Automated Cell Segmentation for Oligodendroglioma

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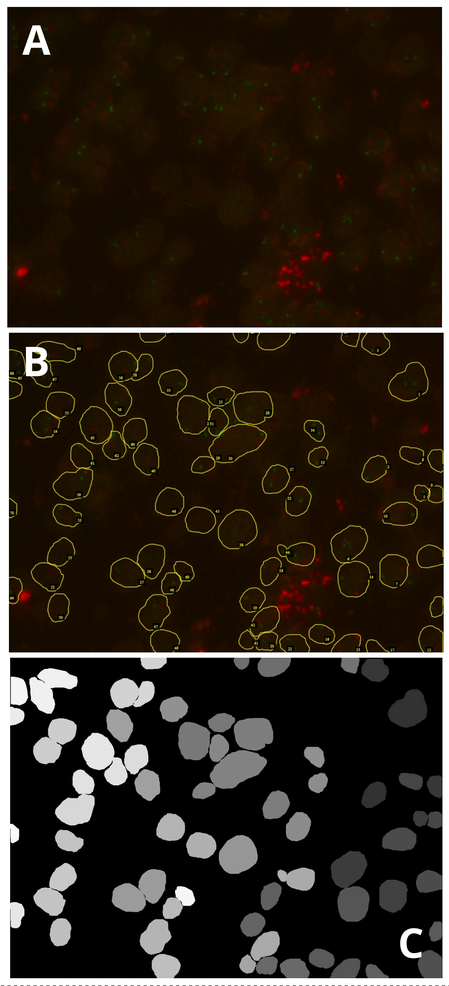
INTRODUCTION

Accurate and timely diagnosis of brain tumors such as oligodendroglioma is critical for guiding treatment decisions and improving patient outcomes. In clinical practice, this diagnosis often relies on fluorescence in situ hybridization (FISH) imaging, where nuclear features are manually analyzed by experts. Traditional approaches such as DAPI nuclear staining and manual cell counting are labor-intensive, prone to inter-observer variability, and require chemical reagents that increase both cost and occupational exposure. To address these limitations, we explore a deep learning–based approach for automated nucleus segmentation and cell quantification in FISH images. By fine-tuning a high-performance segmentation model on a limited dataset of annotated clinical images, we aim to reduce the reliance on manual processing while maintaining diagnostic precision. This strategy enhances both the efficiency and safety of molecular diagnostics in neuropathology.

METHODS & DATASET



This study employed a curated dataset of 25 fluorescence in situ hybridization (FISH) images provided by the University Hospital of Burgos (HUBU), all derived from diffuse glioma cases tested for oligodendroglioma diagnosis by FISH for 1p/19q co-deletion. These high-resolution images, characterized by highly concentrated and frequently overlapping nuclei, were selected to reflect the complexity encountered in real clinical scenarios.

To prepare the data for model training and evaluation, each image (denoted as Image A) was manually annotated (Image B) using the VGG Image Annotator (VIA), an open-source tool that allows precise polygonal segmentation. The annotations were performed by trained personnel, who carefully outlined individual nuclei to ensure morphological accuracy.

A custom Python script was developed to convert the annotation files (in JSON format) into binary segmentation masks (Image C), which served as the ground truth labels. These masks provided the necessary supervision for the fine-tuning process.

No data augmentation techniques were applied, as maintaining the morphological fidelity of the original samples was prioritized. All annotations underwent consistency checks to minimize observer bias and enhance label reliability.

This dataset, though limited in size, proved sufficient for adapting the base model to the specific visual patterns found in FISH images related to oligodendroglioma.

Dataset Split	Number of Images	Percentage
Training	18	72%
Validation	3	12%
Testing	4	16%

