Biological Cell Detection and Tracking in Time-Lapse Microscopy

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I. INTRODUCTION

As known to all, cell tracking becomes more and more important in biological and medical area. This task attracts tremendous research attention and gains quite a lot positive results in recent years. Our project in this course requires us to analyse sequences of time-lapse microscopy images and work as a team to solve three different tasks.

Task one is related to cell detections, cell tracking and cell counting. From the lectures we have learned a lot of segmentation methods and pre-processing techniques, which are very useful to deal with this kind of problems. Task two requires us to detect a specific cell motion, also known as mitosis events. A parameter-combined method should be useful because the features of both cell motion and cell topology are equally important and practical. Task three is mainly about some computations based on the results of task one, such as cell speed, total distance and net distance. Therefore, the accuracy for the cells detection and localization in task one is very important and it directly leads to the accurate results in task three.

The dataset we use comes from Cell Tracking Challenge(http://www.celltrackingchallenge.net). These three datasets, including DIC-C2DH-HeLa, Fluo-N2DL-HeLa, PhC-C2DL-PSC, have different characteristics. The DIC-C2DH-HeLa was captured by Dr.G.van Cappellen in Erasmus Medical Center. There are 84 frames in two sequences and 155 frames in the other two sequences. Every frame is a grayscale image of size 512 × 512. The Fluo-N2DL-HeLa comes from Mitocheck Consortium. Four sequences have the same number of 92 frames and the size of each frame is 1100 × 700. The PhC-C2DL-PSC was captured by Dr.T.Becker in Fraunhofer Institution for Marine Biotechnology. Two of four sequences have 426 frames and the other two have 300 frames and every frame has 720 × 576 pixels. In addition, all three datasets have two mask sequences too.

After analysing the characteristics of each dataset, it can be figured out that the DIC-C2DH-HeLa is difficult in the data pre-processing stage because of the cells cluster features. It is hard to find the boundary between each other when two cells are in the same cell cluster. Therefore, under-segmentation may occur. There are low contrast between the background and the cells in the Fluo-N2DL-HeLa, which means erosion, dilation and other traditional ways to process images can be useful. In comparison with them, the PhC-C2DL-PSC has a relatively larger data and it is harder to evaluate the results because we basically compute the accuracy manually. Further details of method and implementations will be explained in the Method part.

II. LITERATURE REVIEW

A. Segmentation

Image segmentation is the process of dividing an image into different parts with different meanings [1]. For example, an image can be divided into foreground and background. Image segmentation can simplify graphics into a form that is easier to analyse. This technology is widely used in medical imaging, face or fingerprint recognition, machine vision, traffic control, etc. There are many mature methods for image segmentation, according to relevant literature, we have sorted out some typical image segmentation algorithms and summarized their advantages and disadvantages. The accuracy of segmentation is very important in this project because excessive segmentation can easily be confused with cell mitosis.

1) Thresholding: Thresholding is the easiest way to segment image, it converts the grey-scale picture into a black-and-white image. The specific clip-value of this conversion is our threshold. Compare the value of each pixel in the image with the preset thresholding. if the value is more than preset thresholding, the pixel belongs to the foreground, the opposite is the background.

The focus of this method is how to select the threshold. We will introduce two typical methods here. One is K-means algorithm, it choose k objects as the initial cluster centre and determine which cluster it belongs to according to the similarity between the remaining object and the centre point, at last, consider the centre again. Iterate the last two steps to make the cluster stable (no longer change), that is, convergence. The similarity is not only a consideration of distance, but can also be extended to features such as intensity, area, and boundary curvature [2]. Another method is Otsu's method, We can simply understand this algorithm as Traversing the threshold from 0 to 255 to find the optimal t that maximizes the variance g between classes:

$$g = w_0 \cdot (\mu_0 - \mu_1)^2 + w_1 \cdot (\mu_0 - \mu_1)^2$$

$$= w_0 w_1 \cdot (\mu_0 - \mu_1)^2 , \quad (1)$$

where w_0 and w_1 are the ratio of foreground and background pixels to the total number of pixels, and the sum is 1. μ_0 and μ_1 are the average gray values of the foreground and background respectively.

The thresholding method is also a very error-prone algorithm, the heavy noise in live-cell imaging and very large intensity changes will make the thresholding method fail.

