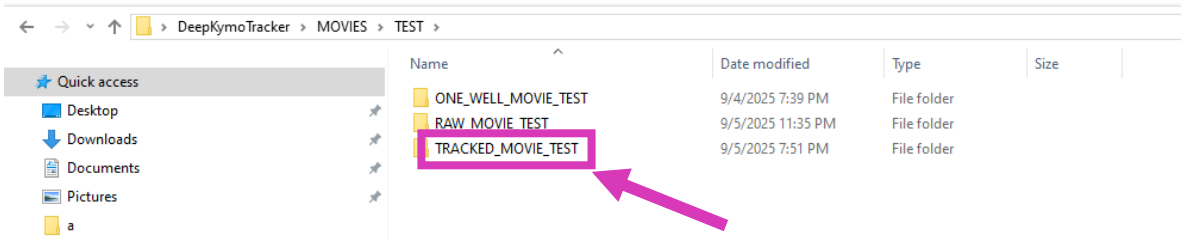
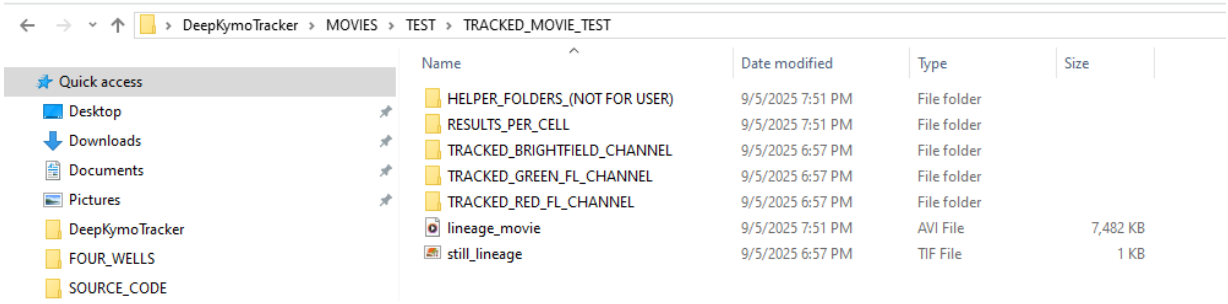
OUTPUT LAYOUT EXPLANATION

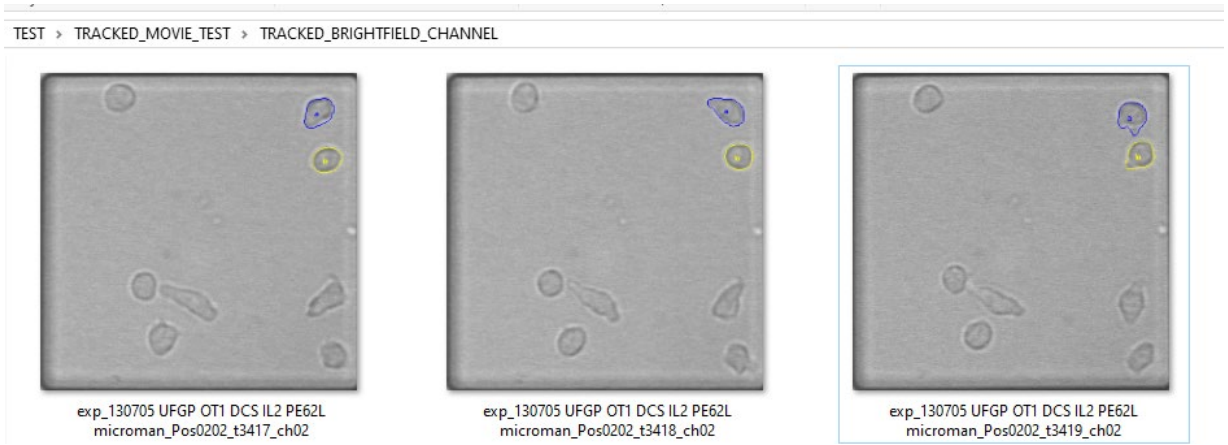
Here is what to expect after applying the whole pipeline of DeepKymoTracker to an example movie named ONE_WELL_MOVIE_TEST. The output is stored in MOVIES\ TEST\ **TRACKED_MOVIE_TEST** folder:



