

# From Images to Knowledge with ImageJ & Friends

virtual conference

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Conferences



## Quantification of 2D/3D multicolor single-molecule localization data

**Tutors:** Florian Levet ([florian.levet@u-bordeaux.fr](mailto:florian.levet@u-bordeaux.fr))

**Session 1:** 2020-12-01 08:00 UTC – 2020-12-01 12:00 UTC

**Session 2:** 2020-12-01 13:00 UTC – 2020-12-01 17:00 UTC

**Bio:**

Computer scientist by training, I joined the BIC (Bordeaux Imaging Center) in 2008. After a few years, I joined as a researcher the Quantitative Imaging of the Cell (QIC) team headed by Jean-Baptiste Sibarita at the Interdisciplinary Institute for Neuroscience (IINS) in Bordeaux. Since 2018, I am heading the computing activity of the QIC. I have developed several analytical tools for the quantification of pixel and localization data applied to cell biology and neuroscience. Amongst these tools, we can list SR-TESELER, the recent COLOC-TESELER and SpineJ. SR- and COLOC-TESELER are standalone software platforms developed for quantification of SMLM data. Noticeably, SR-TESELER has become a method of reference in the field with more than 1,500 downloads of the installer since Sept. 2015 and 200 citations (Google Scholar).

**Title:** Quantification of 2D/3D multicolor single-molecule localization data

**Abstract:**

Over the last decade, single-molecule localization microscopy (SMLM) has revolutionized cell biology, making it possible to monitor molecular organization and dynamics with spatial resolution of a few nanometers. By identifying the molecule coordinates instead of producing images, SMLM holds an important paradigm shift towards conventional fluorescence microscopy. Consequently, dedicated analyzing tools and methods have been developed to properly quantify SMLM data.

In this tutorial we will present various analytical methods designed to quantify single-molecule localization microscopy (SMLM) data directly from the localization coordinates. In particular, we will review clustering, segmentation and colocalization methods, for both 2D and 3D SMLM data. As a support, we will use simulation and experimental data.

At the end of this workshop the participants will be able to choose the most appropriate methods to their problem, whether it be for structural or colocalization analysis.

**Structure of the tutorial:**

The tutorial will not be divided with a x-hour course followed by a x-hour practical. Instead, and to make it more lively, each technique will be first taught with slides and precise examples followed by a direct practical by the participants. I will first explain clustering techniques, then segmentation methods and colocalization analysis. I will then explain how to visualize and analyze 3D SMLM data. Finally, the end of the tutorial will be dedicated to explain how experimental parameters can affect quantifications.

**Technical requirements:**

A Windows computer as only a Windows installer is currently available.