

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: densenet121
- 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	0.109749	0.9801	0.9775	0.9828	0.9797	1.0000	0.9655	0.9825
2	0.063302	0.9900	0.9884	0.9914	0.9898	1.0000	0.9828	0.9913
3	0.118588	0.9650	0.9615	0.9698	0.9644	1.0000	0.9397	0.9689

4	0.070078	0.9849	0.9828	0.9870	0.9846	1.0000	0.9739	0.9868
5	0.052097	0.9899	0.9884	0.9913	0.9897	1.0000	0.9826	0.9912

Summary (Mean ± Std)

Metric	Mean	Std
loss	0.082763	0.026426
accuracy	0.981995	0.009256
precision	0.979714	0.009943
recall	0.984445	0.007974
f1	0.981660	0.009378
pos_precision	1.000000	0.000000
pos_recall	0.968891	0.015949
pos_f1	0.984132	0.008294

Notes

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