*This protocol assumes the user has basic knowledge of Google Colab, Fiji, Trackmate and Cellpose. Instructions and more detailed protocols to those can be found elsewhere and in each app's individual documentation.*

1. Open your ablation file in Fiji. Crop the area to be analyzed.

2. In the first frame, determine the center of the ablation point. Take notes of the X,Y coordinates of the center of the ablation point.

3. Split the stack into individual frames and save them.

4. In the Cellpose environment, segment the cells in the folder by typing in the terminal, substituting path\_to\_folder and path\_to\_model for the windows paths to your folder and model:

python -m cellpose --dir “**path\_to\_folder**" --pretrained\_model "**path\_to\_model**" --save\_png --verbose --exclude\_on\_edges --diameter 0

*models can be found in this folder for download: single cells, tissues*

**Checkpoint**: check if all the segmentations are correct and retrain the model if necessary.

5. Make a stack out of the label images (.png) generated.

**Checkpoint**: ensure that the frames are in the correct order before proceeding to the next step.

6. Using Trackmate, generate the individual tracks for each cell.

**Detector**: Label image detector

**Tracker**: Simple LAP Tracker

When you arrive at **Display Options**, click on Spots and download the csv file and save it to Google Drive.

**Checkpoint**: ensure that the tracks are correct before proceeding to the next step.

**Action**: Export Spots to IJ ROIs (select option: All Spots)

7. Using the ROIs generated by Trackmate, run the ROI->Center of Mass code in Fiji (Credit: [Raju Kada](https://forum.image.sc/t/center-of-mass-imagej-trackmate/73140/7)).

8. Download the generated table, upload to Google Drive as a csv and use it for the next step in Python.