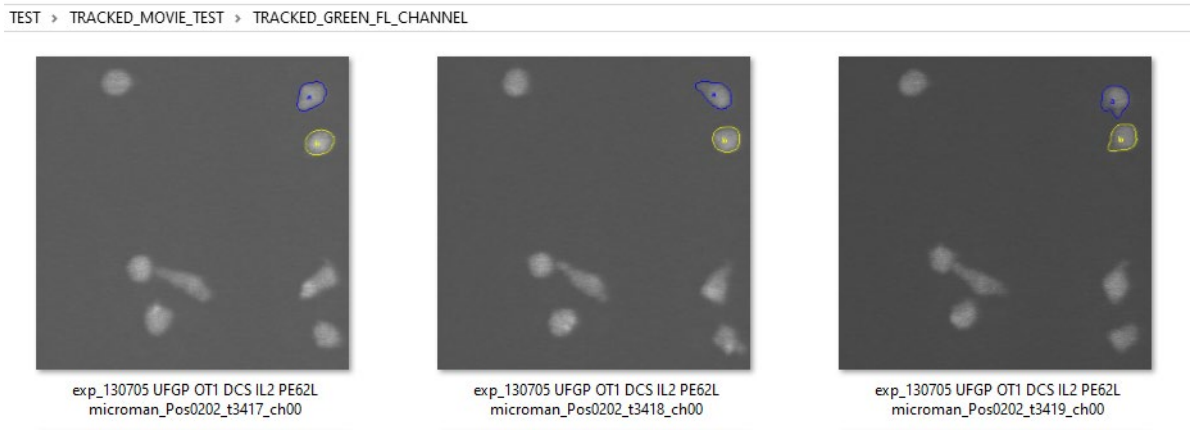
Inside this folder, you will see a number of subfolders. Their contents will be described below. Also, you will see **linage_movie.avi** whose name speaks for itself: this is an animated output cell movie (brightfield channel) coupled with the cell lineage changing dynamically. The file **still lineage.tif**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



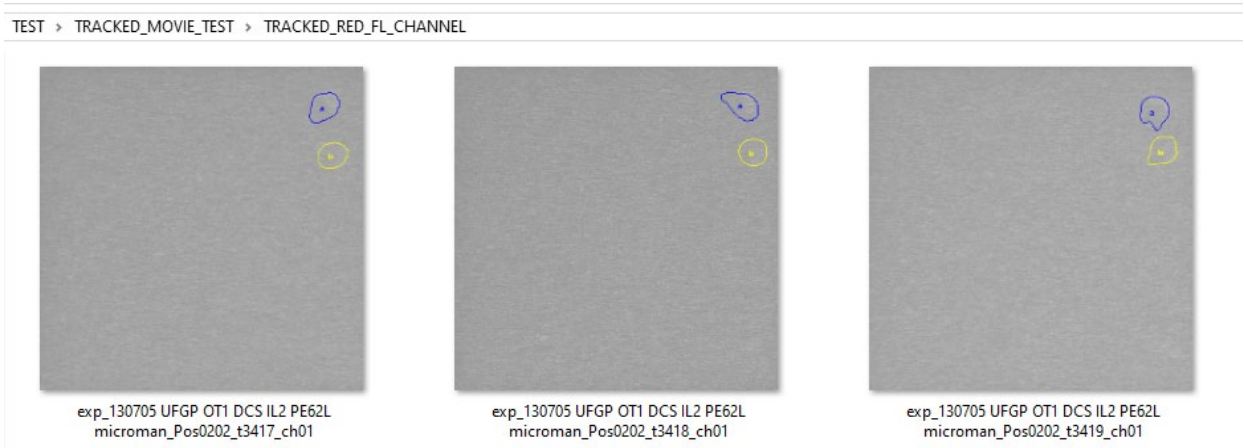
The folder **TRACKED_BRIGHTFIELD_CHANNEL** contains frames with the tracked and segmented cells represented in the brightfield channel. In our example movie ONE_WELL_MOVIE_TEST, we tracked only 2 cells, their names are **a** and **b**.



