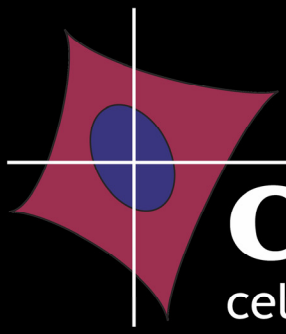
The CellProfiler project



CellProfiler™
cell image analysis software

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

Whitehead Institute for Biomedical Research

Anne E. Carpenter
Whitehead Institute for Biomedical Research:
Laboratory of David Sabatini

Thouis Ray Jones
MIT Computer Sciences/ Artificial Intelligence Laboratory:
Laboratory of Polina Golland

MIT

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

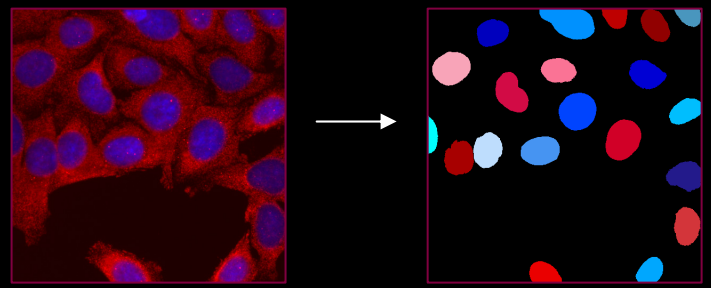
Thouis R. Jones[1], Anne Carpenter[2], and Polina Golland[1]

[1] MIT CSAIL, Cambridge, MA, USA
[2] Whitehead Institute for Biomedical Research, Cambridge, MA, USA

