ASSESSING THE INFORMATION CONTENT OF SINGLE MOLECULE LOCALIZATION MICROSCOPY

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Super-resolution microscopy, by enabling users to see what lies hidden behind the diffraction limit is revolutionizing our understanding of the nano-organization of protein structures. In particular, single molecule localization methods such as (f)PALM, (d)STORM, etc offer an almost unlimited precision on the position of a fluorophore. However, having a very small localization precision does not always translate into a very small resolution since the fraction of localized molecules is also a crucial factor. Unfortunately, this is a much harder value to determine experimentally since it requires a-priori knowledge of the structure, resulting in a whole set of different criteria in the literature that have widely varying requirements on the number of localized molecules, making it hard to distinguish efficiently between true information and artefacts.

We present here a new way of assessing the information content of a super-resolution image using statistical methods, and illustrate it on STORM imaging of different cytoskeletal proteins. Our results highlight the fact that the resolution is very non-uniform, and that some parts of an image can have a much lower resolution that the average, making it very important to monitor the information content locally.