

PancreScan K-Fold Cross-Validation Report

Date: 2026-02-11

Regularization Settings

- Early Stopping Patience: 3
- Dropout: 0.5
- Backbone Frozen: True
- Weight Decay: 0.0001

Configuration

- Data directory: DATASET/train/train
- Model: efficientnet_v2_s
- Folds: 5
- Epochs per fold: 20
- Batch size: 16
- Image size: 224
- Learning rate: 0.0003
- Augmentation preset: strong
- Sampler: weighted
- 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	0.050218	0.9751	0.9739	0.9753	0.9746	0.9826	0.9741	0.9784
2	0.039860	0.9850	0.9854	0.9838	0.9846	0.9829	0.9914	0.9871
3	0.036972	0.9950	0.9941	0.9957	0.9949	1.0000	0.9914	0.9957

4	0.042479	0.9698	0.9727	0.9659	0.9689	0.9580	0.9913	0.9744
5	0.016071	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000

Summary (Mean ± Std)

Metric	Mean	Std
loss	0.037120	0.011409
accuracy	0.984995	0.011420
precision	0.985230	0.010792
recall	0.984134	0.012619
f1	0.984580	0.011752
pos_precision	0.984700	0.015424
pos_recall	0.989640	0.008444
pos_f1	0.987102	0.009784

Notes

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