**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 traj\_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**

**general trajectories**

**#-traj\_scale\_stats.ipynb**

traj\_scale\_contour - trajectory contour divided by sqrt(temporal\_mean(cell area))

traj\_scale\_contour\_with\_vim - contours where vimentin mean intensity ≠ 0

traj\_scale\_haralick - vimentin haralick values of the trajectory that are subtracted by the temporal average of the vimentin haralick values

temporal average is calculated from st:et, where these timepoints are calculated by a stay point algorithm, a period where the time series is relatively stable?

? - why did he scale the haralick features by subtracting the mean?

haralick features may start at different values for different cells

? - why use stay point algorithm to find the mean in that time frame? would that be necessary if there is no emt?

to find a relatively stable period for the mean. emt does not affect weather stay point algorithm is used very much.

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

**1-mitosis\_init\_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\_init.xlsx (and csv as well if needed)

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

\* this is meant to serve as a starting draft to rematch and fill in all intact trajectories

**1-intact\_traj\_fill.ipynb**

extract trajectories that begin and end with cell division

traj labels from mitosis\_labels.csv identified in traj\_object\_num.csv in all positions are dumped into traj\_object\_num-intact.csv

**manual-2\_traj\_rematch.ipynb**

\*saved as xlsx to keep the cell box coloring. red - 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