**SOP Summary of Codes by Ricardo MN**

Kisley Lab – CWRU – 2024

1. RM\_LRG\_ParametersTest.m

-define numFiles

-set initial (e.\_\_) user parameters

-set limits for e.startframe and e.stopframe - define lenght of saved preview movie

-main localization parameter edits are e.sigma,e.wide2; maybe e.Gauss\_width

-super res parameters only matter for final image

-set e.kinetiC = 'false' if low number of events, or not testing adsorption sites

-set correct e.dataTime to match integration time (+ readout time)

-run script; select files; .tiff of localizations automatically saved on file folder

2. RM\_Main\_LRG\_SuperRes.m - includes sub-scripts codes package

- RM\_Main

-define initial parameters, numFiles, etc.

-use values that seem good from ParametersTest

-assumes full area and frames by default unless changed related variables to 'false'

-run ->output stored as file\_analyzed.m in same folder as original data

-RM\_run

-edited version to work with new RM\_Main variables

-TiffReadRM

-loads .tiff data as .m file -runs frame by frame, so it can be slow

-takeROI\_RM

--prompts user to define an ROI, tracing over image of summed data

-will make \_analyzed file and Data1 to match selected ROI

3. XY\_RadialCSP\_Distributions

-Use single slice CSP HILO data

-Provides the cumulative distribution of found adsorption events

-Defines a contour of CSP’s

-Provides area values

4. zScan\_3D\_vol\_simplified

-plots 3D volume of zScan single-molecule data

-takes data and breaks into individual LRG analyzis slices based on metadata z-positions

-outputs \_analyzed.m files for each slice

-uses super-res mapping of each slice, then stitches them together to make a 3D plot