2) Template matching approach: The previous method has poor cutting performance for the adhesive part, and there may be less-segmented or over-segmented. Template matching approach solves this problem very well. First, extract the same number of pixels at the edges of the image to be processed and the template image and these extracted pixels are feature points. Then calculate the variance between each pixel and the feature point. If the variance fluctuates within a certain range, the two points are similar. Repeat the above steps to scan the entire picture and update the position coordinates of the two most similar pixels. But this method does not perform well when the cell morphology changes greatly

3) Watershed transform: The watershed algorithm compares the grayscale space of the image to the geographic structure of the earth's surface. The grayscale value of each pixel corresponds to the altitude, the binarization threshold corresponds to the horizontal plane, and the place lower than the threshold corresponds to the valley. Water is injected into the valley and dams are built on the watershed. In the end, the dams form the dividing line of the image that we are looking for. The most obvious disadvantage of the watershed algorithm is that it is too sensitive to noise, resulting in over-segmentation.

4) Deformable models: Deformable model is also called model-evolution approaches. It combines the information form the pending images with knowledge about biology [2]. This approach is based on Darwin's theory of evolution, it is an artificial intelligence technology used to solve problems by simulating biological evolution processes and mechanisms. It mainly used the selection, reorganization and mutation operations to solve problems. Because this algorithm is too complex, considering the time of the project, we did not conduct in-depth study and research.

B. Bounding

Draw a bounding box for the cell after segmentation. After the cell nucleus is found, a rectangular box is generated according to the cell characteristics. There are DeepCell and U-Net models to detect nuclei [4]. The DeepCell use the neural network to perform the 'general-purpose biological image segmentation', this model is suitable for the small dataset. U-Net model uses an encoder that reduces the resolution of the input image through a multi-layered base layer and a decoder that reconstructs the image by increasing the resolution. U-Net is easy to operate, users can train all kinds of data which they need in the ImageJ (plug-in) interface compared with the DeepCell, U-Net may have detection error on the boundary of the image. Using deep learning can have a good performance in finding nucleus but consume lots of time and memory on training the dataset. In this project, we use the DeepWater model, which will be described in detail in the method part.

C. Tracking

The process of finding the cell trajectory is the process of identifying and connecting each segment of the cell trajectory in the image sequence. According to relevant literature, we have sorted out three ways to track the movement of the cell, namely tracking by detection, tracking by model evaluation and tracking by filtering. Tracking movement by detection is the most common method. After completing the segmentation of different cells, perform tracking by identifying the same cell in subsequent frames. The tracking by model evaluation method tracks cells through features such as image intensity. The tracking by filtering method is a challenging and conquered technology. In the case of low signal-to-noise ratio (SNR), this probabilistic method is not easy to implement.

D. Mitosis Detection

Mitosis is the process by which the mother cell distributes the chromosomes in the nucleus to two daughter cells. In addition to chromosomes, cell structures such as cytoplasm are also equally distributed to the two daughter cells. The information provided by mitosis section can promote the development and progress of biological and medical applications. There are several methods of mitosis detection shows below.

1) Tracking based method: There are three tracking based methods. One is using the specialized mean-shift kernel to identify the cells that started mitosis. After we find the cell trajectory, we can search for mitosis in reverse order from back to front. So just look for two highly similar cells that are gradually approaching [3]. The second method is using a Cellular Tracking framework, this framework, this method track forward and backward with segment drive method, the forward tracking generates the tracking results, the backtracking build a trajectory [4]. Another method is to use Kalman filter to predict the movement of cells and look for mitotic events based on cell boundaries and cell areas near the predicted point [5].

2) Tracking free method: There is a method for mitosis detection using a support vector machine (SVM). This method requires preprocessing of the image, and then extracts candidate spatiotemporal volumes, area, shape, and intensity as features, and finally uses SVM to classify all image sequences [6]. Another method solves the optimization problem through an online learning algorithm. This method uses a sparse representation of mitotic cells to optimization:

$$(\Phi^*, W^*) = arg \min_{\Phi \in \mathbb{C}, W \in \mathbb{R}^{M \times N}} \sum_{i=1}^{N} (\| X_i - \Phi \cdot w_i \|_2^2 + \gamma_1 \| w_i \|_1 + \gamma_2 \| w_i \|_2^2), s.t. w_i \geq 0, \quad (2)$$

where $\Phi = \{\phi_i \in R^{d \times 1}\}_{i=1}^{M}$ is basis set, $X = \{X_i \in R^{d \times 1}\}_{i=1}^{N}$ is the low level features of the input, $w_i \in R^{M \times 1}$ is the sparse vector $W = \{w_i\}_{i=1}^{N}$ between the X_i and basis, γ_1 and γ_2 are the sparsity and consistency respectively， w_i is the input for training in SVM. There are many mature tracking free methods, so I won't repeat them one by one.

