Challenge for benchmarking single-molecule localization microscopy software packages

Daniel Sage

Biomedical Imaging Group, Ecole Polytechnique Férérale de Lausanne (EPFL), Lausanne, Switzerland

We present the second edition of the SMLM software challenge. In this 2016 edition, we are focusing on the three 3D techniques allowing 3D reconstruction of super-resolved images: biplane, astigmatic lens, or double helix. 3D localization microscopy is one of the key areas of growth in the field but still the algorithmic aspects of 3D SMLM are largely unexplored and have never been benchmarked.

Here, we discuss the perspectives of the challenge and the technical aspects of the organization. The key of the challenge is that the authors of the software run the experiment by themselves. We first established a group of experts helping to prepare relevant datasets by simulating the image formation of the microscopy. In this edition, we chose 3D experimental point-spread functions (PSF) to better reproduce experimental conditions. We defined the objective metrics to assess the performance of the software in terms of detection rate, lateral and axial accuracies, resolution, computation time, usability and accessibility. Finally, so, we have encouraged people to take part to the challenge.

At this date, we have attracted the attention of large number of participants, with over 30 software will be evaluated. Based on the submission of the participants, we expose also the preliminary results of our comparative study for 3D localization software packages.