

LOCALIZATION ANALYZER FOR NANOSCALE DISTRIBUTIONS (LAND): A SOFTWARE TOOL FOR SPATIAL POINT PATTERN ANALYSIS OF LOCALIZATION MICROSCOPY DATA

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Single molecule localization microscopy (SMLM) allows the investigation of biological structures and processes with a resolution down to the 10 nm range. Unlike conventional fluorescence microscopy techniques, SMLM generates a list containing the coordinates of each detected single molecule signal, which can be used for quantitative analysis of the underlying distribution and texture. However, there are many algorithms for specific applications such as the analysis of cellular nanostructures [1, 2], but the number of tools that contain a collection of algorithms readily accessible for routine applications is limited [3,4].

Here, we present Localization Analyzer for Nanoscale Distributions (LAND, <https://github.com/Jan-NM/LAND>) a collection of algorithms for the 2D and 3D analysis of the single molecule coordinates as well as the classification of the resulting texture. It contains commonly used algorithms such as Ripley's function, radial density function or density-based spatial clustering of applications with noise (DBSCAN). With LAND we also introduce algorithms specialized for the quantification of the conformation and texture (SMLM-ConText) of the nuclear nanostructure, enabling to differentiate between different chromatin condensation levels. We demonstrate the performance of our software on simulated data as well as its application on the investigation of the nuclear nanostructure and the distribution of membrane receptors.

Since our software is specifically tailored to quickly and reliably evaluate large sample sizes containing high emitter densities, it can be used as a valuable tool for routine applications of SMLM microscopy.

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