

# Automated Object Tracing for Biomedical Image Segmentation Using a Deep Convolutional Neural Network

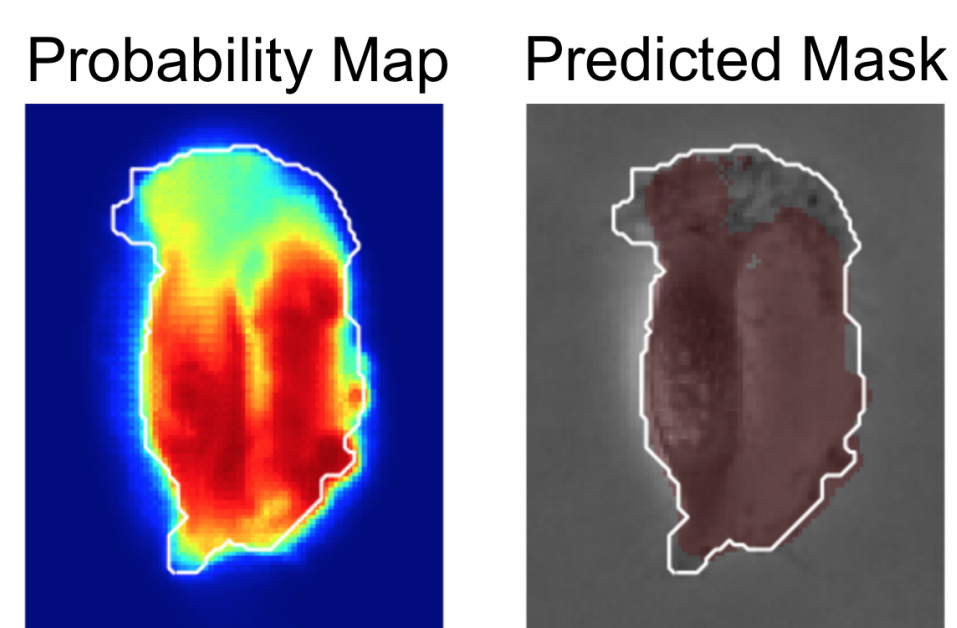
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## Introduction and Background



- Current segmentation techniques (U-Net, etc) may result in patchy and non-contiguous regions.
- Non-contiguous regions may artificially inflate cell counts.