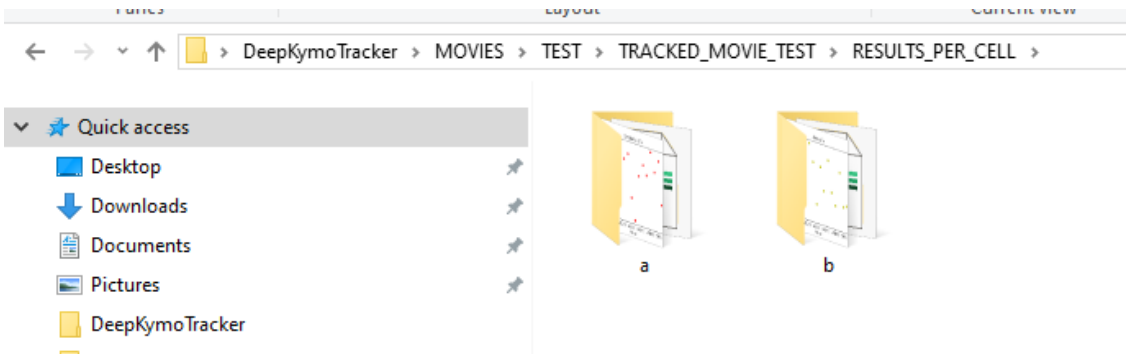
The folder **TRACKED_GREEN_FL_CHANNEL** contains frames with the tracked and segmented cells represented in the green fluorescent channel:



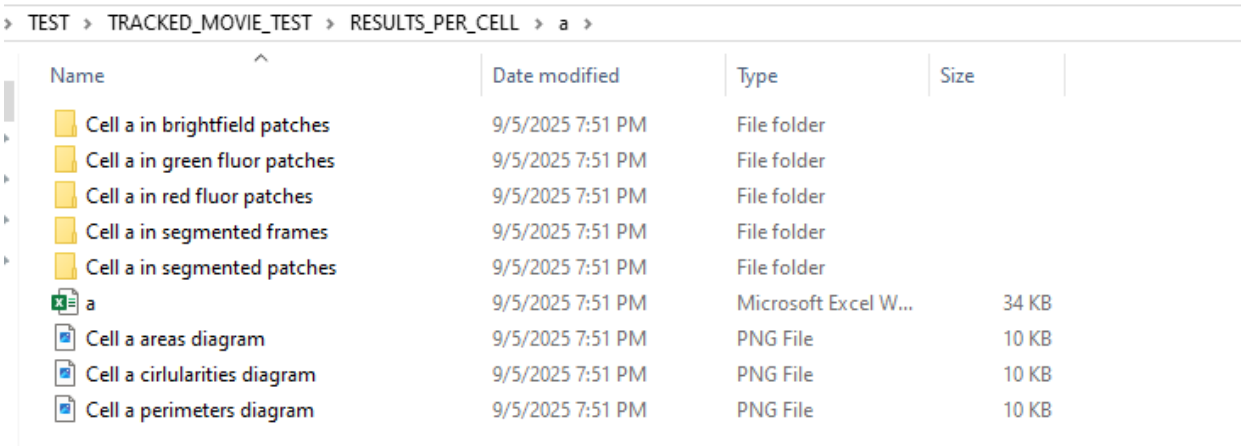
The folder **TRACKED_RED_FL_CHANNEL** contains frames with the tracked and segmented cells represented in the red fluorescent channel:



