

Evaluating Colocalization in Super-resolution Microscopy

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Abstract:

Recently, collectively termed super-resolution microscopy have been developed, and they have the ability to break the optical resolution. 3D structured illumination microscopy (3D-SIM), one of such new technologies, theoretically doubles the optical resolution in both lateral and axial directions, allowing 3D imaging with eightfold volumetric resolution improvement compared with conventional fluorescence light microscopy. On the other hand, methods to evaluate spatial protein-protein proximity at this resolution level have not been established.

In this JC, I'm going to introduce an article, in which several methods for quantification of colocalization have been attempted [1], and review the respective analysis. I'd like to use this opportunity to discuss evaluating colocalization in super-resolution microscopy.

References:

1. Cerase A, et al. (2014) Spatial separation of Xist RNA and polycomb proteins revealed by superresolution microscopy. *Proc Natl Acad Sci U S A* 111(6):2235-2240.
2. Schermelleh L, et al. (2010) A guide to super-resolution fluorescence microscopy. *J Cell Biol* 190(2):165-175.
3. Ronneberger O, et al. (2008) Spatial quantitative analysis of fluorescently labeled nuclear structures: Problems, methods, pitfalls. *Chromosome Res* 16(3):523-562.
4. Dunn KW et al. (2011) A practical guide to evaluating colocalization in biological microscopy. *Am J Physiol Cell Physiol* 300(4):C723-C742.
5. Ollion J, et al. (2013) TANGO: A generic tool for high-throughput 3D image analysis for studying nuclear organization. *Bioinformatics* 29(14):1840-1841.