Two-Stage Learning Approach for Glioblastoma Cell Segmentation

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Introduction & Motivation

Context

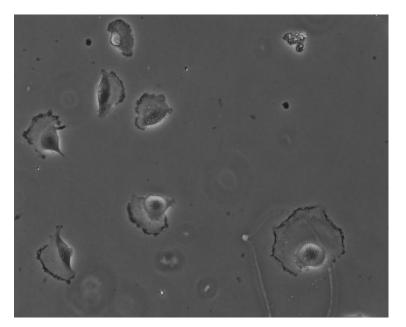
- Glioblastoma is one of the most aggressive brain tumors
- Understanding cell behavior is crucial for treatment and research

• Importance of Segmentation

- Helps track cell division, shape changes, and motion
- Enables analysis of tumor growth and drug response

Challenges

- Images often suffer from low contrast and noise
- Manual labeling is expensive and time-consuming
- Need for automatic and reliable segmentation methods



Glioblastoma-astrocytoma U373 cells image example

Problem Definition & Hypothesis

Annotation Problem

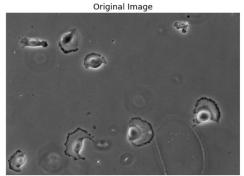
- Gold Truth (GT): highly accurate, but limited and costly
- Silver Truth (ST): abundant, automatically generated, but noisy

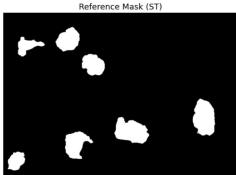
• Core Question

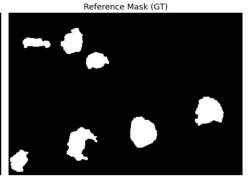
How to train a robust model using many noisy (ST) and few accurate (GT) masks?

Hypothesis

- Two-stage learning can first teach general structure with ST
- Then correct errors and refine with GT for high accuracy
- Reduces dependency on expert labels while maintaining performance







ST Mask vs GT Mask

Literature Review

Model Foundations

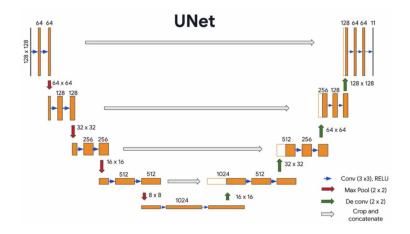
- U-Net: widely used in medical imaging; encoder-decoder with skip connections
- nnU-Net: adaptive configuration for any medical dataset

Labeling Strategies

- Semi-supervised learning: combines labeled and unlabeled data
- Multi-stage pipelines: pretraining and refinement stages

Identified Gap

• Limited studies on using both ST and GT in a structured two-phase pipeline for glioblastoma segmentation



U-Net Architecture Example

Dataset & Preprocessing

Dataset: PhC-C2DH-U373

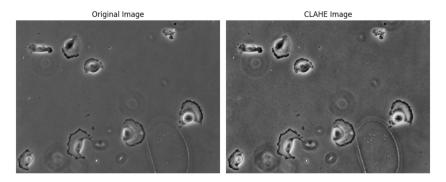
- 230 grayscale phase-contrast microscopy images
- ST masks: auto-generated for all frames
- GT masks: manually annotated, limited subset

Preprocessing Techniques

- CLAHE for contrast enhancement.
- Data augmentations: flip, rotate, elastic transformation
- Padding for U-Net input size constraints

Data Management

 Custom data loader (CTCDataManager) organizes image-mask pairs



Original image vs CLAHE applied image

Two-Stage Learning Pipeline

Stage 1: Pre-Training

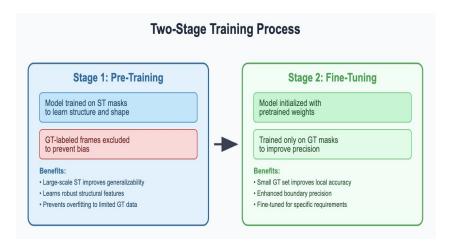
- Model trained on ST masks to learn structure and shape
- GT-labeled frames excluded to prevent bias

Stage 2: Fine-Tuning

- Model initialized with pretrained weights
- Trained only on GT masks to improve precision

Benefits

- Large-scale ST improves generalizability
- Small GT set improves local accuracy and boundary precision



Two-Stage Training Process Flowchart

Model Architecture

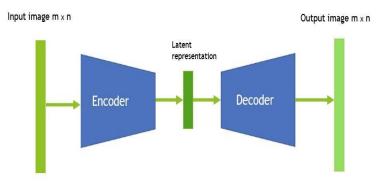
Architecture Overview

- Framework: MONAI (Medical Open Network for AI)
- **Purpose:** Segmentation of Glioblastoma (U373) Cells from PCM Images
- Input: CLAHE-enhanced Grayscale PCM Images
- **Output:** Binary Mask of Cells (Probability Map)

Encoder	Bottleneck	Decoder	
4 Levels: 64→128→256→512	1024 Channels	4 Levels: 512→256→128→64	
Strides (2,2,2,2)	Feature extraction	Restores spatial details	

Why U-Net & MONAI?

