

The CellProfiler project



Free, at: www.cellprofiler.org
Open-source

- Allows quantitative analysis of various cell phenotypes in thousands of images (high-throughput experiments, time lapse, etc.)
- Usable by cell biologists without programming knowledge
- Modular design allows custom image analysis modules to be added (MATLAB source code)
- Flexible: runs on Mac/PC/Unix, can use cluster of computers, and accepts a variety of image formats: tif, jpg, bmp, gif, cur, dib, hdf, ico, pbm, pcx, pgm, png, ppm, ras, stk, xwd, avi
- To keep up with image acquisition rates, processing requires multiple computers



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Variety of algorithms available

Algorithms in CellProfiler are from the literature or donated to the project

```
function [rgOut, varargout] = ImDAPI2Rg(imDAPIin, LoGDim, LoGHW, MinArea)
```

```
wiendim=[5 5];
```

```
rgLoG=fspecial('log',LoGDim,LoGHW);  
imLoGout=imfilter(double(imDAPIin),rgLoG);  
imLoGoutW=wiener2(imLoGout,wiendim);  
rgNegCurve=imLoGoutW<-1;
```

```
%set outsides
```

```
rgNegCurve([1 end],1:end)=1;  
rgNegCurve(1:end,[1 end])=1;
```

```
%Throw out noise, label regions
```

```
rgArOpen=bwareaopen(rgNegCurve,MinArea,4
```

Voronoi-Based Segmentation of Cells on Image Manifolds

Thouis R. Jones¹, Anne Carpenter², and Polina Golland¹

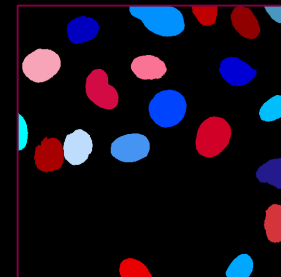
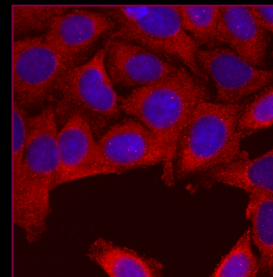
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Abstract. We present a method for finding the boundaries between adjacent regions in an image, where "seed" areas have already been identified in the individual regions to be segmented. This method was motivated by the problem of

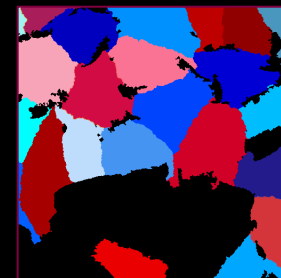
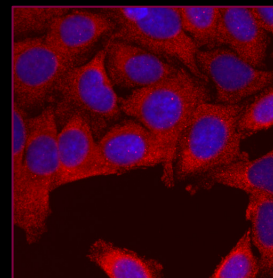
Primary identification

- Meyer & Beucher 1990
- Malpica...del Pozo 1997
- Wahlby...Bengtsson 2004
- Wahlby PhD Thesis 2003
- Ortiz de Solorzano
...Lockett 1999

