Computational aspects of super-resolution microscopy

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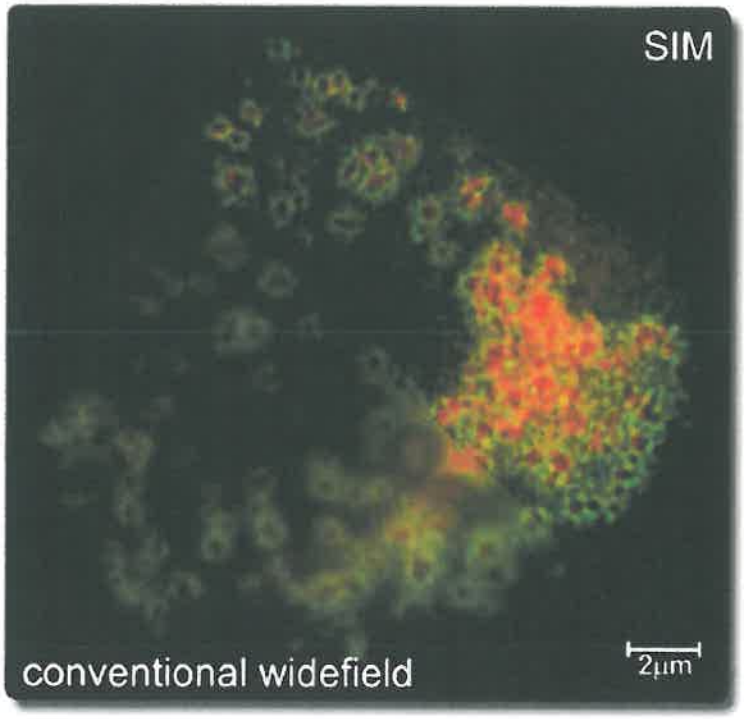
Abstract

In 2014 the Nobel Prize in Chemistry was awarded for fluorescence-based superresolution imaging. Even though stimulated emission depletion (STED) imaging can acquire images in a single-beam scanning configuration, many modern superresolution approaches such as structured illumination (SIM), pointillistic microscopy (PALM, STORM) or image scanning microscopy (e.g. the Airy Scan system) need computers to translate the acquired data into images being presented to the user. Just as in many medical imaging modalities such as CT-scan, magnetic resonance imaging (MRI) or positron emission tomography (PET), the raw data of many modern superresolution approaches needs image reconstruction algorithms.

In this talk, first an introduction into the framework of maximum-likelihood based inverse modelling will be given. Then the computational aspects of reconstructing data of fluorescence structured illumination microscopy will be treated. Finally a reconstruction algorithm (Matlab and CudaMat implementation) will be presented, which is capable of reconstructing the object along with unknown illumination structures.



Podosomes of a cell image with structured illumination (SIM). f-actin shown in red and vinculin in green. Image courtesy of Marie Walde, Gareth Jones and James Moneypenny.