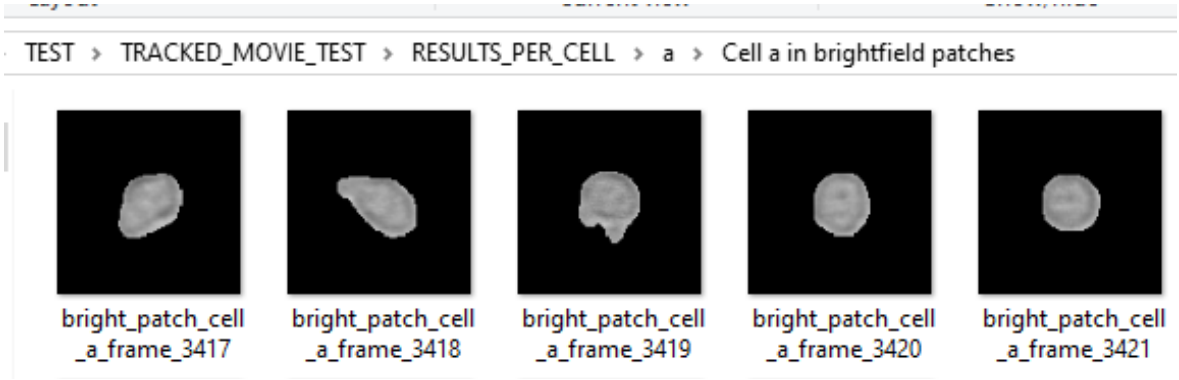
Let us walk through the contents of **RESULTS_PER_CELL** folder. As can be seen from the screenshot below, it contains a separate folder for each cell – in our case, these are folders named **a** and **b**, according to the cell names.



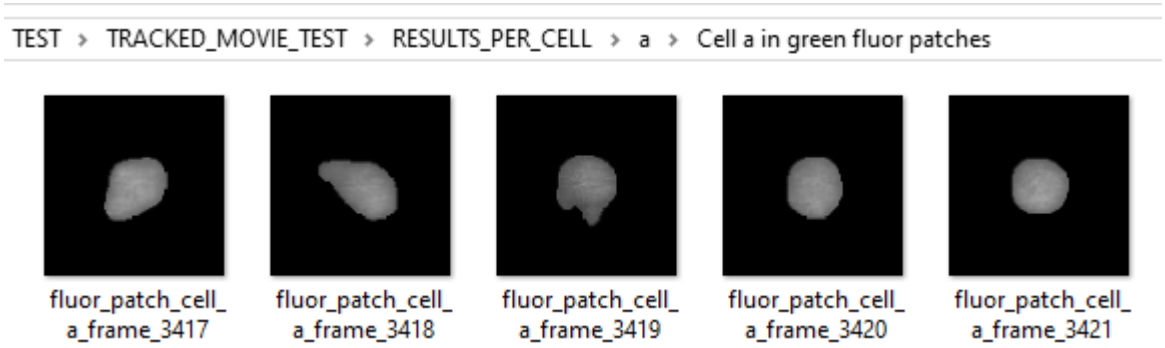
Let us take a look inside folder **a**. As you can see, it contains a number of folders and files:



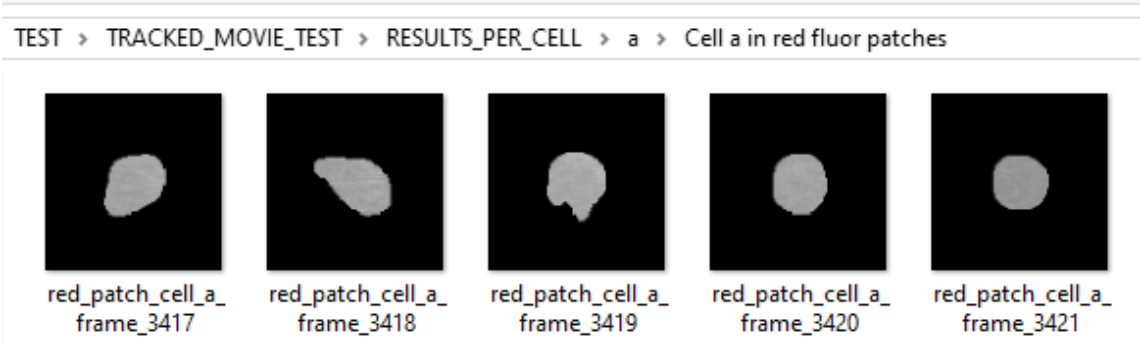
Cell a in brightfield patches: these are patches with the cell (cell **a** in our example), where the body of the cell is taken from the brightfield channel and the background is black.



