Conference Paper Title*

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***Abstract*—This document is a model and instructions for LaTeX. This and the IEEEtran.cls file define the components of your paper [title, text, heads, etc.]. *CRITICAL: Do Not Use Symbols, Special Characters, Footnotes, or Math in Paper Title or Abstract.**

***Index Terms*—component, formatting, style, styling, insert**

I. Introduction

A good understanding of living things needs various analyses of its anatomic and dynamic properties, which can be gained from live-cell imaging experiments [**?**]. The more data these experiments generate, the better the behaviour of cell populations can be represented. Therefore, for better result, these experiments often produce a great number of time-lapse image data. It helps in high-throughput spatiotemporal measurements of cell behaviors like migration, mitosis, apoptosis and the reconstruction of cell lineages [**?**], [**?**], but makes the computing complex. Other challenges are related to the quality and content of the image data like poor contrast with high noise levels, irregular cell contours, entry and exit of the cells [**?**], [**?**]. To deal with these large amount of data with different quality and content, people have developed many kinds of cell detecting and tracking techniques.

For detecting, the easiest way is to use threshold if cells in images have different intensities than their neighbouring areas [**?**]. However, due to its simplicity, it is one of the most error-prone method and often fail when noise levels are high, contrast are low or the cells overlap. A complex and popular method for detecting and segmentation is template matching, but it only performs well when cell contours are simple and regular [**?**]. Another popular but more robust approach is watershed transformation, which can completely separates cells but are prone to over-segmentation. Model-based segmentation can produce more sensible results, but are prone to under-segmentation. Therefore, both of the approaches mentioned before need some postprecession [**?**].

As for tracking techniques, finding the nearest cell in last frame based on their centroid position is a straightforward approach. It works well if the cells in the images move in a slow pace and not close to the other cells. In the cases that cells are intensively populated or move fast, this method should be extended to include some other basic properties such as areas, contours, overall mean distances, curvature and intensities [**?**]. But it still can not deal with the movement and apoptosis of some cells. In 2013, the rank-based filtering mechanism are refined in maximum cardinality minimum weight bipartite matching [**?**]. The matched pairs are sorted based on their matching cost and only the top q percentage of the pairs are selected as correct matches, which can deal with the exit or apoptosis of the cells with higher probability. Another trend intending to use stochastic knowledge are called probabilistic methods, including Bayesian inference, Kalman filtering and Particle filtering. They are also powerful techniques for tracking cells.

Our task is to try as many computer vision methods as possible, compare their difference and select the most appropriate way to detect, track and analyse cells. We have three data sets with different quality and face three kinds of challenges. Firstly, cells in DIC-C2DH-HeLa set are so big and closer to each other that it is a little difficult to detect them and make a segmentation. We mainly use two different ways to generate marks for later segmentation. The first method we exploited is called J-net, which is a multiresolution neural network for semantic segmentation. Based on the masks produced by this approach, we then use some basic image processing operations, like threshold, Gaussian blur, erosion, dilation and watershed, to improve the segmentation. And the other one is called deep water transformation, which can deal with this data set perfectly as well. Cells in Fluo-N2DL-HeLa set have low contrast and need some basic image pre-processing strategies. We use Gaussian blur to remove noises in the images and use threshold to increase the contrast for better visualization. After that, we use erode and dilate to separate the cells. Cells in PhC-C2DL-PSC set are intensively populated and some of them move in a high pace. We firstly use erode operator and Gaussian blur to get rid of the noises. Then we use threshold to increase the contrast. This data set can also be dealt with the deep water transformation mentioned above. As for the tracking part, we choose the nearest-neighbor linking approach based on the distances and areas, which is not so sophisticated and can match most of the cells correctly.

In summary, the contribution of this paper include:

- We propose a model that can deal with all three different kinds of data sets.
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II. Literature Review

A. Cell segmentation in computer vision.

Cell segmentation distinguishes individual cells from images [1] and could be regarded as the most significant and

Identify applicable funding agency here. If none, delete this.

the most fundamental task in cell analysis. The reason is that subsequent cell analysis, such as mitosis and motion, often require cell boundary as an essential feature to do further processes [2].

