A SEEDED FRAMEWORK FOR TRACKING OF GENE EXPRESSION DYNAMICS IN INDIVIDUAL CELL COMPARTMENTS

Du C.-J., Marcello M., Spiller D.G., White M.R.H., Bretschneider T.

1. Abstract

For tracking of gene expression dynamics in individual cell compartments, we propose to initialize a few keyframes with a novel constrained interactive segmentation method, which uses the constrained density weighted Nyström method for eigenvector decomposition and the geodesic commute distance for pixel classification. The tracking is achieved by both forward and backward propagating from two keyframes using a group of overlapping subwindow segmenters around nuclei and cytoplasm boundaries. Experiments demonstrate that the system is able to track quite complex cell sequences reasonable well.

2. Introduction
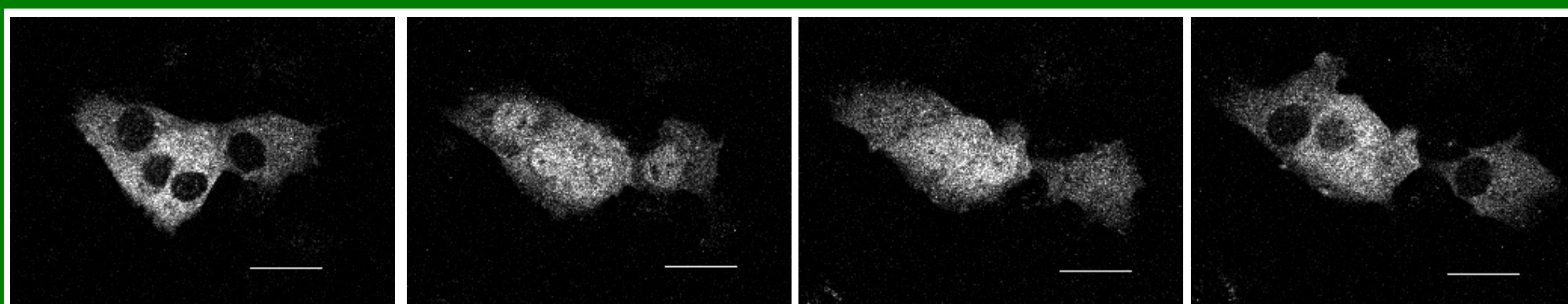
The 1st, 11th, 21st, 31st, frames in an example sequence

- A better understanding of gene regulation requires tracking the spatiotemporal relationships of transcription factors in individual cell compartments.
- The cells in the current study are quite complex.
- We propose to use the constrained density weighted Nyström method and geodesic commute distances for segmentation.
- For tracking, we adopt a keyframe-based system which combines both forward and backward propagation using a group of overlapping subwindow segmenters around nuclei and cytoplasm boundaries.

