

High Content Cellular Analysis and Their Applications

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Abstract

The biomedical research community faces for the first time the prospect of identifying and understanding the functions and interactions of macromolecules in human cells with high throughput, large scale approaches owing to the rapid advances of optical fluorescence microscopy in the past decade. Automated digital microscopy, coupled with a large arsenal of fluorescent and other labeling techniques, offers tremendous values to localize, identify and characterize cells and molecules. It has become a quantitative technique for probing cellular structure and dynamics and is increasingly used for cell-based assays and screens. The new development, in turn, generates many new informatics challenges in requiring innovative algorithms and tools to extract, classify, model, and correlate image features and content from

massive amounts of images for both hypothesis-driven analysis and hypothesis-generated tasks.

High content cellular analysis (HCCS) concerns the automation and quantitation of cellular information in a scale that is not achievable by the conventional manual microscopic approach. HCCS couples automated microscopy imaging and image analysis with biostatistical and data mining techniques to provide a system biologic approach in studying the cells, the basic unit of life, and potentially leads to many exciting applications in life and health sciences; beyond the scope of current high throughput screens. In this talk, I will introduce the concept of high content cellular analysis and briefly describe selected HCCS applications in genomic-wide screens, drug discovery, neuroscience, and signaling pathway perturbations, being investigated at Harvard.