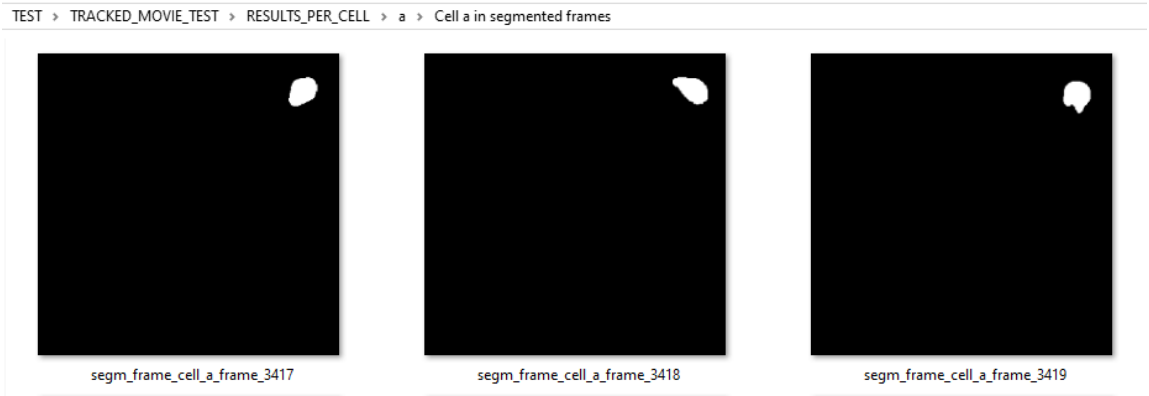
Cell a in green fluor patches: these are patches with the cell (cell **a** in our example), where the body of the cell is taken from the green fluorescent channel and the background is black.



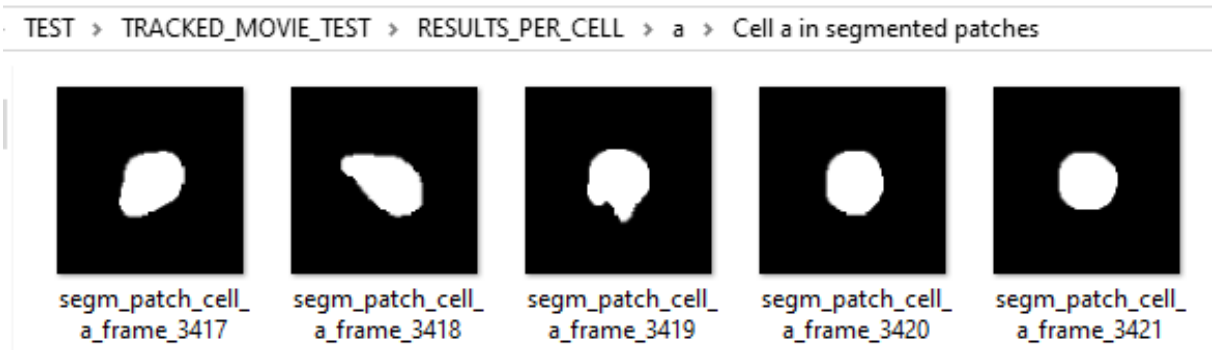
Cell a in red fluor patches: these are patches with the cell (cell **a** in our example), where the body of the cell is taken from the red fluorescent channel and the background is black



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.



