Cell Tracking according to Biological Needs - Strong Mitosis-aware Multi-Hypothesis Tracker with Aleatoric Uncertainty

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Platform: Linux, Windows

Prerequisites: Python 3(.10), CUDA 11 with NVIDIA 3090ti or similar

SUMMARY

This submission is the official result to "*Tracking according to Biological Needs - Strong Mitosis-aware Multi-Hypothesis Tracker with Aleatoric Uncertainty"[1]*

We use test time augmentation and EmbedTrack [2] to estimate instance-wise segmentation and motion together with the aleatoric prediction uncertainty. Compared to [2], we do not only get a discrete position and a discrete motion vector per cell but 2D Gaussian spatial densities that describe both, the position and the motion. Additionally, we derive the probability of detection and multiple segmentation proposals based on test time augmentation and uncertainty estimation. The 2D Gaussians, the segmentation proposals, and the probability of detection are used to calculate association costs between cell instance segmentations of subsequent frames. With this information, we introduce an extended Multi-Bernoulli Mixture Tracker that can handle multiple segmentation inputs and model mitosis events explicitly. Within this framework, multiple likely association hypotheses are extracted per frame and re-evaluated a-posteriori to extract the most likely tracking hypothesis. Our basic framework is explained in detail in [1]. An overview and extensions are explained in the next sections.

PREPROCESSING

Equally to [2], we generate image crops of size crop_size and min-max normalize each image crop to the range [0, 1], where the minimum and maximum are set to the percentiles 1 and 99 respectively.

SEGMENTATION

To extract association features, we use the segmentation framework as reported in [2] with their original pre-trained models and apply test time augmentation to extract uncertainty distributions. Augmentations are applied as in [2] (flip, rotate) and we add scaled_images for some datasets, resulting in N augmentations. The N augmentations are used to calculate 2D Gaussian densities for the per-pixel offsets in the segmentation branch of [2]. The discrete cell centroid estimation from [2] is also relaxed to a 2D Gaussian using the offset predictions of all pixels belonging to the cell. Details can be found in [1].

TRACKING

We use a random finite sets (RFS) tracker very similar to the one described in [1]. The RFS tracker creates multiple association hypotheses per frame and models the probability of object existence implicitly. Instead of using a Poisson multi-Bernoulli Mixture tracker (PMBM), we use a comparable but less complex multi-Bernoulli Mixture tracker (MBM). For every frame and hypothesis h_sampling new hypotheses are sampled and pruning is applied until h_total hypotheses are left. Our MBM tracker uses the same mitosis-aware association as the PMBM tracker in [1], but we use different hyperparameters k_M to calculate the mitosis costs. Moreover, the MBM introduces the hyperparameters “Probability of Birth (pB)” and “Probability of Survival (pS)” which are set according to the datasets. Moreover, in our implementation, pB is different outside the field of interest as described by the CTC and is denoted as pB_ofoi.

POSTPROCESSING

We remove trajectories that are smaller than 3 frames. Furthermore, if a trajectory contains gaps, we bilinear interpolate cell masks.

References:

[1] Kaiser T, Schier M, Rosenhahn B. Cell Tracking according to Biological Needs - Strong Mitosis-aware Multi-Hypothesis Tracker with Aleatoric Uncertainty. IEEE Trans Med Imaging. 2025 Jun 25;PP. doi: 10.1109/TMI.2025.3583148. Epub ahead of print. PMID: 40560714.

[2] Katharina Löffler, Ralf Mikut. EmbedTrack—Simultaneous Cell Segmentation and Tracking Through Learning Offsets and Clustering Bandwidths. IEEE Access, 2022