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LS-1-P-2871 3D reconstruction of live cell organelles from information entropy point of view

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A major challenge of live cell imaging is keeping cells alive and functioning as naturally as possible for the duration of the experiment [1]. A single 2D image only provides a small part of the complete context of the research and the relationship between structures in the sample cannot be fully determined in 2D. 3D imaging gives researchers more information about cellular structure and function. Our goal is to investigate images of observed objects' positions that as possible credibly copy their positions and determine the states of elementary units which determine the state of the organism: in our case, organelles. A microscopic image thus must be understood as information about the sample, and the microscope must be seen as an information channel. If we want to reconstruct an organelle in three-dimensional space we have to have a method for automatic features extraction. Computational image analysis allows us to provide rapid and automated processing of large datasets.

In order to understand the development of the image at various levels of de-focus, we introduce the point divergence gain PDG. We examine the change in the information which occurs when the particular point is replaced by the point from the next image. This may result in both an increase and decrease in the information. The change in an image series due to a z-scan is the result of either an object's appearance or disappearance from the image or changes in the point spread function of the object with the distance from its ideal focal plane. To determine the borders of the determinable point spread function, we calculate image points which carry the same information in consequent images captured upon moving the object along the lens' optical axis (z-scan). In this way, we may precisely identify the border of the point spread function for different identifiable objects [2, 3].

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