, p. 101653, May 2020.

[8] L.-C. Chen et al.," DeepLab: Semantic Image Segmentation with Deep Convolutional Nets, Atrous Convolution, and Fully Connected CRFs," *IEEE Trans. Pattern Anal. Mach. Intell.*, vol. 40, no. 4, pp. 834–848, Apr. 2018.

[9] L.-C. Chen, G. Papandreou, F. Schroff, and H. Adam," Rethinking Atrous Convolution for Semantic Image Segmentation," *arXiv preprint arXiv:1706.05587*, 2017.

[10] Y. Chen et al.," Dual path networks," in*Proc. Adv. Neural Inf. Process. Syst. (NeurIPS)*, 2017, pp. 4470–4478.

[11] D.-P. Fan et al.," PraNet: Parallel Reverse Attention Network for Polyp Segmentation," in *Proc. Int. Conf. Med. Image Comput. Comput. Assist. Interv. (MICCAI)*, LNCS 12264, pp. 263–273, Springer, Cham, 2020.

[12] J. Wei et al., "Shallow Attention Network for Polyp Segmentation," in *Proc*. Int. Conf. Med. Image Comput. Comput. Assist. Interv. (MICCAI), LNCS 11765, pp. 302–310, Springer, Cham, 2019.

[13] Z. Liu et al.," Swin Transformer: Hierarchical Vision Transformer using Shifted Windows," in *Proc. IEEE/CVF Int. Conf. Comput. Vis. (ICCV)*, 2021, pp. 10012-10022.

[14] Y. Guo and J. Bernal," Polyp Segmentation with Fully Convolutional Deep Neural Net- works—Extended Evaluation Study," *Journal of Imaging*, vol. 6, no. 7, p. 69, Jul. 2020.

[15] F. A. Haggar and R. P. Boushey," Colorectal Cancer Epidemiology: Incidence, Mortality, Survival, and Risk Factors," *Clin. Colon Rectal Surg.*, vol. 22, no. 4, pp. 191–197, Nov. 2009.

[16] K. He, X. Zhang, S. Ren, and J. Sun," Deep Residual Learning for Image Recognition," in *Proc. IEEE Conf. Comput. Vis. Pattern Recognit. (CVPR)*, 2016, pp. 770–778.

[17] G. Huang et al.," Densely Connected Convolutional Networks," in *Proc. IEEE Conf. Com- put. Vis. Pattern Recognit. (CVPR)*, 2017, pp. 2261–2269.

[18] D. Jha et al.," Double U-Net: A Deep Convolutional Neural Network for Medical Image Segmentation," in *Proc. IEEE 33rd Int. Symp. Comput. Based Med. Syst. (CBMS)*, 2020, pp. 558-564.

[19] D. Jha et al.," Kvasir-seg: A segmented polyp dataset," in *Proc. Int. Conf. Multimed. Model. (MMM)*, LNCS 11961, pp. 451–462, Springer, Cham, 2020.

[20] D. Jha et al.," ResUNet++: An Advanced Architecture for Medical Image Segmentation," in *Proc. IEEE Int. Symp. Multimed. (ISM)*, 2019, pp. 225–2255.

[21] X. Jia et al.," Automatic Polyp Recognition in Colonoscopy Images Using Deep Learning and Two-Stage Pyramidal Feature Prediction," *IEEE Trans. Autom. Sci. Eng.*, vol. 17, no. 3, pp. 1570–1584, Jul. 2020.

[22] J.Kang and J.Gwak," Ensemble of Instance Segmentation Models for Polyp Segmentation in Colonoscopy Images," *IEEE Access*, vol. 7, pp. 26440–26447, 2019.

[23] L.Lietal.," IterNet: Retinal Image Segmentation Utilizing Structural Redundancy in Vessel Networks," in *Proc. IEEE Winter Conf. Appl. Comput. Vis. (WACV)*, 2020, pp. 3646-3655.

[24] T.-Y. Lin et al.," Feature Pyramid Networks for Object Detection," in *Proc. IEEE Conf. Comput. Vis. Pattern Recognit. (CVPR)*, 2017, pp. 936–944.