- High performance on biomedical segmentation
- Efficiently learns from small datasets
- Skip connections preserve spatial resolution
- MONAI's optimized medical imaging modules



Basic U-Net Diagram

Evaluation Metrics

Quantitative Metric

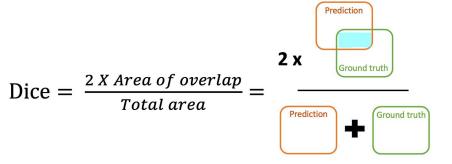
- Dice Coefficient
 - Measures overlap between prediction and ground truth

Qualitative Evaluation

- Visual inspection by overlaying masks on raw images
- Helps interpret false positives, under-segmentation, boundary issues

Why Dice?

More informative than accuracy for imbalanced data (small object regions)



Experimental Setup

Environment

Google Colab Pro with CUDA-enabled GPU

Training Details

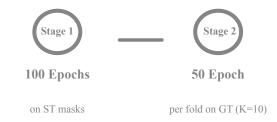
- Stage 1: 100 epochs on ST masks
- Stage 2: 50 epochs per fold on GT (K = 10)

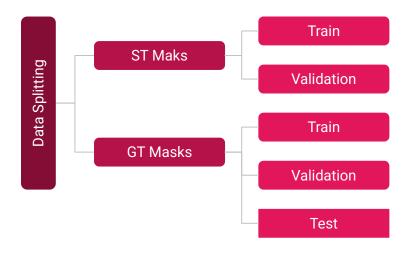
Data Splitting

- ST-only images for pretraining
- GT-only images for fine-tuning and testing
- GT set split into train/val/test with no overlap

Hyperparameters

- ST: LR = 1e-4, threshold = 0.6
- GT: LR = 1e-5, threshold = 0.8





Model Comparisons & K-Fold Validation

Tested Variants

- MONAI U-Net vs Pure U-Net
- With/without augmentation
- CLAHE on/off
- Loss functions: BCEDiceLoss vs BCEWithLogitsLoss

Best Setup

• MONAI U-Net + CLAHE + augmentation + BCEDiceLoss

K-Fold Results (GT)

- K=10 performed mean Dice of 0.9492 ± 0.0321
- Consistent generalization across folds

Mode	Loss Function	Augmentati on	Preprocessi ng	Val Score (Pre)	Val Score (Fine)	Threshold
MONAI U-Net (K-Fold)	BCEDiceL oss (0.3)	Yes	CLAHE	0.9685	0.9469	0.60 (Pre) 0.8 (Fine)
MONAI U-Net	BCEDiceL oss (0.3)	Yes	CLAHE	0.9770	0.9273	0.7
MONAI U-Net	BCEDiceL oss (0.3)	No	CLAHE	0.9631	0.9172	0.7
MONAI U-Net	BCEDiceL oss (0.3)	No	No	0.9689	0.9207	0.7
Pure U-Net	BCEDiceL oss (0.3)	No	No	0.9798	0.9375	0.5
Pure U-Net	BCEWithL ogitsLoss	Yes	No	0.9290	0.8947	0.5

Ensemble Learning & Results

Why Ensemble?

- Models from K-folds have slightly different strengths
- Reduces overfitting from individual folds

Ensemble Method

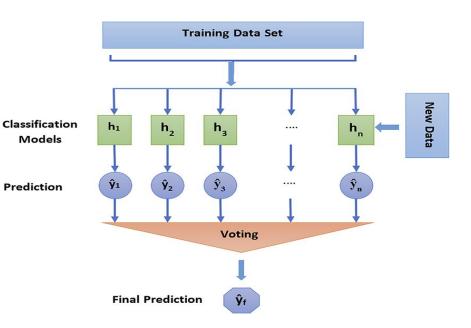
Pixel labeled as "cell" if at least eight of ten models agreed.

