Commentary: Tracking Biological Cells in Time-Lapse Microscopy

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Introduction

This paper is aim to describe a approach in cell tracking which is crucial in analyzing biological processes and diseases diagnosing. manual analysis of cells images is a long time consuming and uninteresting thing for human. It would be a great workload when a larger number of cells picture need to be analyse.in this way, the auto cell tracking would play a important role in increasing the analyzing efficiency.

however, there are some challenges need to be deal with. which are most caused by the different image gaining techniques, complicated cellular topology, and irregular cell motion. some ways to get the image would limit the image quality or lead to another noisy.in the topological part, the overlap of cells, close contact and various cell cycle events like mitosis and so on would also grow the complexity of the tracking. and in order to minimize the effect of phototoxicity, the images would be captured infrequently. This would cause total different cells in consecutive frames.

For dealing the challenges, the paper would describe a method to deal the challenges when tracking cells. It would uses a morphological top-hat filter and the h-maxima transformation and fits an ellipse in the segmentation part. Then this method would compute by combining the motion features and topological features of cells to increasing the cell matching and tracking accuracy in cell tracking.

Finally, the method might be a robust approach to automatic cell detection and tracking .so that it would be helpful in the different kinds' situation. In the medical area, this would help to test and analyze the function of new drugs. In the hospital side, this method would help them to diagnose disease and repair tissue and other cell analyze activities.

Methods

This methods mainly combine three parts, which is detection, tracking, and trajectory recovery.

In the detection part, it inverts image to bright the cell, followed by a morphological opening operation, this would erode the small peaks like noise. Then subtract by original image so that the nonuniform illumination would be correct. For the h-maxima transformation part, using Gaussian filtering first to make an individual intensity maximum of each cell. then use the h-maxima transformation to get the segmentation of the nuclei. Finally, it uses an ellipse for localizing the nucleus in the cell which would decrease the influence of high dense cells.

In the tracking part, it would combine the cell topological features, color compatibility, degree of area overlaps, and deformation to be used as motion parameters to increase the accuracy of tracking. Furthermore, a global optimization technique based on weighted bipartite matching is added to minimize the overall cost. however, all the function describe before cannot deal with the mitosis problem, it would be deal with by follow function.

the trajectory recovery part is added to the model which is based on a template matching and can deal with the problems like mitosis that could cause the broken trajectory.be more specific ,this function part would deal with cell division in their basic form, and avoid changing the relationship between cells which could cause the tracking error. This would realize by set three category which contain different appearance types cell then calculate the trajectory forward or backward of cells to link their trajectory.

In the detection part, there is have place to improve. set a suitable scale σ of the Gaussian filter and replace the h-maxima transformation as extended maxima transform would have a better divided performance, which is tested in the [1]. And for the cells like honeycomb, it would have not great divided ability because of the peak of the cell may not be the nuclei. So that one cells would be divided as multinumber cell. This function would perform better when cells have relatively simple structure inside and clear nuclei.

In the tracking part , use a unique planar graph could let the relation of node independent on the topology between them. this Delaunay triangulation can efficiency encode the neighboring relationship between cells which also lead to a better performance on tracking cells. this is already compared in [1].

Results

In the segmentation part, when compare to the watershed, hybrid merging and compactness, this proposed-method would have the best precision and accuracy. This result can prove the method by detecting some types of cell clearly.
In the tracking part, when compare to the compactness and hybrid merging, this proposed-method would have the greatest tracking accuracy. at the same time the tracking accuracy would decrease when the cells number in image increase. furthermore, the accuracy decrease rate is also lower than other two method.
For evaluating the segmentation result, it uses the parameters true positive (TP), false positive (FP), false negative (FN), precision (P), and recall (R). and the parameter P is a measure of the exactness of the cell detection, and the parameter R used to measure the completeness. and for the frame choose, it picks 700 frames form videos sequences. this evaluate method would give a complete evaluation of the method because it would describe the right class type and wrong class type clearly. So, it would be convenient to observe the flaw or advantage of the method. Since the accuracy is high and the method can deal with different types of cell, this function could make contribute to the cells analyze in hospital or biological lab.
For evaluating the tracking result, it is measured by the ratio of the detected track route to the actual track segments observed in the image sequence. This method can get an accurate result when the observed result is precise. because of the lower accuracy in high density cells image. This tracking method would still benefit the movement of cells research when the background cells number is limited, this may be suitable for some research who analyze the cells with low density.
For the experiment, it may add more types of samples to test. For the detection part, may use more types of cells to test And for the tracking part, because the frame is pick random, so that some situation may not occur. to compensate this, some extra test sample should be created. like made some combination, mitosis and new cells, mitosis and cells disappearance, new cells and cells disappearance and so on.

Conclusions

This paper has clearly described the approach to divide the cells and cells tracking. The divided method can keep separate cells well when the cells partial overlaps or have dynamic changes in the cell-shape while migration. In the tracking part, the features of the cell used to calculate is displacement, skewness, color compatibility, area overlap, and deformation. Count more feature in would lead higher accuracy. The trajectory recovery part can also process the problem of broken trajectory. And most important, this method is a robust one which means it can deal with many types of cells situation.
However, there are still some place the method can increase. The segmentation part may be not able to deal with some special cells without clear nuclei well. And because the tracking part have combined many features that would cause the intensive calculation of the method.

Finally, about the problem be addressed in before, the cells could be captured irregularly so that there may have no cells in consecutive frames was not pointed in the method. in this way, the problem of infrequence capture problem may need more attention in the future research. Furthermore, the future research should focus more on the different cells divided, and the optimization of the tracking method to be with less feature needed, less calculation and higher accuracy. in order to achieve this goal, the deep learning model might be considered to apply in some process part.

References

[1] K. Thirusittampalam, M. Hossain, O. Ghita, and P. Whelan, "A novel framework for cellular tracking and mitosis detection in dense phase contrast microscopy images," *IEEE J. Biomed. Health Inform.*, vol. 17, no. 3, pp. 642–653, May 2013.