

Supplementary Material

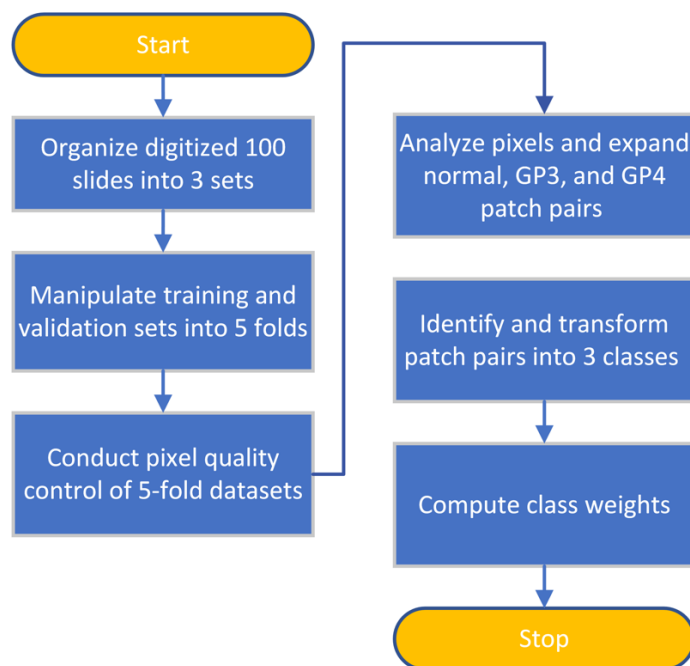


Fig. 1 Flowchart illustrating the preprocessing steps for the PCa slide dataset, including division into sets, fold manipulation, and class weight calculation.