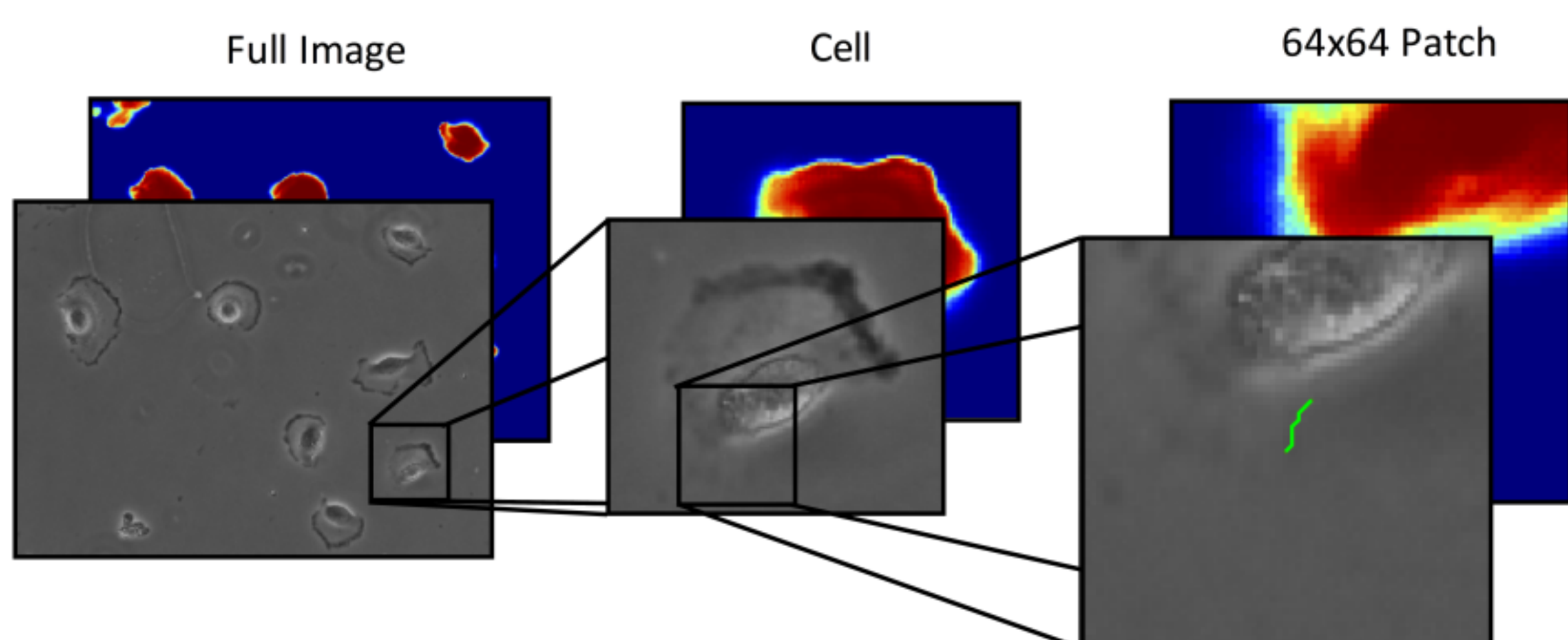
### Research Questions

- Can we ensure contiguously segmented regions?
- Can we leverage existing CNNs to improve segmentation?
- Can we obtain state-of-the-art accuracy by reformulating the segmentation task as a boundary tracing one?

## Network Architecture

Our CNN takes as input a square patch of the raw image with an 8-pixel-long contour of the previously traced path overlaid on top. Optionally, U-Net predictions can be added as a 2nd channel. The outputs are the relative  $x$  and  $y$  coordinates of the next  $m$  pixels along the cell boundary. We train the regression loss between the predicted and true relative coordinates.

### Input to CNN



### Output

	$\Delta x$	$\Delta y$
$p_{+1}$	-1	-1
$p_{+2}$	-2	-1
$p_{+3}$	-3	-1
$\vdots$	$\vdots$	$\vdots$
$\vdots$	$\vdots$	$\vdots$
$\vdots$	$\vdots$	$\vdots$
$p_{+m}$	-8	1

### Tracing

**Initialization:** Contours are initialized with either ground truth or the contiguous 8-pixel path with highest U-Net predicted scores.

**Choosing the Next Pixel:** Each of the  $m$ -pixel-ahead predictions “vote” for the location of the next pixel to be traced based on the angle ( $\theta$ ) of the vector made by its coordinates relative to the center pixel. Each vote is weighted according to how close it is to the center location:

$$w(i) = e^{-\alpha i}, \quad i = 1, \dots, m$$

where  $\alpha$  is a hyper-parameter. The pixel with the largest vote is added to the trace, provided it has not already been traced.

**Ending the Trace:** When the most recent predicted pixel is within 5 pixels of the starting contour, the tracing ends and a Bresenham line is used to close the trace.

## Results

Method	Ground Truth Initialized	U-Net channel	$m$	Jaccard Score (mean $\pm$ std)	Jaccard Score (median)
Tracer	No	No	10	0.8091 (0.04216)	0.8443
	No	No	20	0.8268 (0.03749)	0.8579
	No	Yes	10	<b>0.8407</b> (0.03873)	<b>0.8742</b>
	No	Yes	20	<b>0.8460</b> (0.04764)	<b>0.8841</b>
	Yes	No	10	<b>0.8479</b> (0.03485)	<b>0.8776</b>
	Yes	No	20	<b>0.8626</b> (0.01497)	<b>0.8942</b>
	Yes	Yes	10	<b>0.8621</b> (0.02785)	<b>0.9070</b>
	Yes	Yes	20	<b>0.8611</b> (0.02414)	<b>0.9044</b>
	Yes (HITL)	Yes	10	<b>0.8629</b> (0.0244)	<b>0.9074</b>
Yes (HITL)	Yes	20	<b>0.8797</b> (0.0171)	<b>0.9054</b>	
U-Net [1]	-	-	-	0.8370 (0.03329)	0.8624

Table: 10-fold cross validated Jaccard scores on the testing set for the current state-of-the-art segmentation algorithm (U-Net) and our tracing network. Jaccard scores higher than state-of-the-art are in bold font. HITL denotes retraced human-in-the-loop.