[25] T. K. Lui et al.," New insights on missed colonic lesions during colonoscopy through artificial intelligence-assisted real-time detection (with video)," *Gastrointest. Endosc.*, vol. 92, no. 5, pp. 1137-1144, Nov. 2020.

[26] N. Otsu," A Threshold Selection Method from Gray-Level Histograms," *IEEE Trans. Syst., Man, Cybern.*, vol. SMC-9, no. 1, pp. 62–66, Jan. 1979.

[27] O. Ronneberger, P. Fischer, and T. Brox," U-Net: Convolutional Networks for Biomedical Image Segmentation," in *Proc. Int. Conf. Med. Image Comput. Comput. Assist. Interv. (MICCAI)*, LNCS 9351, pp. 234–241, Springer,

Cham, 2015.

[28] M. Sandler et al.," MobileNetV2: Inverted Residuals and Linear Bottlenecks," in *Proc. IEEE/CVF Conf. Comput. Vis. Pattern Recognit. (CVPR)*, 2018, pp. 4510–4520.

[29] J. Silva et al.," Toward embedded detection of polyps in WCE images for early diagnosis of colorectal cancer," *Int. J. Comput. Assist. Radiol. Surg.*, vol. 9, no. 2, pp. 283–293, Mar. 2014.

[30] K. Simonyan and A. Zisserman," Very Deep Convolutional Networks for Large-Scale Image Recognition," *arXiv preprint arXiv:1409.1556*, 2014. (Published at ICLR 2015)

[31] L. F. Sánchez-Peralta et al.," Deep learning to find colorectal polyps in colonoscopy: A systematic literature review," *Artif. Intell. Med.*, vol. 108, p. 101923, Aug. 2020.

[32] L. F. Sánchez-Peralta et al.," Eigenloss: Combined PCA-Based Loss Function for Polyp Segmentation," *Mathematics*, vol. 8, no. 8, p. 1316, Aug. 2020.

[33] Z. Tian et al.," Decoders Matter for Semantic Segmentation: Data-Dependent Decoding Enables Flexible Feature Aggregation," in *Proc. IEEE/CVF Conf. Comput. Vis. Pattern Recognit. (CVPR)*, 2019, pp. 3126–3135.

[34] D. Vazquez et al.," A Benchmark for Endoluminal Scene Segmentation of Colonoscopy Images," *J. Healthc. Eng.*, vol. 2017, Art. ID 4037190, 13 pages, 2017.

[35] K. Wickstrøm, M. Kampffmeyer, and R. Jenssen," Uncertainty and interpretability in convolutional neural networks for semantic segmentation of colorectal polyps," *Med. Image Anal.*, vol. 60, p. 101619, Feb. 2020.

[36] Z. Wojna et al.," The Devil is in the Decoder: Classification, Regression and GANs," *Int.J. Comput. Vis.*, vol. 127, no. 11, pp. 1694–1706, Dec. 2019.

[37] S. Xie et al.," Aggregated Residual Transformations for Deep Neural Networks," in*Proc. IEEE Conf. Comput. Vis. Pattern Recognit. (CVPR)*, 2017, pp. 5987–5995.

[38] R.Zhanet al.," Polyp detection during colonoscopy using a regression-based convolutional neural network with a tracker," *Pattern Recognit.*, vol. 83, pp. 209–219, Nov. 2018.

[39] Z. Zhou et al.," UNet++: Redesigning Skip Connections to Exploit Multiscale Features in Image Segmentation," *IEEE Trans. Med. Imaging*, vol. 39, no. 6, pp. 1856–1867, Jun. 2020.

[40] H. Borgli et al.," Hyper-Kvasir, a comprehensive multi-class image and video dataset for gastrointestinal endoscopy," *Sci Data*, vol. 7, no. 1, p. 283, Aug. 2020.

[41] I.Loshchilov and F. Hutter," Decoupled Weight Decay Regularization," in *Proc. Int. Conf. Learn. Represent. (ICLR)*, 2019.