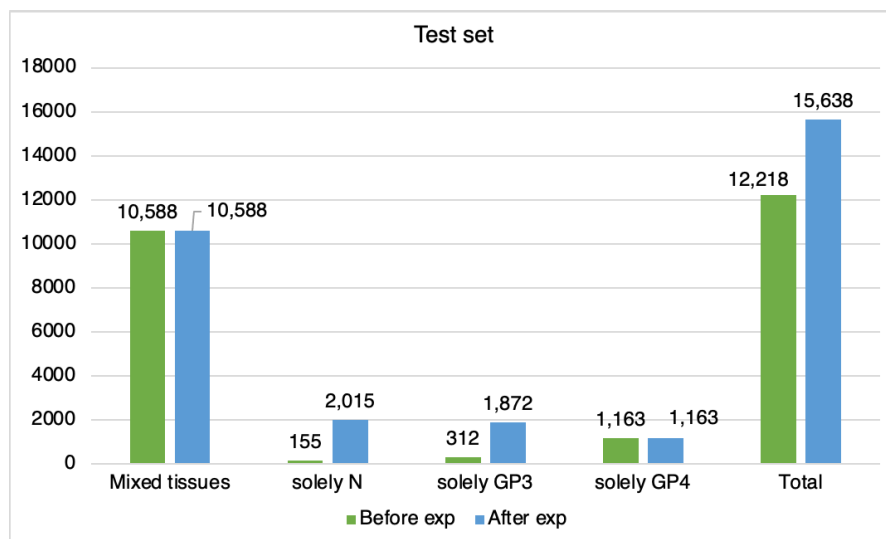


Fig. 2 Patch pair counts in the test set before and after expansion

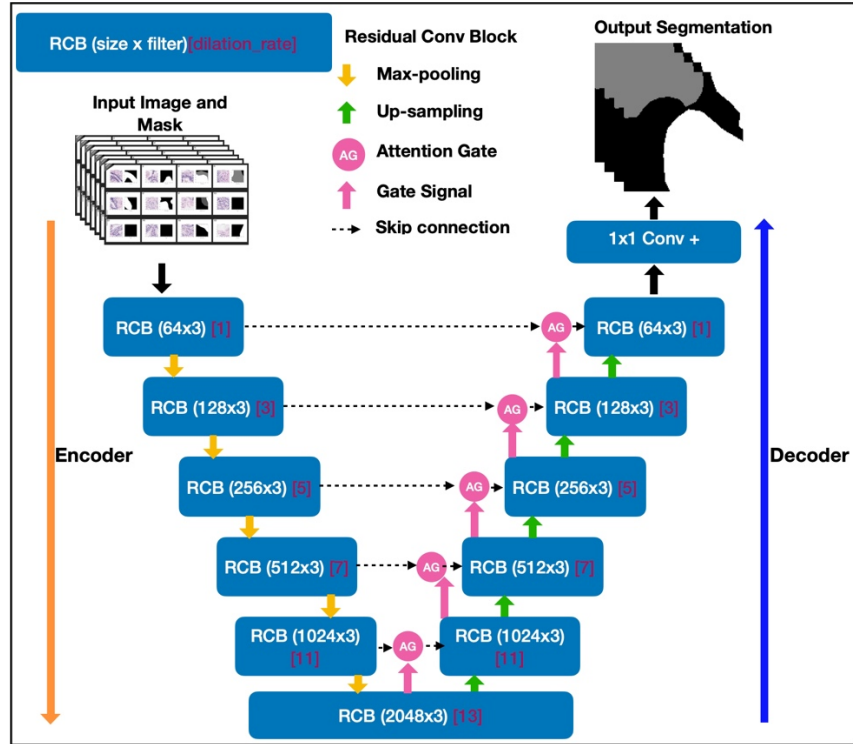


Fig. 3 Enhanced model architectural design of the proposed DARUN model

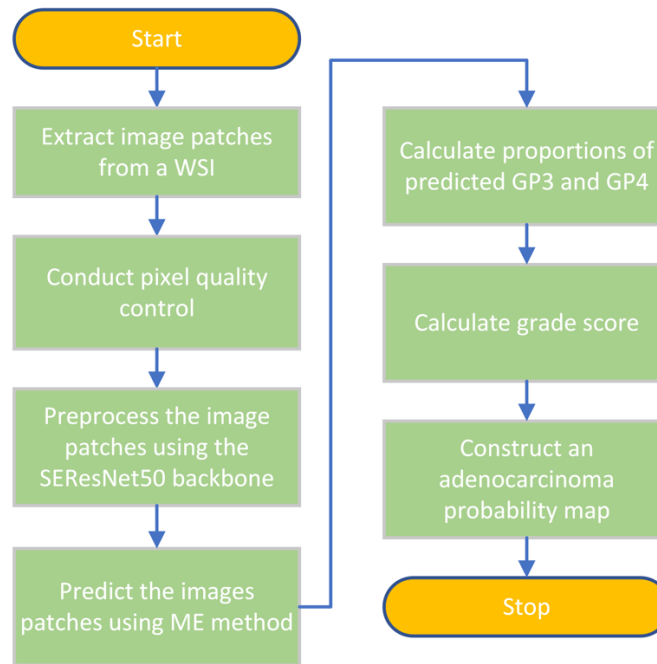


Fig. 4 Inference steps outlining the process for generating adenocarcinoma probability maps specifically targeting GP3 and GP4 tissues.

