

# A Fiji Tool for Automatic Fusion of Segmentation and Tracking Labels

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## Abstract:

Tracking all objects in a time-series of migrating and dividing cells is a frequent task in bioimage analysis. In order to minimize efforts, tracking outputs often use cell markers to represent the rough location of cells over time. The spatial extent of such markers is not consistent with the spatial extent of the tracked cells (it might only be a single pixel, voxel, or a small subregion inside the cell).

In this work we address the problem of extending a marker-based tracking in such a way that every cell label is assigned to (ideally) all image elements that respective cell consists of. To this end, we assume to be given a collection of segmentations per time-point. The goal is to replace every marker by a dense segmentation of the respective cell. At the heart of this task lie the problems of (i) combining multiple assigned cell segmentations to a single, fused segment, and afterwards (ii) resolving potential overlaps between segments of different cells.

The power of this approach is that a marker-based tracking can be extended to a densely segmented tracking by computing and fusing fully tracking unaware segmentations. Our algorithm is made available as an open source tool which we disseminate within Fiji, a well known image processing tool that is routinely used for bioimage analysis around the world.

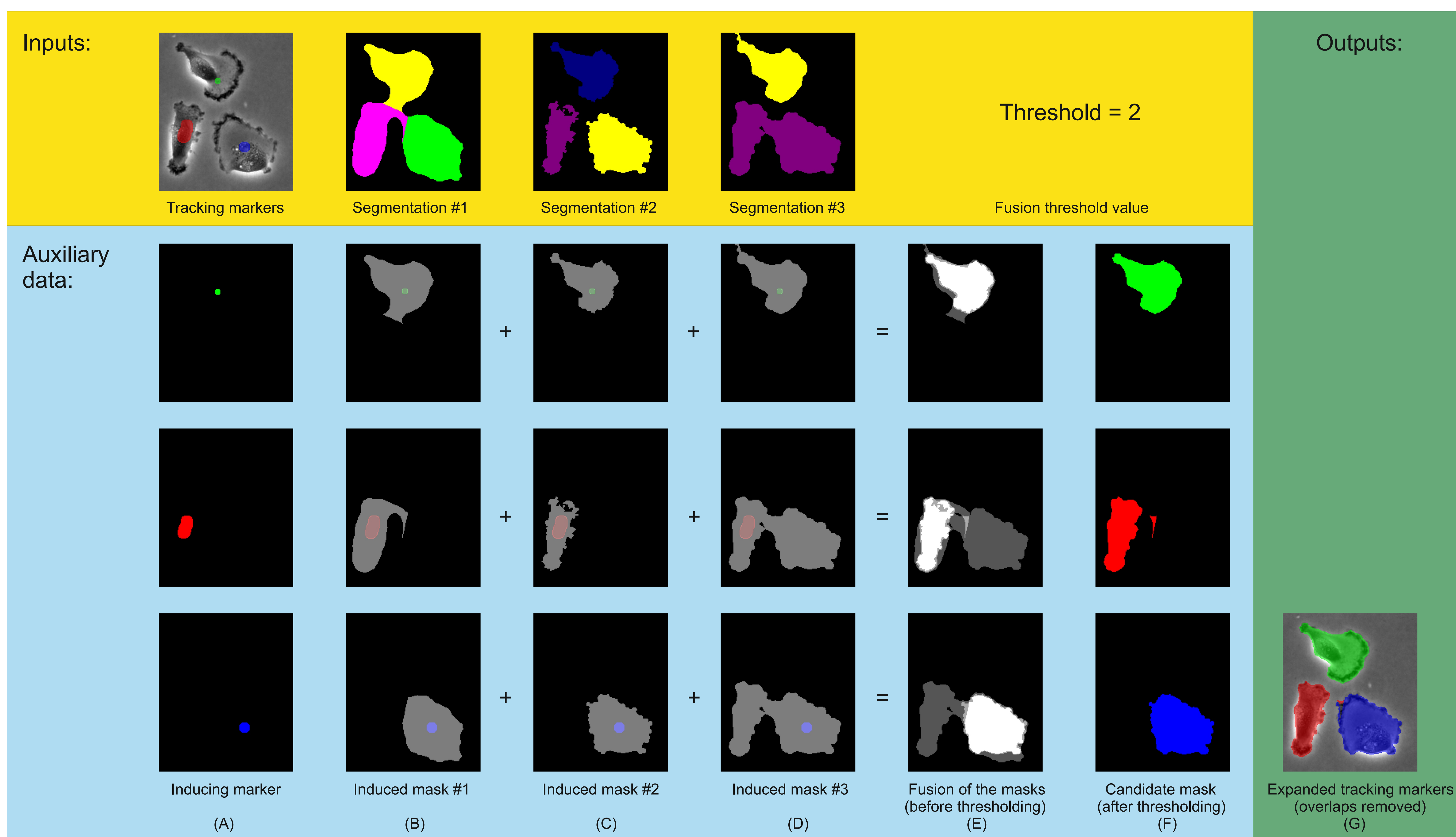
## Keywords:

