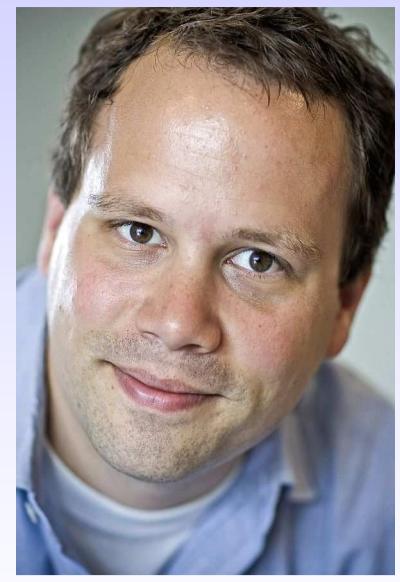
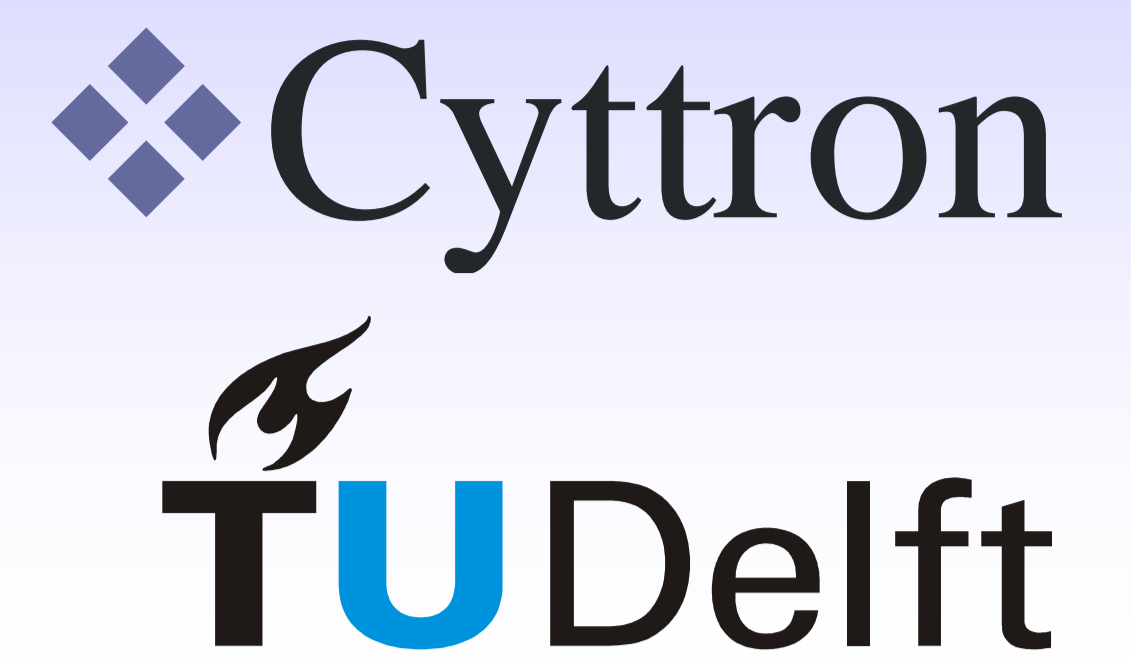


TeloView: dot-like segmentation using a Gaussian scale space approach and application



space approach and application

Bart J. Vermolen^{1,2}, Ian T. Young², Vered Raz³, Yuval Garini^{2,4}



University of Twente
Enschede - The Netherlands

1. Biophysical Engineering Group, University of Twente, The Netherlands, [b.j.vermolen@utwente.nl]
2. Quantitative Imaging Group, Delft University of Technology, The Netherlands
3. Department of Molecular Cell Biology, Leiden University Medical Center, The Netherlands
4. Department of Physics and Institute of Nanotechnology, Bar-Ilan University, Israel

Introduction

The 3D genome organization in the nucleus is important for both research and diagnostics. It can be studied by analyzing the telomeres, centromeres and other nuclear bodies. Here we present:

1. A novel detection method for dot-like signals.
2. Comparison with the previously implemented TopHat method.
3. Determinate radial redistributions of nuclear components in hMSC.