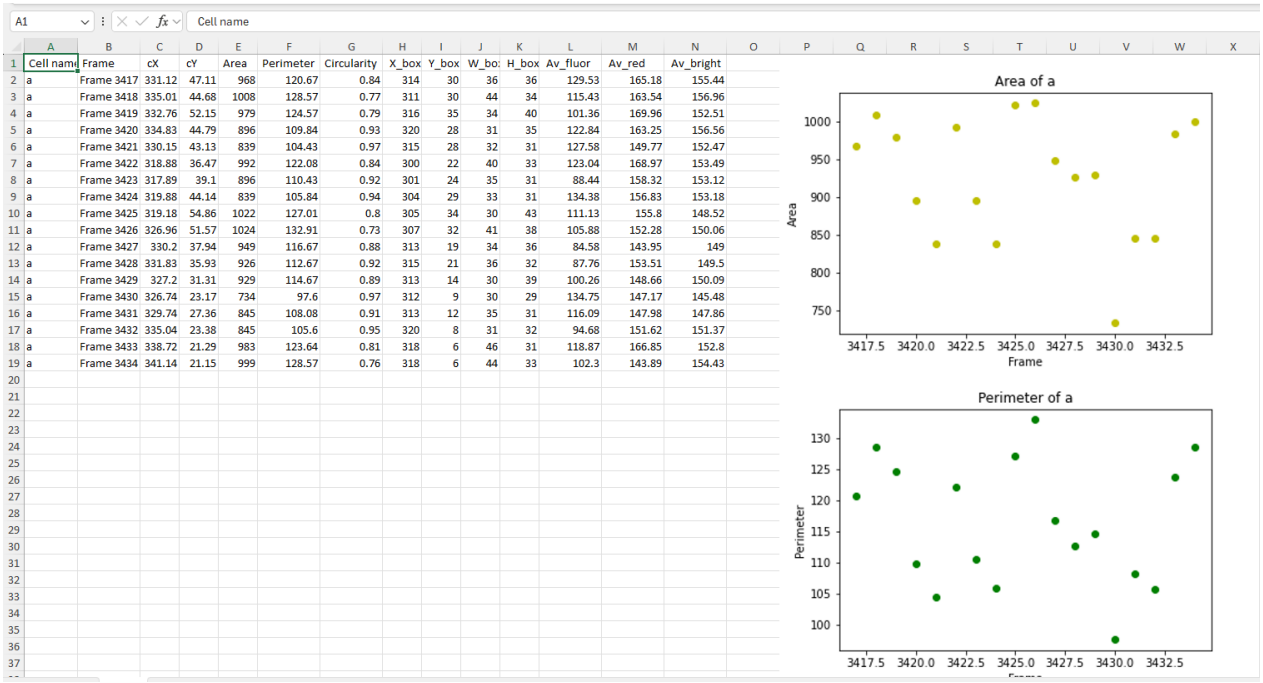
a. .xlsx : this Excel file contains the numerical information about cell **a** in each frame:

- **(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,

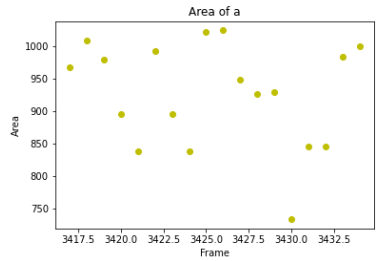
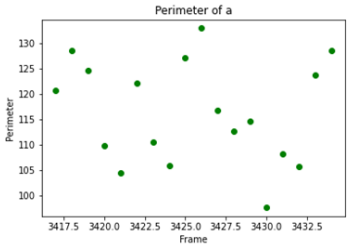
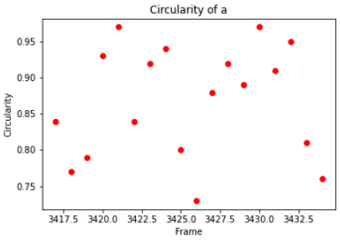
  W_box, H_box – are the width and the height of the bounding box;