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

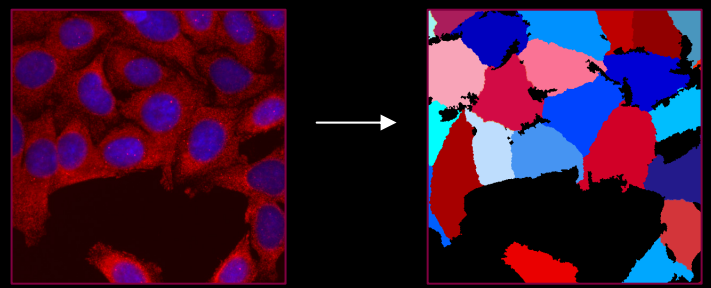
Primary identification

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

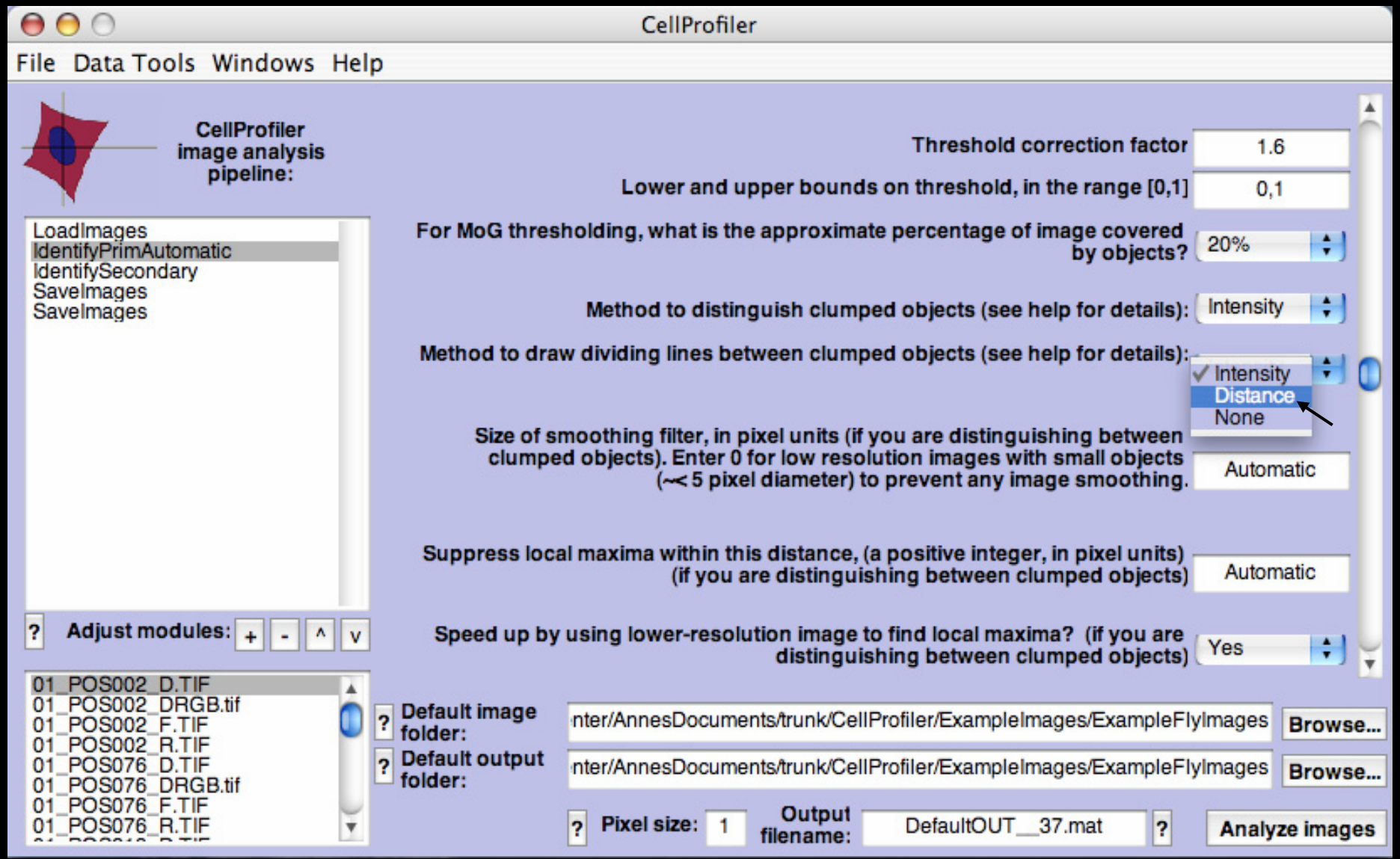


Secondary identification

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



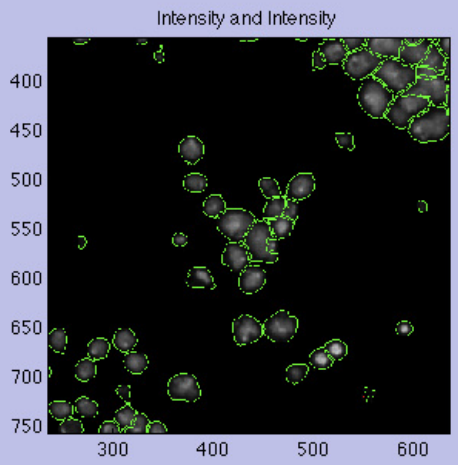
Variety of algorithms available

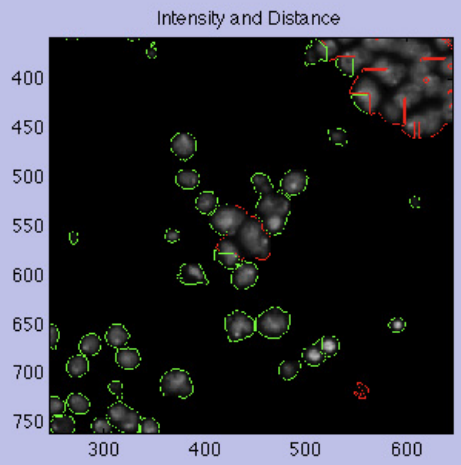


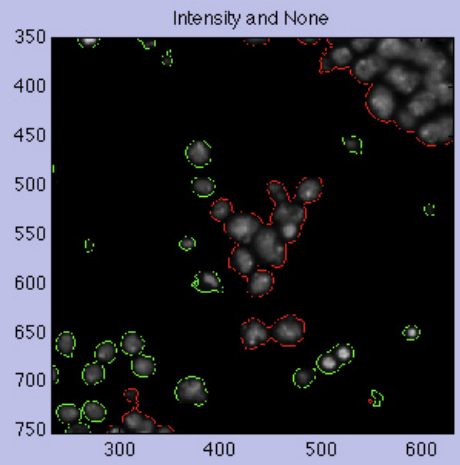
Algorithms can be compared in test mode:

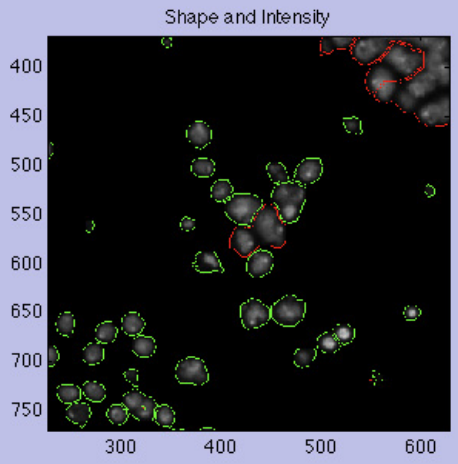
Figure 4

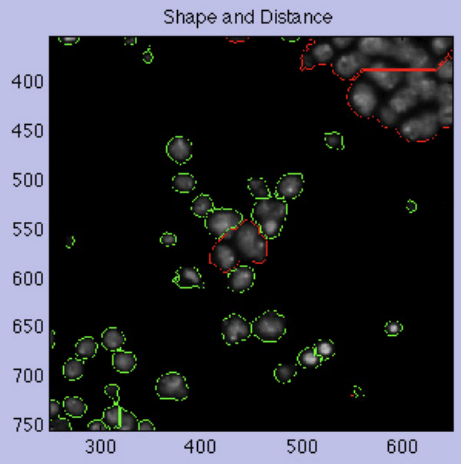
File Edit View Insert Tools Desktop Window Help











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: