

AMIT: A high performance segmentation and tracking framework for migration and confrontation assays

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01/11/2021

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AMIT: A high performance segmentation and tracking framework for migration and confrontation assays

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Method

The algorithm for migration and interaction tracking (AMIT) [1, 2] provides a novel and automated framework for analyzing (label-free) experimental time-lapse microscopy data, in addition to improved detection of whole cell tracks [4]. The approach enables a high throughput processing based on parallel batch processing through the implementation in the machine-oriented and performance-optimized C++ language. The framework is able to detect nearly all objects in the image sequence, including nuclei and organelles. This makes the tracking method not rely on any geometric characteristics and can be applied to a wide variety of cell morphologies. The user-friendly application and definition of parameters works via a standardized JSON interface.

AMITSegmentation is based on

- Image contrast enhancement using top- and bottom-hat transformation
- Image denoising by suppression of background variability
- Enhance high intensity signal by standard deviation filtering
- Morphology post-process to suppress artifacts in object

AMITTracking connects single cells through

- Nearest neighbor based
- Identification of cell clusters by monitoring events of cell-cell fusion and cluster fission
- Hierarchical cluster splitting based on watershed segmentation

GitHub <https://github.com/applied-systems-biolog/amit>

Performance evaluation

(A) Comparison of the new Segmentation (AMIT-v3) with the previous AMIT version (AMIT-v2) [4] (C). It becomes clear that the new version detects more overall and undetected areas than the old version. This is visually evident in (C) third row, where AMIT-v3 performs particularly well in low contrast areas, leading to better overall visual quality and quantitative improvement from the new segmentation algorithm.

In addition, we compare AMIT with deep learning based methods (B) such as the Yolact [5] and MU-CZ [6], which require much more time-consuming data preparation, such as creating manual annotation. Again, AMIT-v3 performed the best results overall in terms of an accurate segmentation (see Jaccard index).

(B) Comparison of AMIT-v3 with other segmentation algorithms. The figure shows the Jaccard index, the percent index, and the track fragmentation error (TFE) for different methods. The legend indicates: AMIT-v2 (red), AMIT-v3 (blue), MU-CZ (green), Yolact (orange), and SegNet (yellow).

Tracking: AMIT-v3 was also compared with AMIT-v2 [4]. The new tracking achieved significantly better results with regard to the total coverage (TC) of cells. We could also reduce the track merging error (TME) and provide comparable results in terms of the track fragmentation error (TFE).

Summary

AMIT-v3 includes:

- ✓ Accurate segmentation on low contrast cells
- ✓ Detection of fluorescently labelled cells in 2D image data
- ✓ Enables analysis of cell cluster (splitting)
- ✓ Analysis of migration / confrontation assays
- ✓ Detection of cell tracks
- ✓ Fast applicability to few image data
- ✓ Parameters are interactively adjustable
- ✓ Application to label-free microscopy
- ✓ Analysis of high-resolution images on laptops
- ✓ State-of-the-art parallelization
- ✓ Open source availability for everyone

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References

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