Active contours for cell tracking

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Summary

Modern bioimaging technologies have shed light on numerous biological processes directly or indirectly involving the cell morphology, requiring adequate methods to precisely extract and track its outline over time. In contrast to the "detect-then-link" paradigm classically found in particle tracking applications, our approach to cell tracking, based on the theory of deformable models, directly addresses this question, by permitting a precise analysis of the cell shape in 2D and 3D, in addition to keeping their identity and determining their center of mass. Here, each cell contour is pre-detected automatically in the first image of each video, then optimised by minimising an energy-functional composed of various terms related either to the image (homogeneous regions, image gradients, etc.) and regularisation terms (contour smoothing, shape constraints, etc.). This process is then repeated for every subsequent frame, while the pre-detection step is re-used to detect objects entering the field of view. Such methods do require that a minimal overlap exists between the successive position of each cell, which is now easily achieved with today's imaging hardware. While active contours are known to be computationally demanding, we implement a discrete formalism, whereby the contour is defined as a closed polygonal line (in 2D) or mesh (in 3D) to enable fast computations and small memory footprint [1,2].

Protocol

Our analysis protocol comprises several steps, described below (parameters in bold font):

1. Intensity stabilisation: this step reduces the high intensity variations in the image data, by capping the lower and upper **nI%** pixel values.
2. Median filtering: this step reduces image noise by replacing each pixel value by the median intensity value calculated within a neighbourhood or radius **rM**
3. For each frame:
    a. Pre-detect cells using a Hierarchical K-Means approach [3]:
        i. Gaussian filter of large radius **rG**
        ii. Quantise the image intensities into an arbitrarily large number of classes by K-Means (here 10, although results converge for larger values)
        iii. Extract connected components in each class in ascending order, falling within a pre-defined size range [**aMin** – **aMax**]
    b. Initialise a contour of spatial sampling **s** for each previously unknown cell
    c. Deform a contour according to image gradients (weighted by **wg**), image homogeneity (weighted by **wh**) and regularisation (weighted by **wr**). Divisions are automatically detected and tracked when a contour splits

The protocol is implemented using the "Protocols" framework of the Icy software (icy.bioimageanalysis.org), and illustrated in Fig. 1.

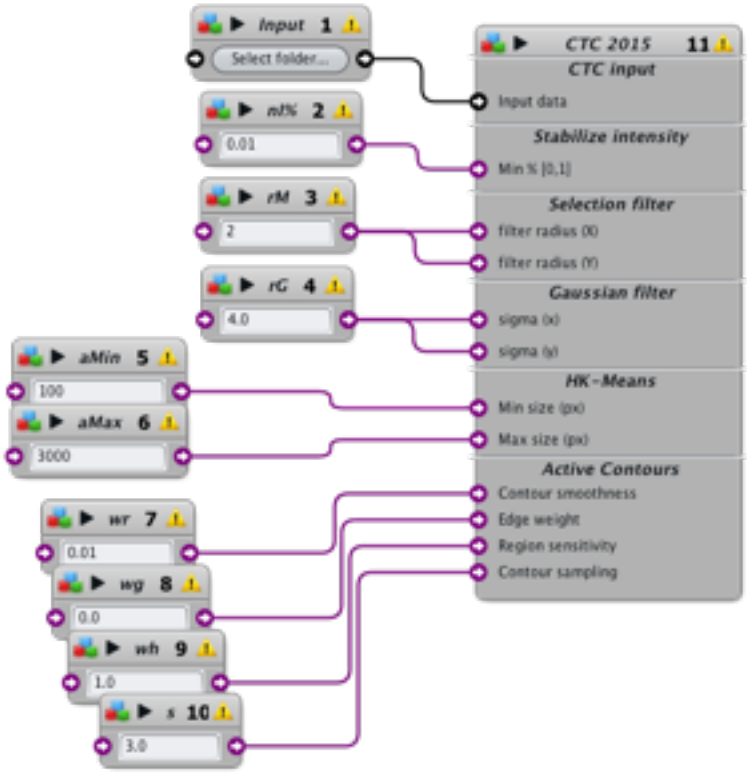

Fig. 1. Typical image analysis protocol for the 2015 Cell Tracking Challenge, implemented and freely reproducible in the Icy software (icy.bioimageanalysis.org). Parameters are described in the text, and their variation per dataset is listed in Table I.

Data set	nl%	rM	rG	[aMin – aMax]	wr	wg	wh	s
Fluo-N2DH-SIM-01	0.01	2	4	[100 – 3000]	0.01	0	1.5	3
Fluo-N2DH-SIM-02	0.01	2	4	[100 – 3000]	0.02	0	1.5	3
Fluo-N2DH-SIM-03	0.01	2	4	[100 – 3000]	0.04	-0.1	1	3
Fluo-N2DH-SIM-04	0.01	2	4	[100 – 3000]	0.04	0	1.1	3
Fluo-N2DH-SIM-05	0.01	2	4	[100 – 3000]	0.07	0	1	3
Fluo-N2DH-SIM-06	0.01	2	4	[100 – 3000]	0.04	0	1	3
Fluo-N2DH-SIM+-01	0.01	2	4	[100 – 3000]	0.04	0	1.4	3
Fluo-N2DH-SIM+-02	0.01	2	4	[100 – 3000]	0.2	0	1.5	5

Table I. Parameter set used for the 2015 Cell Tracking Challenge datasets analysed

References

[1] Zimmer & Olivo-Marin, Coupled parametric active contours, IEEE PAMI, 2005.

[2] Dufour et al., 3D Active Meshes: Fast discrete deformable models for cell tracking in 3D time-lapse microscopy, IEEE TIP, 2011

[3] Dufour et al., Automated quantification of cell endocytosis using active contours and wavelets, Proc. ICPR, 2008