Label fusion, Image annotation, Segmentation labels, Tracking labels

Free, open source and ready to use Fiji plug-in:



<https://github.com/xulman/CTC-FijiPlugins>



## Principle:

For every tracking marker (A), the merging process considers at most one segmentation mask that covers more than 50 % of its size from every corresponding input segmentation image (B)-(D). Consequently, a cumulative gray-scale image with counts of how many times an image element was observed in the considered masks is computed (E). Such fused image is thresholded, labeled accordingly (F), and inserted into an output image as an expanded marker. During the insertions, it may happen that expanded markers are overlapping. Therefore, the overlapping parts of all colliding markers are removed after all insertions are done (G). If the marker size is reduced by more than 10 %, the marker is removed completely.

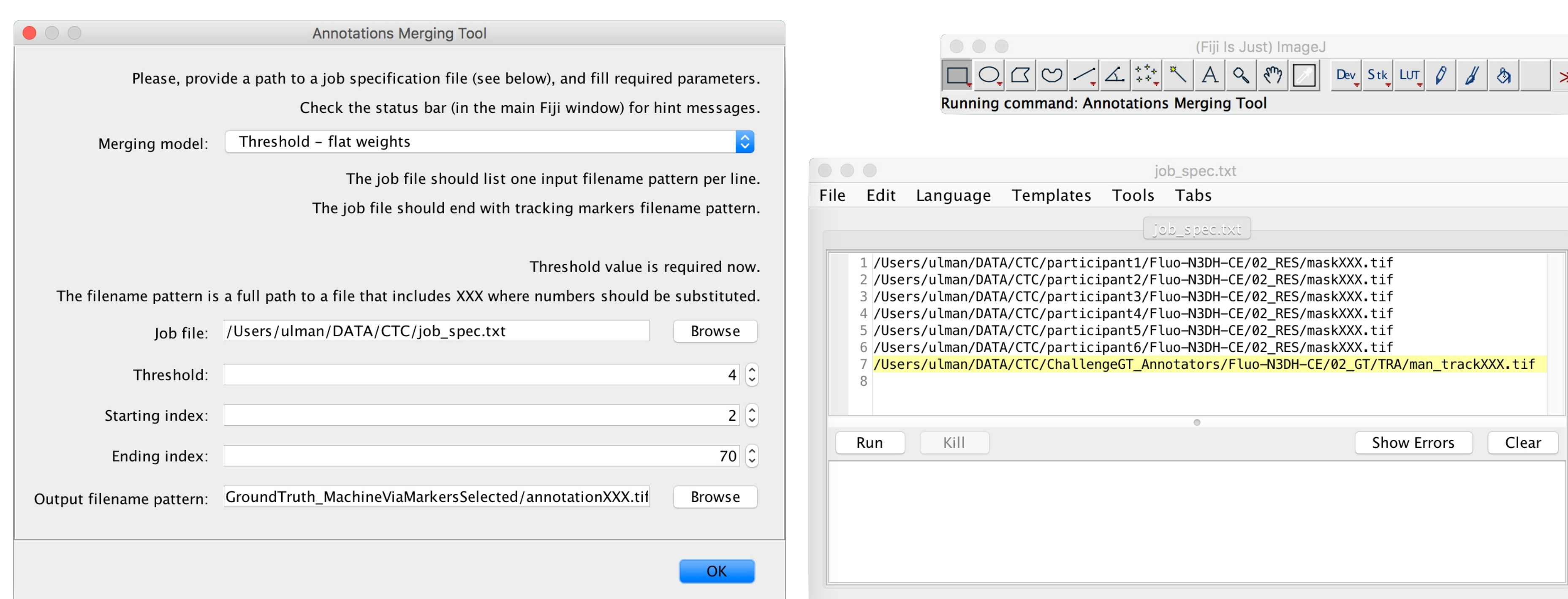


Fig: Sample screenshot of the tool control dialog (left panel) and sample of the fusion job specification file (right bottom).

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 [1], SIMPLE [2], or their image-based alternatives such as iSTAPLE [3] or iaSTAPLE [4].

## References:

- [1] S.K. Warfield et al.: Simultaneous truth and performance level estimation (STAPLE): an algorithm for the validation of image segmentation. IEEE TMI, 2004.
- [2] T.R. Langerak et al.: Label fusion in atlas-based segmentation using a selective and iterative method for performance level estimation (SIMPLE). IEEE TMI, 2010.
- [3] X. Liu et al.: iSTAPLE: improved label fusion for segmentation by combining STAPLE with image intensity. SPIE Medical Imaging, 2013.
- [4] D. Schlesinger et al.: Crowd sourcing image segmentation with iaSTAPLE. IEEE ISBI, 2017.

## Results:

The tool has been applied for processing of the datasets from the Cell Tracking Challenge ([www.celltrackingchallenge.net](http://www.celltrackingchallenge.net)), 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.

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