xing-vimentin-dic-pipeline

**1 - preprocess**

**2 - cell identification**

**3 – compute**

pipe\_4\_traj\_reorganize\_2nd.py

Glossary

traj\_start / traj\_end: starting / ending img number & obj number

traj\_start\_area / traj\_end\_area: starting / ending areas of the trajectory cells

traj\_start\_xy / traj\_end\_xy: starting / ending positions of the trajectories

F / L: numpy arrays containing all information from raj\_start / traj\_end, traj\_start\_area / traj\_end\_area, traj\_start\_xy / traj\_end\_xy, F for start, L for end

pipe\_5\_traj\_reorganize\_3rd.py

Outputs

+mitosis\_record.csv, contains all instances of detected mitosis. Contains trajectory labels, image numbers, and object numbers of mother, sister1 & sister2

-same as input mitoses.npy, except for mitoses.npy does not have the trajectory labels

**4 – trajectories**

**pcna-intact** (extracting trajectories that only begin & end with cell division)

1\_mitosis\_traj\_fill.ipynb

extract trajectories that begin immediately after cell division traj labels from mitosis\_labels.csv identified in traj\_object\_num.csv and dumped into traj\_object\_num-mit.xlsx

manual-2\_traj\_rematch.ipynb

\*saved as xlsx to keep the cell box coloring. pink - non-intact; green - intact

**memes (imported scripts)**

track\_modules

get\_mitotic\_triple\_scores( F,L,mitosis\_max\_distance,size\_simi\_thres)

outputs

mitoses - mother img num, mother obj num, sis1 img num, sis1 obj num, sis2 img num, sis2 obj num. This variable is changed and curated by some algorithm that was really complex and I couldn’t decipher it. Weikang can you write a more detailed description of this part?