3) Hybrid method: The hybrid method is divided into three steps. First, extract the candidate sequence from the whole dataset. this step can filter out images that may have a mitotic event. Secondly, extract features to do the classification. We can use Histogram of Oriented Gradient (HOG), GIST, Scale Invariant Feature Transform (SIFT), Unique Scale Gradient Histogram or even Convolutional Neural Network (CNN) to extract features [7-12]. The third step is to use the graphic model for mitosis detection. For example, these mature graphical models developed by predecessors can be used for mitosis detection: Hidden Markov Model (HMM), Conditional Random Field (CRF), Hidden Conditional Random Field (HCRF), Event Detection Conditional Random Field (EDCRF), Two Labeled Hidden Conditional Random Field(TL-HCRF), Max-Margin Hidden Conditional Random Field and Max-Margin Semi-Markov Model (MM-HCRF+MM-SMM) and Hidden State Conditional Neural Field (HSCNF).

4) Deep learning: Hierarchical Convolutional Neural Network (HCNN). The input of HCNN is the original images and the difference image between frames, and features composed of appearance and motion information are trained with the help of a three-layer architecture. The 3D Convolutional Neural Network (3D-CNN) has five volume base layers and two fully connected layers. It takes the original image as input and uses 3D convolutional kernels to extract features. But as the 3D convolutional kernel becomes deeper and deeper, the network becomes more and more complex, and the result is prone to overfitting [13].

III. METHODS

Some microscopy images are of poor quality due to the controlled environment required by different image acquisition systems. There might be shading artifacts and noises appear on the image due to inconsistent illumination, different sensitivity of camera, or even dust on the lens of the image acquisition systems[14]. In addition, the contrast between the cells and the background is sometimes low which will make the selection of a threshold for the segmentation of cells extremely difficult. Therefore, some form of preprocessing is necessary and a reasonable preprocessing will facilitate the detecting process.

A. Preprocessing Dataset

1) Preprocessing Dataset 1: The images in dataset 1 are not ideal for detection. The contrast between the cells and the background is low and there are many noises and cellular structures inside the cell which makes the detection of cells difficult. We've tried some morphology methods such as gamma correction, Gaussian filtering, morphological opening operation with erode and dilate operation, and Sobel gradient. None of them resulting in a reasonable image for detection using traditional methods. Therefore we decided to apply a method combining convolutional neural network and a marker-controlled watershed segmentation for dataset 1. Before CNN training, all the images are normalized using histogram equalization. Then data augmentation is done by using randomized rigid geometric transformations and scaling to prevent overfitting. After that, full annotation and weak annotation are trained so that two reference outputs, one for cell detection by markers and another for the recognition of an image foreground, could be calculated.

2) Preprocessing Dataset 2 and Dataset 3: The images in dataset 2 are extremely bright such that we can't even detect cells by our eyes. So gamma correction is applied. Gamma correction will map luminance levels to compensate the non-linear luminance effect of display devices so that the human perceptive bias on brightness is synchronized. With gamma = 1.5, the over-bright situation of images in dataset 2 is solved and we were able to clearly see all the cells. After that, there are still some noises remaining in the images. In order to remove all the unnecessary noises and details, Gaussian filtering is applied. Gaussian filter will generate a unique local maximum inside the cell if a cell has a uniform intensity distribution and reduce unnecessary noises and details, which will make the cells clearer and easier to detect. After performing Gaussian filtering, a binary plus otsu threshold is applied to make the images only black and white so that the cells are obvious and focused.

The images in dataset 3 are fairly clear. We still perform gamma correction followed by Gaussian filter and a binary plus otsu threshold in terms of uniform.

After performed all the preprocessing methods, all the images are converted with only black and white, and all the cells are clearly shown which are ideal for using traditional detection methods.

B. Cell Detection

1) Detection of Dataset 1: A pair of fully convolutional CNNs are trained using the two reference outputs, with one network predicting cell marker pixels and the other network predicting the image foreground [15].

