High-content screening (HCS) systems have become increasingly important with the move towards more quantitative investigations in biology. The typical HCS system consists of a laser-scanning microscope with an extensive suite of image-processing software to identify cells or tissue and extract the desired fluorescence information. HCS allows the measurement of parameters of individual cells, such as DNA content or expression levels of fluorescent proteins, much like flow cytometry. However, HCS also includes spatial information, which allows each cell to be monitored over an extended period of time. The disadvantage of current HCS techniques is the large number of high-resolution images that contain portions without any cells, which produces large amounts of data with little meaningful content. These many gigabytes of data must be processed offline, which may take several hours to produce meaningful results. Therefore, we have outlined a new data-acquisition strategy to improve the use of data storage, in an effort to obtain a throughput comparable to flow cytometry, while maintaining the information content available to HCS. Difficulty encountered in the automatic identification of budding yeast cells has demonstrated the need for such a higher-throughput, HCS instrument.

Here, we discuss the image-processing approach that will identify individual cells through bright-field illuminated images, extracting the center and size of each cell. The output of this image-processing step could be the control of a laser-steering mirror, which would scan only those areas identified as cells. Methods will also be presented that improve cell identification by elimination of false-positives (non-cells identified as cells).