

Tracking-Assisted Segmentation of Biological Cells

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Introduction

Being able to detect individual cell and track its trajectory through time helps to automate treatment observation and disease spread detection.

Due to the constant change in shape, position and status of the cells in the data, even the best methods fail to accurately detect cells that combine, split or die.

We propose to improve segmentation by augmenting with Siamese matching.

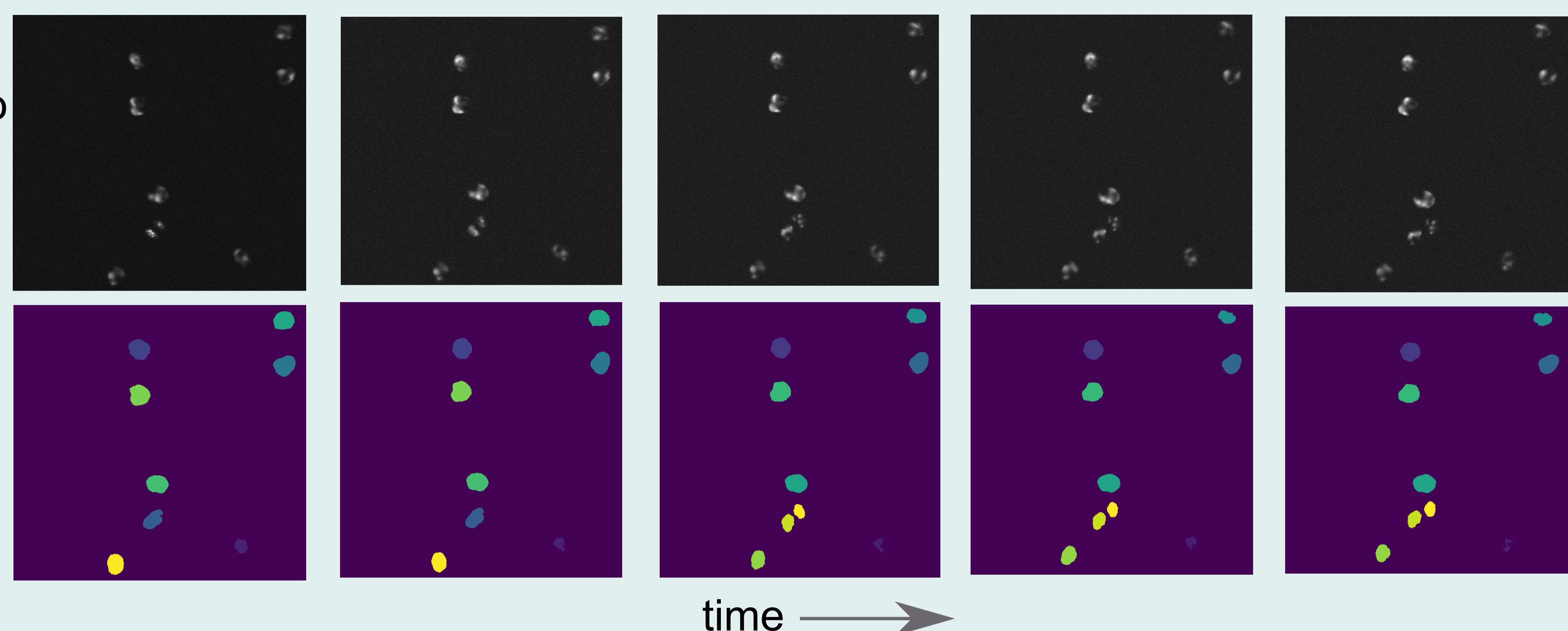


Figure: Demonstration of cell splitting and ground-truth segmentation

Approach

The 4-step procedure involves:

- **Initial Segmentation**

- Segmentation done using U-Net model
- Resolution adjusted using nearest-neighbor

- **Siamese Tracking**

- Tracking done in forward as well as backward directions
- For cell C_t^i predictions by the tracker in I_{t+1} and I_{t-1} are denoted as F_t^i and B_t^i