After training, the prediction of whether a pixel is a marker is used to compute the watershed marker function that is a binary image with each connected pixel stands for a cell marker. Then, the marker function is used to define segmentation seed in a marker-controlled watershed segmentation.

The prediction of the foreground is transformed to the watershed segmentation function and a mask of cell regions. Finally, a marker-controlled segmentation is applied using computed marker function and segmentation function only to pixels within the cell regions.

2) Detection of Dataset 2: Considering the cells in Dataset 2 are kind of hollow causing the remaining cytoderms are not well connected, we decided to fill the hollows first using the FloodFill function imported from OpenCV. Then an erosion operation is applied to reduce the connection of touching cells so that they could be detected easily.

Finally, we use cv2.findContour to find all the contours of each cell so that the corresponding bounding box could be calculated and drawn. All the cells are now detected.

3) Detection of Dataset 3: The cells in Dataset 3 are not hollow but complete so the FloodFill function applied in dataset 2 is not necessary. Besides, the contrast between the cells and the background is relatively high, so it is easy to detect the cells by finding all the region maxima and the maxima will be the nuclei. We applied regmax function imported from mahotas to finish the task. After finding all the nuclei, we could simply draw the bounding box using the contours computed by findContour function.

C. Cell Tracking

Instead of choosing mature tracking models to do the tacking task, we use our own method to get a substantial result. In the previous tasks, we have successfully processed bounding boxes for each image in the time-laps microscopy sequences. Therefore, we take the first frame of one sequence as an initiation and allocate an ID and frame number to every center of all the bounding boxes. In the next image, for each center, we compute the distances of this center to all the other centers. Then we define a threshold and this can determine whether the center in the next image is the same center by comparing the minimum distance and the threshold. If it is the same cell, we allocate the same ID and current frame number to this center, otherwise we consider it a new cell and allocate a new ID and frame number to it. We also draw the path in the next image. After applying this algorism to all the images, we can get a final result of the moving path in the last frame.

D. Detection of Cell Division (Mitosis)

Although in methods above, we have detected normal individual cells, there still may be some cases that cell division events take place, namely mitosis events. It is a processing that one mother cell splits into two daughter cells, even along with cell motion. In order to detect cell division events, we combine cell motion and cell topology parameters. In detail, we use distance ($E_{distance}$) and area (E_{area}) as parameters.

The parameter $E_{distance}$ measures the distance the distance between the center of mother cell's boundary in frame N and the center of daughter cell A's boundary in frame N+1,

$$E_{distance}(A, M) = \sqrt{(x_A - x_M)^2 + (y_A - y_M)^2}, \qquad (3)$$

where (x_M, y_M) refers to the mother cell nucleus M's position in frame N and (x_A, y_A) refers to the daughter cell nucleus A's position in frame N+1.

The parameter E_{area} is defined as the area difference between the mother cell M and sum of two daughter cells, namely A and B,

$$E_{area}(M, a, b) = |S_M^{N-1} - (S_a^N + S_b^N)|, \qquad (4)$$

where S_M^{N-1} refers to the mother cell M's area in frame N-1, S_a^N and S_b^N refer to daughter cell A and B's area in frame N respectively.

We use the above two parameters to estimate and judge if there are mitosis events take place. This method is based on a hypothesis that if a mother cell has finished dividing into two daughter cells, the distance between either one of the daughter cell's nucleus and the mother cell's nucleus is close enough. As mentioned above, when we track each cell's motion path, we identify them by their IDs and frame number N if they appear in the N^{th} frame. We use distance between cell nuclei to distinguish old and new cells in different frames, aiming to ensure that each cell has its own ID. In other words, we set a threshold distance D_{th} that if the real distance between each pair of cells D is larger than the threshold distance D_{th}, we will assign both the cells different IDs. Otherwise, if the distance between the pair of cells is smaller

than the threshold distance D_{th}, it results in one ID containing two cells, and we judge the two cells in this case as a possible mitosis event.

In order to detect mitosis events more accurately, we introduce E_{area} parameter to the method. We suppose when a mother cell splits into two daughter cells, the sum of the daughter cells' area is close to the mother cell's area. Hence, we set a threshold area difference S_{th} that if the area difference E_{area} is less than the threshold area difference S_{th}, we judge the two daughter cells as a possible mitosis event.

Hence, under the condition that the $E_{distance}$ parameter is satisfied, if the E_{area} parameter also satisfies the above condition, we determine the two daughter cells in the current frame N come from the mitosis event in previous frames.

