**Cell Segmentation and Tracking:**

To automate the segmentation of the cells within the time-lapse images we retained an existing segmentation model using cellpose 2.0 [1]. The graphical user interface (GUI) of cellpose was used to manually segment 9 randomly selected frame from the experiment images, the subsequent cell masks were saved as .npy files. The cell masks acted as a ground-truth that was used to retrain the “live cell” model that is part of the model zoo that comes as a part of cellpose 2.0 [1]. The model was retained using the default parameters of the training function within the cellpose GUI (100 epochs, learning rate = 0.1 and weight decay = 0.001).

The analysis of the images was performed using a jupyter notebook [2]. The images are segmented using the user-trained model, and the resultant cell masks are saved into a numpy array. Cell shape parameters for each cell are extracted from the segmentation masks using user-defined functions based on the shape parameters avaliable in Fiji/ImageJ [3]. The shape parameters are saved into a data-frame frame containing the central position, frame number and mask-number of the cell. The cell tracks are generated from the cell-masks using the btracks package [4].

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[2] B. E. Granger and F. Pérez, "Jupyter: Thinking and Storytelling With Code and Data," in Computing in Science & Engineering, vol. 23, no. 2, pp. 7-14, 1 March-April 2021, doi: 10.1109/MCSE.2021.3059263.

[3] Schindelin, J., Arganda-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T., … Cardona, A. (2012). Fiji: an open-source platform for biological-image analysis. Nature Methods, 9(7), 676–682. doi:10.1038/nmeth.2019

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