- **Collision Detection**

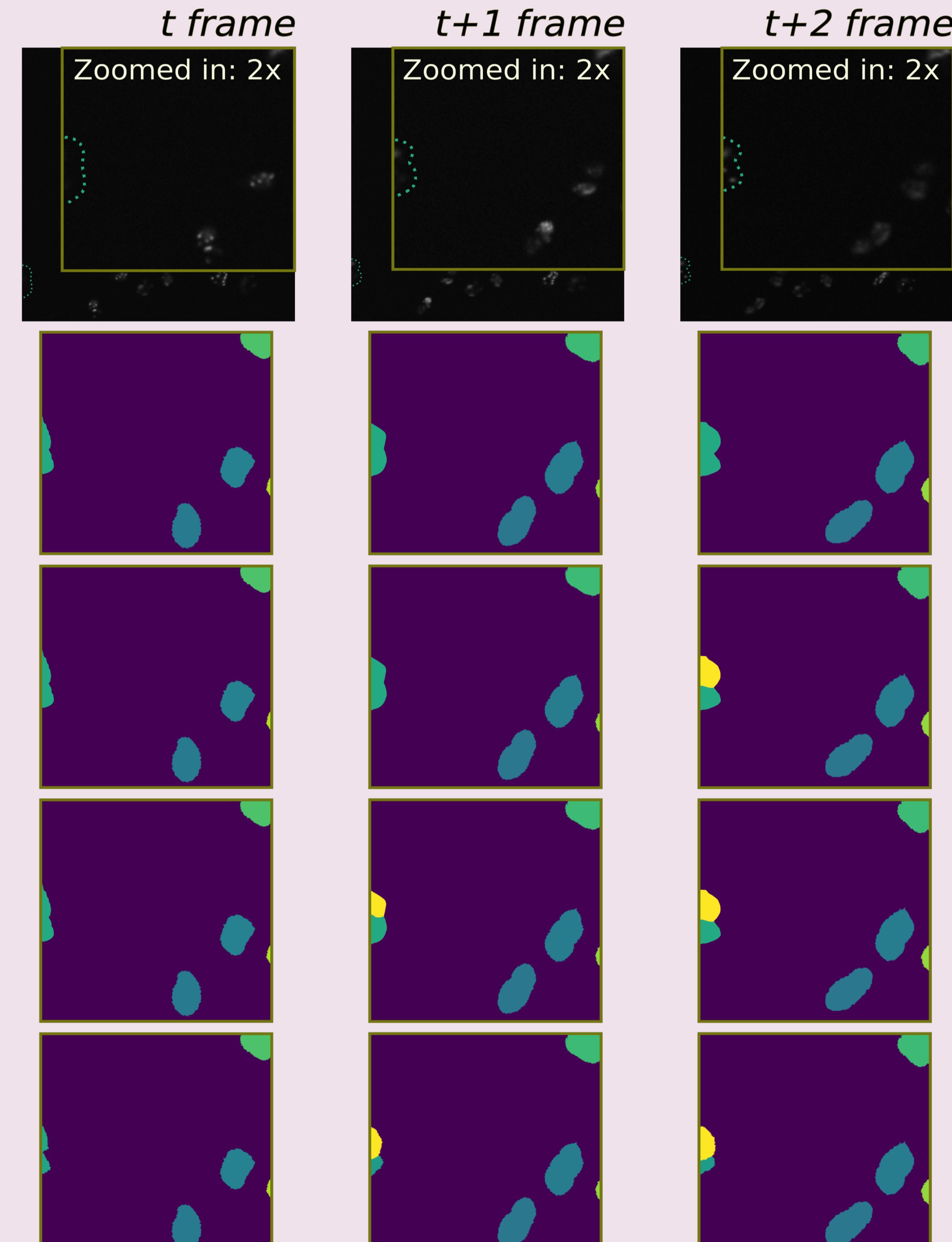
- Cell C_t^i is a lump of multiple cells if the centroids of two or more cells from the previous frame lie in B_t^i .
- Re-segmentations are performed until each cell is mapped to atleast one cell in the previous frame.

- **Mitosis Detection**

- Centroids of two cells lie within F_{t-1}^i .
- If matching area is
 - 0, then apoptosis
 - 1, no change,
 - else, mitosis.

Demonstration

Fluo-N2DH-SIM+ Cell images:



U-Net Segmentation:

U-Net Segmentation and Watershed deconvolution:

Ours:

True labels:

Preliminary results and Conclusion

Dataset	Segmentation accuracy		Tracking accuracy	
	U-Net	Our method	U-Net + SiamTracker	Our method
Fluo-N2DH-SIM+ 01	0.919	0.924	0.986	0.992
Fluo-N2DH-SIM+ 02	0.800	0.838	0.922	0.956
Fluo-N2DH-GOWT1 01	0.739	0.746	0.973	0.978
Fluo-N2DH-GOWT1 02	0.827	0.837	0.869	0.875

- Improvement of 3.8% on U-Net for segmentation.
- Improvement of 3.4% on U-Net for tracking.
- Interpretation of mitosis, apoptosis and cell collision help the cell tracker.

Recent improvement of this method outperforms other approaches on Fluo-N2DH-SIM+ 02 and two other datasets.