

## CytoSurfer—Deal with Large Data Sets Generated by Image Segmentation Using ImageJ

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### Abstract

High Content Screening (HCS) technologies are used in drug discovery to identify hits and characterize lead candidates from large compound libraries. In HCS, cells grown multi-well plates are imaged using automated microscopes resulting in the production of very large sets of images.

Handling and interpreting such image datasets are recurrent bottlenecks in the HCS workflow. HCS analysis is composed of (i) an image analysis step intended for segmentation of the cellular objects, followed by (ii) a feature extraction/data processing step meant for profiling the compound's biological effects. In addition to the dedicated HCS platform softwares, ImageJ is a perfect environment to proceed to customized cell segmentation and feature extraction. This solution allows to easily automate complex image analyses using ImageJ tools and macros.

ImageJ's segmentation and feature extraction results in millions of cells depicted by dozens of quantitative features. To correlate these data with compound effects, population analysis and visualization can be easily performed in CytoSurfer®. This user-friendly software allows datasets to be visualized as population scattergrams, histograms and density maps.

Subpopulations of cells can be defined by drawing polygons in scattergrams or histograms. Cells within the gates (defined polygon) are then analyzed in all samples. Images of the cells within the gates can be directly visualized. CytoSurfer includes 96/384 wells plates capability, heatmap, dose response, IC50, ZFactor, t-test and multi-plates processor. ImageJ brings a flexible segmentation toolbox to CytoSurfer®, leading to a modular and versatile HCS profiling application.

### Keywords

High content screening, data processing, large data set, population analysis, cytometry

