Genomic loci to compartment distance ImageJ plugin

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Goal

We are often interested in finding the relative distance of a genomic loci with respect to a nuclear compartment (e.g Nuclear Speckles, Nucleoulus) in our microscopic experiments. The goal of this document is describe the algorithm used in an ImageJ plugin. This algorithm is developed based on conversations between Dr. Andrew Belmont lab members.

Process

loci indentification

1. User draws a ROI containing the genomic loci and the closest nuclear compartment.
    - The loci identification is done by the user. (Can automate it but it would be challenging for low SNR)
    - The closest nuclear is guess by the user, user can repeat the process if there close ties.

User input

ImageJ user defines following parameters 1. Channel number containing nuclear comartment signal a number between 1-4. 1. Channel number containing genomic loci signal a number between 1-4. 1. Threshold value for compartment boundary detection based on percent of maximum signal: a number between 0.0-1.0 . 1. Method to define the genomic loci - Maximum intensity pixel: The pixel location of maximum intensity in loci signal. - Boundary: for huge diffuse signal (e.g. amplified TetO array). This can be done by defining a border for signal based on thresholding. Requires a Threshold value between 0-1. - Center of mass: The pixel location of the center of mass. Defined based on the binary thresholded signal. Requires a Threshold value between 0-1. (under development)

Algorithm

Compartment bounary detection

1. **Noise subtraction:**

Defining nuclear compartment boundary

1.