

cell tracking challenge, 2019

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the leverjs engine for segmentation, tracking, lineaging and validation

leverjs is a collection of software tools and algorithms for segmenting, tracking, lineaging and validating 5-D time-lapse microscopy image data. leverjs includes a storage architecture (SQLite), a custom WebGL raycasting engine for visualization (javascript/gsl), segmentation algorithms (matlab/any language), tracking (c++) and a UI for controlling the processing and for correction of the results (javascript). See <https://leverjs.net> for details. leverjs is free and open source. The program can be run client-server, or as a stand-alone executable available for mac, PC or linux. All of the present results were generated using the same software package, available at <https://leverjs.net/git>. All of the results, together with the images and the parameter settings, can be viewed at <https://leverjs.net/ctc2019>.

leverjs is based on the previously developed LEVER algorithms (Wait et al., 2014; Winter et al., 2016; Winter et al., 2011; Winter et al., 2015). The segmentations are written in MATLAB, and are driven by an interactive nodejs control module that sequences between the segmentation, tracking and classification algorithms in a manner that allows the system to integrate temporal context and to learn from classification results and user input to improve subsequent processing. This approach has been shown to reduce error rates by up to 8X compared to existing state-of-the-art algorithms (Winter et al., 2015; Winter et al., 2012; Winter et al., 2017). The leverjs tools use a C++ and the MAT tracking algorithm (Chenouard et al., 2014; Winter et al., 2012). The segmentation algorithm is completely unsupervised. Like the segmentation, the mitotic detection is “model-based”, using expected temporal characteristics of dividing cells including track initiation, cell texture and parent-daughter geometry.

segmentation parameters

The leverjs segmentation incorporates six different parameters:

1. `minimumRadius_um` – the expected object radius, in um. This is a size scale parameter. If a range is provided, then the segmentation runs as a multi-resolution approach, evaluated at each of the specified radii. The results are then bucketed into overlapping cell regions, and the best segmentation is chosen using a technique based on algorithmic statistics (manuscript in preparation), (Cohen, 2014; Vitanyi, 2006).
2. `useCuda` – whether to use the “Hydra Image Processor” (HIP) GPU (CUDA) accelerated image processing filters (Wait et al., 2019, in revision).
3. `denoise` – whether to apply the denoising algorithm first proposed in (Michel et al., 2007) and later refined in (Wait et al., 2014).
4. `isPhase` – indicates phase contrast images
5. `bCytoplasmic` – set to indicate the segmentation should preserve all fine processes of non convex shapes

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