TRACKING OF ENDOTELIAL CELLS OF CRYO-MICRO PREPARATIONS, BASED ON TRANSFORMATION OF CELLS

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Modern research in the area of the analysis of the endothelial cells is largely used not automated and manual work. This situation does not allow for all-out research on the long video sequence. When the number of tested parameters such as area, perimeter, aspect ratio, orientation, direction of movement, speed, distribution of the pixel intensity histogram, the cell shape of the edge, the time required is further increased. Therefore, an automated tracking of endothelial cells of crio-mikro preparations is an important task [1].

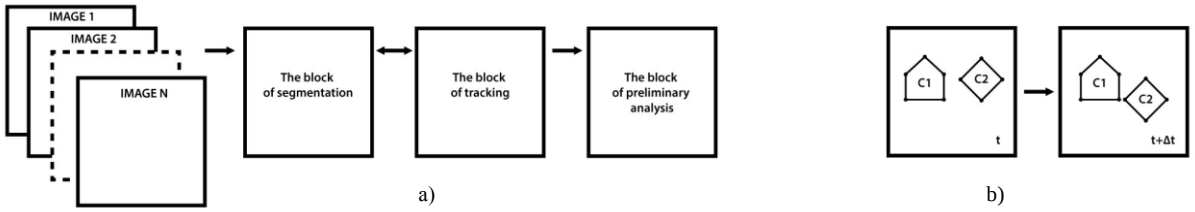

Fig. 1 Video analysis process a series of images of endothelial cells of cryo-micro preparations (a), two adjacent time-frame of video sequence (b)

The video sequence is fed to the input of the segmentation (Fig. 1a), which made the process of separating of the elements of cells from the other pixels. Next the segmented region of cells shown in outline form to the input unit tracking, which in turn has a feedback with a block segmentation process to correct segmentation. The main objective of the unit tracking is a tracking of the "cell life" during the entire video sequence. The block of preliminary analysis, according to the received data, collects the entire use information about all cells throughout the full sequence. These preliminary data analysis are an excellent source of knowledge for a comprehensive study of the processes contributing to cell survival during freezing and thawing.

This work is devoted to the tracking unit, namely, problems, algorithms that have been identified, delivered, and used resolved [2]. To solve the problem of tracking primarily identified source data. These data paths are the set of normalized cells in complex form, in the two adjacent time frames (Fig. 1*b*).

As can be seen from Fig. 1b, by normalizing the contours at time t experienced the transformation (moving). Circuit $C1$, describes cell 1 has moved in the horizontal direction with a certain length, in turn circuit 2 represents the cell 2 is also shifted by a certain distance. Thus, the decision comes down to the issue of the conformity $C1_t \to C1_{t+\Delta t}$, $C2_t \to C2_{t+\Delta t}$.

The simplest solution is based on the analysis of the center of mass. That is, the circuit for the time t, is associated with the contour at time $t+\Delta t$, which is the shortest distance of the center of mass relative to the contour of time t. But in this way, there are inconsistencies in certain movements. Therefore, it is appropriate to use shape analysis (measure of similarity) of the two circuits. In conformity becoming only the contours that are closest in form. However, the use of shape analysis requires some time-consuming. When the number of loops at time t is n, and for the time $t+\Delta t$ is obtained equal to m, we have $n \cdot m$ measures of similarities. It should also be borne in mind that similar cells may be present in a completely different place, so you need to use both features (and the position of the center of mass and a measure of similarity) to determine matches. For this purpose decided to enter the threshold T, which would define the maximum distance change. In addition, there is necessary threshold Tf, which determines the permissible change shape. Based on the foregoing, we determine the matching string for full video sequence on the output.

Perspective of the work is designing a graphical soft for automatically processing, segmentation and tracking cells on crio-microscopically datasets.

References

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[2]. Gonzales R., Woods R. *Digital image processing*. Prentice Hall.- 1070 p.- 2002.