UVA-NL

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Platform: Linux

Prerequisites: None

UVA-NL: SUMMARY

We used an end-to-end cascade neural architecture able to model the movement behavior of biological cells and predict collision and mitosis events. Our approach uses **MU-Lux-CZ** for an initial segmentation which is then improved through processing by a Siamese tracker capable of matching each cell along the temporal axis. By facilitating the re-segmentation of collided and mitotic cells, our method demonstrates its capability to handle volatile trajectories and unpredictable cell locations while being invariant to cell morphology and image properties.

UVA-NL: SEGMENTATION

The initial segmentation relaxes further any constraint of dataset-tuned segmentation and applies the water deconvolution method [1]. The output of the initial segmentation produces finely segmented cells where the actual cell behaviors might not be correctly expressed. To be able to correctly reason about cell movement over time, cells need to be correctly tracked.

UVA-NL: TRACKING

The location of the cell in subsequent frames is identified using Siamese tracking. For tracking purposes, a SiamFC tracker [2], pre-trained on the GOT-10k dataset [3], is used. Tracking is done in the forward as well as the backward direction to predict the new location of a cell from the current frame to the previous and next frames. The cell segmentation is refined through tracking by detecting the occurrences of mitosis and collision events, using the same approach but in opposite directions along the temporal dimension. The working of the tracking module is as follows. Let I_t denote the t-th frame in a sequence of length T, and $S_t = \{C_t^1, \ldots, C_t^K\}$ be the set of detected cells in this frame. These are used to initialize the tracker at step t. For cell C_t^i, the predicted locations by the tracker in I_{t+1} and I_{t-1} are referred as forward (F_t^i) and backward (B_t^i) predictions, respectively. Collision and mitosis are then detected, descriptions of which follow below. Note that the movement prediction model explained here does not depend on the

morphology of the cell or on any other image property. Hence, it is directly applicable on top of any segmentation algorithm without the need for additional tuning.

Collision detection. Collision occurs when two cells share a fraction of their boundary , and this can be mistaken as a single cell during segmentation. When processing a new frame I_t, where $t > 1$, collision detection is performed first in which a cell C_t^i is considered to be a lump of multiple individual cells if the centroids of two or more cells in S_{t-1} lie within the tracked region B_t^i. If this is the case, C_t^i is re-segmented using the centroids of the two cells in the previous frame I_{t-1}. This collision detection procedure continues until each cell in I_t matches at most one cell in I_{t-1}.

Mitosis detection. Henceforth, a similar procedure as for the collision detection is performed for mitosis but in the opposite direction for t in the sequence of frames. Cells are matched in S_{t-1} to the detected cells in I_t. Namely a cell C_{t-1}^i is matched to a cell C_t^i if the centroid of C_t^i is inside the region F_{t-1}^i. Different from collision detection, however, C_{t-1}^i is also matched to C_t^i if the centroid of the region F_{t-1}^i lies within the boundaries of the cell C_t^i. This matching procedure yields a set of matches for each cell C_{t-1}^i, which we denote as M_{t-1}^i and its size as $|M_{t-1}^i|$. The state of cell C_{t-1}^i is then determined as apoptosis if $|M_{t-1}^i| = 0$, M_{t-1}^i if $|M_{t-1}^i| = 1$, or mitosis otherwise. In case of mitosis, the cell splits, thus the tracking of C_{t-1}^i ends and the cells in M_{t-1}^i are initialized with two new tracks, with C_{t-1}^i being their parent. The new cells in S_t that are not linked to any cell in I_{t-1} are interpreted as newly detected cells which start their life in I_t without link to a parent cell.

Re-segmentation. In case of a detected collision of two or more cells into a cell C_t^i, the cell C_t^i is re-segmented in such a manner that the new number of segments matches the number of colliding cells. This is achieved using watershed deconvolution [4]. To prevent over-segmentation of the cell C_t^i, which adversely affects segmentation accuracy, the relative position of the centroids of the cells in I_{t-1} are used as the seeds for the segmentation algorithm.

REFERENCES

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