# Fully-automated image processing software to analyze calcium traces in populations of single cells

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## ARTICLE INFO

## ABSTRACT

Advances in fluorescence live cell imaging over the last decade have revolutionized cell biology by providing access to single-cell information in space and time. One current limitation of live-cell imaging is the lack of automated procedures to analyze single-cell data in large cell populations. Most commercially available image processing softwares do not have built-in image segmentation tools that can automatically and accurately extract single-cell data in a time series. Consequently, individual cells are usually identified manually, a process which is time consuming and inherently low-throughput.

We have developed a MATLAB-based image segmentation algorithm that reliably detects individual cells in dense populations and measures their fluorescence intensity over time. To demonstrate the value of this algorithm, we measured store-operated calcium entry (SOCE) in hundreds of individual cells. Rapid access to single-cell calcium signals in large populations allowed us to precisely determine the relationship between SOCE activity and STIM1 levels, a key component of SOCE. Our image processing tool can in principle be applied to a wide range of live-cell imaging modalities and cell-based drug screening platforms.

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## 1. Introduction

Live imaging offers the unique advantage of watching a biological system function over time. With the emergence of automated instrumentation and genetically encoded fluorescent biosensors, it is now theoretically possible to measure dynamic changes of multiple single-cell parameters, such as protein–protein interactions, signaling events, or transcriptional regulation, in large cell populations [1–5]. However, because of the complex nature of such single-cell readouts, data analysis is usually performed manually or semi-automatically for a few individual cells, raising the possibility of personal bias and inadequate statistical sampling.

Most commercially available image processing softwares lack built-in segmentation algorithms that can automatically detect individual cells and extract single-cell parameters in a time series. Some imaging softwares, such as MetaMorph for example, offer applications that segment cells based on a threshold intensity, but lack the ability to separate cells that are contacting one another, and thus perform poorly in dense cell populations. Consequently, most users typically draw regions of interest (ROIs) manually to label individual cells, which dramatically lengthens data analysis and thus precludes analysis of large cell populations. Software packages that come with automated fluorescence microscopy platforms have more elaborated cell segmentation algorithms, but these are expensive and usually not integrated in applications that extract single-cell data in a time series.

Here, we present an image segmentation algorithm that reliably identifies individual cells in a field and measures fluorescent intensity over time. Our software uses the watershed transform to individuate cells touching each other, and thus performs well in dense cell populations. Our script is applicable to a wide range of live-cell imaging modalities, such as calcium imaging, bimolecular fluorescence complementation (BiFC), fluorescence energy transfer (FRET) or transcription reporter assays.

To demonstrate the use of our algorithm, we chose to measure Store-Operated Calcium Entry (SOCE) in hundreds of individual cells. SOCE is the major $Ca^{2+}$ entry pathway in non-excitable cells and is critical for a number of important cellular functions including motility, secretion and gene expression [6]. SOCE is regulated by $Ca^{2+}$ depletion from the endoplasmic reticulum (ER), which is detected by the ER-localized $Ca^{2+}$ sensor STIM1 [7,8]. STIM1 oligomerizes and migrates to ER-plasma junction sites upon store depletion, where it activates the $Ca^{2+}$ channel ORAI1 at the plasma membrane, resulting in $Ca^{2+}$ influx [7,9–14]. To demonstrate the value of automated single-cell analysis in large populations, we

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silenced STIM1 using a short hairpin RNA (shRNA) construct and correlated SOCE activity with STIM1 concentration in hundreds of individual cells.

## 2. Materials and methods

### 2.1. Reagents

The psiLv-H1$^{TM}$ shRNA expression vectors (co-expressing mCherry) were purchased from GeneCopoeia$^{TM}$. The sequence of the scrambled shRNA is CGATACTGAACGAATCGAT. The shRNA sequence against rat STIM1 is TCCAGGCAGGAAGAAGTTT. The STIM1 pAb was from Cell Signaling (#4916).

### 2.2. Cell culture and electroporation

Neuroscreen-1 cells (a clone derived from rat pheochromocytoma cells) were purchased from ATCC and grown in Dulbecco's Modified Eagle's Medium (high glucose) with 10% horse serum and 5% Fetal Bovine Serum (Invitrogen). To transfect Neuroscreen-1 cells with shRNA constructs, $1 \times 10^5$ cells were electroporated with 3 μg of the respective DNA using the Neon$^{TM}$ Transfection System in 100 μl of the Neon$^{TM}$ electroporation buffer (Invitrogen). The settings for the electroporation were as follow: 1410 V Pulse Voltage, 30 ms Pulse Width, 1 Pulse Number. The cells were then seeded onto Lab-Tek Chambered Coverglass (Bio Lab/NUNC) and maintained for another 3 days in 5% $CO_2$ before imaging.

### 2.3. Live cell confocal imaging and image processing

See on-line supplementary methods.

