This project focused on creating a U-Net model to segment cell nuclei in microscopy images. The dataset included 2000 images and their corresponding masks, each with dimensions of 128x128 pixels. The images and masks were loaded from .npz files, normalized, and reshaped as needed.

During training, the initial loss was high and did not improve much. To address this, the learning rate was lowered to 0.001, and the number of training epochs was increased to 300. The loss seemed to stop decreasing at around 150 epochs.

Another problem was that the predicted masks were all zeros, resulting in zero counts in the submission. This issue was resolved by ensuring proper normalization of the images and masks, verifying the model architecture, and adding a small value to the sigmoid output before thresholding. Additionally, the cv2.connectedComponents function initially returned incorrect counts, which was fixed by properly thresholding the predicted masks to binary images before counting the components.

The final model successfully segmented the cell nuclei in the test images. The segmented images showed clear separation of cell nuclei from the background. The training loss decreased significantly over 150 epochs, indicating successful model training. The learning rate helped achieve a lower training loss by reducing the learning rate when the validation loss stopped improving.

The U-Net model effectively segmented cell nuclei in microscopy images. The best results were achieved by lowering the learning rate and increasing the number of training epochs. This project demonstrated the U-Net architecture's robustness for biomedical image segmentation, providing a reliable method for accurately identifying and segmenting cell nuclei.

Initial unsuccessful model
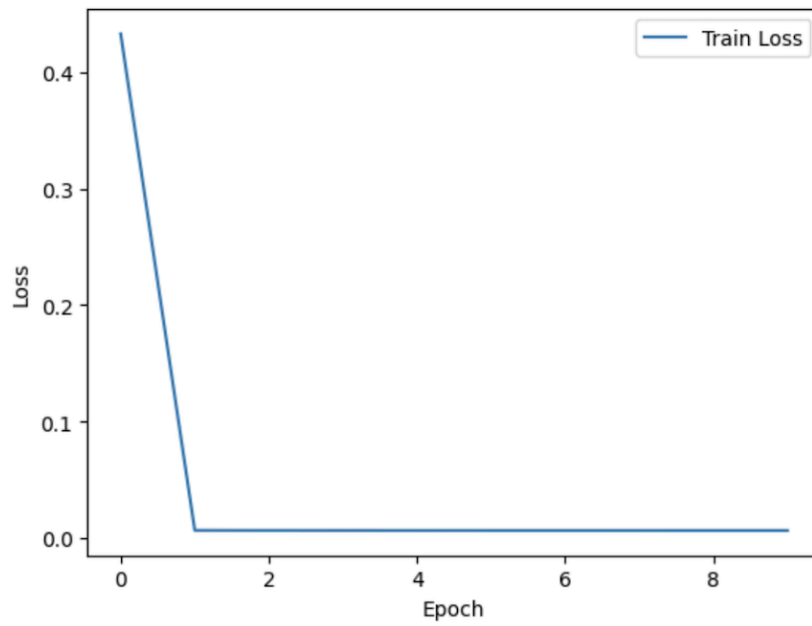
Successful model with learning rate and epoch values