

BROWN

Cell Segmentation Using a CNN-Based Classification Algorithm

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Introduction

Cell segmentation, a technique for defining and distinguishing individual cells' boundaries in biomedical images, has benefited increasingly from DL approaches as opposed to traditional methods.

The paper we chose introduced a CNN-based, state-of-the-art architecture for the cell segmentation problem, which led them to win the ISBI tracking challenge in 2015. Their architecture outperformed the prior best method (a sliding-window convolutional network) on the ISBI challenge dataset using 30 annotated training images. For reference, segmentation of a 512x512 image takes less than one second on a GPU.

Dataset

Pancreatic Stem Cells



- Phase-contrast time-lapse images of human pancreatic stem cells migrating and dividing on a standard polystyrene dish.
- Temporal resolution: 10 min / frame
- Volume: 2 sequences, 300 frames each (572×572 px) — 124 MB

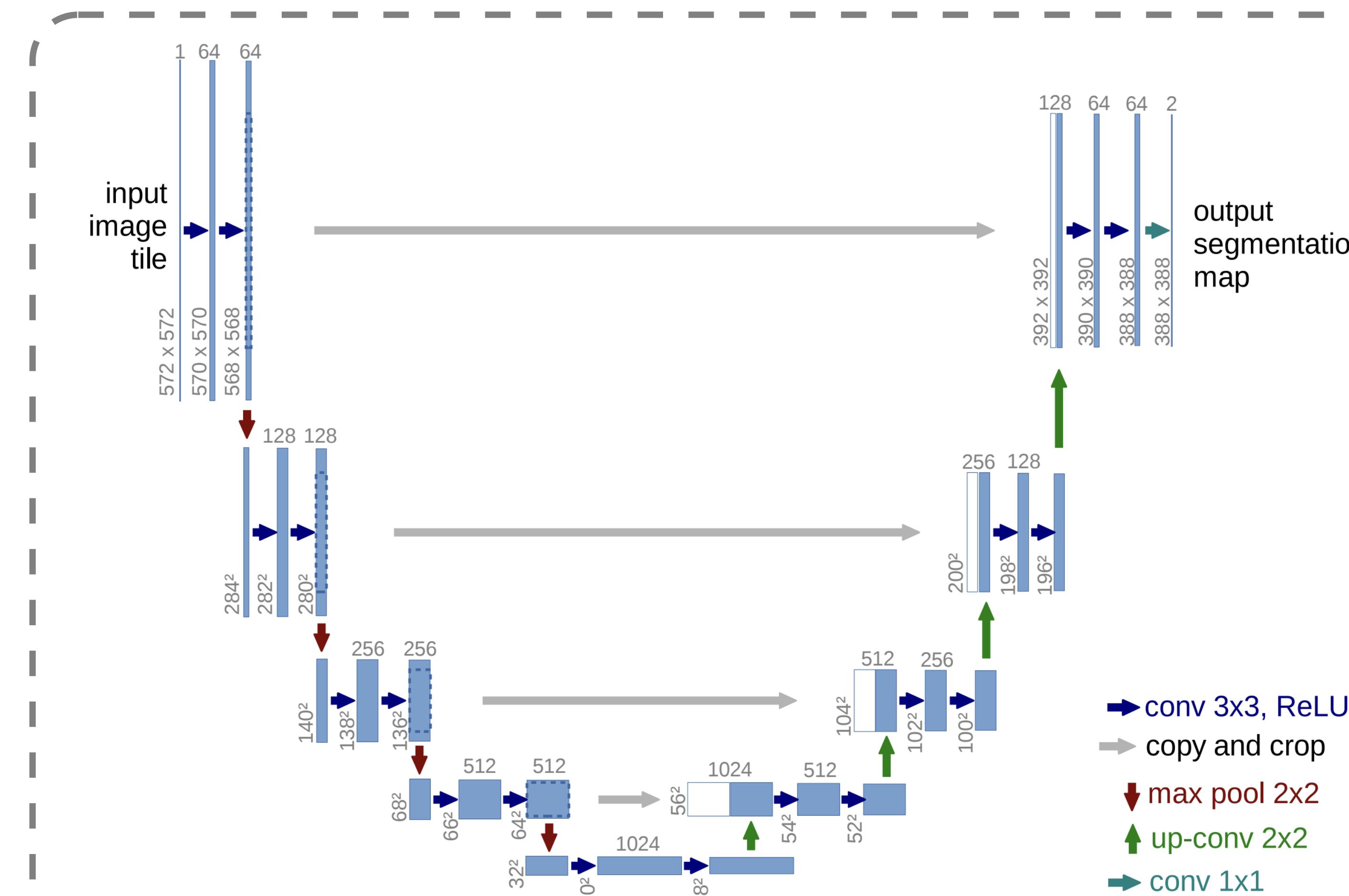
Preprocessing

Pipeline

- Load TIFF pairs with rasterio
- Histogram stretch (2 %–98 %)
 - rescales each image to $[0, 1]$
- Mask binarisation:** mask $> 0 \rightarrow \{0, 1\}$.
- Add channel dim
- On-the-fly augmentations**
 - random $0^\circ/180^\circ$ rotation + flip
 - elastic deformations ($\sigma = 30$ px, $\alpha = 1000$).

