Mitochondria Segmentation in EM Images using U-Net

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Github link

Introduction

Accurate segmentation of mitochondria from electron microscopy (EM) images is essential for understanding cellular structures and diagnosing diseases related to mitochondrial dysfunction. In this project, I implemented a U-Net-based deep learning model to perform binary segmentation of mitochondria on a publicly available EM dataset. The dataset comprises high-resolution grayscale images and corresponding manually annotated masks. To handle large image sizes and improve model generalization, I applied patch-wise training and extensive image augmentation techniques. The model is trained using the binary cross-entropy loss function and evaluated using pixel-wise accuracy, Dice coefficient, and Intersection over Union (IoU). The best model achieved a Dice score of **0.8563** and an IoU score of **0.7487**, demonstrating its effectiveness in segmenting complex biological structures. This work showcases the utility of deep learning in biomedical image analysis and serves as a foundation for future improvements using advanced architectures or domain-specific enhancements.

Problem Statement

Mitochondria play a critical role in various cellular processes, including energy production, apoptosis, and metabolic regulation. Abnormalities in mitochondrial structure or quantity are linked to numerous diseases such as cancer, neurodegenerative disorders, and metabolic syndromes. Accurate identification and segmentation of mitochondria in electron microscopy (EM) images are therefore essential for biomedical research and clinical diagnostics.

To address this, I aim to develop an automated deep learning-based segmentation model that can learn to accurately segment mitochondria from raw EM images. The goal is to leverage the U-Net architecture—widely adopted in medical image segmentation—combined with robust preprocessing and augmentation strategies, to achieve high segmentation accuracy while being computationally efficient and generalizable across EM samples.

Dataset used

The dataset used in this project is an **Electron Microscopy (EM) dataset for mitochondria segmentation**, sourced from Kaggle. It consists of grayscale EM images capturing cellular structures, with corresponding pixel-wise binary masks labeling mitochondria regions.

Preprocessing Steps

- **Patch Extraction**: Large images were divided into non-overlapping **256×256** patches using the *patchify* library, increasing the dataset size and making training feasible on a local machine.

- **Normalization**: All images were scaled to the range `[0, 1]` to stabilize model training.
- **Mask Binarization**: Masks were ensured to be strictly binary using thresholding functions.

Data Augmentation

To address class imbalance and boost model generalization, aggressive data augmentation was applied, including:

Rotation (up to 90°)

Horizontal/vertical flipping

Zooming

Shifting

Shearing

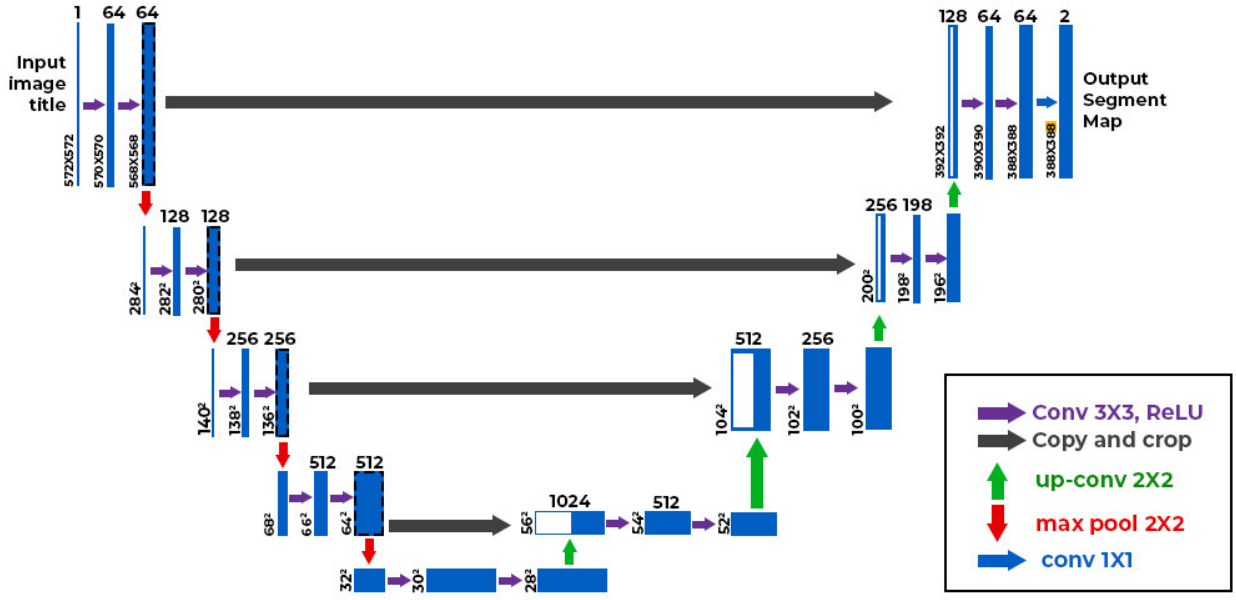
Augmentation was performed using Keras' *ImageDataGenerator* for both images and masks with synchronized seeds to maintain alignment.

