SINGLE-MOLECULE LOCALIZATION MICROSCOPY: PERFORMING 3D SUPER-RESOLUTION RECONSTRUCTION USING OPEN-SOURCE SOFTWARE

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The 3D SMLM reconstruction is a challenging computational task in term of performances, parametrization and runtime. The goal of this workshop is to present and to experiment some of the existing software solutions. We selected some software based on their usability and their accessibility (open-source) on ImageJ or Matlab. We will experiment software in four different modalities: 2D, astigmatism, double-helix, and biplane, both on simulated datasets and real datasets.

- Introduction of techniques for 3D SMLM and software
- Analysis methods, performances, limitations, density
- Calibration (3D)
- Post-processing: wobble correction, drift correction, temporal grouping, rendering
- Presentation of QuickPLAM or ThunderSTORM
- Presentation of SMAP by Jonas Ries, EMBL
- Presentation of ZOLA-3D by Benoît Lelandais, Pasteur Institute
- Demonstration on selected software (if time allows): QuickPALM, ThunderSTORM, EasyDHPSF, SMAP, ZOLA-3D