Quantitative Results

- Pre-trained (ST only): 0.9030 ± 0.0980
- Only-GT (single stage on GT masks): 0.8317 ± 0.1204
- Mixed (single stage on ST + GT masks): 0.9063 ± 0.1081
- Fine-tuned (GT): 0.9128 ± 0.0951
- Ensemble of 10 folds (majority vote): 0.9202 ± 0.0792

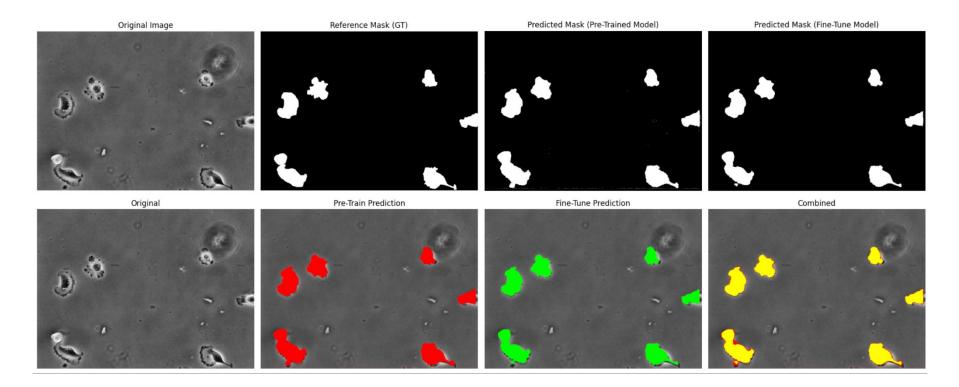
Significance

• Wilcoxon test: p = 0.015625 (improvement is statistically significant)

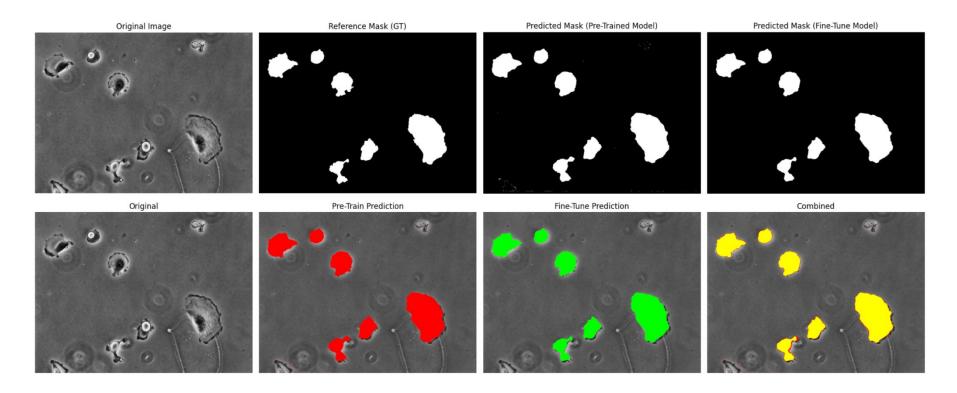


Majority Voting Example

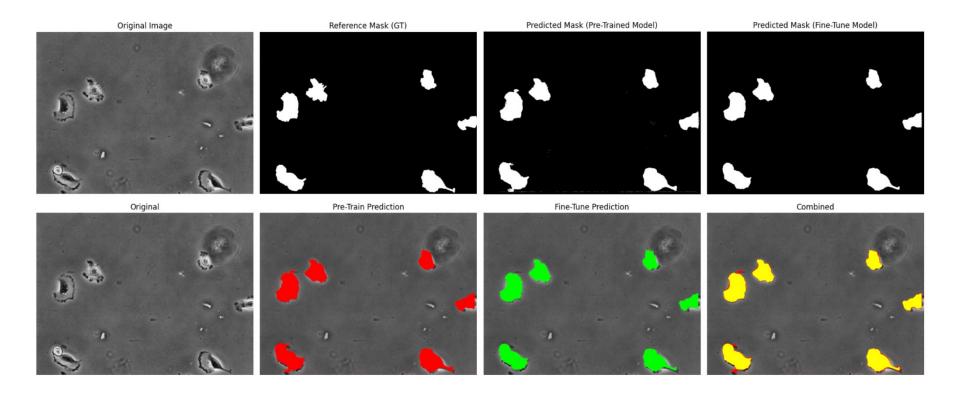
Results



Results



Results



Discussion & Conclusion & Future Work

Summary

- Two-stage training approach is effective and efficient
- Combines strengths of both ST (quantity) and GT (quality)
- Ensemble learning increases stability and accuracy

Final Dice Score

0.9202 on test set with GT masks

Future Directions

- Adaptive ensembling strategies such as weighted voting or stacking based on pre-model confidence could push the ensemble's performance beyond simple majority voting
- Larger and more diverse datasets
- Post-processing (morphological ops, watershed) to refine masks