## 3. Results and discussion

### 3.1. An image segmentation algorithm to identify individual cells in a field

We set out to develop a versatile image segmentation tool that reliably identifies cells in an image, based on a fluorescence signal. Our algorithm was designed to meet the following four criteria. (1) Touching cells should be accurately separated, allowing single-cell analysis of dense cell populations. (2) Cell segmentation should not require nuclear staining (a segmentation strategy that is widely used in commercial imaging processing algorithms), since this is not always compatible with live-cell imaging. (3) Segmentation should be easily implementable in time series, in order to extract time-dependent changes in single cell parameters. (4) The code should be user friendly and flexible (the user should have the possibility, if desired, to set segmentation parameters based on visual inspection). The script, termed ISA (for Image-based Segmentation Algorithm) was written in MATLAB using built-in functions of the image processing toolbox.

Fig. 1b shows a typical confocal fluorescence image of cells labeled with the calcium dye Fluo-4. There are ~150 cells in this field displaying a range of fluorescence intensities, many of which are in direct contact with neighboring cells. Separating touching objects in an image can be a challenging task in image processing. We applied the watershed transform to solve this problem. The watershed transform finds "catchment basins" and "watershed ridge lines" in an image by treating it as a surface where light pixels are high and dark pixels are low [15,16]. The workflow for marker-based watershed segmentation is depicted in Fig. 1a (see methods). The result of the watershed transform is shown in Fig. 1g. Each detected object is displayed using a pseudocolor scale

(Fig. 1g) or is numbered (Fig. 1h). Note that the software accurately separates cells that are in direct contact with each other (compare Fig. 1c with g and h). ISA detects 151 out of 153 cells present in this image, and separates touching cells with 89% accuracy.

### 3.2. Automated analysis of single-cell $Ca^{2+}$ traces

We next used ISA to automatically detect single-cell $Ca^{2+}$ changes in a time-lapse experiment. We chose to monitor store-operated $Ca^{2+}$ entry (SOCE), an important $Ca^{2+}$ entry pathway in non-excitable cells, which is regulated by $Ca^{2+}$ depletion from intracellular stores [17]. SOCE is classically measured by a $Ca^{2+}$ addback assay [7]. Cells loaded with the $Ca^{2+}$ dye Fluo-4 are treated with thapsigargin to release $Ca^{2+}$ from stores and activate SOCE (in the absence of extracellular $Ca^{2+}$), which is then measured by addition of extracellular $Ca^{2+}$. The $Ca^{2+}$ addback assay exhibits a bimodal $Ca^{2+}$ profile, the first peak corresponds to thapsigargin-evoked $Ca^{2+}$ mobilization from stores, while the second peak represents $Ca^{2+}$ entry through SOC channels (Fig. 2a–c). We modified our software to extract the average fluorescence intensity of each individual segmented cell, and compute changes of $Ca^{2+}$ signals in a time series (see methods) (Fig. 2b). To determine how our software performs, we manually drew regions of interest (ROIs) in each of these cells and measured $Ca^{2+}$ responses using metamorph (Fig. 2c). ISA-derived $Ca^{2+}$ traces are quantitatively and qualitatively comparable to these obtained manually.

### 3.3. Single-cell correlation analysis of SOCE activity and STIM1 levels

We then used ISA to precisely determine the relationship between SOCE activity and levels of STIM1, an ER-localized calcium sensor that detects store depletion and activates SOCE [7,8]. To alter endogenous STIM1 concentration, we silenced STIM1 using a short hairpin RNA (shRNA) sequence co-expressed with the red fluorescent protein mCherry. When assayed by qRT-PCR, this shRNA reduces in average the STIM1 transcript in Neuroscreen-1 cells by ~65% (Supplementary Fig. 1a). Importantly, single-cell analysis of STIM1 knock down by immunocytochemistry shows that the extent of knock down strongly correlates with mCherry intensity (Supplementary Fig. 1b and c). Both Fluo-4 (green) and mCherry images (red) were acquired during the $Ca^{2+}$ addback assay and cells were segmented based on mCherry fluorescence (Fig. 3a). Fluo-4 $Ca^{2+}$ traces (for mCherry-expressing cells only) were then computed as described above. Since mCherry-expressing cells exhibit a wide-range of fluorescence intensities, analysis of a sufficiently large cell population should give access to single-cell SOCE responses for a broad spectrum of STIM1 concentrations. To increase the number of cells for this experiment, we acquired time-lapse data for up to four different fields in parallel using multi-position imaging (see methods). Fig. 3b shows single-cell and average $Ca^{2+}$ profiles for a control shRNA sequence. The bimodal response is similar to that shown in Fig. 2. shRNA-mediated knock-down of STIM1 has no effect on thapsigargin-evoked $Ca^{2+}$ release, but leads, in average, to a 60% reduction of the $Ca^{2+}$ addback peak, indicating SOCE inhibition (Fig. 3c). Note, however, that single-cell responses upon $Ca^{2+}$ addback are quite heterogeneous. Some cells show unaffected SOCE responses, while others exhibit no SOCE activity (Fig. 3c). To further explore the relationship between SOCE activity and STIM1 concentration, we plotted the maximum Fluo-4 intensity after $Ca^{2+}$ addition ($Ca^{2+}$ addback peak), as a function of mCherry intensity for each individual cell (Fig. 3e). We observed a strong negative correlation between SOCE activity and mCherry concentration. SOCE was unaffected, or mildly affected in cells weakly expressing mCherry