Germarium_Meiosis

These ImageJ plugins are highly specific to the image data used here (Hatkevitch et al., 2019) – please contact Vincent Boudreau (viboud@gmail.com) for more information. A first plugin prepares raw confocal germarium images by uniformly adjusting image brightness and contrast, and manually rotating images. The second and third plugins allow for the manual identification of meiotic stage-specific nuclei and saving images to a user-defined folder. The fourth plugin runs image segmentation and multiple fluorescence intensity measurements on a folder of meiotic nuclei. The output of these plugins is a Microsoft Excel document with multiple fluorescence intensity measurements for all identified meiotic nuclei in a given meiotic stage.

Before using these plugins, you must install the Canny-Deriche filtering edge detection plugin in your ImageJ "plugins" folder. The plugin is provided as image_edge.jar. Simply drop the .jar file in your plugins folder. Additionally, custom background subtraction macros (MaskC1_SubC1_.ijm, MaskC1_SubC2_.ijm, MaskC1_SubC3_.ijm) must be added to your ImageJ "macros" folder. Once these files have been added, restart ImageJ and they should be installed.

Image requirements:

Images must be triple channel, grayscale images with several optical slices and a single time-point. These plugins were designed for use with DAPI staining in the first channel, CID staining in the second channel and a meiotic marker such as C(3)G in the third channel.

Plugins:

1) Germaria_proc_.ijm
2) Germaria_nucleus_box_.ijm
3) Save_All_Open_.ijm
4) Germaria_measure_.ijm

REFERENCES:

If you use this plugin, please cite:

Hatkevich T., Boudreau V., Rubin T., Huynh J.-R., Maddox P.S., Sekelsky J. (2019) Centromere clustering promotes meiotic homolog pairing and synapsis. bioRxiv 612051; doi: https://doi.org/10.1101/612051.

ImageJ macro installation:

https://imagej.nih.gov/ij/docs/guide/146-31.html