Dataset Distribution for Model

MODEL & PLATFORM INTEGRATION

Model Architecture

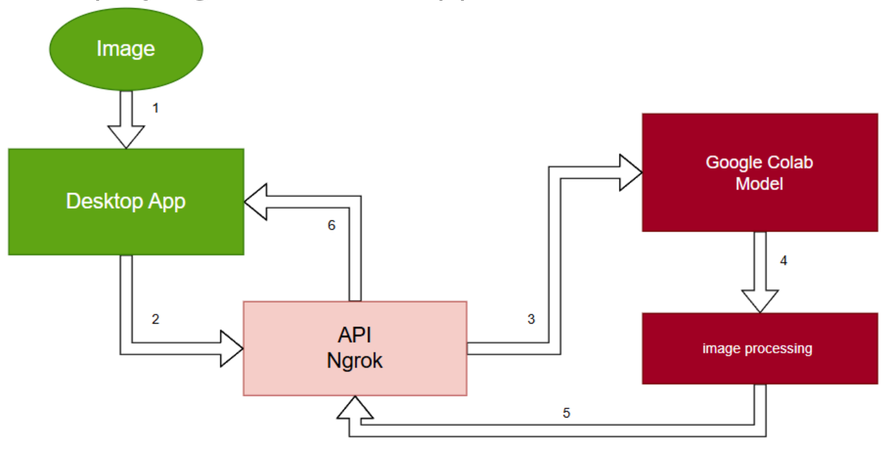
We employed the MEDIAR architecture a transformer-based deep learning model originally designed for medical image segmentation and pre-trained on a large dataset of over 70,000 images as the foundation of our system. The model was fine-tuned using our domain-specific dataset to enhance its accuracy in segmenting nuclei in FISH images, adapting it to the unique characteristics of this imaging modality. Fine-tuning and training were conducted using Google Colab's GPU resources, which allowed quick and efficient processing.

Platform Integration and Clinical App

For practical application, the fine-tuned model was integrated into a lightweight, user-friendly desktop application developed with Python and PyTorch. This platform enables clinicians to upload microscopy images and obtain immediate segmentation results and cell counts, without the need for DAPI staining or manual intervention. Designed to support diagnostic workflows, the tool offers a fast, reproducible, and interpretable alternative to traditional segmentation methods.

Workflow Overview

The user uploads an image to the app, which sends it via API to the model hosted on Google Colab. The model processes the image and returns the results through the API, displaying them in the app for the user.



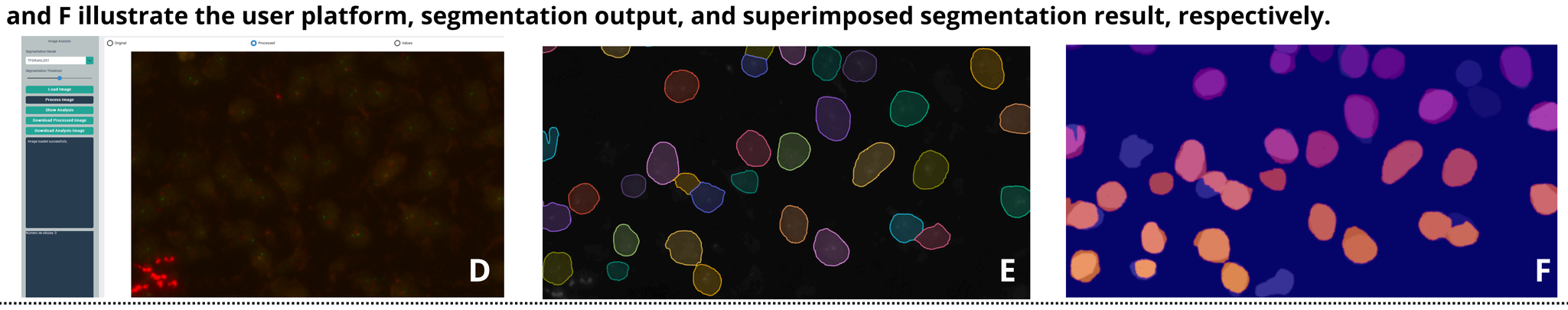
RESULTS & CONCLUSION

Image ID	Precision	Accuracy	BCE Loss
cell_00007	0.4531	88.54%	1.8921
cell_00008	0.4570	90.20%	0.8355
cell_00007	0.4234	94.01%	0.7627

Segmentation Performance Summary

The developed segmentation model successfully identified and outlined individual nuclei in FISH images, even in challenging conditions of high cellular density and overlapping regions. Fine-tuned on a limited, manually annotated dataset, the model demonstrated strong performance in detecting and separating adjacent cells. Although it slightly underestimated cell size, it reliably detected the correct number of nuclei, indicating robustness for cell counting and cell segmentation without DAPI analysis or manual intervention. Integrated into a user-friendly desktop application, the system enables clinicians to obtain real-time segmentation. The application developed is a first step that could be easily incorporated in routine oligodendroglioma FISH slides in both digital pathology scanned or microscopy images without requirements of DAPI evaluation, offering an accessible and fast alternative to traditional diagnostic methods.

Figures D, E, and F illustrate the user platform, segmentation output, and superimposed segmentation result, respectively.



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Github repository

Video of the Demo App

Walid 's Agency