Semantic Segmentation of WM989 Cells with U-NET

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Introduction

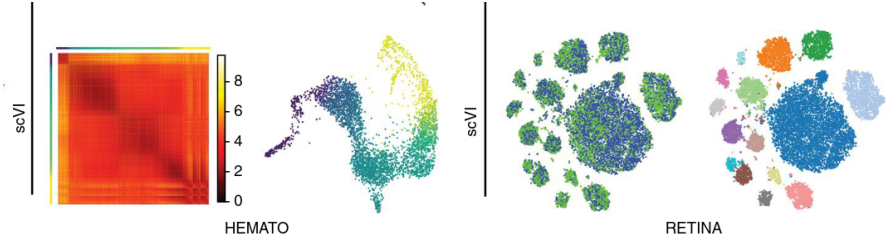


Figure 1: U2OS nuclei from BBBC039 dataset

Segmentation problem

Single-cell RNA expression has sample, batch, and real biological variability. Need a lot of data

Motivation: Automating segmentation, simple thresholding/watershed do not work well over large FOV and make imprecise estimates of cell boundaries

But... probably need a new model for every sample type. Worth the effort if we can achieve low validation loss with few training samples (few-shot learning)

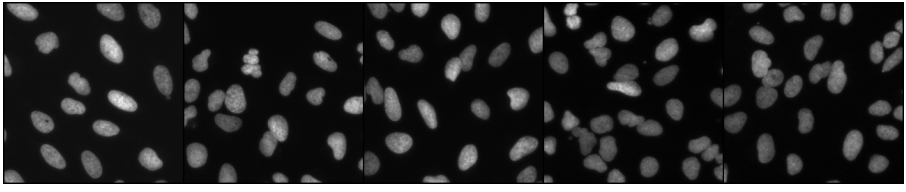
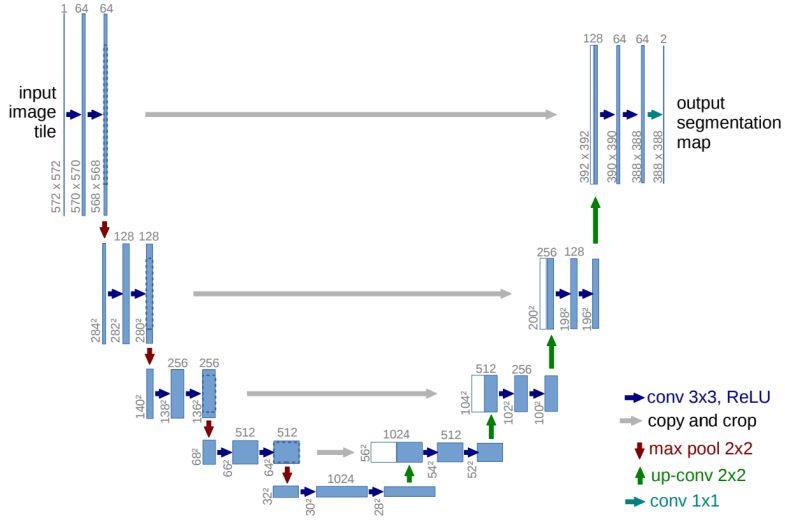


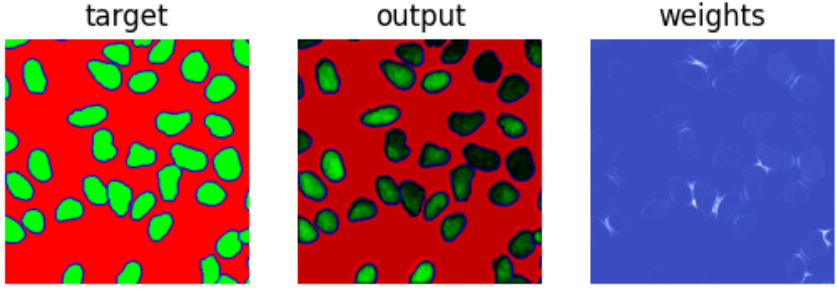
Figure 2: U2OS nuclei from BBBC039 dataset