E. Analysis of Cell Motion

When analyzing the distance of cell movement, we all analyze the movement of the center of the bounding box. For task3-1, calculate the cell movement rate at a certain point using the displacement of the cell in the current frame and the previous frame, divided by the time interval between frames, here we assume it is 1.

Task3-1 needs to calculate the speed of the cell at that time point. The distance of this part is the difference between the position of the same cell in two adjacent frames.

Task3-2 is to calculate Total distance travelled up to that time point. This is obtained by summing the displacement (Euclidean distances) between every two consecutive frames.

$$total\ distance\ =\ \overrightarrow{AB}\ +\ \overrightarrow{BC}\ +\ \overrightarrow{CD}\ +\cdots, \tag{5}$$

where the letter represents the position of the cell in each frame.

Task3-3 is to find net distance travelled up to that time point. This step is to find the linear distance between the cell position in the current frame and the cell position in the initial frame.

$$net\ distance\ =\ \overrightarrow{AZ}, \tag{6}$$

where A is the position from the initial frame, Z is the position from the current frame.

Task3-4 is to find the confinement ratio of the cell motion. This is to find the ratio of the results of the first two steps.

$$confinement\ ratio\ =\ \frac{net\ distance}{total\ distance}, \tag{7}$$

IV. EXPERIMENTAL SETUP

Our experiments are based on four time-lapse video sequences of fluorescent counterstained nuclei or cells (Fluo) moving on top or immersed in a substrate, along with Phase Contrast (PhC), and Differential Interference Contrast (DIC) microscopy videos of cells moving on a flat substrate.[16] We perform the experiments on an Intel Core i5-8300H 2.30 GHz processor with DDR4 2666MHz of RAM. The working environment we used is Python 3.7. We combine the graphical presentation and count of cells detected as qualitative and quantitative evaluation metrics.

A. Evaluation of Cell Detection

For qualitative evaluation, we visually observe whether there is a misjudgment of cell segmentation, such as under-segmentation or over-segmentation. As mentioned above, we have drawn a bounding box around each cell after segmentation, thus, for the presented graphical output, we need to observe whether there are multiple cells in one bounding box and whether the cell in each bounding box is complete.

For quantitative evaluation, since we have calculated the count of cells detected, it is reasonable to verify the performance of cell detection by calculating the accuracy of count of cells. The parameter accuracy is carried out to evaluate our method.

$$accuracy = \frac{count\ of\ detected\ (dividing)\ cells}{total\ count\ of\ (dividing)\ cells}, \tag{8}$$

B. Evaluation of Cell Motion (Tracking Path)

When a cell moves, we have tracked its moving path by drawing lines. For qualitative evaluation, we visually observe whether the path is correctly drawn when the same cell moves in different frames. Moreover, we need to observe when a new cell appears in the current frame because of sudden entry or mitosis event happen, the path of the new cell should be drawn from the next frame instead of the current frame.

C. Evaluation of Cell Mitosis Detection

For qualitative evaluation, if a mother cell is divided into two daughter cells, we can visually observe that the new split cell has its new ID, and there will be a new path drawn from the next frame for the daughter cell.

For quantitative evaluation, since we have calculated the count of dividing cells, we can evaluate the performance of cell mitosis detection by calculating the accuracy of count of cells, using parameter accuracy as mentioned above.

V. RESULTS AND DISCUSSION

As mentioned in Experimental setup part, we combine qualitative and quantitative analysis methods to evaluate our project.

A. Results of Cell Detection

For a qualitative result, the segmentation images of each dataset are shown in Fig. 1. As shown in the image, there is

only one cell in each bounding box and the cell is complete with no part of the cell outsides the bounding box.

