A Novel Framework for Tracking In-vitro Cells in Time-lapse Phase Contrast Data

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1. Introduction

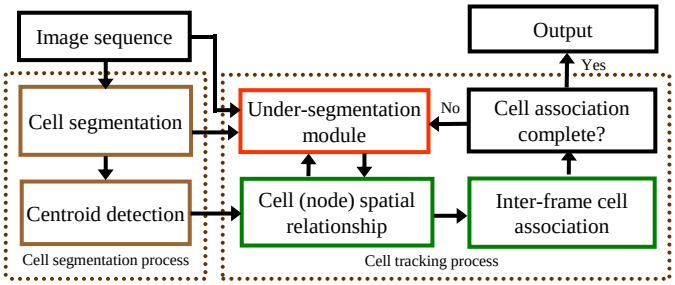
• Computer vision based tracking to analyse spatial and temporal patterns of living cells, such as mitosis, morphology, and motility. This analysis facilitates the discovery of new clinical therapies.

• The major challenges that need to be addressed in automatic cell tracking include Brownian motion, cell division, agglomeration, and under-segmentation.

• In this work, a vision based automatic tracking framework has been developed to handle the above mentioned challenges where tracking accuracy is increased by redressing the under-segmentation.

• The proposed framework has been evaluated on dense phase-contrast cellular images that are characterised by low contrast and high level of noise.

2. Proposed Cell Tracking Framework: An overview



3. Processing Steps and Results

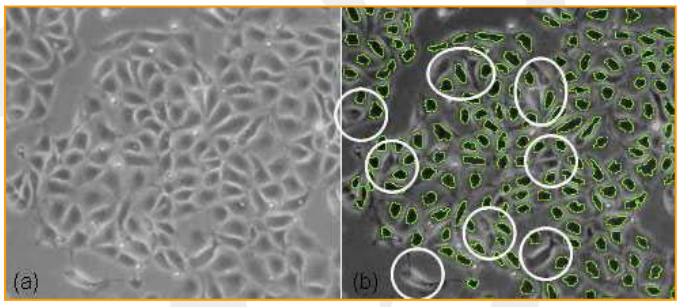


Figure 1. The input cell image and segmentation result. a) Phase contrast MDCK cell image. b) Segmentation result where the missing cells (under-segmentation) are marked by circles.

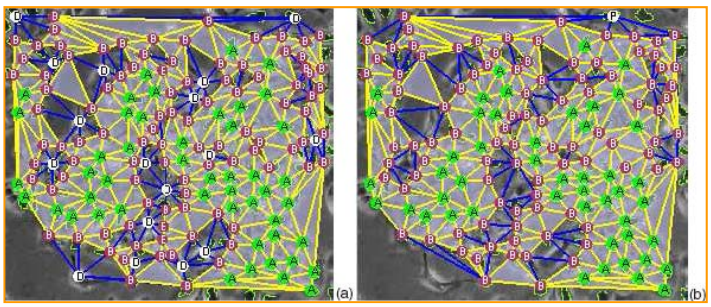


Figure 2. Cell association process. a) Image at time t, b) Image at t+1. The labels A & B indicates the associated cells, while the cells labeled with D in (a) are not associated due to under-segmentation in image t+1.

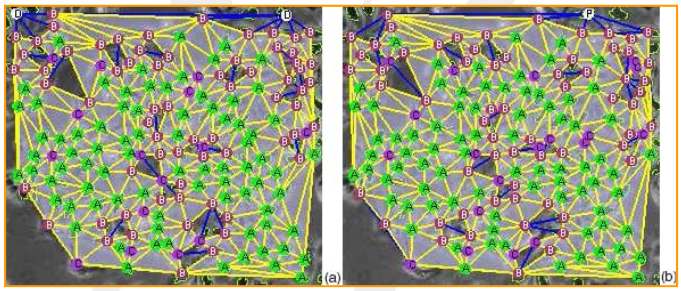


Figure 3. Cell association process after redressing the under-segmentation. The under-segmented cells in image t+1 are identified using pattern matching along with spatial & temporal information and are labeled with 'C' in (b).

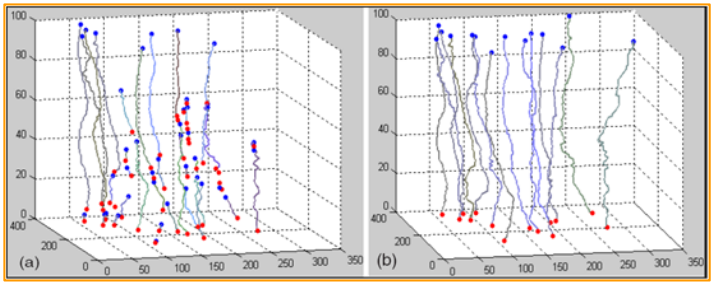


Figure 4. 2D+Time trajectory of tracked cells over 100 frames. (a) Tracking results when the *under-segmentation* module is not included in the cell tracking algorithm. (b) Tracking results after the inclusion of the *under-segmentation* module.

Table 1. Quantitative tracking result.

Cell image sequence	Number of frames	# of cells tracked throughout the sequence (manually)	Delaunay Matching		Delaunay & Pattern Matching	
			# of cell tracked throughout the sequence	Percentage	# of cell tracked throughout the sequence	Percentage
1	100	190	96	51%	170	89%
2	100	120	59	49%	105	88%
3	100	174	94	54%	143	82%
4	100	135	58	43%	112	83%

Conclusions

• The major objective of our work was the development of an adaptive cell tracking algorithm that is able to accommodate challenges including the occurrence of segmentation errors, unstructured motion, mitosis and cellular agglomeration.

• Experimental results indicate substantial improvements in tracking accuracy after redressing problems caused by under-segmentation.

Acknowledgements

• This research is funded by the National Bio-Photonics and Imaging Platform (HEA-PRTLI IV).

• Prof András Czirók, Department of Anatomy and Cell Biology University of Kansas Medical Center.