## Results

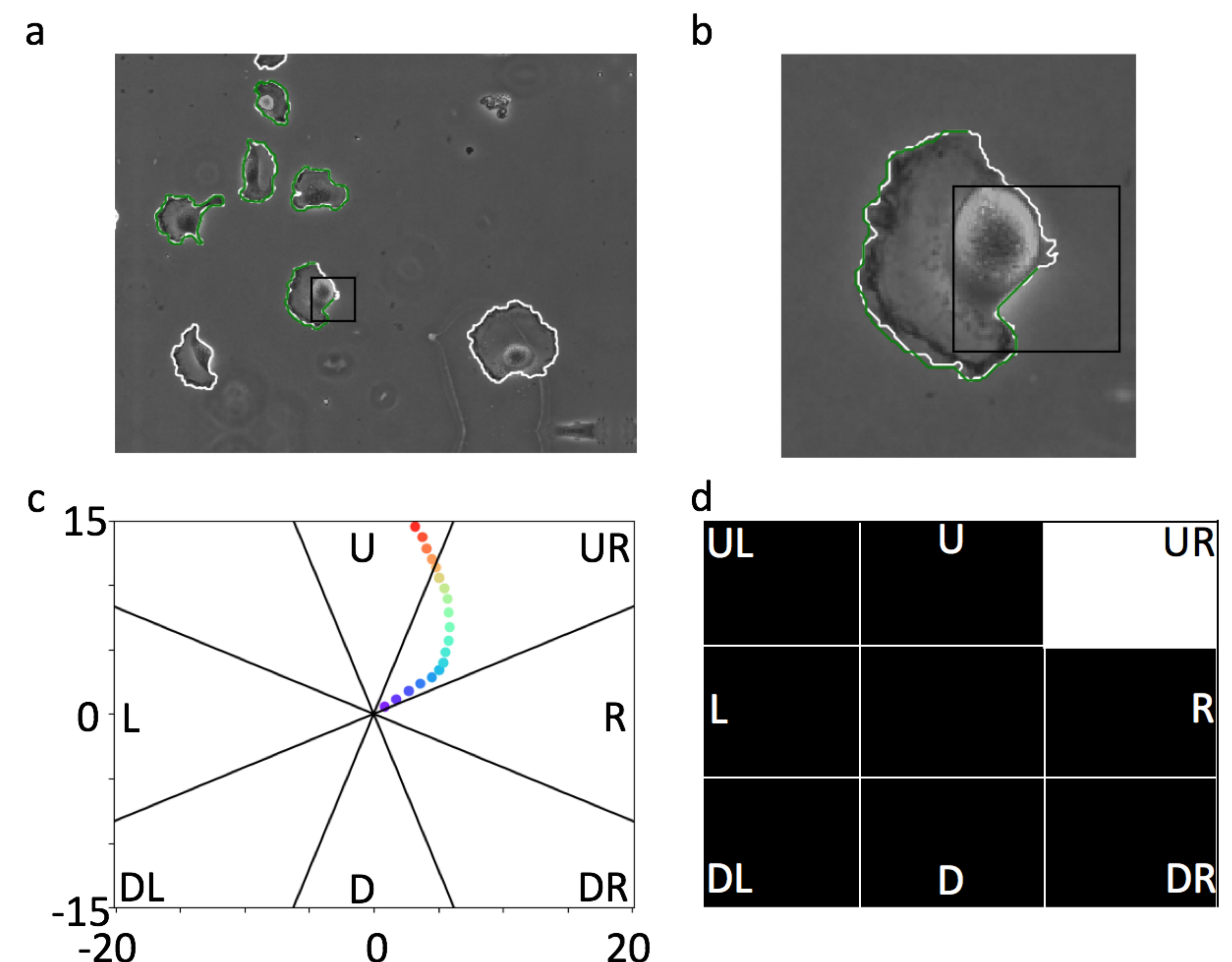