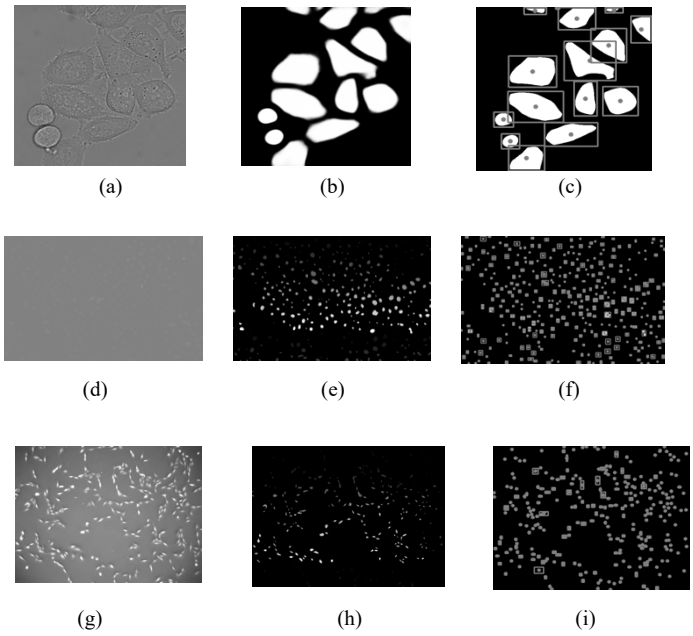

Fig. 1. Original image, segmented image, segmented image with bounding box for three datasets. (a), (b), (c) for Dataset 1. (d), (e), (f) for Dataset 2. (g), (h), (i) for Dataset 3.

For a quantitative result, the performance evaluation table is shown as belows. The accuracy is calculated by the number of true detection of cells dividing the total number of detected cells, using (8) in Experimental setup part.

TABLE I. ACCURACY OF CELL DETECTION

Dataset	Total Frames	Ground Truth	Count of Detected Cells	Accuracy(%)
Dataset 1	83	1411	1340	94.96%
Dataset 2	91	26160	24115	92.18%
Dataset 3	299	69851	61937	88.67%

It is obvious that the accuracy of Dataset 1 using deep learning is fairly high, meaning the deep learning method is robust in such situation. The accuracy of Dataset 2 and Dataset3 are fine, which means the traditional method still works in such cases but could be improved.

B. Results of Cell Tracking

For the results of cell tracking, from a qualitative aspect, the results are shown in Fig. 2. In addition, The final tracking path of existing cells is in the last frame of every sequence. It can be figured out that the tracking path is clear and reasonable. The reason is that we manually observe some of the paths drown to check if they are generated by the same cells. We also consider the special conditions when mitosis occurs or some new cells suddenly come into the image. In these cases, new path will be generated in the subsequent frame. These results are also the keys to compute the distances in task three. As the results in teak three shows in the next part, the tracking results are substantial.

However, we do not have evaluation matrix to do quantitative analysis and due to the method we use, cells with high moving speed are hard to detect which decrease the real accuracy of tracking.

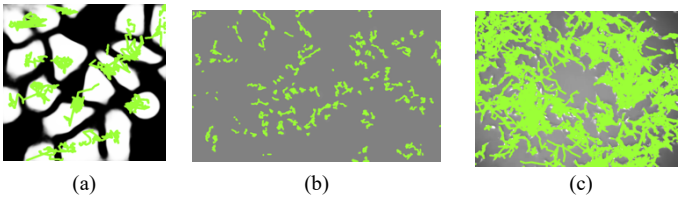

Fig. 2. Cell tracking paths for three datasets in different frames. (a) Dataset 1, Sequence 2, (b) Dataset 2, Sequence 3, (c) Dataset 3, Sequence 1.

C. Results of Detecion of Cell Division (Mitosis)

For a qualitative result of detecting cell division, we based on the dictrionary we built to find the frame which has mitosis events, recording the divided cell's ID as well. When we get the frame and cell ID, we can validate if there are divided cells in the specified frame. The example results is shown in Fig. 3. It is obvious that in Fig. 3(b), Cell 0 didives into Cell 0 and Cell 17, compared to Fig. 3(a).

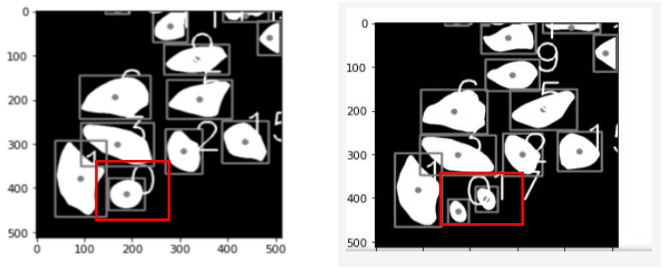

Fig. 3. Detected cell division between the two frames. (a) Frame 10 in Dataset 1, (b) Frame 11 in Dataset 1.

As for the count of dividing cells, we can calculate by the length of the new-built dictionary, which records the division of cells.