TopHat (TH) and MultiScale Product (MSP)

$$\text{TopHat}(A, B) = A - \max_B(\min_B(A))$$

A: image
B: structuring element

background features
> B
> size signal of interest

The maxmin operation estimates the background

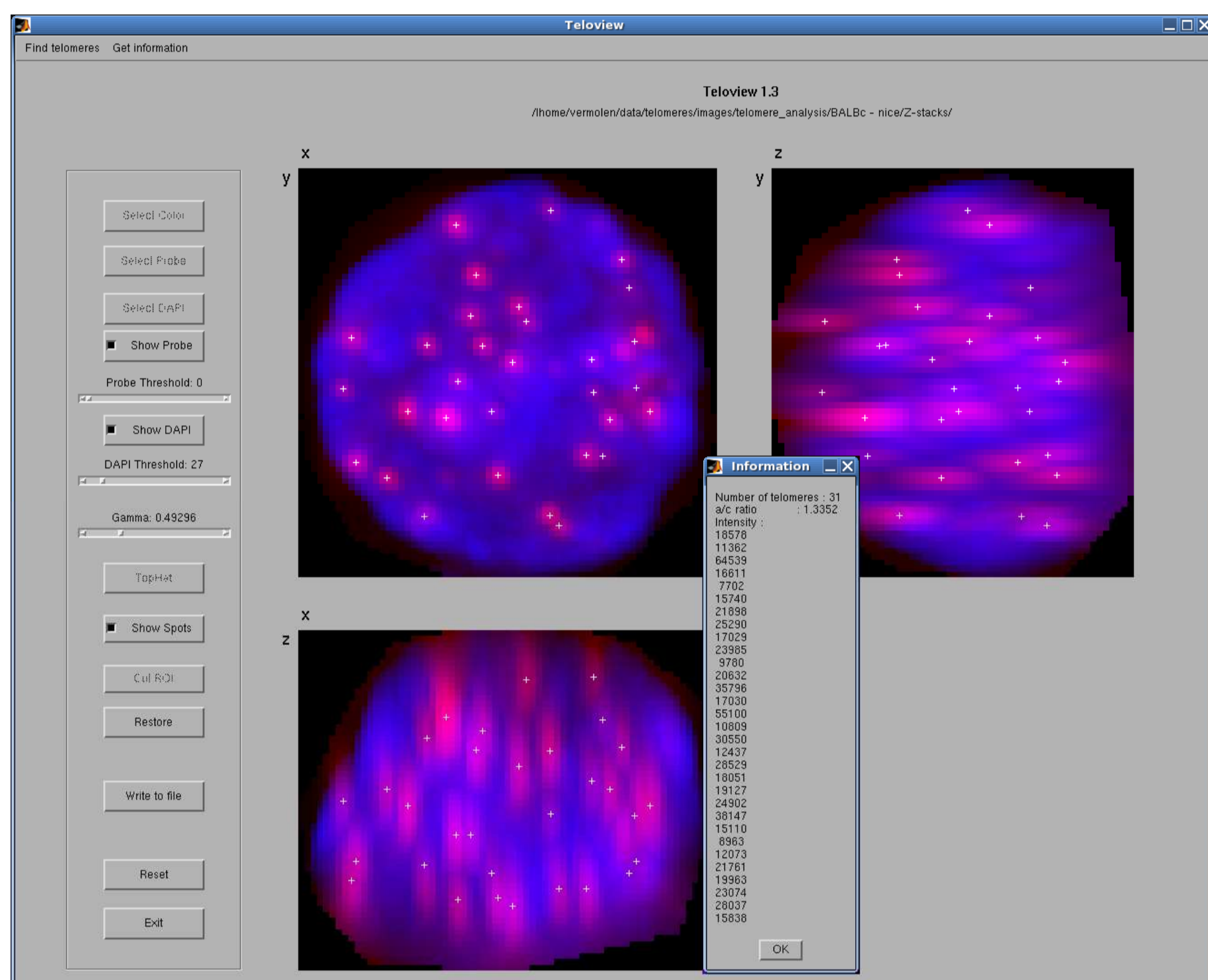
TeloView: a set of DIPimage tools in MatLab

