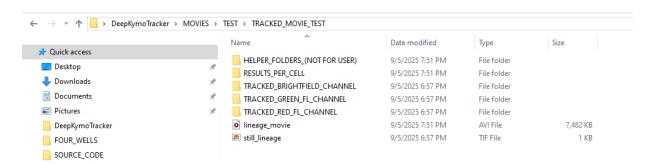
5. OUTPUT LAYOUT EXPLANATION

(User Guide)

Here is what to expect after applying the whole pipeline of DeepKymoTracker to an example movie named ONE_WELL_MOVIE_TEST. The output is stored in MOVIES\ TEST\ TRACKED_MOVIE_TEST folder:

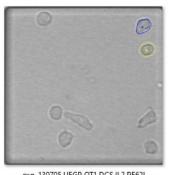


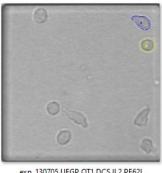
Inside this folder, you will see a number of subfolders. Their contents will be described below. Also, you will see **linage_movie.avi** whose name speaks for itself: this is an animated output cell movie (brightfield channel) coupled with the cell lineage changing dynamically. The file **still lineage.tif** is just an image of the whole lineage.

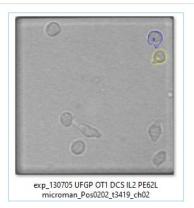


The folder **TRACKED_BRIGHTFIELD_CHANNEL** contains frames with the tracked and segmented cells represented in the brightfield channel. In our example movie ONE_WELL_MOVIE_TEST, we tracked only 2 cells, their names are **a** and **b**.

TEST > TRACKED_MOVIE_TEST > TRACKED_BRIGHTFIELD_CHANNEL



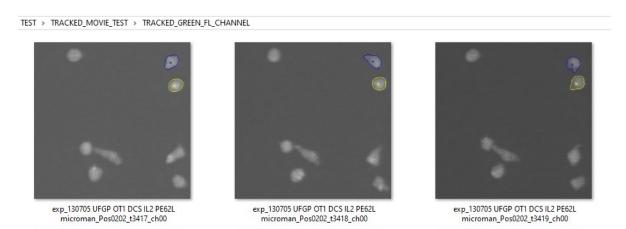




exp_130705 UFGP OT1 DCS IL2 PE62L microman_Pos0202_t3417_ch02

exp_130705 UFGP OT1 DCS IL2 PE62L microman_Pos0202_t3418_ch02

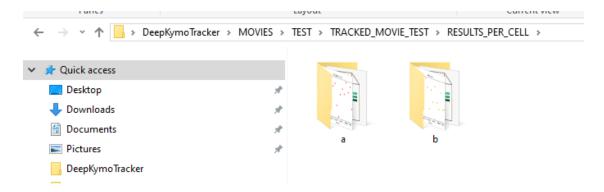
The folder **TRACKED_GREEN_FL_CHANNEL** contains frames with the tracked and segmented cells represented in the green fluorescent channel:



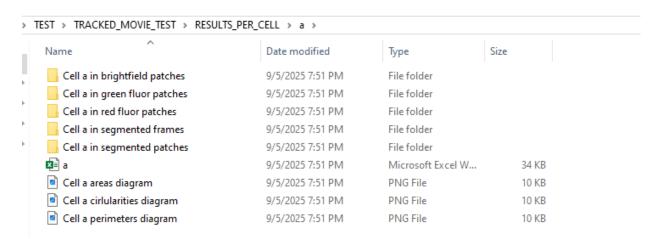
The folder TRACKED_RED_FL_CHANNEL contains frames with the tracked and segmented cells represented in the red fluorescent channel:



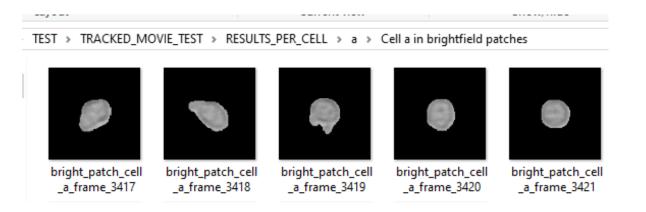
Let us walk through the contents of **RESULTS_PER_CELL** folder. As can be seen from the screenshot below, it contains a separate folder for each cell – in our case, these are folders named **a** and **b**, according to the cell names.



Let us take a look inside folder **a**. As you can see, it contains a number of folders and files:

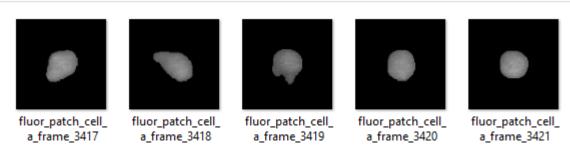


Cell a in brightfield patches: these are patches with the cell (cell **a** in our example), where the body of the cell is taken from the brightfield channel and the background is black.

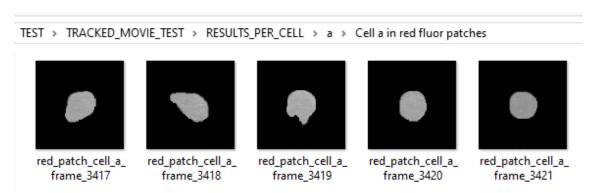


Cell a in green fluor patches: these are patches with the cell (cell **a** in our example), where the body of the cell is taken from the green fluorescent channel and the background is black.