Transform	Implementation (per batch)	Hyper-parameters
Random rotation & mirroring	rotate by $k \in \{0, 180^\circ\}$ then random horizontal flip Simard et al. routine: 1. draw iid displacement field $\sim U(-1, 1)$ 2. Gaussian-blur $\sigma = 30$ px 3. scale $\alpha = 1000$ 4. warp raw & mask with bicubic / nearest-neighbour interpolation	—
Elastic deformation		$\alpha = 1000$, $\sigma = 30$, grid-free

Architecture



U-net architecture (example for 32×32 pixels in the lowest resolution). Each blue box corresponds to a multi-channel feature map. The number of channels is denoted on top of the box. The x-y-size is provided at the lower left edge of the box. White boxes represent copied feature maps. The arrows denote the different operations.

- Architecture:** replicated the original U-Net layer-by-layer (5 down/5 up, skip connections, "valid" convolutions)
 - Contracting path (encoder)
 - Bottleneck: deepest block with highest feature depth.
 - Expansive path (decoder)
- Framework:** rewrote the network from scratch in TensorFlow/Keras instead of the paper's Caffe/CUDA code.

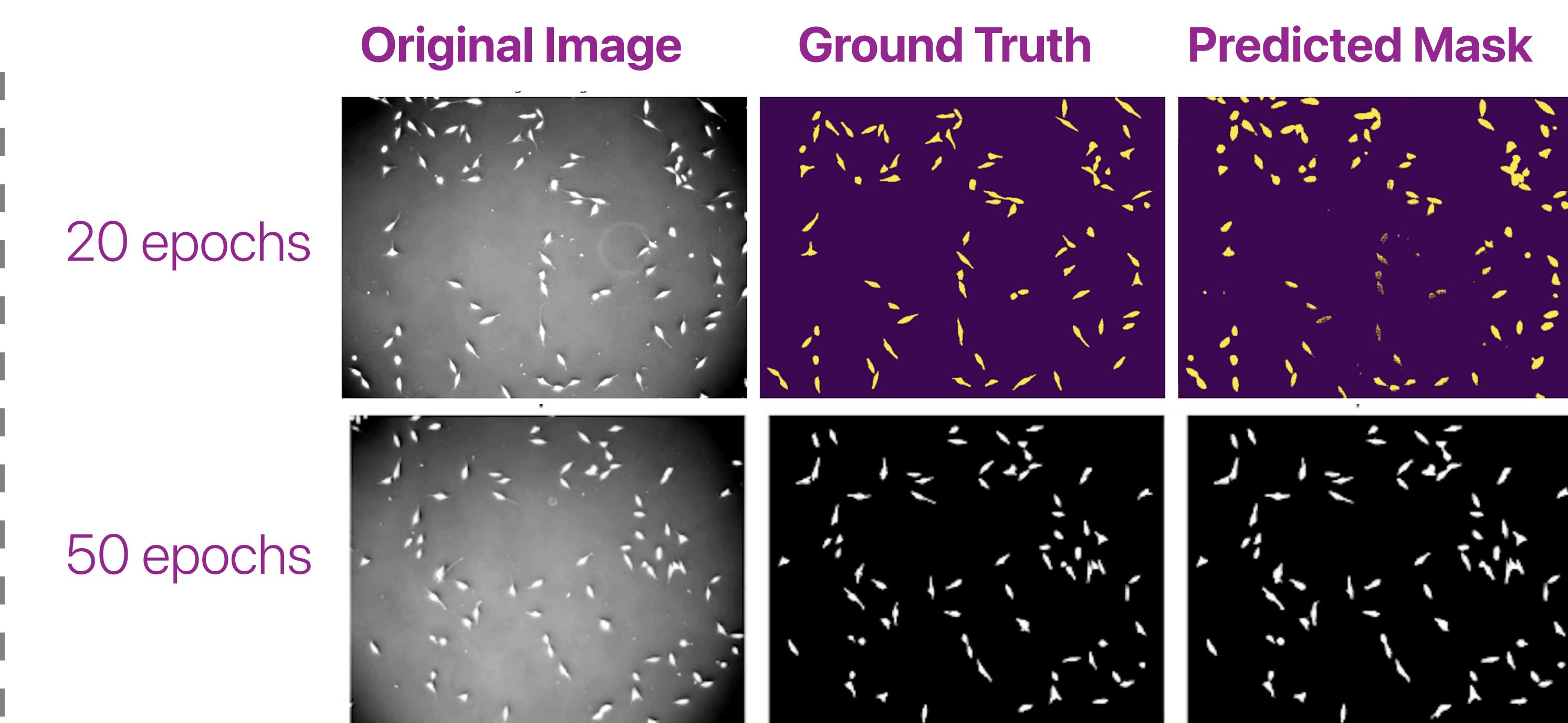
Challenges

The extreme class-imbalance ($\approx 93\%$ background) let the model exploit it—early runs reported 93 % binary accuracy simply by labelling every pixel as background, missing all nuclei.