3. Constrained interactive segmentation

Key Idea

- The labeled seeds provided by the user can be used to construct instance-level constraints on pairs of subset points, including must-link and cannot-link constraints.
- The solution is to explicitly propagate the instance-level constraints from a few specified pairs to the remaining pairs, thus increasing the effects the constraints.
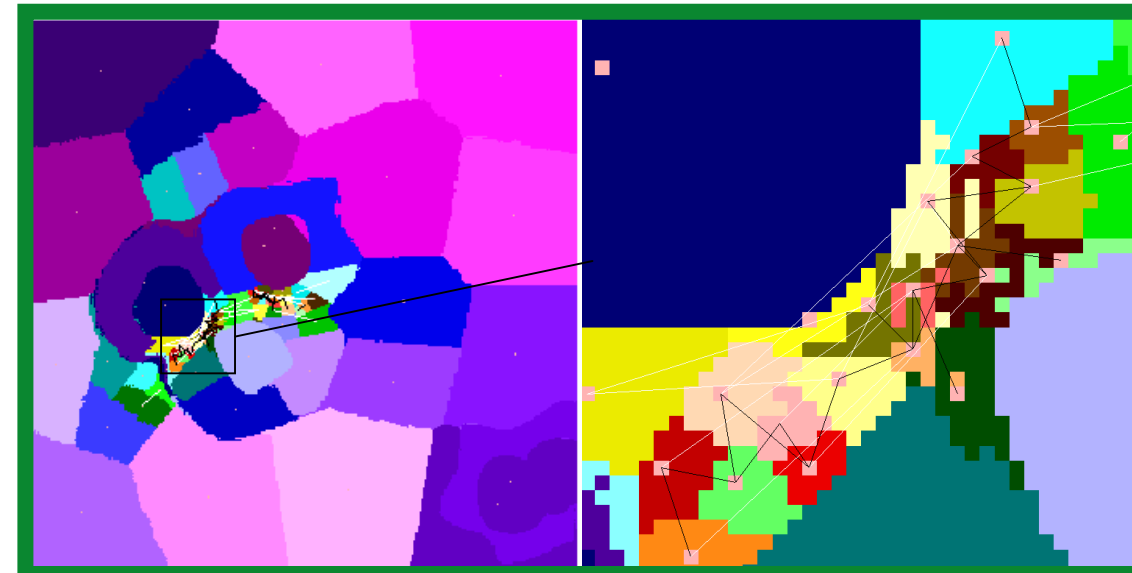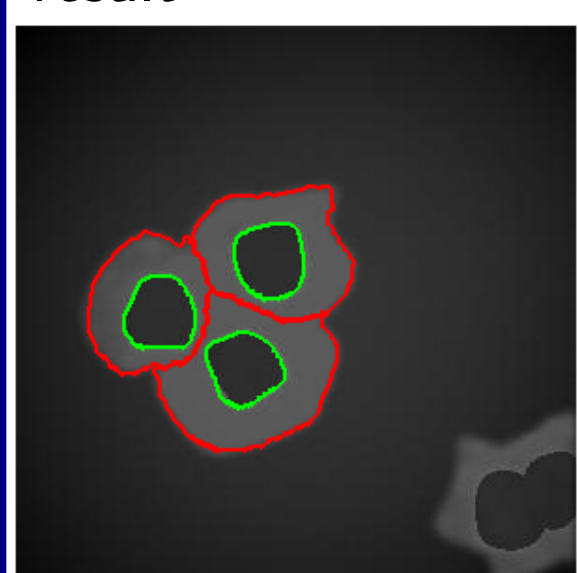
Demonstration