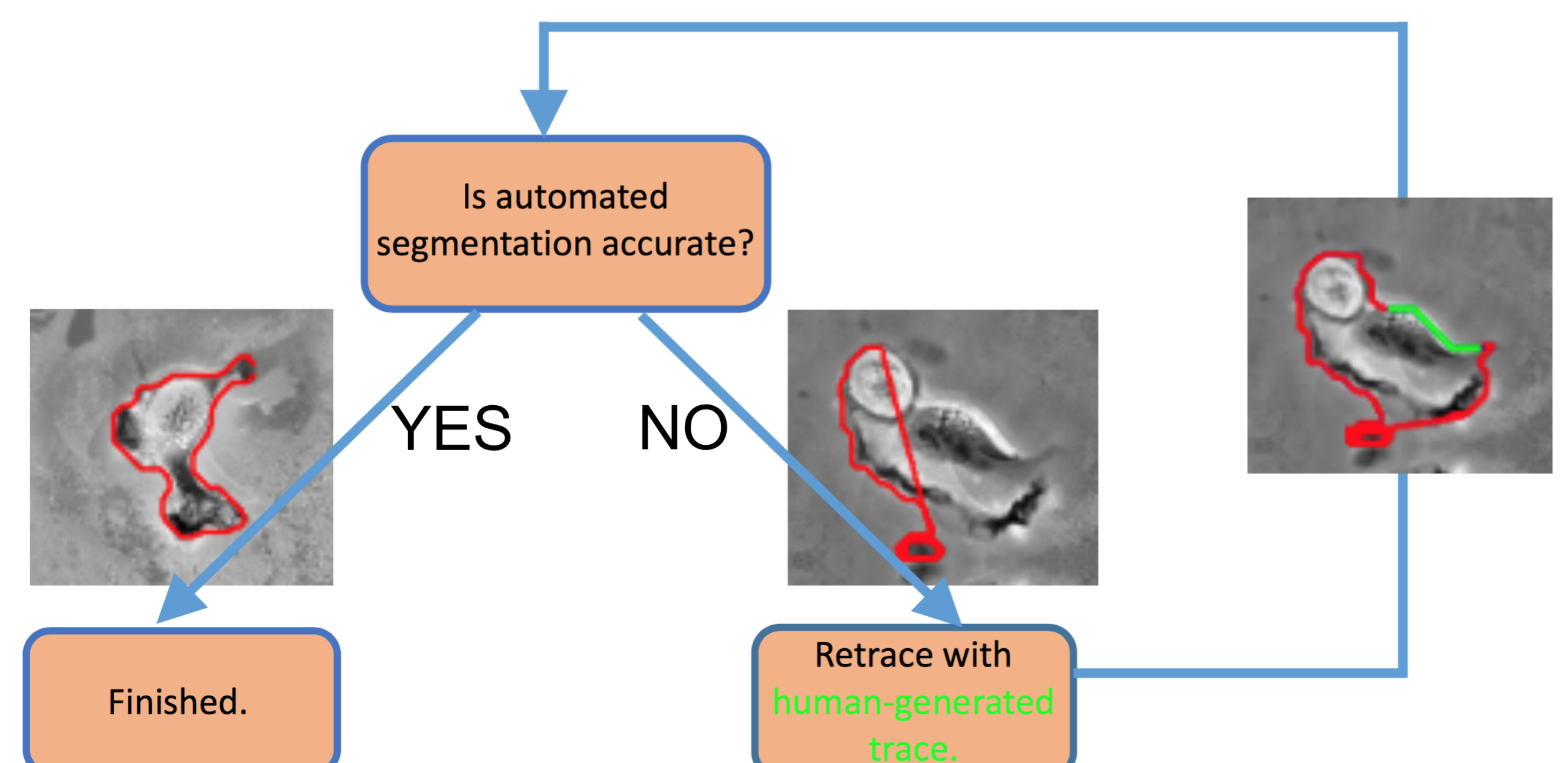