Load images

Automatic localization of probe signals

Interactive correction

Analyze probe signals:
e.g. calculate intensities, organizational parameter, find aggregates etc.



$$g_i = g \otimes G(\sigma_i) \quad G(\sigma_i) = \frac{1}{3\sigma_i^3(2\pi)^{\frac{3}{2}}} \exp\left(-\frac{1}{2}\left(\frac{x^2}{\sigma_i^2} + \frac{y^2}{\sigma_i^2} + \frac{z^2}{9\sigma_i^2}\right)\right)$$

$$\sigma_i = \text{base} * \sqrt{2}^i \quad g_{\text{product}} = (g - g_0)(g_0 - g_1)(g_1 - g_2)$$

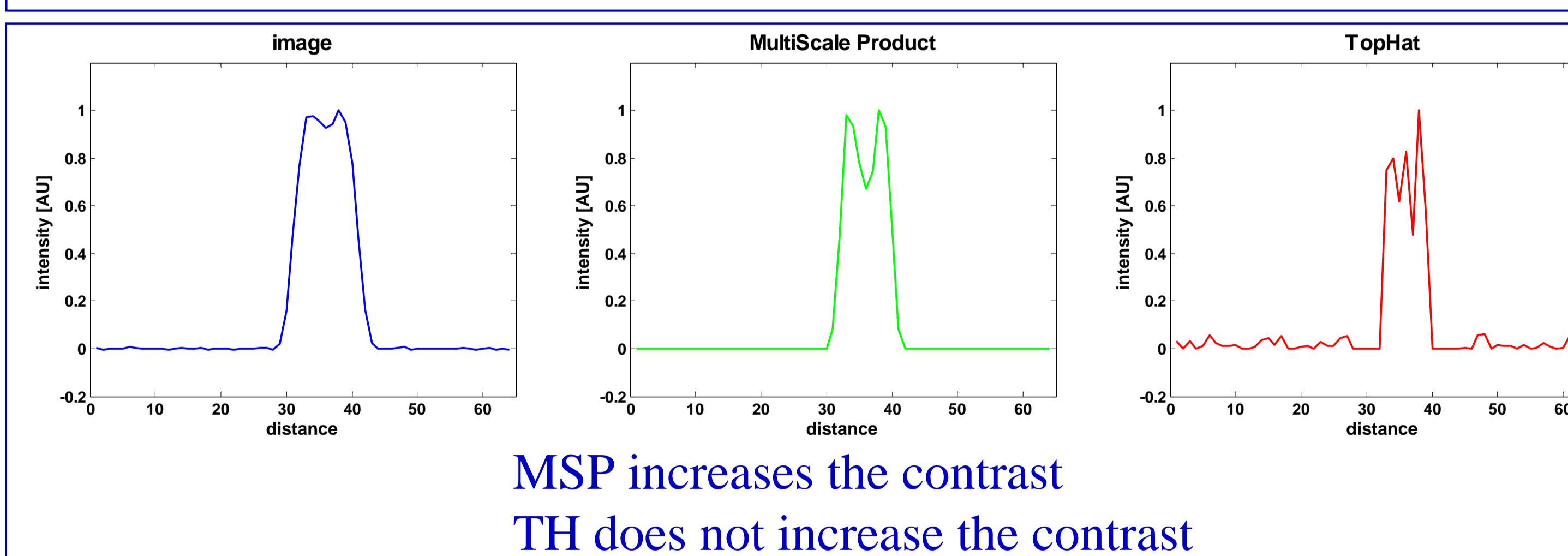
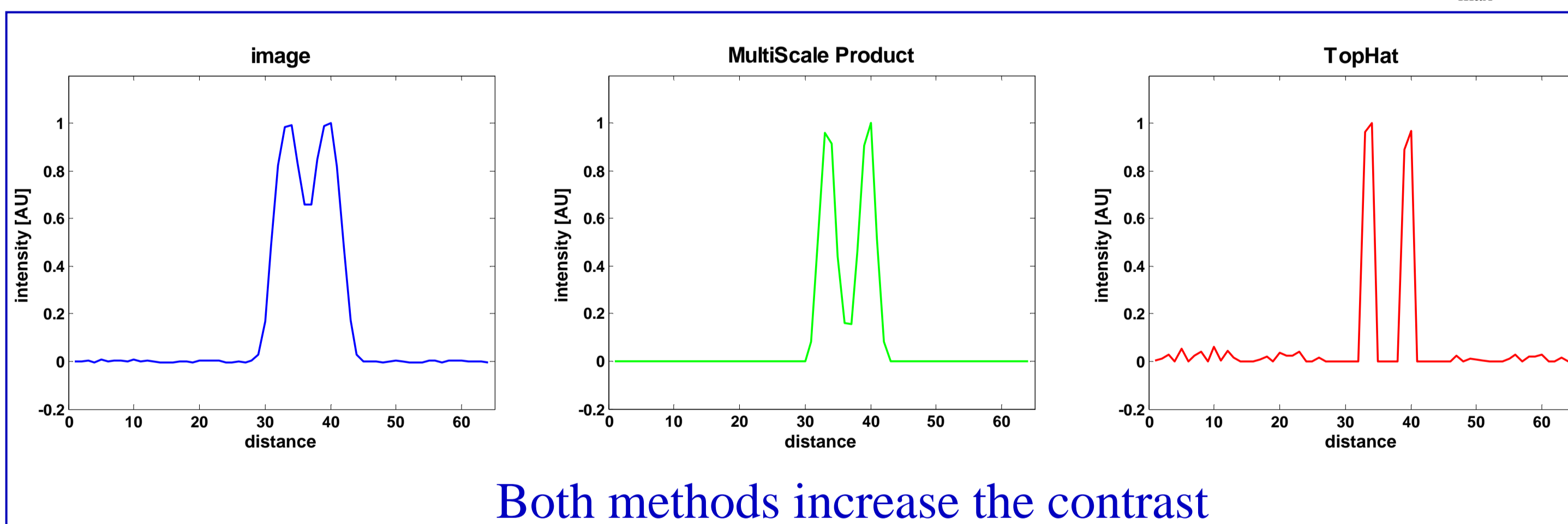
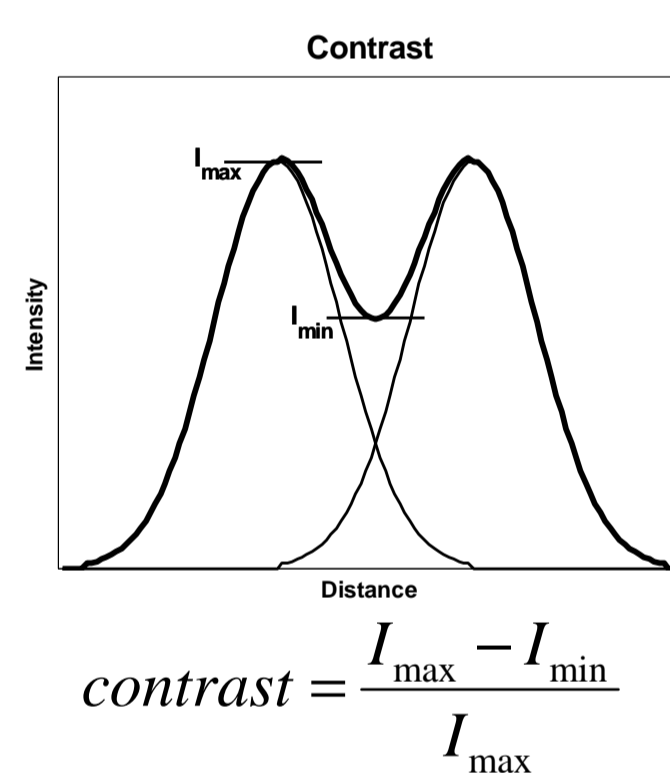
base ~ size signal of interest