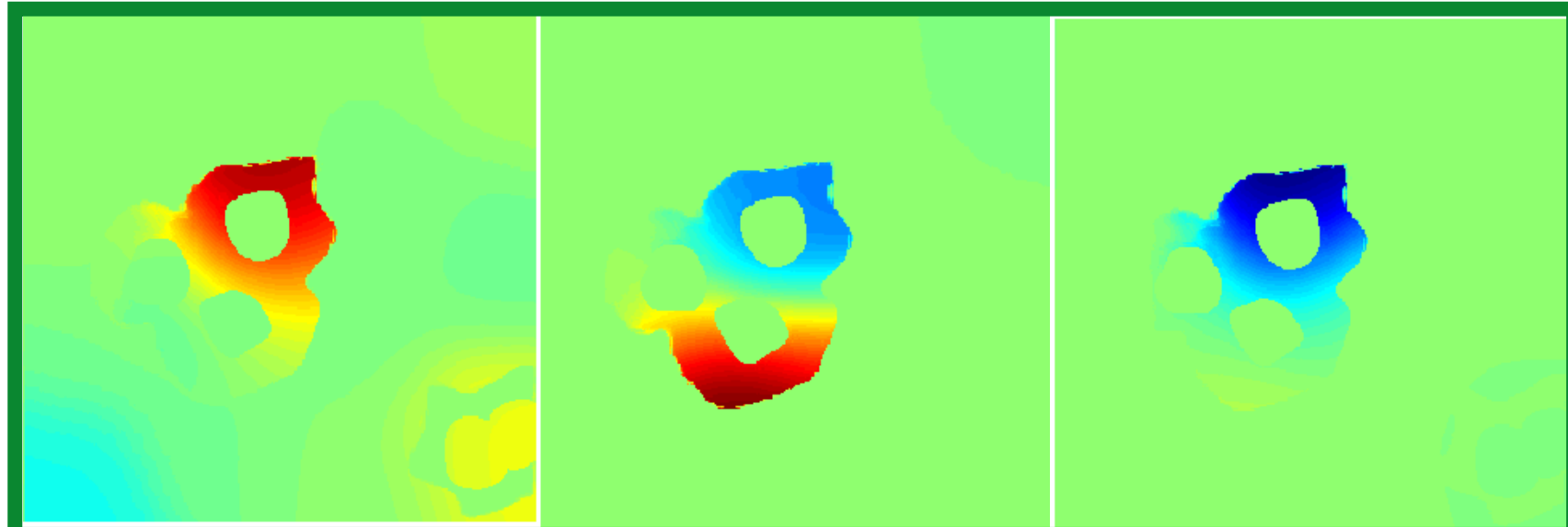Input image and seeds

2a. Subset selection via k-means

2b. Constraints generation

2d. Segmentation result

2c. Eigenvector decomposition via constrained density weighted Nyström method

4. Tracking with subwindow segmenter

Approach

- Selecting a few keyframes for interactive segmentation to yield a set of cell contours.
- Based on the initial shape alignment by the SIFT flow method, a set of overlapping subwindows is uniformly sampled along the cell boundary.
- Each subwindow is segmented using the automatically generated seeds.
- The final probability of a pixel is a linear combination of the probabilities computed from each covered subwindow.
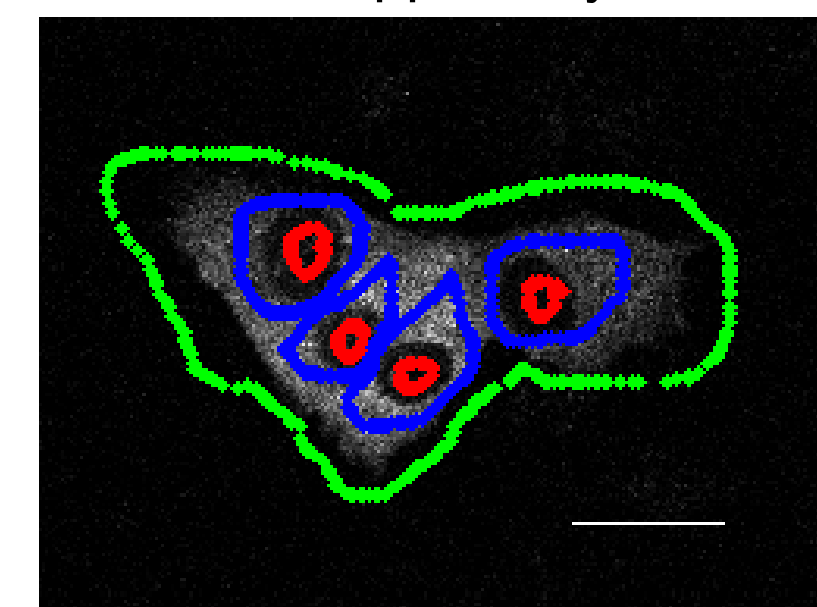
Illustration