However, instead of detecting dividing cells in each frame, we could only find the frames which the cells has already divided. Our results is based on the hypothesis that the mother cell is dividing from the first frame it appears to the last frame before it finished division completely. Moreover, it is hard to distinguish mitosis events manually, so we do not have quantitative results of detecting cell division.

C. Results of Cell Motion Analysis

In the cell motion section, we generated four files to record the results, called motion, net, ratio, total. These four files correspond to the results of the four questions in task3. The

following tables are part of the data in the DIC-C2DH-HeLa folder.

TABLE II. PART OF MOTION ANALYSIS OF DATASET 1

	Cell ID	Speed	Net distance	Total distance
t001	-			
t002	0	4.24	0.28	0.28
	1	3.0	0.1	0.1
	2	4.47	1.75	1.75
	3	3.16	0.41	0.41
	…	…	…	…
…	…			
t012	0	3.16	41.16	1079.46
	1	4.47	4.61	889.70
	2	6.32	35.71	2016.67
	3	2.0	2.0	837.24
	…	…	…	…
…	…			
t083	2	1.41	43.37	4.76×10^{24}
	27	2.0	32.62	1.62×10^{14}
	35	1.0	27.24	7716540.0
	47	2.0	19.60	4297.07
	54	0	1.14	1.14
	…	…	…	…

TABLE III. PART OF DISTANCE RATIO OF DATASET 1

	t001	t002					
Cell ID	-	0	1	2	3	…	…
Ratio	0	1	1	1	1	**…**	

	t012					
Cell ID	0	1	2	3	…	…
Ratio	0.04	5.18×10^{-3}	0.02	2.39×10^{-3}	**…**	

t083				
2	27	35	47	54
4.76×10^{-24}	2.01×10^{-23}	3.53×10^{-6}	4.56×10^{-3}	1

The first frame is the starting frame without displacement and speed. All data in the table are to two decimal places. For cells with the same net distance and total distance (e.g t083 cell 54), these kind of cells may have been inactivated.

There are some errors in this part of the data. The cells in the PhC-C2DL-PSC data set move faster. When calculating distance, we need to judge the distance between cells with the same ID in different frames, but when we judge whether cells in different frames should have the same ID, our method will set a threshold. When the distance between two similar cells is less than this threshold, they are the same cell and will have the same ID; if the distance between two similar cells is greater than this threshold, it may be caused by mitosis, so it will have New ID. This method of assigning cell IDs may identify a fast-moving cell as two cells.

VI. CONCLUSION

Task1 and Task3 were completed with reasonable accuracy and it is shown that for different images, different techniques should be applied. The traditional method, e.g. morphology opening operation followed by erosion and dilation along with some sort of filtering, for cell detection is trustable in certain situations. However, it has its limit. The traditional method can not correctly detect cells with complex cellular structure inside cause the complex cell structure might be considered another cell. That's when the deep learning technique comes in. With deep learning techniques, the pixels of cells could be predicted and be used in a marker controlled watershed function so that the inside structures would not be considered new cells anymore.

Task 2 is the most challenging task and it is partly finished. Although we could detect divided cells, we could not find a way to know exactly which frame the cell starts to divide. This might be improved by developing a new algorithm for detecting nuclei rather than the center of the bounding box. Because some overlapping cells which are just starting to divide are considered one cell using our method cause there is one bounding box. If we could know there are two nuclei, we will be able to detect those two cells.

All the methods we used are evaluated both qualitatively and quantitatively. The results have demonstrated that our methods are reasonably stable and accurate given provided datasets.

VII. CONTRIBUTION

Hexuefeng Xiang (z5100589):
Read the reference documents. Preprocessing Dataset 2 and Dataset 3, Code for Task 1-2. Finish the methods, results, conclusion part in the report and prepare for the demo.

Anqige Wu (z5199351):
Read the reference documents. Preprocessing Dataset 1 and code for Task 2. Finish the methods, results, experimental setup part in the report. Prepare the demo PPT.

Yuao Jiang (z5217274):
Read the reference documentss. Code for Task 3. Finish the introduction, methods, results part in the report and prepare for the demo.

Rong Zhen (z5225226):
Read the reference documents. Preprocessing Dataset 1 and code for Task 2. Finish the methods, experimental setup part in the report and prepare for the demo.

Dan Su (z5226694):
Read the reference documents. Code for Task 3. Finish the literature review, methods, results part in the report and prepare for the demo.

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