In recent years, various state-of-the-art approaches have been proposed to improve cell segmentation. Existing traditional methods such as thresholding, region growing, seeded watershed segmentation, and edge-base segmentation [9] mainly focus on features of images. For instance, Chen et al. proposed a method to segment cells by performing global thresholding based on Otsu's algorithm [7]. However, this method only has an excellent performance in images with separated cells, not for those in which cell contours touch or overlap with others. Wählby et al. proposed an edge detection method based on the region, in which they use the gradient magnitude of objects pixels and background pixels in the image to do watershed segmentation [8]. The result of these methods is, respectively, prone to be influenced by the noise and would be segmented overly [1]. More sophisticated methods often apply deep learning technologies to improve the accuracy of cell segmentation [3]. For example, Ronneberger et al. proposed a U-Net architecture based on the annotated datasets after data augmentation and use autoencoder to reconstruct image to obtain neuronal structures segmentation [4]. Van Valen et al. proposed a framework named DeepCell, which used optimized deep convolutional neural networks to segment biological images and could be performed in different kinds of biological cell types [5]. Nath et al. proposed a time-saving approach based on four or fewer level set algorithm to segment moving epithelial cells [6]. However, the performance of the approaches mentioned above precisely depends on the types and shapes of cell datasets we would process. Hence, it is unrealistic to achieve proper cell segmentation by only one way, and we propose to combine deep learning technology and traditional computer vision methods to segment different cell datasets.

B. Cell tracking in computer vision.

Researching cells' activities like moving, dividing, and their health conditions in a certain period manually is an extremely time-consuming and inefficient work. In recent years, experts in the computer vision area have proposed some methods to automatedly track and analysis cell activities. These approaches could be presented in three broad categories [10]. The first one is establishing a tracking model to detect cells path. For example, Debeir et al. proposed to build a cell tracking path by Vitro phase-contrast in video based on the mean shift algorithm [11]. Ray et al. proposed tracking cells automatically by combing active contour and Kalman filter [12]. One tricky thing is that the fundamental structure of those model evaluation methods above cannot be used in mitosis directly [10], which means that other transformation needed to be done to get good tracking results. The second category is based on the result of the cell after segmenting. For example, Yan et al. proposed to use a classic watershed transform algorithm for cell segmentation first and then use its distance and cells' size to track their path [14]. The tracking result of this method lies in the performance of segmentation in no small extent. The last group is a framework based on Bayesian probabilistic. Kachouie et al. proposed a probabilistic model-based cell tracking method to locate separated cells [13]. In this method, one problem is that it does not have enough assumptions to establish models for different cells [10]. Inspired by the approaches above, we propose to track cells based on segmentation and use the distance between cells and their areas to identify cell activities.

III. Methods

A. Cell Segmentation

1) overview: The proposed network combines two existing network designs. The first one DeepWater network [1] is a combination of a convolutional neural network and a marker-controlled watershed segmentation. The other one is J-net [2], a multi-resolution neural network for semantic segmentation. The DeepWater network works for DIC-C2DH-HeLa dataset and PhC-C2DL-PSC dataset. And the J-net network only works for the DIC-C2DH-HeLa dataset. Moreover, normal watershed algorithm is introduced for the segmentation of Fluo-N2DL-HeLa dataset and PhC-C2DL-PSC dataset. Comparison of segmentation effects between different methods will be discussed in the experiment section.

