A General Framework for Fitting an Arbitrary Model to SMLM Data

Y.L. Wu[1], P. Hoess[1], M. Mund[1,2], A. Tschanz[1], and J. Ries[1]
1. European Molecular Biology Laboratory, Meyerhofstrasse 1, Heidelberg, Germany
2. Department of Biochemistry, University of Geneva, Quai Ernest-Ansermet 30, Geneva, Switzerland
Email: yu-le.wu@embl.de

Keywords: super-resolution microscopy, SMLM, quantitative analysis, model fitting

Quantitative analysis of superresolution microscopy data is currently a major bottleneck, specifically for single molecule localisation microscopy (SMLM) where the data consists of lists of localisation coordinates. Structures of interest are usually analysed by simple geometric analysis or by averaging. In many cases, we can postulate an underlying basic geometry for the structures and are interested in the values of the parameters describing the model. However, an approach for fitting a parametrized model at the level of localisations is still missing.

Here, we present a new general framework for fitting an arbitrary model to SMLM data at the level of localisations. This framework is inspired by maximum likelihood estimation, which is commonly used to fit point clouds: the model is a probability density function and localisations are assumed to be observations drawn from the density function (distribution). We implemented a standardized framework to easily incorporate own continuous or discrete models for both 2D and 3D data and included visualization routines to assess the quality of the fit.

We demonstrate the power, versatility and flexibility of the framework by fitting models to various biological structures including clathrin-mediated endocytosis, nuclear pore complexes (NPCs; Fig.1), and microtubules. Our results show that the framework enables a precise quantification of structural features in SMLM images.

This framework is implemented as an open-source Matlab tool and will be available along with instructions and model templates.

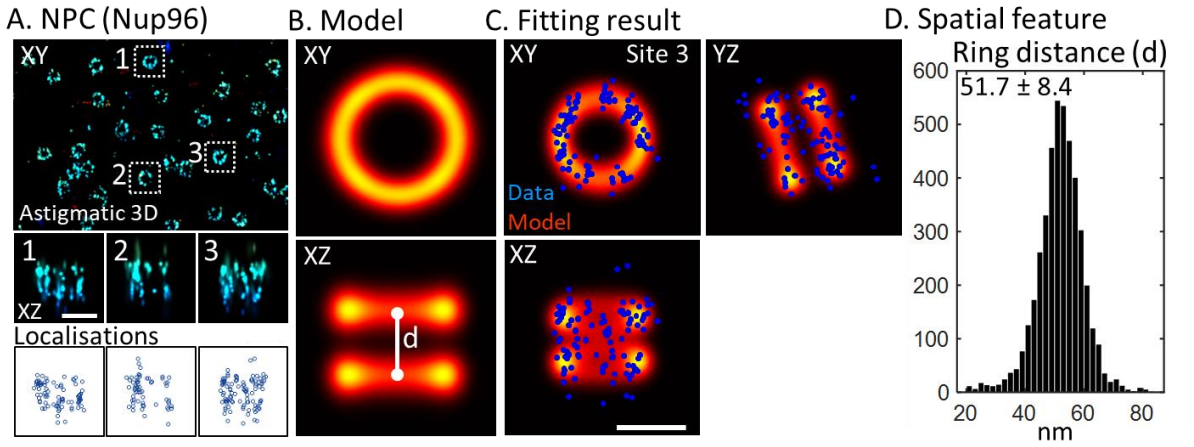

Figure 1. Fitting a dual-ring model to NPCs at the level of localisations to measure the distance between Nup96 in the cytoplasmic and nucleoplasmic ring (parameter d). Scale bars: 100 nm.