Replaced weighted crossentropy with weighted BCE + Tversky loss to heavily penalise missed foreground.

- Outcome: binary accuracy rose to 97 % and predicted masks delineated nuclei correctly.
- Lack of details in the original paper: no information regarding kernel sizes, strides, activation functions, or epoch count.

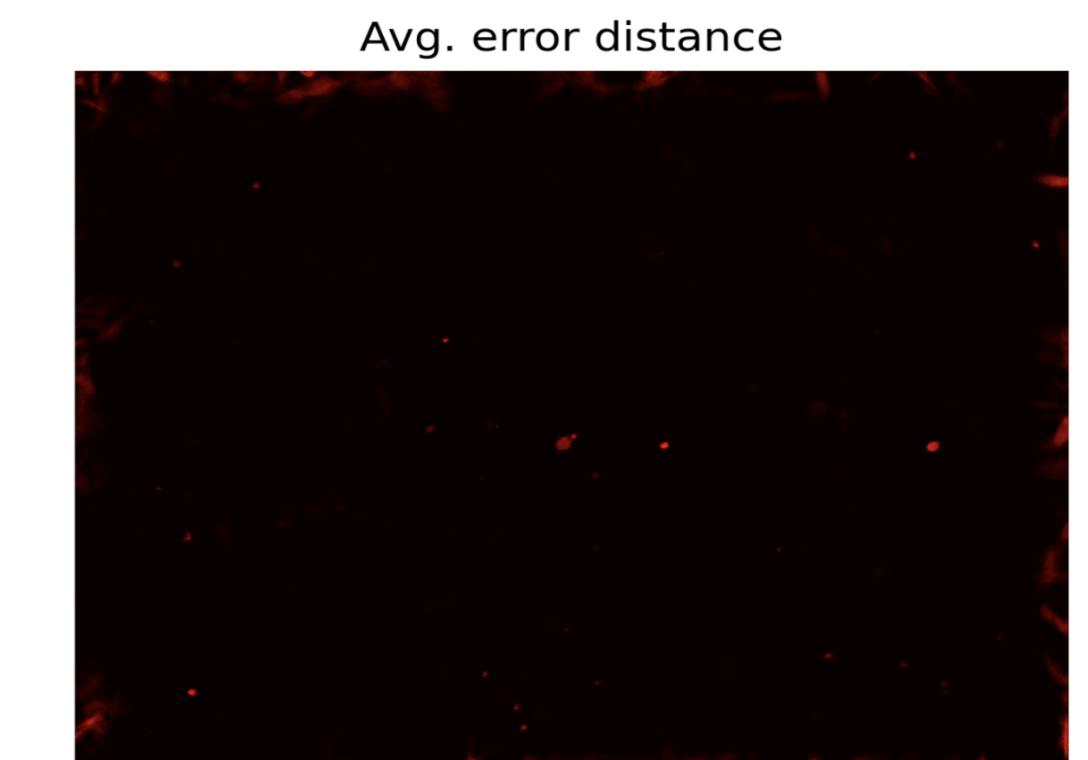
Results



20 epochs

50 epochs

- Validation Dice reaches $\approx 98\%$ after ~ 50 epochs. As opposed to $\approx 97\%$ at 20 epochs.
- Performance exceeds our target ($\geq 98\%$) while keeping training time modest.



Average Error Distance map shows where mistakes typically occur and how many pixels they stray from the true cell edge—small spots represent fuzzy boundaries and larger represent real split/merge errors.

Conclusion & Future Directions

Implemented a from-scratch U-Net that reaches 98.65% accuracy on two challenging, highly imbalanced cell datasets.

Unlike the paper's weighted crossentropy, BCE + Tversky loss was critical to overcome all-background predictions.

Boost performance by tuning hyperparameters and loss weights to push validation accuracy past 98.65%.

Implement time-lapse tracking using cell displacement and velocity paths.

- Fine-tune the trained U-Net on additional imaging modalities.

Sources

- Ronneberger, Olaf, et al. "U-Net: Convolutional Networks for Biomedical Image Segmentation." Medical Image Computing and Computer-Assisted Intervention – MICCAI 2015, Springer International Publishing, 2015, pp. 234–41. Crossref,