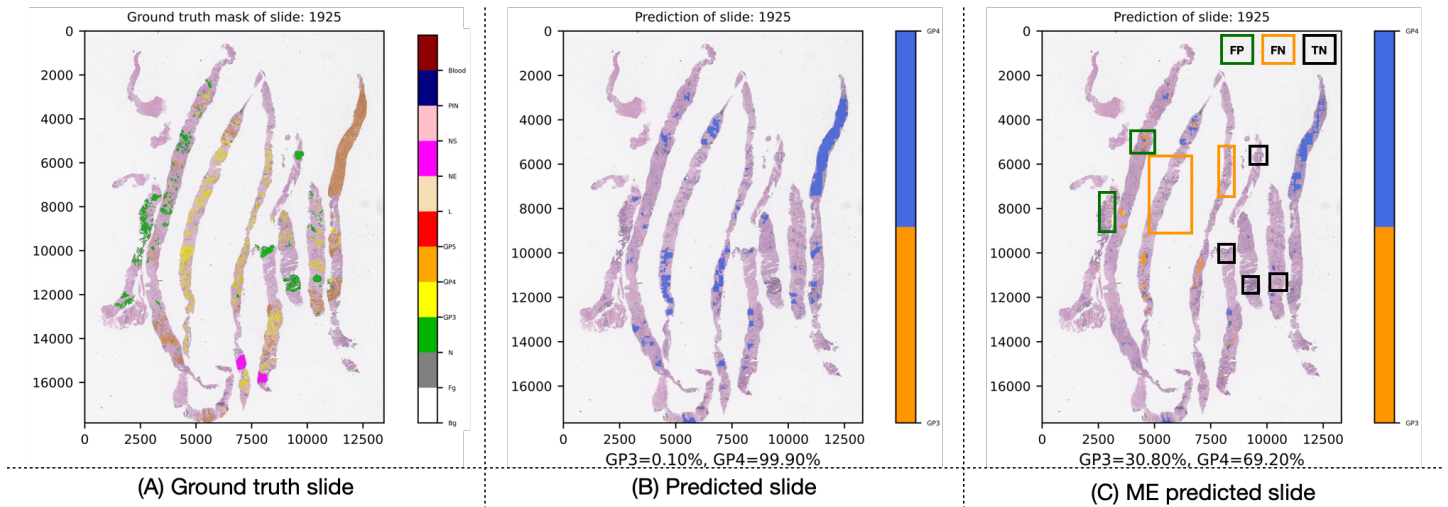


Fig. 5 Adenocarcinoma segmentation prediction and GP percentages for slide ID 1925 of Fold-4 validation set; black indicates TN for benign, orange indicates FN for GP3, and green indicates FP for benign.

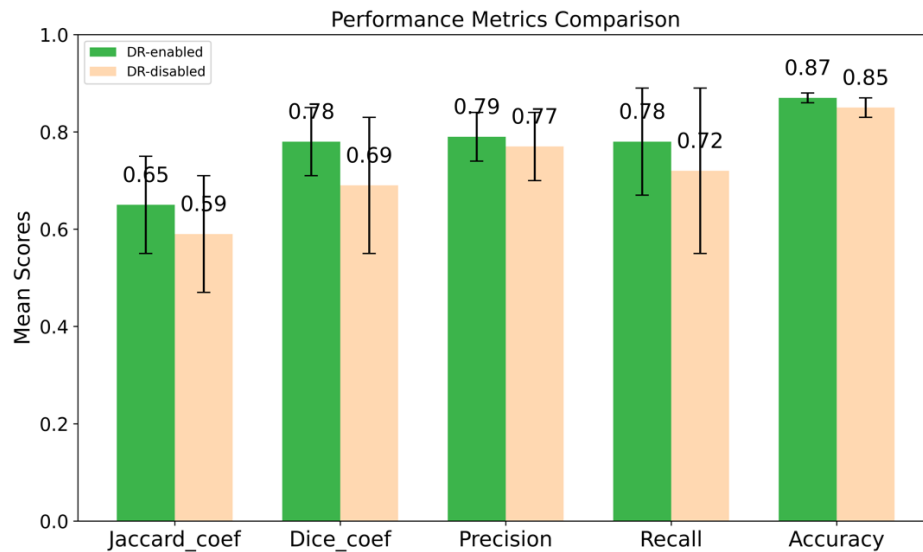


Fig. 6 Comparison of performance metrics: DR-enabled vs. DR-disabled models for the Fold-1 dataset. The DR-enabled model performed significantly better across all metrics, with a p-value of 0.039 (t-value = 2.145).

