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: convnext_tiny
- 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	0.043276	0.9751	0.9739	0.9753	0.9746	0.9826	0.9741	0.9784
2	0.040556	0.9950	0.9941	0.9957	0.9949	1.0000	0.9914	0.9957
3	0.068797	0.9800	0.9773	0.9828	0.9796	1.0000	0.9655	0.9825

4	0.042428	0.9849	0.9828	0.9870	0.9846	1.0000	0.9739	0.9868
5	0.040624	0.9799	0.9794	0.9794	0.9794	0.9826	0.9826	0.9826

Summary (Mean ± Std)

Metric	Mean	Std
loss	0.047136	0.010881
accuracy	0.982990	0.006758
precision	0.981482	0.006948
recall	0.984022	0.006982
f1	0.982611	0.006910
pos_precision	0.993043	0.008520
pos_recall	0.977511	0.008792
pos_f1	0.985175	0.005886

Notes

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