Model Architecture

To perform binary segmentation of mitochondria from electron microscopy (EM) images, we implemented a **U-Net** architecture — a convolutional neural network designed specifically for biomedical image segmentation. U-Net's encoder-decoder structure with skip connections allows it to capture both contextual and fine-grained spatial information, making it ideal for segmenting mitochondria, which often exhibit subtle texture differences from the background.

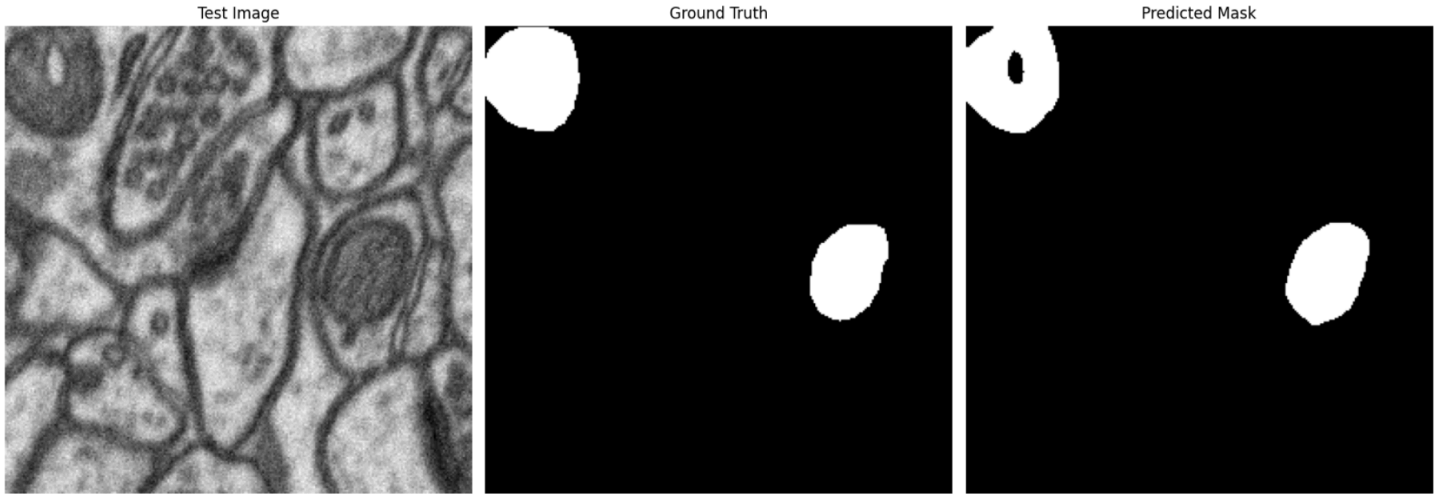
Input: 256×256 grayscale image patches

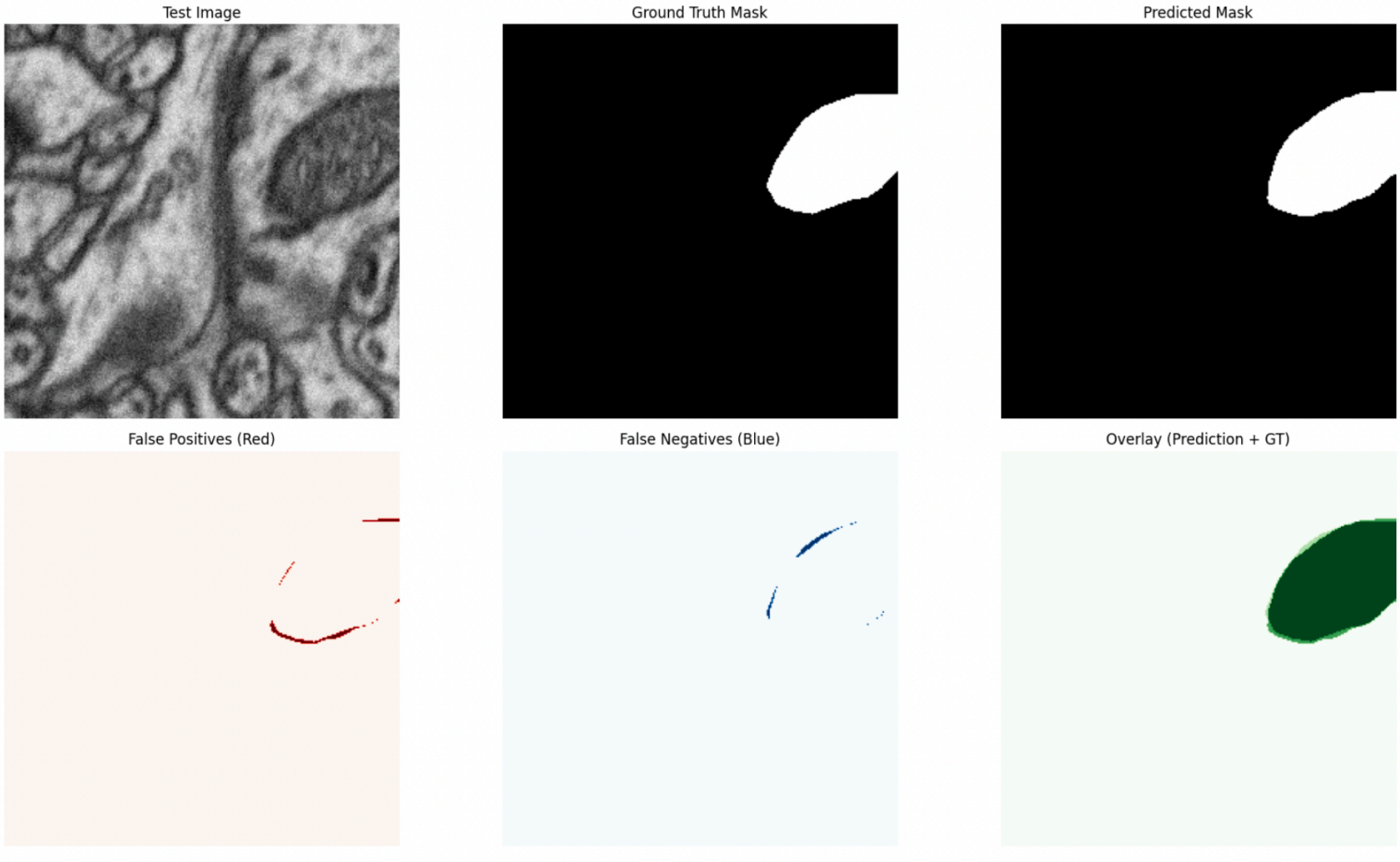
Output: 256×256 binary mask (1 for mitochondria, 0 for background)