2) DeepWater Network: In DeepWater network, two convolutional neural networks are trained. One (CNN_m) is for cell marker prediction, and the other one (CNN_c) is for image foreground (cell regions) prediction. With the outputs of the two CNN, marker-controlled watershed transformation is applied to generate the final segmentation. Both CNNs are in the same structure. Each network is made of 18 convolutional layers with kernel size 3×3. Hour-glass topology with skip connections is applied to the design. The last convolutional layer has a kernel of size 1×1 and a soft-max activation function. A weighted cross-entropy loss function

$$L(p, y) = -\frac{\sum_{q \in \Omega} w(q) \log \left(p_{y(q)}(q)\right)}{\sum_{q \in \Omega} w(q)} \tag{1}$$

where w is a pixel weight function that is unique for every training sample is used in the network design. Assume we have a cell mask ϕ and a set of masks of all cells Φ, to each pixel q we have in the image, we assign a weight $w(q) \in \mathbb{R}^+$ by the formula:

$$w(q) = \left[1 + a \sum_{\phi \in \Phi} \max(d - \|q, \phi\|, 0)\right] \cdot b \tag{2}$$

where $||q, \phi||$ is the Euclidean distance from q to the closest pixel ϕ.

With predictions from CNN_m, we treat them as markers and put them into the watershed transformation. The watershed only focus pixels within the cell regions. The segmentation function which distinguishes the predictions from CNN_m and CNN_c controls the segmentation process. In the final segmentation, only one segment is associated with one marker.

3) J-net: J-net is a simplified version of U-net [3], which merely includes the expansive path. This network assembles the second half of the U-net, therefore, it is named after its shape. In the design of J-net for the DIC-C2DH-HeLa dataset, three segments are included. Each segment is a combination of a CNN and either a deconvolution layer [4],which upsamples the output of the previous layer by the factor of two, or the final layer which creates the segmentation output.

In the first segment, the

IV. Experimental Setup

Explain the experimental setup and evaluation methods.

V. Results and Discussion

Provide statistical and visual results, along with a discussion of method performance and outcomes of the experiments.

VI. Conclusion

Summarise what worked / did not work and recommend future work.

VII. Contribution of Group Members

State each group member's contribution in brief. In at most 3 lines per member, describe the component(s) each group member contributed to.

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VIII. Introduction

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A. Maintaining the Integrity of the Specifications

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A. Abbreviations and Acronyms

Define abbreviations and acronyms the first time they are used in the text, even after they have been defined in the abstract. Abbreviations such as IEEE, SI, MKS, CGS, ac, dc, and rms do not have to be defined. Do not use abbreviations in the title or heads unless they are unavoidable.

B. Units

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Number equations consecutively. To make your equations more compact, you may use the solidus (/), the exp function, or appropriate exponents. Italicize Roman symbols for quantities and variables, but not Greek symbols. Use a long dash rather than a hyphen for a minus sign. Punctuate equations with commas or periods when they are part of a sentence, as in:

$$a + b = \gamma \tag{3}$$

Be sure that the symbols in your equation have been defined before or immediately following the equation. Use "(**??**)", not "Eq. (**??**)" or "equation (**??**)", except at the beginning of a sentence: "Equation (**??**) is . . ."

D. LaTeX-Specific Advice

Please use "soft" (e.g., `\eqref{Eq}`) cross references instead of "hard" references (e.g., `(1)`). That will make it possible to combine sections, add equations, or change the order of figures or citations without having to go through the file line by line.

Please don't use the `{eqnarray}` equation environment. Use `{align}` or `{IEEEeqnarray}` instead. The `{eqnarray}` environment leaves unsightly spaces around relation symbols.

Please note that the `{subequations}` environment in LaTeX will increment the main equation counter even when there are no equation numbers displayed. If you forget that, you might write an article in which the equation numbers skip from (17) to (20), causing the copy editors to wonder if you've discovered a new method of counting.

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- The word "data" is plural, not singular.
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- In American English, commas, semicolons, periods, question and exclamation marks are located within quotation marks only when a complete thought or name is cited, such as a title or full quotation. When quotation marks are used, instead of a bold or italic typeface, to highlight a word or phrase, punctuation should appear outside of the quotation marks. A parenthetical phrase or statement at the end of a sentence is punctuated outside of the closing parenthesis (like this). (A parenthetical sentence is punctuated within the parentheses.)
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An excellent style manual for science writers is [**?**].

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TABLE I
TABLE TYPE STYLES

Table Head	**Table Column Head**		
	Table column subhead	***Subhead***	***Subhead***
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[a]Sample of a Table footnote.

Fig. 1. Example of a figure caption.

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