Overlapping subwindow segmenters

An example of subwindow segmenter, seeds for cytoplasm and background, and the segmentation result
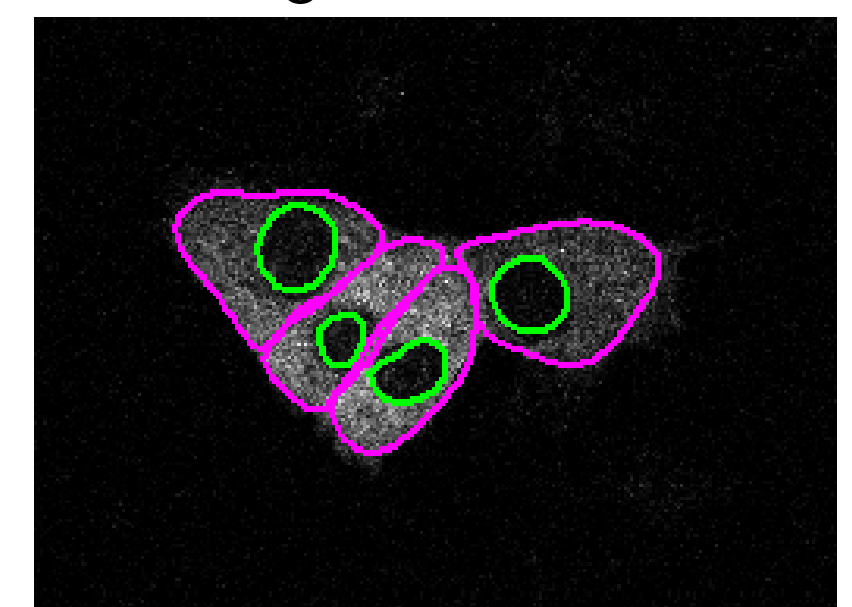
Tracking result
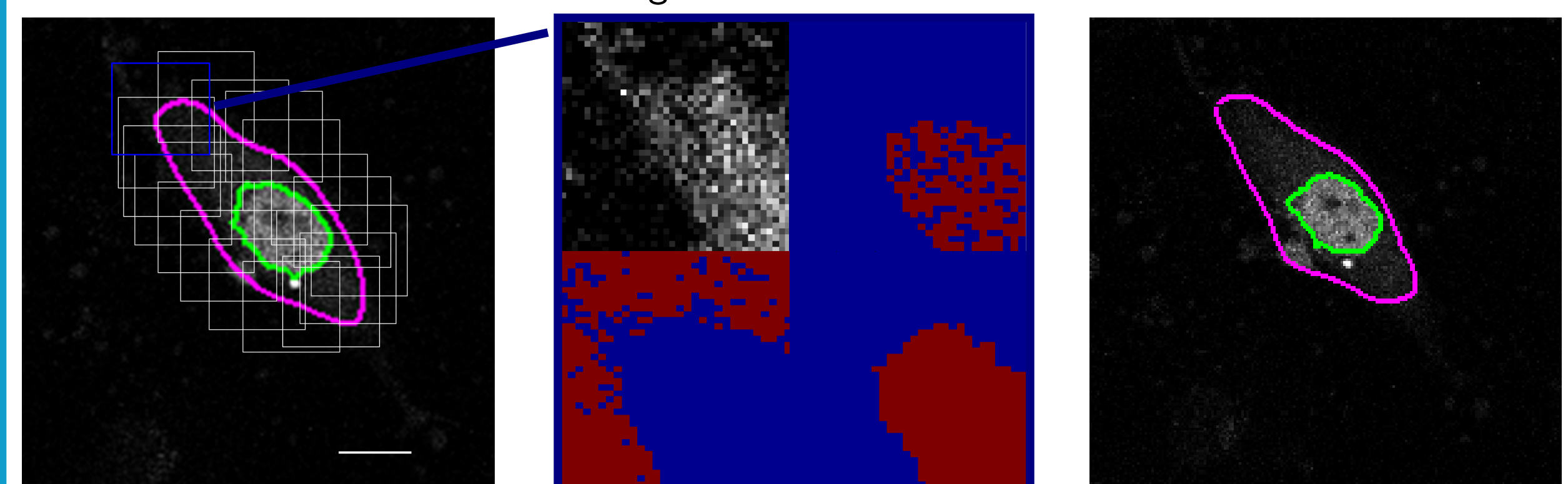
5. Results