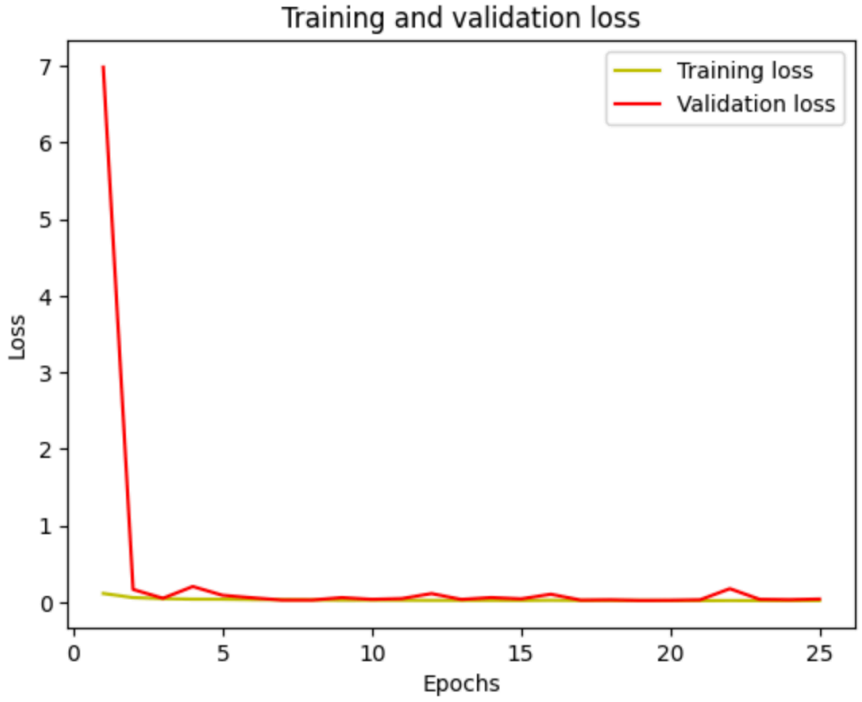
Results

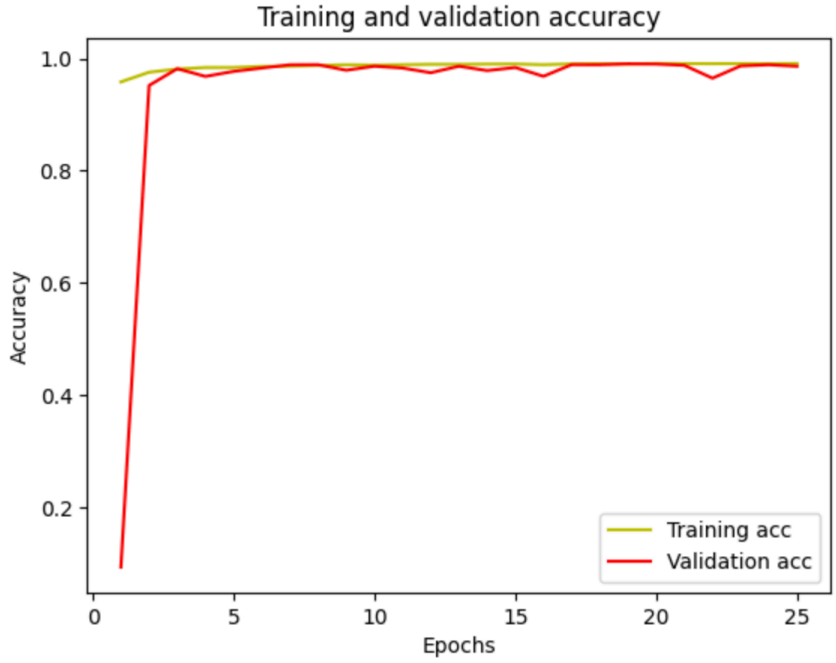
Metric	Value
Pixel-wise Accuracy	98.61%
Dice Coefficient	0.8563
IoU Score	0.7487





Change	Why It Was Made	Effect
Patchify images to 256×256	To handle large images and fit into memory	Allowed efficient training on MacBook
Normalization	To scale pixel values between [0, 1]	Stabilized and sped up training
Aggressive augmentation	Prevent overfitting on small dataset	Boosted generalization accuracy
Dice/IoU Evaluation	Better reflect segmentation performance	Provided realistic evaluation of region overlap





Conclusion

The training and validation curves showed stable convergence without signs of overfitting, confirming that the model generalized well on unseen data. Visualization of the predicted masks along with false positives and negatives validated the spatial accuracy of segmentation.

These results demonstrate that U-Net, even with a relatively shallow architecture and limited training epochs, is highly effective for biomedical image segmentation tasks.