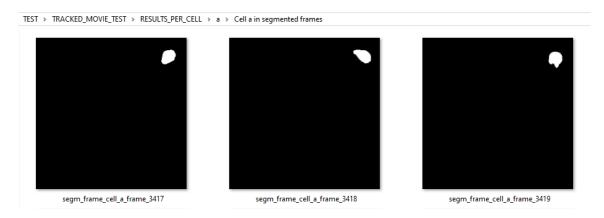
TEST > TRACKED_MOVIE_TEST > RESULTS_PER_CELL > a > Cell a in green fluor patches



Cell a in red fluor patches: these are patches with the cell (cell **a** in our example), where the body of the cell is taken from the red fluorescent channel and the background is black

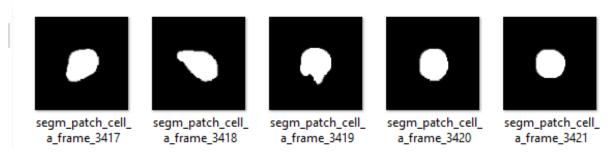


Cell a in segmented frames: black frame where only segmented cell a is represented.



Cell a in segmented patches: patches with segmented cell a in the centre.

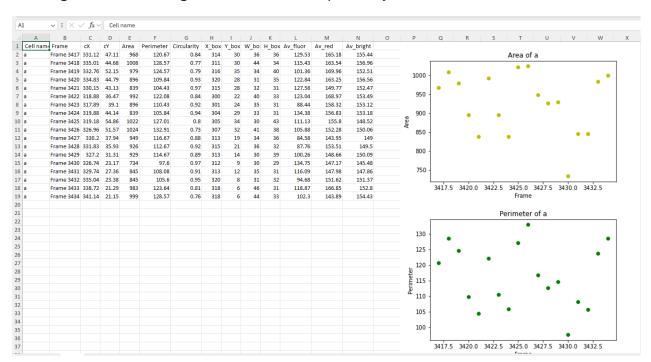
TEST > TRACKED_MOVIE_TEST > RESULTS_PER_CELL > a > Cell a in segmented patches



- a. .xlsx: this Excel file contains the numerical information about cell a in each frame:
 - (cX, cY) coordinates of cell centroid;
 - (X_box, Y_box, W_box, H_box)-the parameters of the bounding box for cell a, namely,

X_box, Y_box are the coordinates of the top left corner of the bounding box, W_box, H_box – are the width and the height of the bounding box;

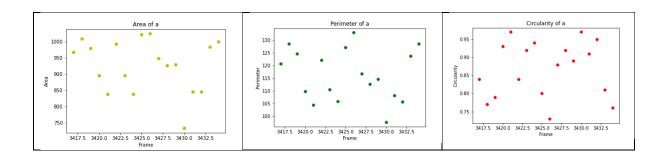
• Av_fluor, Av_red, Av_bright are the average intensities of the cell body in the green, red and brightfield channels, respectively.



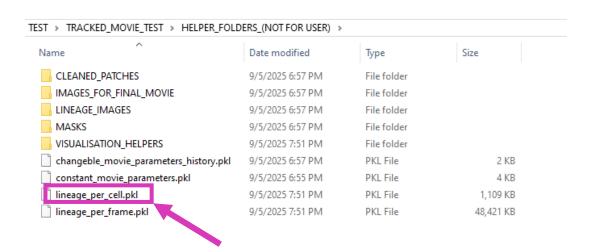
The files Cell a areas diagram.png, Cell a perimeters diagram.png and

Cell a circularities diagram.png are the diagrams as shown below:

Cell a areas diagram:	Cell a perimeters	Cell a circularities
	diagram:	diagram:



Finally, if you for some reason prefer to extract the numerical information about each cell from .pkl file (rather than . .xlsx), you can find lineage_per_cell.pkl file inside HELPER_FOLDERS_(NOT FOR USER):



In Python, you can extract the lineage_per_cell with the snippet of code below:

```
Import pickle
outpath=r"C:\Users\helina\Desktop\DeepKymoTracker\MOVIES\TEST\TRACKED_MOV
IE_TEST\HELPER_FOLDERS_(NOT FOR USER)"
pedigree_path=os.path.join(outpath,"lineage_per_cell.pkl")
with open(pedigree_path, 'rb') as handle:
    lineage_per_cell = pickle.load(handle)
```

Lineage_per_cell is a dictionary with cell names as the keys (in our example, there are "a" and "b":

Lineage_per_cell={"a": [cell_a_params_for_frame_1, ..., cell_a_params_for_frame_k, ...],

"b": [cell_b_params_for_frame_1, ... ,cell_b_params_for_frame_k, ...]}.

where

cell_a_params_for_frame_k=[cell_name, frame_number, patch_with_cell_in_colour, [cX,cY], area, perimeter, circularity, colour, bounding_box, av_fluor, av_red, av_bright].

Here

- bounding_box=X_box, Y_box, W_box, H_box
- colour=[r,g,b]
- patch_with_cell_in_color:

