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

Ketheesan Thirusuttampalam
kethesan@eeng.dcu.ie

M. Julius Hossain
julius@eeng.dcu.ie

Ovidiu Ghita
ghitao@eeng.dcu.ie

Paul F. Whelan
paul.whelan@dcu.ie

The advent of modern microscopy imaging technologies has made possible the acquisition of cellular image sequences with high temporal and spatial resolutions [2, 3]. While the availability of high resolution image acquisition opened the possibility to study a large spectrum of biological processes, on the other hand it has generated a substantial problem as the amount of data to be interpreted by biologists is constantly increasing. Consequently, in many situations the manual data annotation process has become impractical and this has generated a substantial interest in the development of automatic approaches that are able to track cellular structures in dense time-lapse images [1]. However, the development of accurate cell tracking algorithms is a challenging task due to factors such as non-structured motion patterns, cellular agglomeration and proliferation. To address these challenges, in this paper the cellular tracking has been formulated as a sequential process where the inter-frame cell association is attained by assessing the variation in the local structures contained in consecutive frames of the image sequence.

The proposed cell tracking algorithm has been designed in a multi-step modular fashion and a schematic that shows its main constituent components is illustrated in Figure 1. The first component of the algorithm implements the cell segmentation process where the detected cells are used to generate a Delaunay mesh in each frame of the sequence. The most sophisticated component of the proposed algorithm is represented by the cellular tracking process that has been specifically designed to accommodate the under-segmentation errors that occur during the cell segmentation process.

As illustrated in Figure 1, the cell tracking is performed in three phases. In the first phase, the nodes that exhibit the most similar local structures in the Delaunay meshes in consecutive frames are identified using equation (1).

$$M(u'_i, u^{+1}_j) = \frac{S(F'_i, F^{+1}_j)}{|F'_i|} \quad (1)$$

where $F'_i$ and $F^{+1}_j$ are the triangular structures that are associated with the nodes $u'_i$ and $u^{+1}_j$ in the two Delaunay meshes, $|F'_i|$ denotes the number of triangles associated with the node $u'_i$, and $S(\bullet)$ defines the number of triangles that are matched with respect to Hausdorff distance. In the second step of the cell association algorithm we attempt to match the un-associated nodes that are adjacent to the nodes that are identified in the first step (i.e. the nodes that are determined with the highest confidence level). This is carried out using equation (2) in this process we use the information that is similar in the Delaunay meshes to aid the identification of the corresponding nodes in the $t$ and $t+1$ frames whose local structure is changed due to unstructured cell motility or degenerations that may occur in the Delaunay meshes.

$$M(u'_i, u^{+1}_j) = \frac{S(P'_i, P^{+1}_j)}{|F'_i|} + \frac{R(E'_i, E^{+1}_j)}{|E'_i|} + \left(1 - D(c'_i, c^{+1}_j)\right) \quad (2)$$

where $R(\bullet)$ counts the number of most similar links between the nodes $u'_i$ and $u^{+1}_j$, $D(\bullet)$ is the $L_2$ distance between the centroid points $c'_i$ and $c^{+1}_j$, and $D_{max}$ is a parameter that defines the maximum cell movement that can occur in adjacent frames.

The last phase of the cell tracking algorithm attempts to redress the problems caused by under-segmentation and cellular agglomeration that induce large distortions in the Delaunay mesh. This has been implemented using normalised cross-correlation that is applied to locate in the frame $t+1$ a pattern that approximates the un-associated cell in frame $t$.

![Figure 1: Overview of the proposed cell tracking framework.](image)

![Figure 2: Illustration of the cell association process where the left and right images depict the $t$ and $t+1$ frames. (a) and (b) Cell association results - the nodes that are associated in the first and second steps are labelled with A and B, respectively. With D and P are marked the nodes in (a) and (b) that do not obey the matching criteria enforced with Eqsns. (1) and (2). These nodes are not associated due to factors such as under-segmentation and large distortions in their local Delaunay meshes.](image)

![Figure 3: The effect of under-segmentation on the cell tracking process. (a) Cell tracking results - DM. (b) Cell tracking results - DPM.](image)

