

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 \pm 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.