

Semi-automated mRNA counting in single cells

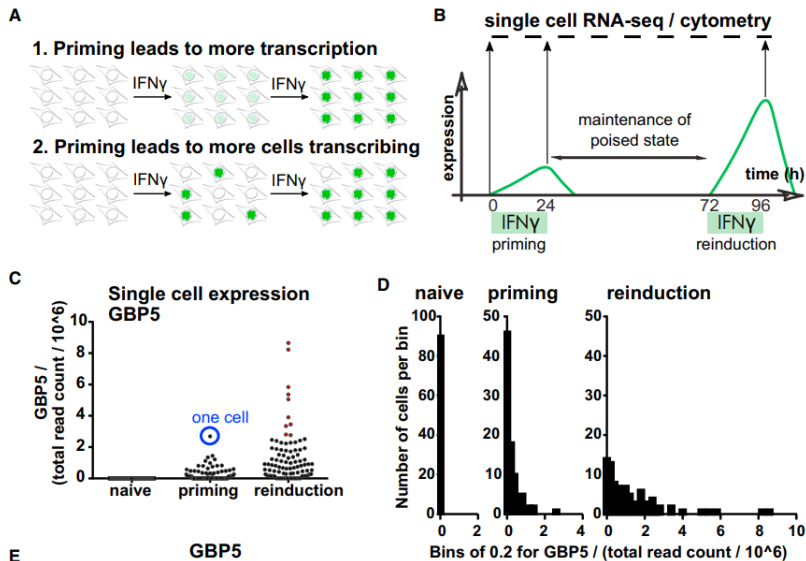
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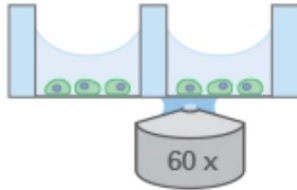
Summary

- ▶ 10× 10 grid acquisition of DAPI, GAPDH, GBP5 in Hela cells on #1.5 chambered coverglass
- ▶ Cell segmentation using UNET implementation in PyTorch
- ▶ Spot detection using LoG filter
- ▶ Spot calling using Fisher information filter
- ▶ Kinetic models.. (TBD)

Single-cell RNA-seq identifies GBP5 as a memorized gene

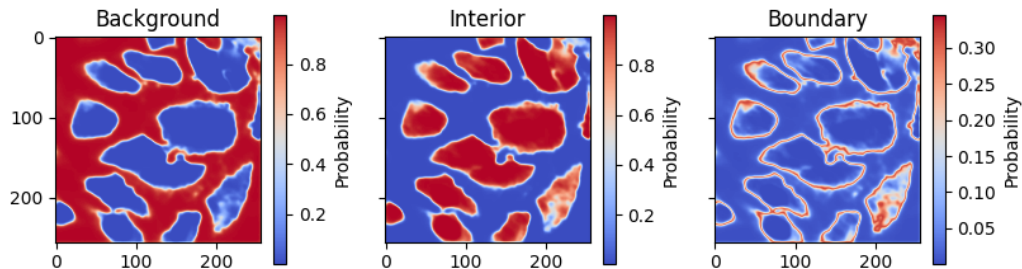


Imaging approach



Training a semantic segmentation with cross-entropy loss (log loss)

100 256 x 256 images, 80 train + 20 validation,



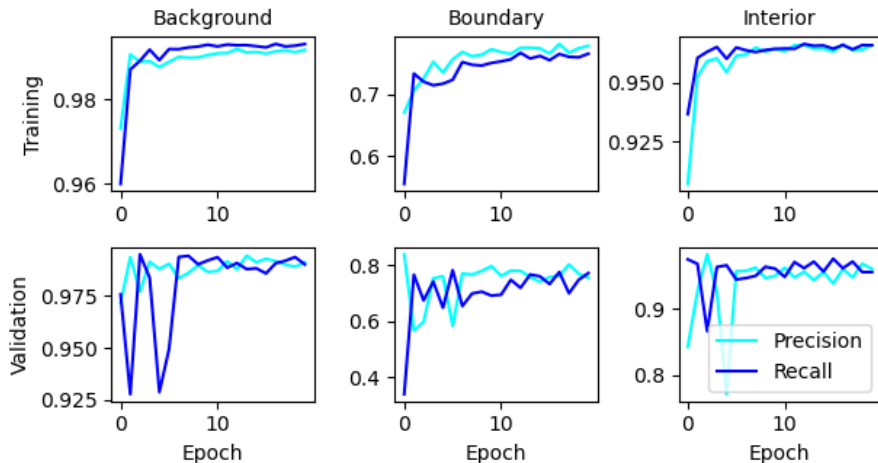
We train a 3-class semantic segmentation model with cross-entropy loss:

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

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

Training on HeLa GAPDH channel

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



Spot calling using Fisher information filter

Results