U-NET Architecture



Training on BBBC039 U2OS Cells

BBBC039: 200 images, 160 train + 40 validation, 256 x 256 random crop

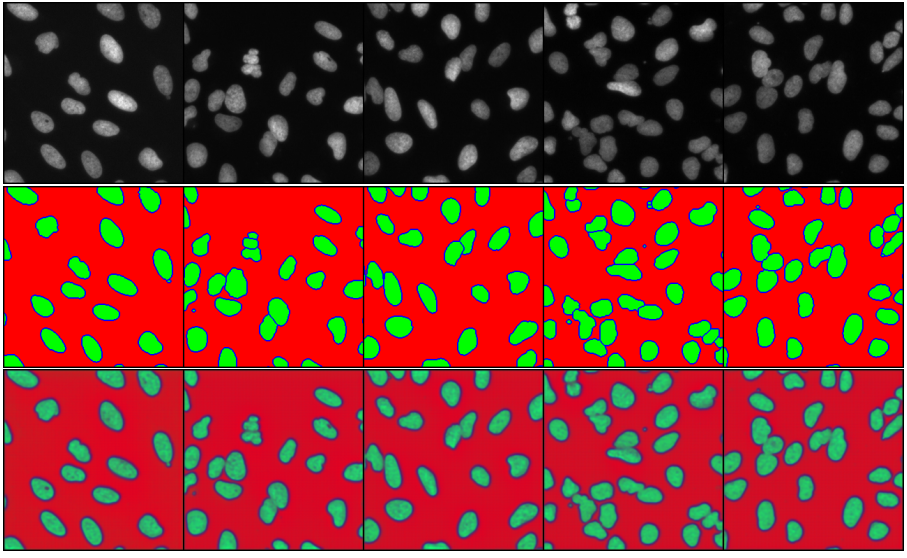


We train a 3-channel semantic segmentation model with **weighted** cross-entropy loss:

$$\mathcal{L} = \sum_{i,j} w_{ij} \log p_{ij}(\tilde{x}) = \sum_{i,j} w_{ij} \log \frac{\exp(-s_{ij}(\tilde{x}))}{\sum_{x \in \chi} \exp(-s_{ij}(\tilde{x}))}$$

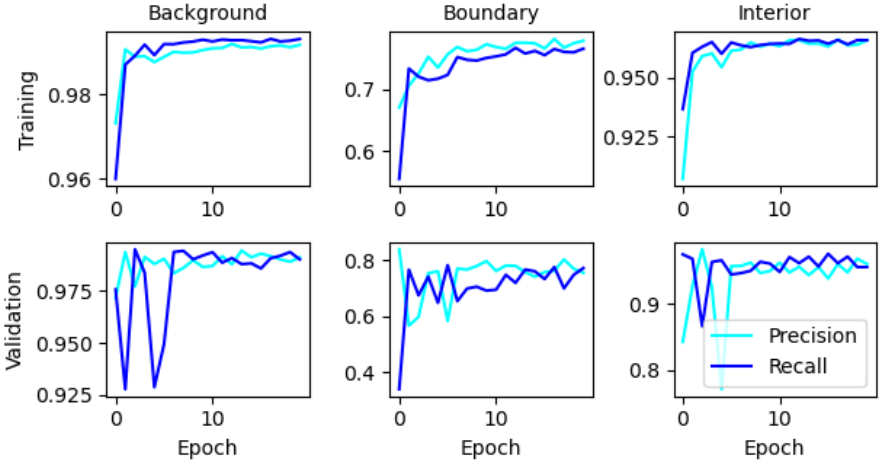
p_{ij} is the probability the model assigns a pixel to the true class $\tilde{x} \in \{\mathrm{a}, \mathrm{b}, \mathrm{c}\}$

Training on BBBC039 U2OS Cells



Training on BBBC039 U2OS Cells

Learning rate $\eta = 0.01$, Batch-size $B = 5$ (32 train iterations, 8 validation)



Boundary-only model