Segmentation

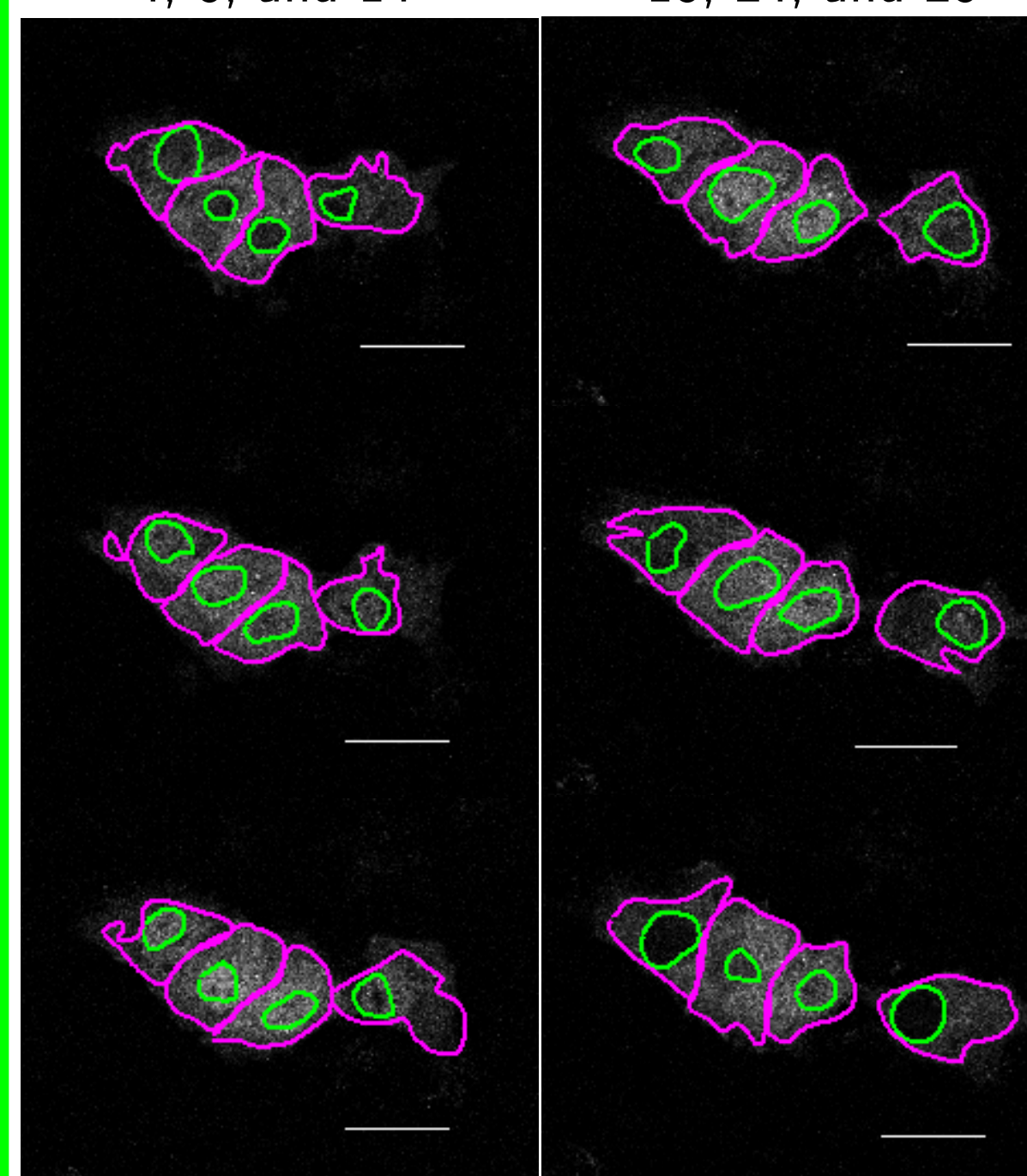The seeds supplied by the user

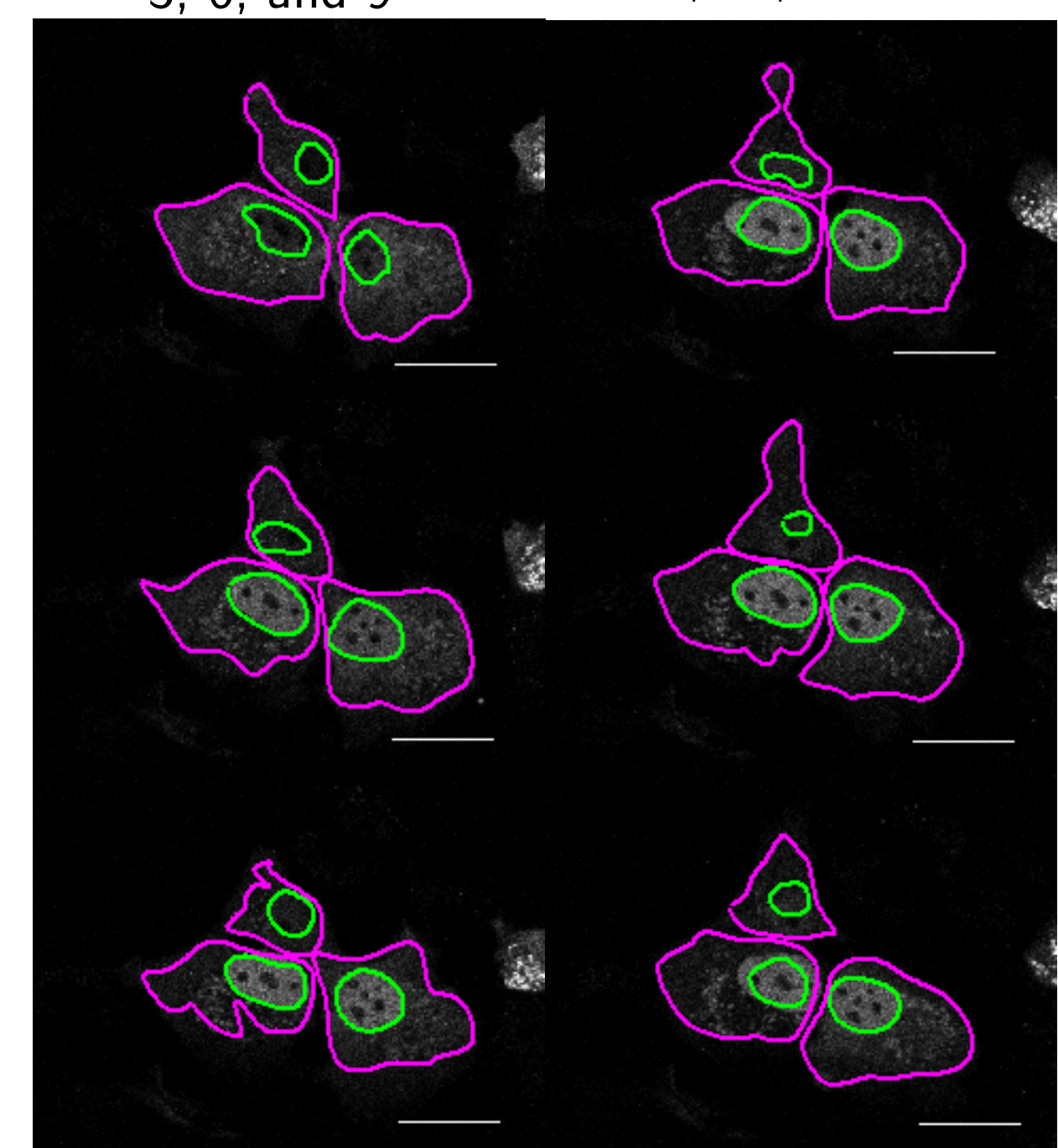The segmentation result

Tracking

Tracking results of sequence one at positions
4, 8, and 14 ; 18, 24, and 28

Tracking results of sequence two at positions
3, 6, and 9 ; 13, 16, and 19

6. Acknowledgements