The differences attenuates features affected equally by the convolution with Gaussians with subsequent widths

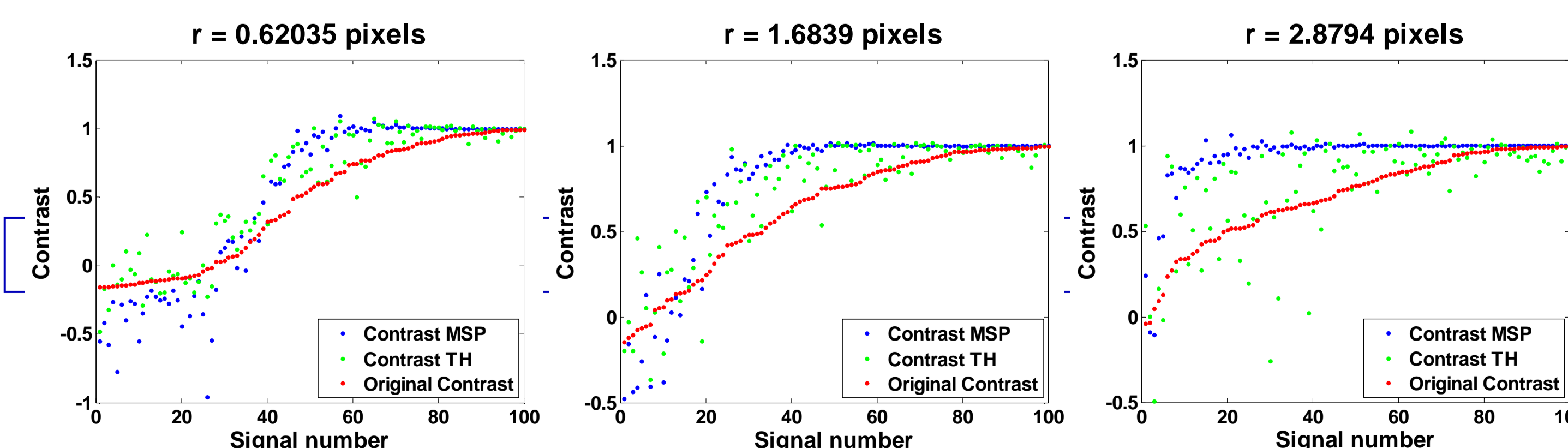
The product enhances features affected by the convolution

Simulation results

- Two dots in close vicinity
- Model Poisson noise
- Assumption: a higher contrast make it easier to segment the individual signals