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

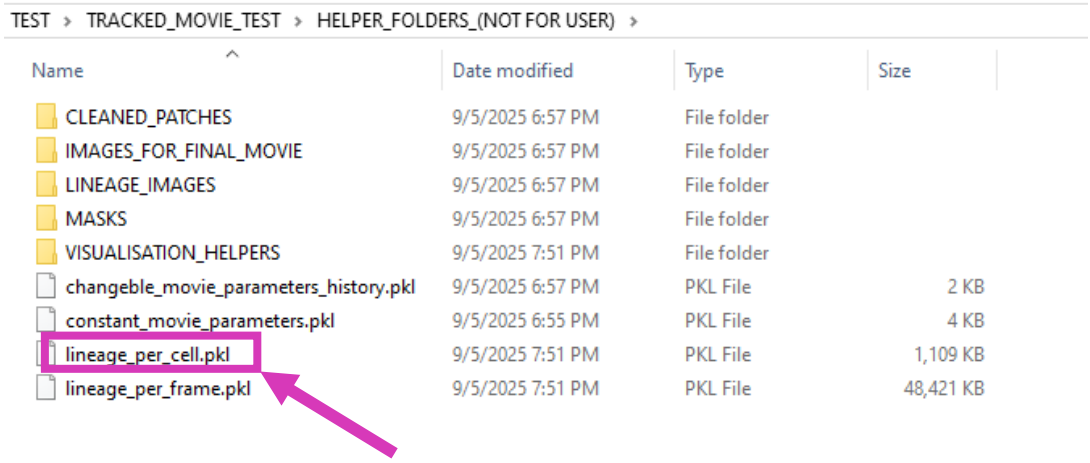


Cell name	Frame	cX	cY	Area	Perimeter	Circularity	X_box	Y_box	W_box	H_box	Av_fluor	Av_red	Av_bright
a	Frame 3417	331.12	47.11	968	120.67	0.84	314	30	36	36	129.53	165.18	155.44
a	Frame 3418	335.01	44.68	1008	128.57	0.77	311	30	44	34	115.43	163.54	156.96
a	Frame 3419	332.76	52.15	979	124.57	0.79	316	35	34	40	101.36	169.96	152.51
a	Frame 3420	334.83	44.79	896	109.84	0.93	320	28	31	35	122.84	163.25	156.56
a	Frame 3421	330.15	43.13	839	104.43	0.97	315	28	32	31	127.58	149.77	152.47
a	Frame 3422	318.88	36.47	992	122.08	0.84	300	22	40	33	123.04	168.97	153.49
a	Frame 3423	317.89	39.1	896	110.43	0.92	301	24	35	31	88.44	158.32	153.12
a	Frame 3424	319.88	44.14	839	105.84	0.94	304	29	33	31	134.38	156.83	153.18
a	Frame 3425	319.18	54.86	1022	127.01	0.8	305	34	30	43	111.13	155.8	148.52
a	Frame 3426	326.96	51.57	1024	132.91	0.73	307	32	41	38	105.88	152.28	150.06
a	Frame 3427	330.2	37.94	949	116.67	0.88	313	19	34	36	84.58	143.95	149
a	Frame 3428	331.83	35.93	926	112.67	0.92	315	21	36	32	87.76	153.51	149.5
a	Frame 3429	327.2	31.31	929	114.67	0.89	313	14	30	39	100.26	148.66	150.09
a	Frame 3430	326.74	23.17	734	97.6	0.97	312	9	30	29	134.75	147.17	145.48
a	Frame 3431	329.74	27.36	845	108.08	0.91	313	12	35	31	116.09	147.98	147.86
a	Frame 3432	335.04	23.38	845	105.6	0.95	320	8	31	32	94.68	151.62	151.37
a	Frame 3433	338.72	21.29	983	123.64	0.81	318	6	46	31	118.87	166.85	152.8
a	Frame 3434	341.14	21.15	999	128.57	0.76	318	6	44	33	102.3	143.89	154.43

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 diagram:	Cell a circularities 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_MOVIE_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: