DREX-US

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Platform: Linux

Prerequisites: MATLAB Compiler Runtime 2019b (x64)

DREX-US: SUMMARY

leverjs is a free and open-source collection of software tools and algorithms for segmenting, tracking, lineaging and validating 5-D time-lapse microscopy image data. It includes a storage architecture (SQLite), a custom webgl raycasting engine for visualization (javascript/glsl), segmentation algorithms (matlab/any language), tracking (C++) and a UI for controlling the processing and for correction of the results (javascript). 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/ctc2021.

leverjs is based on the previously developed LEVER algorithms [1-4]. The *leverjs* tools use an MPI-based multi-processing C++ implementation of the MAT tracking algorithm [5, 6]. The segmentation algorithm is completely unsupervised [7]. 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. The segmentation makes use of a new CUDA-based filtering architecture that improves accuracy of functions including Laplacian of Guassian filtering and non-local means filtering compared to other available approaches [8].

REFERENCES

1. Winter MR, Liu M, Monteleone D, Melunis J, Hershberg U, Goderie SK, Temple S, Cohen AR. Computational image analysis reveals intrinsic multigenerational differences between anterior and posterior cerebral cortex neural progenitor cells. *Stem Cell Reports* **5**, 609-620 (2015).
2. Wait E, Winter M, Bjornsson C, Kokovay E, Wang Y, Goderie S, Temple S, Cohen AR. Visualization and correction of automated segmentation, tracking and lineaging from 5-D stem cell image sequences. *BMC Bioinformatics* **15**, 328 (2014).

3. Winter M, Mankowski W, Wait E, Temple S, Cohen AR. LEVER: Software tools for segmentation, tracking and lineaging of proliferating cells. *Bioinformatics* **32**, 3530-3531 (2016).
4. Winter M, Wait E, Roysam B, Goderie KS, Ali RAN, Kokovay E, Temple S, Cohen AR. Vertebrate neural stem cell segmentation, tracking and lineaging with validation and editing. *Nature Protocols* **6**, 1942-1952 (2011).
5. Winter M, Mankowski W, Wait E, De La Hoz EC, Aguinaldo A, Cohen AR. Separating touching cells using pixel replicated elliptical shape models. *IEEE Transactions on Medical Imaging* **38**, 883-893 (2019).
6. Winter MR, Fang C, Banker G, Roysam B, Cohen AR. Axonal transport analysis using multitemporal association tracking. *International Journal of Computational Biology and Drug Design* **5**, 35-48 (2012).
7. Cohen AR. Extracting meaning from biological imaging data. *Molecular Biology of the Cell* **25**, 3470-3473 (2014).
8. Wait E, Winter M, Cohen AR. Hydra image processor: 5-D GPU image analysis library with MATLAB and Python wrappers. *Bioinformatics* **35**, 5393-5395 (2019).