

PancreScan K-Fold Cross-Validation Report

Date: 2026-02-10

Configuration

- Data directory: DATASET/train/train
- Model: efficientnet_b0
- Folds: 2
- Epochs per fold: 1
- Batch size: 16
- Image size: 224
- Learning rate: 0.0003
- Augmentation preset: basic
- Sampler: shuffle
- Positive class: pancreatic_tumor
- Positive threshold: 0.4
- Classes: normal, pancreatic_tumor

Fold Metrics (Validation)

Fold	Loss	Accuracy	Precision (macro)	Recall (macro)	F1 (macro)	Precision (pos)	Recall (pos)	F1 (pos)
1	0.049943	0.9820	0.9795	0.9844	0.9817	1.0000	0.9689	0.9842
2	0.037007	0.9800	0.9794	0.9794	0.9794	0.9827	0.9827	0.9827

Summary (Mean ± Std)

Metric	Mean	Std
loss	0.043475	0.006468
accuracy	0.980980	0.001020

precision	0.979495	0.000050
recall	0.981937	0.002492
f1	0.980548	0.001103
pos_precision	0.991349	0.008651
pos_recall	0.975779	0.006920
pos_f1	0.983441	0.000742

Notes

- Metrics are computed on the validation split of each fold.
- Positive-class metrics use the selected threshold.