Developments of the ongoing 3D SMLM software challenge

Thanh-an Pham[1], Daniel Sage[1], Seamus Holden[2]

[1]Biomedical Imaging Group, Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland

[2]Centre for Bacterial Cell Biology, Newcastle University, Newcastle, United Kingdom

In this symposium SMLMS 2016, we have presented the second edition of challenge for benchmarking the SMLM software. This edition was focussed on the 3D localisation for which we have proposed simulated datasets in three modalities: astigmatism, double-helix and biplane. The proposed datasets share the same 3D underlying pseudo-biological structures imaged in 3 different modalities that allow us an inter-modality comparison. A large number of participants and developers ran their software that we have automatic evaluated with our knowledge of the ground-truth. The results of the participants were collected and formatted to perform the automatic assessed in order to get pertinent information for the multiple-criteria system.
Here, we briefly recall the pipeline for the generation of realistic data, including the experimental 3D point-spread functions (PSF), the photo-physic model of activation. We also discuss the issues encountered in order to fairly compare the modalities. Notably, the photon count in the double-helix modality was normalised with respect to the other modalities. We evaluated the results on these new datasets for which all the participants with a double-helix modality reran their software. We present our choice of quantitative and qualitative metrics, in particular the new metrics that we have introduced for assessment in the axial direction.
We also expose early results and some general outlines based on this preliminary comparative study for 3D localisation software.