A Fiji Tool for Automatic Fusion of Segmentation and Tracking Labels

Vladimír Ulman[1,2], Martin Maška[2], David Svoboda[2],
Michal Kozubek[2], and Florian Jug[1]

[1] Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany
[2] Centre for Biomedical Image Analysis, Masaryk University, Brno, Czech Republic

Keywords: label fusion, image annotation, segmentation labels, tracking labels

Abstract

In biomedical image analysis, it is generally known that obtaining reliable segmentation results is difficult. As a consequence, often a set of diverse segmentation results is obtained when multiple raters (human annotators or segmentation algorithms) attempt to segment the same imaged object (be it an organ, tissue, cell, or nucleus). In order to obtain presumably more reliable segmentation result of the object, careful merging of segmentation results from multiple sources has become a common solution [6, 2, 1].

While fusion of labels in static images is already an established field, dealing with labels in time-lapse imaging remains to be explored. While obtaining gold corpus for segmentation is a difficult and time consuming task, creating gold corpus for tracking of observed objects is often easier as long as simplified markers are used to denote individual objects. Whenever a proper segmentation of the tracked objects is required, integration of the gold corpus for tracking with a silver corpus for segmentation seems to be a reasonable solution.

Here, we address the problem of obtaining segmentation results for a time-resolved 2D and 3D light microscopy images of multiple tracked cells. For every such video, the gold tracking corpus is an image sequence of quintessential markers with a unique label for all markers of the same cell, and the input for the silver segmentation corpus is a collection of sequences of segmentation masks containing inconsistently labeled objects. The goal is to *expand* the tracking markers with *fused* segmentation results while preserving the tracking labels. We present a tool to achieve that — a free, open source and ready to use Fiji plug-in[3].

The principle of the tool is rather straightforward, following a majority or weighted majority voting scheme. For every tracking marker, the merging process considers at most one segmentation mask that covers more than 50% of its size from every corresponding input segmentation image. Consequently, a cumulative gray-scale mask with counts of how many times an image element was observed in the considered masks is computed. Such fused mask is thresholded, labeled accordingly, and inserted into an output image as an expanded marker. During

[3] The tool is available at the URL https://github.com/xulman/CTC-FijiPlugins .

the insertions, it may happen that expanded markers are overlapping. As a post-processing, the overlapping parts of all colliding markers are removed. If the marker size is reduced by more than 10% after the post-processing, it is removed completely.

The tool has been already applied for processing of the datasets from the Cell Tracking Challenge [4], for which the gold tracking corpus is available. The silver segmentation corpus was created from 3 to 21 computed segmentation results across 22 real videos, using traditional majority voting scheme with the threshold value of 2/3 of the number of input segmentation results. The fused silver segmentation and gold tracking corpora allowed us to calculate various spatio-temporal characteristics (e.g., the average cell overlap due to its movement between consecutive images) of the real videos.

Since the merging of selected segmentation masks happens independently per one object, it is easy to extend the tool with additional merging schemes such as STAPLE [6], SIMPLE [2], or their image-based alternatives [3, 5].

Acknowledgements

This work was supported by the German Federal Ministry of Research and Education (BMBF) under the code 031L0102 (de.NBI), and by the Czech Science Foundation (GACR), grant P302/12/G157.

References

1. Lampert, T.A., Stumpf, A., Gançarski, P.: An empirical study into annotator agreement, ground truth estimation, and algorithm evaluation. IEEE Transactions on Image Processing 25(6), 2557–2572 (2016)
2. Langerak, T.R., van der Heide, U.A., Kotte, A.N., Viergever, M.A., Van Vulpen, M., Pluim, J.P.: Label fusion in atlas-based segmentation using a selective and iterative method for performance level estimation (SIMPLE). IEEE Transactions on Medical Imaging 29(12), 2000–2008 (2010)
3. Liu, X., Montillo, A., Tan, E.T., Schenck, J.F.: iSTAPLE: improved label fusion for segmentation by combining STAPLE with image intensity. In: SPIE Medical Imaging. pp. 86692O–86692O. International Society for Optics and Photonics (2013)
4. Maška, M., Ulman, V., Svoboda, D., Matula, P., Matula, P., Ederra, C., Urbiola, A., España, T., Venkatesan, S., Balak, D.M., et al.: A benchmark for comparison of cell tracking algorithms. Bioinformatics 30(11), 1609–1617 (2014)
5. Schlesinger, D., Jug, F., Myers, G., Rother, C., Kainmüller, D.: Crowd sourcing image segmentation with iaSTAPLE. In: Biomedical Imaging (ISBI), 2017 IEEE 12th International Symposium on. pp. 401–405. IEEE (2017)
6. Warfield, S.K., Zou, K.H., Wells, W.M.: Simultaneous truth and performance level estimation (STAPLE): an algorithm for the validation of image segmentation. IEEE transactions on medical imaging 23(7), 903–921 (2004)