

Visualization and analysis of single-molecule localization microscopy data in R (SMoLR)

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We developed SMoLR (Single Molecule Localization in R)[1][2]: a flexible framework that enables exploration and analysis of single-molecule localization data within the R programming environment. SMoLR is a package aimed at extracting, visualizing and analyzing quantitative information from localization data obtained by single-molecule microscopy. SMoLR is a platform not only to visualize nanoscale subcellular structures but additionally provides means to obtain statistical information about the distribution and localization of molecules within them using various clustering methods. This can be done for individual images or SMoLR can be used to analyze a large set of super-resolution images at once. Additionally, SMoLR can be used for image feature-based particle averaging, resulting in identification of common features among nanoscale structures.

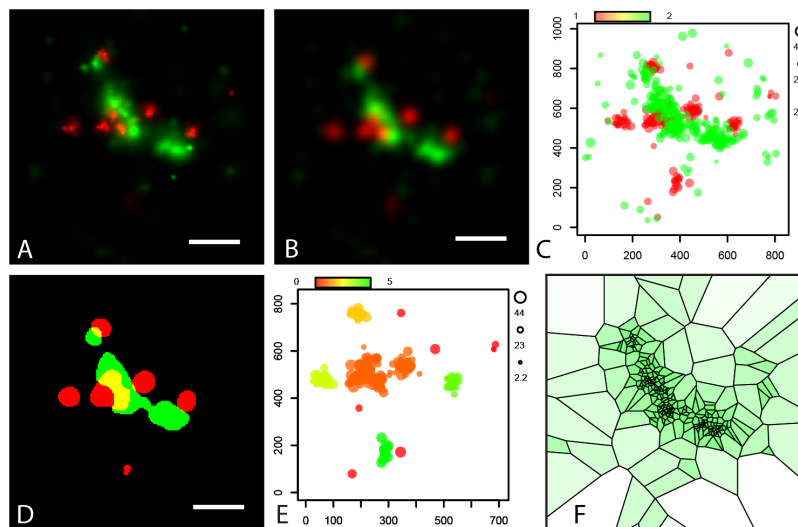


Figure 1. Visualization of single molecule microscopy data using (A) plotting precision dependent gaussians, (B) Kernel density estimation, (C) plotting Cartesian coordinates with extra information (color, size). Clustering using (D) Kernel density estimation, (E) density based clustering (dbscan) and (F) voronoi tessellation.

Embedded in the extensive R programming environment, SMoLR allows flexible ways to study the nanoscale organization of biomolecules in cells by extracting and visualizing quantitative information and hence provides insight in a wide-variety of different biological processes at the single-molecule level.

[1]. Paul, M.W., de Gruiter, H.M., Lin, Z., Baarends, W.M., van Cappellen, W.A., Houtsmuller, A.B., and Slotman, J.A. (2019). SMoLR: visualization and analysis of single-molecule localization microscopy data in R. *BMC bioinformatics* 20, 30.

[2] <https://github.com/ErasmusOIC/SMoLR>