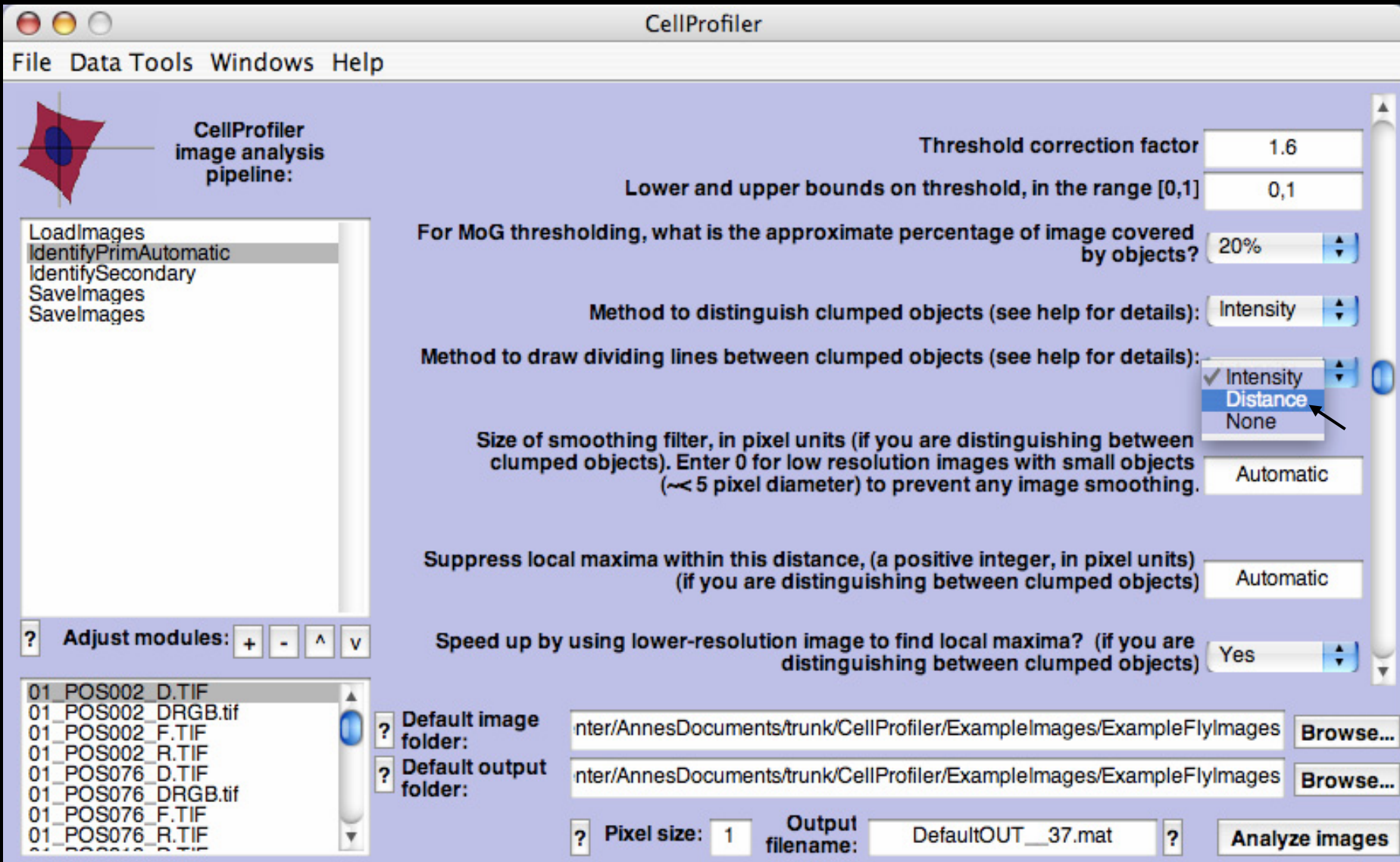


Secondary identification

- Jones, Carpenter, Golland (2005) ICCV Workshop on Computer Vision for Biomedical Image Applications
- Vincent, Soille (1991) IEEE Transactions of Pattern Analysis and Machine Intelligence