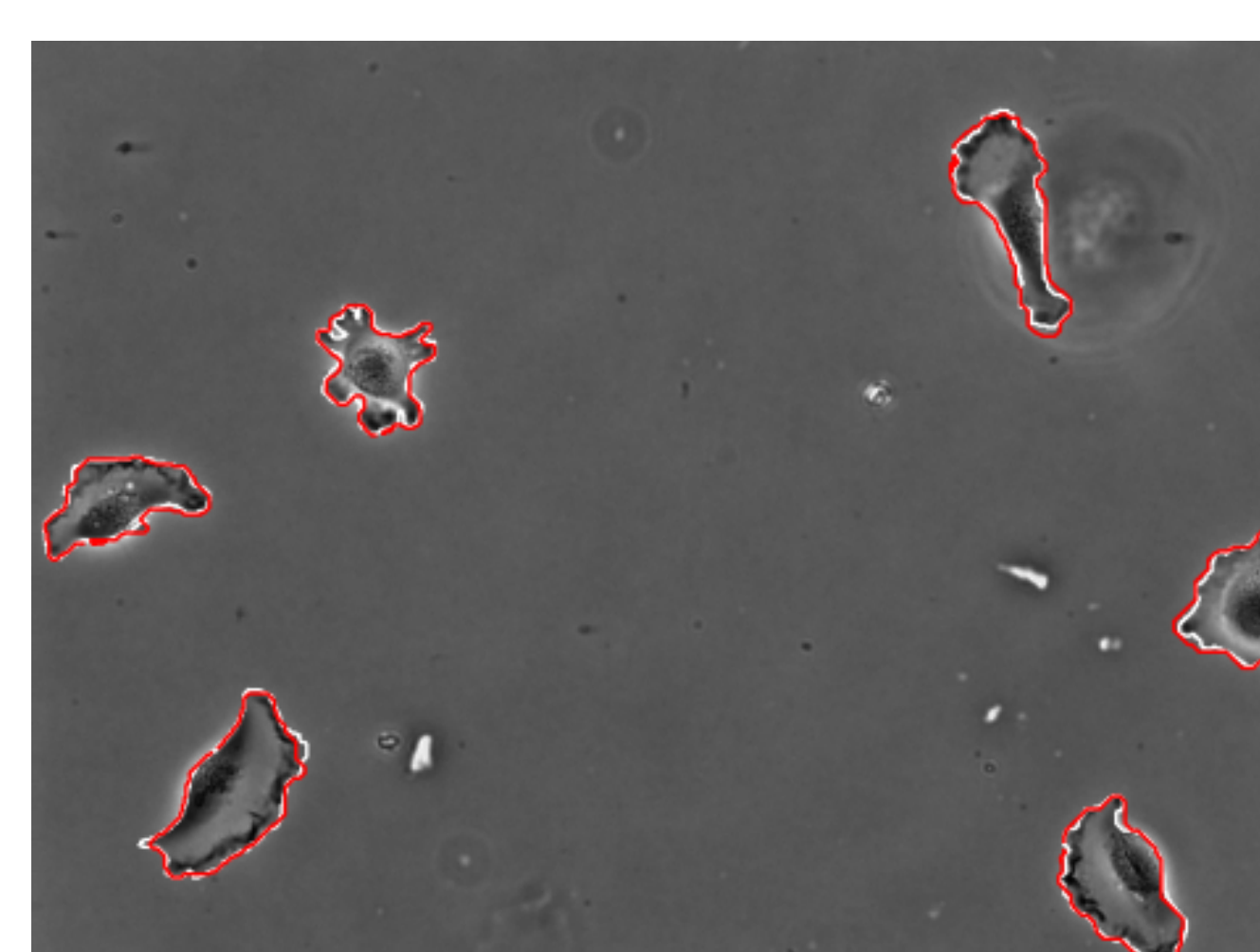
Figure: (a) An example of an image in the process of being segmented. Ground truth contours in white, CNN-traced contours in green. (b) A zoom of the current cell being traced. The black square in (a) and (b) is the current  $64 \times 64$  input patch to the CNN, centered at the currently traced pixel. (c) The predicted locations of the next 20 pixels relative to the center pixel of the patch, and the corresponding angles,  $\theta$ . (d) The score map used by the tracing algorithm to determine the location of the next pixel in the trace, e.g., the upper right (UR).

