HIT-CN

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Platform: Windows

Prerequisites: Python

HIT-CN: SUMMARY

Tracking-by-detection methods are widely used in multi-cell tracking. We perform multi-cell tracking based on the cell centroid detection. In the detection, cells are categorized into normal cells and mitotic cells, and multi-frame is used as input of the network. When tracking, cell associations is performed with the overlap intersection-over-union. A local cell status matrix is established to detect mitosis and then cell lineage is built up. Primary cell segmentation results are combined with cell centroid detection results to acquire more accurate results.

HIT-CN: PREPROCESSING

In this stage, six tasks are performed:

(a) After cell semantic segmentation using the U-Nnet [1], sizes between input and output images are inconsistent. To address this problem, the original image is expanded by adding a flipping version, to make sure the size of output image is consistent with that in the original image.

(b) Since the ground truth (GT) of the edge part of the image is ignored, the image border of the ignored part is completely black filled.

(c) Horizontal or vertical flipping operations are performed to expand the train TRA dataset.

(d) TRA GT of cell tracking can be categorized into a normal state and a mitotic state. Here the mitotic state is defined as the n_{mitotic} frames before and after mitosis. In our method, TRA GT for each pixel is redefined as 0 for background, 1 for normal cells, and 2 for mitotic cells.

(e) The amount of SEG GT is scarce, original images and SEG GT are cropped centered on each cell centroid with a size of $s_{\text{crop}} \times s_{\text{crop}}$. Furthermore, horizontal or vertical flipping operations are performed.

(f) SEG GT for each pixel is redefined as 0 for background and 1 for cells.

HIT-CN: SEGMENTATION

Cropped small samples which have two categories are used for training, and U-Net is used for primary cell segmentation. In test sets, the whole image is used to inference.

HIT-CN: DETECTION

Samples which have three categories are used to train, and another U-Net is trained for cell centroid detection. Since there is an interframe association in the mitotic stage, multi-frame is used as inputs, which makes the network more robust to detect mitotic cells. Here, the current frame is incorporated to previous n_{input} frames as inputs. The experiment results show this method acquire higher accuracy on mitotic cell detection, compared with single-frame input method. In our experiments, the loss weight w_{loss} is defined. Increasing the proportion of mitotic cells loss weight can make the network learn and detect better.

HIT-CN: TRACKING

The interframe cell associations are performed according to the overlap IOU [2]. According to cell centroid detection, an external box for each cell of size $m_{\text{size}} \times m_{\text{size}}$ is created, and relationships of candidate cells are matched according to the overlap IOU of the external box between frames. If tracking is lost, i.e., there is no matching detection in the current frame, the position of the previous frame is used as a replacement of the position in current frame. If there is still no matching detection in the after max_{miss} frames, the tracking is terminated.

HIT-CN: POST-PROCESSING

Combining cell centroid detection results of n_{detect} frames before and after the current frame, a local cell status matrix is created for a new trajectory. In the matrix, each element is marked as 0, 1, or 2, corresponding to background, normal cells and mitotic cells. When the number of elements marked as 2 is greater than a threshold min_{mitotic}, a mitosis may occur here. Then we assign the cell lineage, and mark tracking trajectory appropriately. All trajectories shorter than min_{track} are deleted. Jointing cell centroid results with primary segmentation results, we can acquire more accurate tracking results. Primary segmentation results are divided into individual cells according to cell centroid detection.

REFERENCES

1. Ronneberger O, Fischer P, Brox T. U-net: Convolutional networks for biomedical image segmentation. In *Proceedings of Medical Image Computing and Computer-Assisted Intervention*, 234-241 (2015).

2. Bochinski E, Eiselein V, Sikora T. High-speed tracking-by-detection without using image information. In *Proceedings of the 14th IEEE International Conference on Advanced Video and Signal Based Surveillance*, 1-6 (2017).