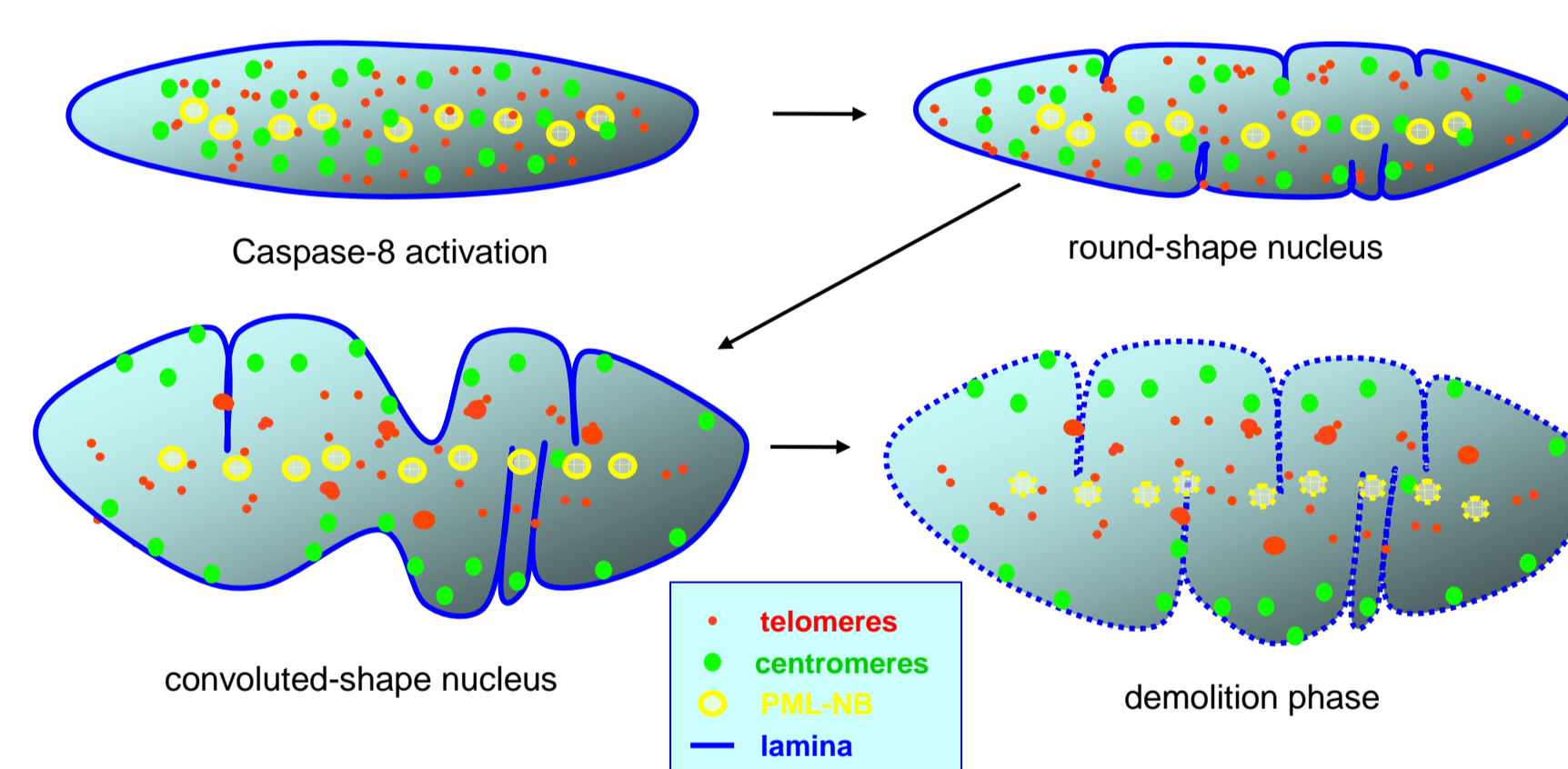


Two dots with random distances and therefore random initial contrast



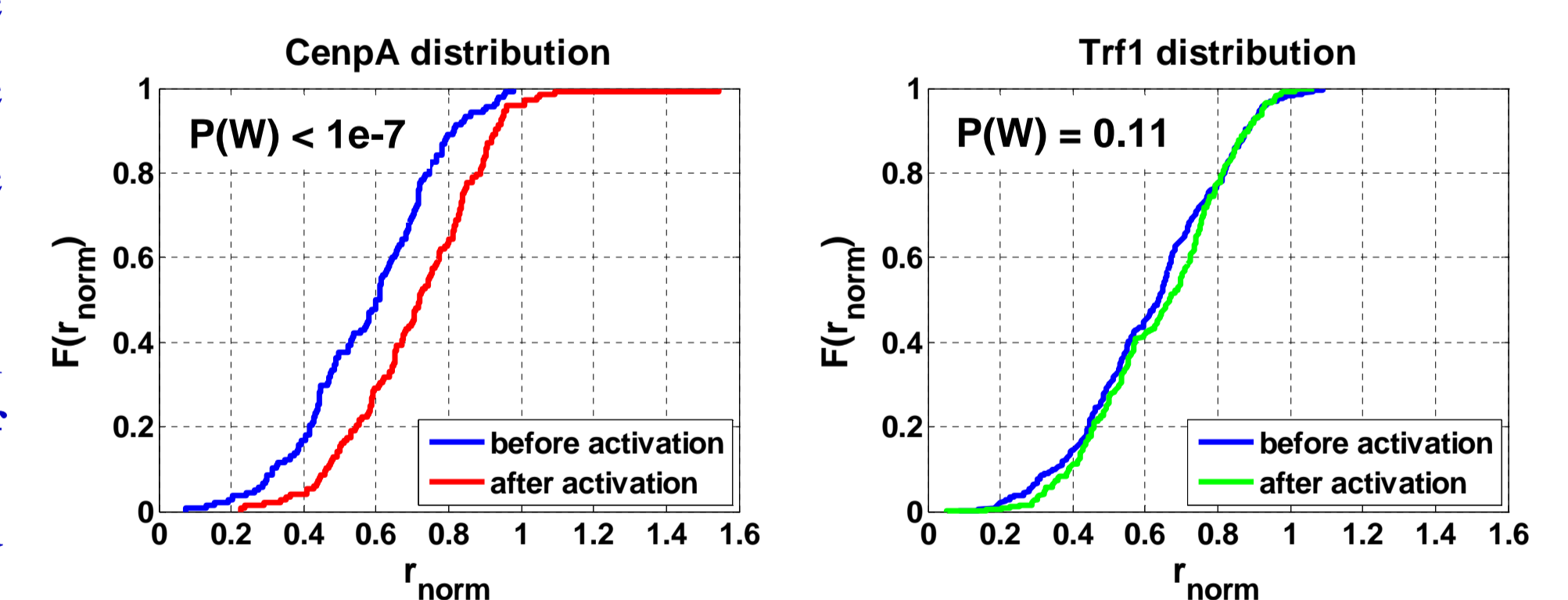
MSP more consistent results
MSP higher contrast for larger dots

Changes in nuclear spatial organization induced by the caspase-8 pathway



Here we have activated apoptosis in human mesenchymal stem cells, by expressing an inducible caspase-8 (1). Left we see a cartoon of the changes appearing in the nucleus.

The signals are segmented using the MSP approach and we find that caspase-8 triggers the spatial reorganization of telomeres (Trf1) and centromeres (CenpA)



Conclusion

Here we have presented a novel method with MultiScale Products to enhance the contrast of dot-like signals based on a method by Olivo-Marin (2). We show an improvement compared to the previously implemented TopHat method (3). Both the TH and the MSP method have been implemented into TeloView and is being used in several labs. Using the MSP method we have segmented fluorescent signals from several nuclear components showing redistribution of these components after caspase-8 activation.

References:

1. Vermolen, B.J. *et al*, Segmentation and analysis of the three-dimensional redistribution of nuclear components in hMSC, *submitted*.
2. Olivo-Marin, J-C., Extraction of spots in biological images using multiscale products, *Pattern Recognition*, 35, 2002.
3. Vermolen, B.J. *et al*, Characterizing the three-dimensional organization of telomeres, *Cytometry Part A*, 67A:2, 2005.