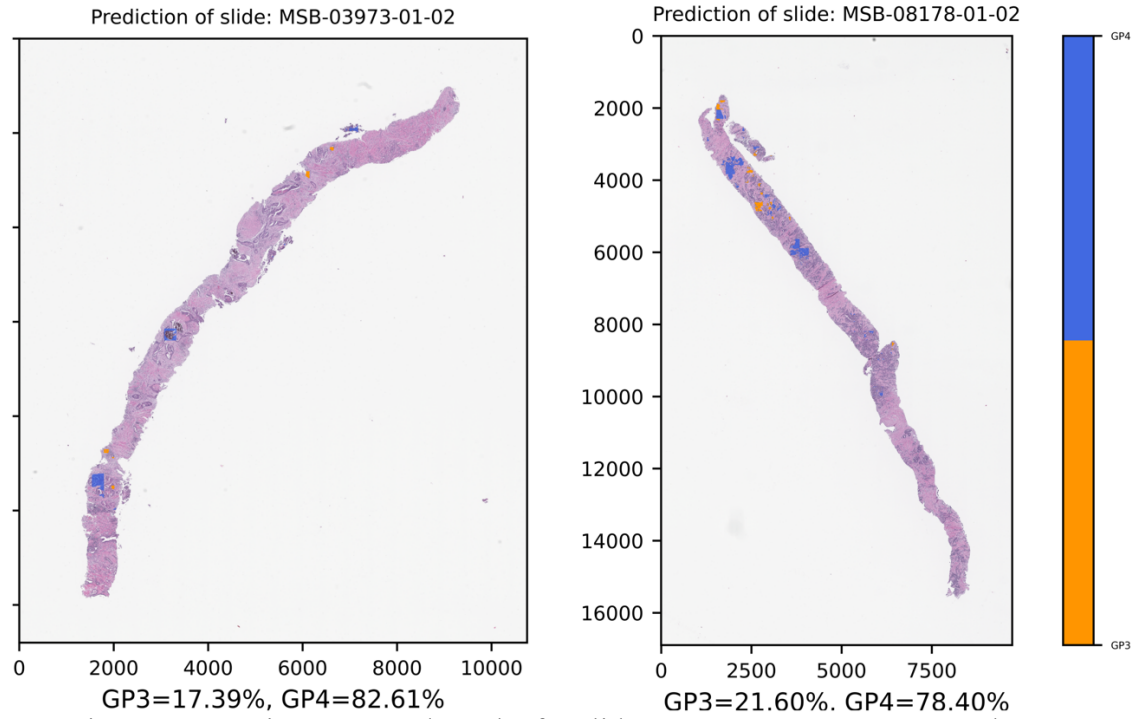


Fig. 7 Adenocarcinoma semantic segmented results for slide IDs MSB-03973-01-02 and MSB-08178-01-02 of the CMB-PCA as an external validation dataset.

Table 1. Hyperparameters and their configurations for the proposed DARUN model

Parameter	Configuration
Image patch preprocessing	Utilized the SEResNet50 of Segmentation Models version 1.0.1
Patch size	256 x 256
Kernel size	3 x 3
Dilation rate	1, 3, 5, 7, 11, 13
Batch size	8
Epochs	120
Dropout rate	0.25
Activation function	ReLu for all CNN-based layers and Softmax for the prediction layer
Loss function	Defined in the Equation 8 where $\alpha=0.25$, $\beta=1.0$, $\gamma=2.0$
Optimizer	Adam with initialized learning rate
Learning rate (LR)	$1e-4$
Class weights	Computed
Data augmentation	Horizontal flip (selection probability of 0.5) and vertical flip (selection probability of 0.5)
ReduceLROnPlateau	Monitor on validation of the Total loss with factor = 0.8, patience = 5, min_lr = LR/Epochs