## Human-in-the-Loop (HITL)



## Examples

### U-Net Initialized



### Human Initialized

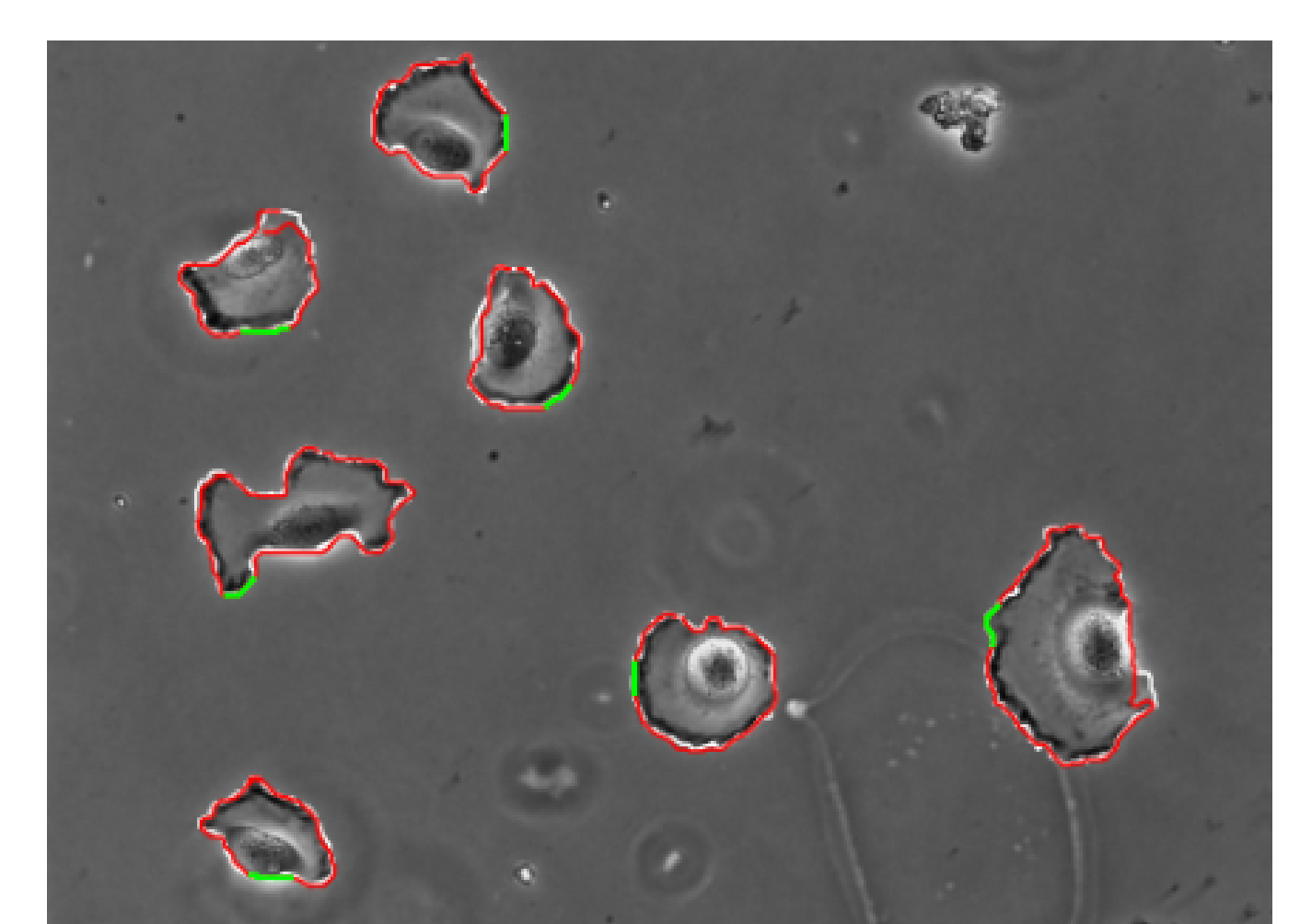


Figure: White contours are ground truth, red are predicted, green are human initialized. Jaccard scores are 0.9079 (U-Net initialized, left) and 0.9328 (human initialized, right).

## Conclusions

- We reformulated the segmentation task as a tracing task by using boundary optimization.
- Obtained SOTA accuracy on an ISBI cell tracking dataset [2,3].
- Flexible to use in conjunction with other CNNs such as U-Net to increase accuracy.
- Capable of human-in-the-loop segmentation with higher accuracy than segmentation alone.

[1] Ronneberger et al. “U-Net: Convolutional networks for biomedical image segmentation.” *MICCAI*, 2015.  
[2] Maška, et al. “A benchmark for comparison of cell tracking algorithms.” *Bioinformatics*, 2014.  
[3] Ulman, et al. “An objective comparison of cell-tracking algorithms.” *Nature methods*, 2017.