LTMaker: a tool for semiautomatic reconstruction of the embryonic lineage tree from 4D-microscopy

F.J. Vico[1], D. Lobo[1], A. Gómez[1], S. Burrezo[1], J.D. Fernández[1], L. Duloquin[2], B. Maury[2] & N. Peyrieras[2]

[1]Dep. Lenguajes y Ciencias de la Computación, Universidad de Málaga, 29071 Málaga, Spain
[2]CNRS-DEPSN, Avenue de la Terrasse, 91198 Gif sur Yvette, France

Studies of animal development using a 4D-microscopy system generate an immense amount of image data. In order to properly analyze the recorded embryogenesis, a computer-aided systematic process of categorization of cells from the image data should be accomplished.

We present a software tool named *LTMaker* for the systematic semiautomatic identification of embryonic cells centers and also to determine the underlying linage tree. The program saves the generated data to a file so that further analysis of the embryo can be performed with external tools.

LTMaker is operated by a specialist that determines, through the use of a monitor, a mouse, and a keyboard, the center position of each cell nuclei in the embryo, and the mitoses that occur in the recorded interval. Once the first volume is identified, the specialist needs only to correct the identification in the subsequent volumes, instead of repeating the process. In this way, the spatial-temporal correlation of the embryogenesis data between volumes is exploited for the improvement of identification speed. Additionally, the software interface has been designed to optimize the speed of manual correction of cells positions and mitosis. The program outputs the identified experiment information in a data file that includes cells positions, tracking and lineage tree for further analysis with other tools.

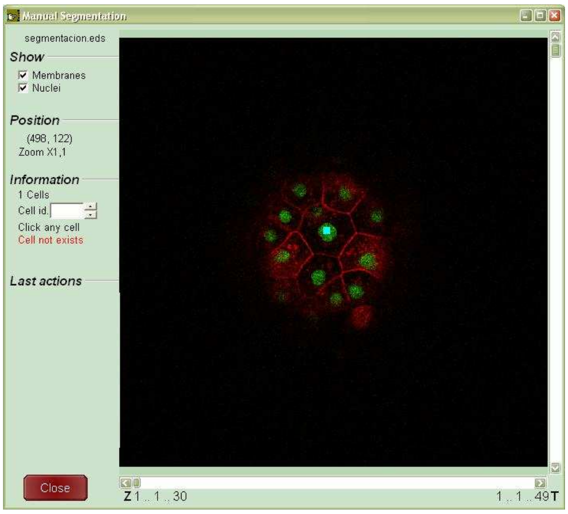
The main advantage of the program is that speed is optimized in the manual identification of the embryo cells by exploiting the spatial-temporal correlation of them. Other related software tools are available, but the spatial-temporal correlation of data is not exploited [1], or they are not designed specifically for manual identification [2].

While initially designed to cover the basic needs of research centers in embryology, a number of functionalities were identified that could be of interest for the industry in this scientific area: debugging a lineage tree, matching the lineage trees obtained by different users, automatic identification of nuclei, tablet-based version, etc. The integration of these functionalities will provide future versions of *LTMaker*.

References

1. Hejnol, A. & Schnabel, R. *What a couple of dimensions can do for you: Comparative developmental studies using 4D-microscopy – examples from tardigrade development*, Integ Comp Biol 46, 151-162, 2006

2. Boyle, T.J. *et al. AceTree: a tool for visual analysis of Caenorhabditis elegans embryogenesis*, BMC Bioinformatics 7:275, 2006



segmentacion.eds

☑ Membranes
☑ Nuclei

(498, 122)
Zoom X1,1

1 Cells
Cell id.
Click any cell
Cell not exists

Z 1 .. 1 .. 30
1 .. 1 .. 49 T

Fig. 1. Screenshot of the main *LTMaker* window.