Variety of algorithms available



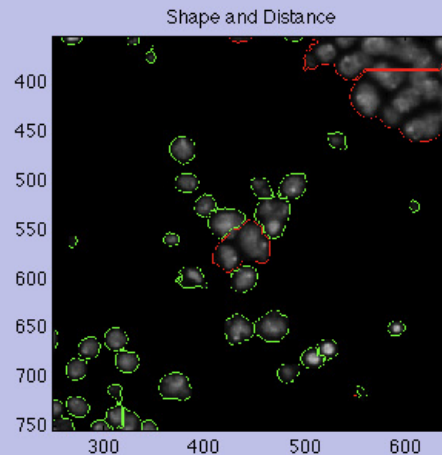
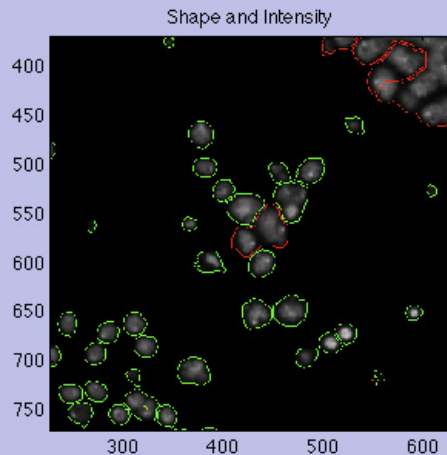
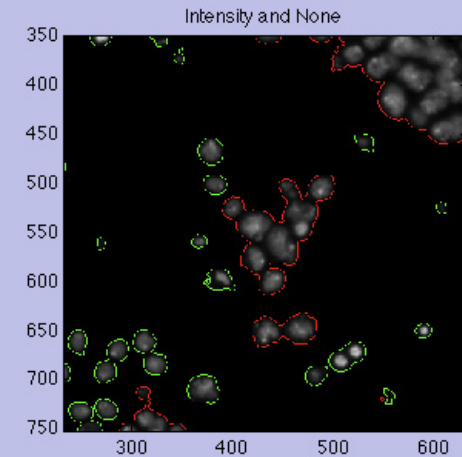
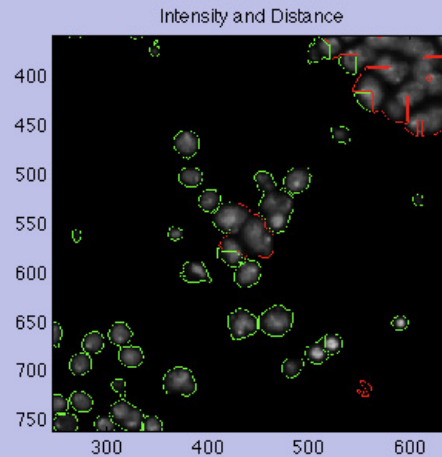
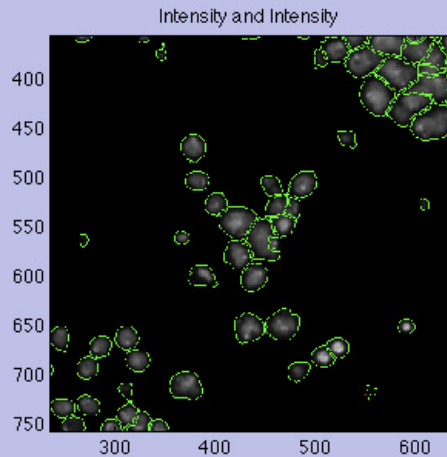
The screenshot displays the CellProfiler software interface, specifically the 'CellProfiler image analysis pipeline' configuration window. The window title is 'CellProfiler'. The menu bar includes 'File', 'Data Tools', 'Windows', and 'Help'. On the left, there is a 'CellProfiler image analysis pipeline:' section with a red and blue logo. Below this is a list of modules: 'LoadImages', 'IdentifyPrimAutomatic', 'IdentifySecondary', 'SaveImages', and 'SaveImages'. A 'Adjust modules:' section contains buttons for '+', '-', '^', and 'v'. Below the module list is a list of image files: '01_POS002_D.TIF', '01_POS002_DRGB.tif', '01_POS002_F.TIF', '01_POS002_R.TIF', '01_POS076_D.TIF', '01_POS076_DRGB.tif', '01_POS076_F.TIF', and '01_POS076_R.TIF'. The main configuration area on the right contains several settings:

- Threshold correction factor:** 1.6
- Lower and upper bounds on threshold, in the range [0,1]:** 0,1
- For MoG thresholding, what is the approximate percentage of image covered by objects?:** 20%
- Method to distinguish clumped objects (see help for details):** Intensity
- Method to draw dividing lines between clumped objects (see help for details):** Intensity, Distance, None (Distance is selected)
- Size of smoothing filter, in pixel units (if you are distinguishing between clumped objects). Enter 0 for low resolution images with small objects (~< 5 pixel diameter) to prevent any image smoothing.** Automatic
- Suppress local maxima within this distance, (a positive integer, in pixel units) (if you are distinguishing between clumped objects)** Automatic
- Speed up by using lower-resolution image to find local maxima? (if you are distinguishing between clumped objects)** Yes
- Default image folder:** nter/AnnesDocuments/trunk/CellProfiler/ExampleImages/ExampleFlyImages (Browse...)
- Default output folder:** nter/AnnesDocuments/trunk/CellProfiler/ExampleImages/ExampleFlyImages (Browse...)
- Pixel size:** 1
- Output filename:** DefaultOUT__37.mat
- Analyze images** button

Algorithms can be compared in test mode:

Figure 4

File Edit View Insert Tools Desktop Window Help



Status Details

	Time(sec) for 1st Cycle	Avg Others
Module 1:	2.2	1.2
Module 2:	1.0	0.9
Module 3:	1.0	0.8
Module 4:	1.3	1.1
Module 5:	11.5	7.0
Module 6:	1.0	1.0
Module 7:	0.5	0.4
Module 8:	3.5	0.9
Module 9:	0.9	0.4
Module 10:	1.5	0.7
Module 11:	0.1	0.1
Module 12:	2.6	2.6
Avg Totals:	27.1	17.1
TOTAL TIME:	61.5	

Different measured features can be compared:

Cell images

↓ Identify modules

Identified cells

↓ Measure modules

Image and cell measurements

↓ Calculate Statistics module

V and Z scores for each measured feature

↓
Decision about how to score the assay