Mathematical image-processing methods for the automated segmentation of yeast cells in transmission images

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The extraction of quantifyable information from measured data is often an important subtask in the investigation of natural phenomena. In many situations, this data consists of digital images or image stacks as it is the case for microscopy data. The automated and reliable extraction of quantities of interest from images, however, is a challenging task: On the one hand, the relevant information may only be indirectly available, for instance the shape of an object, and the need to bring this information into a proper representation arises. On the other hand, the image usually contains features, such as irrelevant information, noise or clutter from measurements, which affect the stability of data-extraction algorithms. In the recent years, many novel mathematical tools have been developed, ranging from the abstract theory to actual computer implementations, in order to address the above-mentioned difficulties in automated image processing [1-4].

Here, we present the application of such tools to the yeast Saccharomyces cerevisiae, a widely used model organism in biomedical research. In particular, a data-processing pipeline is proposed aiming at the extraction of the quantities of interest from transmission microscopy images which depict dense populations of these yeast cells. The main problem in this setting is the sufficiently reliable detection of the cell boundaries in the presence of other cell features such as organelles or vacuoles. It is shown how non-linear diffusion-based denoising techniques can be utilized to reduce unwanted features while preserving the essential information at the cell boundaries. Moreover, we discuss a modified active contour model which is able to segment a single yeast-cell from their boundary information. Eventually, it is presented how these components enter a data-processing pipeline to obtain cell-based quantitative information in conjunction with associated fluorescence microscopy data. Finally, we show, by some examples, the application of the method to some data with known characteristics and discuss its potential for other applications.

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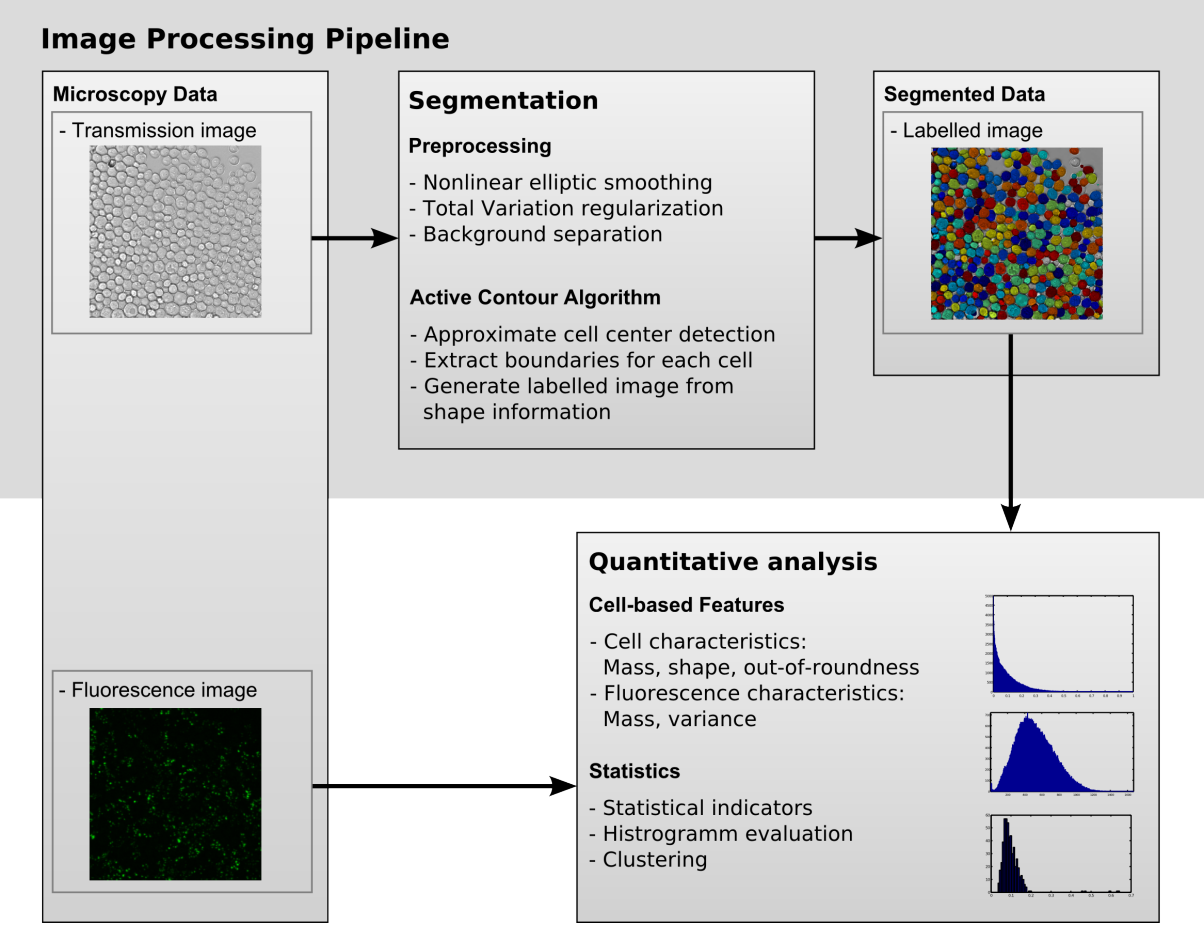

Figure 1. Prototypical image processing pipeline for transmission microscopy images of yeast cells. Such a pipeline can, for instance, be embedded into the quantitative analysis of data given by respective fluorescence images.

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