# Visual Computing for Quantifying the F-actin Pattern Changes in response to drug type and concentration

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## •Introduction

Advanced Microscopy and Fluorescent imaging technology bring biologists the possibility to use visual information to perform cellular quantification with a decent accuracy. Therefore it is desirable to apply computer vision and machine algorithms to extract interesting cellular patterns for the quantification purpose. In this work we mainly focus on one protein, say the F-actin, which is a **filamentous protein and the main constituent of the thin filaments of muscle fibers..** The goal is to quantify its appearance in the cells under different pharmaceutical treatment. The visual quantification could be used to validate the early hypothesis made on the interaction mechanism between the cells and the added drugs. It could also be used for predicting the functioning pattern of newly discovered drugs. We mainly concerns on the following aspects: What features to extract . How precise these algorithms are . Which quantification measurement could truly highlight the inter-treatment differences..

## •Related Work

Recent work in this area, which is quite similar to ours includes recognition of the locations of different kinds of proteins in a single cell or multiple cell images [1] done Prof. Robert Murphy's group from CMU and the "cell profiler" [2] a machine learning powered interface which extract rules from user specified data-set and distinguish positive samples from the negative ones. While our work shares some similarities with these two previous work we would like highlight the difference here as shown in Table. 1 In this work we are addressing the challenge to determine patterns in unlabeled confocal microscopy images. Our main objective is not classification but a descriptive quantification to profile the response of F-actin to different pharmaceutical treatments. Our analysis framework can deal with quite complex images and can highly generalize the F-actin organization patterns into a few numerical quantification measurements.

| | cell profiler | Protein localization | Our work |
|---|---|---|---|
| Feature Extraction | cell based | cell based | image based |
| Result Format | Binary Indicator | Discrete Class labels | Continuous Numerical Results |
| Classification Goal | Tell positive from negative | Different kinds of proteins | Different organization pattern of a single protein (F-actin) |
| Motivation | Highlight the difference | Highlight the difference | Show the conditional variation trend |

Table 1. *This Table gives a comparison between our work and previous work*

## •Methodology

### 1. Analysis Framework

We did the image analysis in a top down fashion. There are two layers in the main structure. In the first layer the image is segmented into 3 parts: white bright actin (WBA), which has a much higher intensity than the rest of an image, cytoplasm which has an intensity in between and background. In the second layer we did Sub-classification to the white bright actin and cytoplasm based on the differentiating features presented in the sub-regions, such as the cellular location of the structure for WBA and line shape textures for cytoplasm. The flow chart of our analysis framework is shown in Fig. 1.

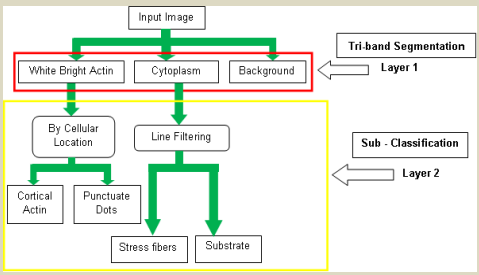


**Fig 1.** *This figures shows our analysis framework for doing the quantification*

### 2. Tri-band Segmentation

The procedure for doing the tri-band segmentation is shown in Fig 2. on the left and an example showing the result is presented in Figure below. Here the blue regions denote the background, the green region denotes the cytoplasm and the red regions denote white bright actin(WBA)

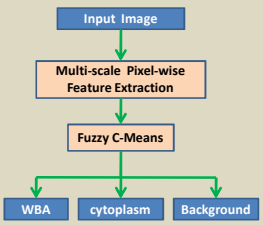


**Fig 2.** *Flow chart for doing tri-band segmentation*

### 3. Sub-classification

When working on the F-actin patterns the biologists are mostly interested in identifying the following sub-regions: punctuate dots, cortical actin and stress fibers. Fig.4 gives a visual definition for cortical actin and punctuate dots in the cells while Fig.5 shows how stress fibers appear. In this section we shows the algorithm for doing the sub-classification for white bright actin(WBA) region and Cytoplasm region. Fig 6. shows the flow chart for the sub-classification in WBA regions and Fig 7. shows the flow chart for doing sub-classification in the cytoplasm region. Fig 8. shows an example of stress fiber extraction.

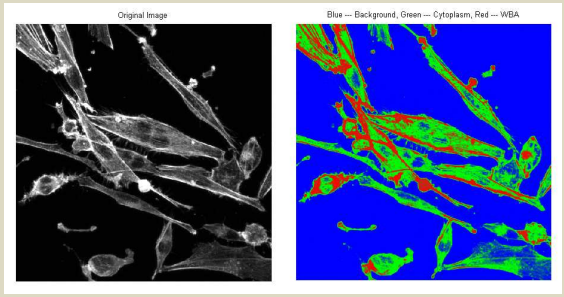


Fig 3. *An example showing the tri-band segmentation result, the figure on the left is the original image and the figure on the right is the segmented and color labeled image.*

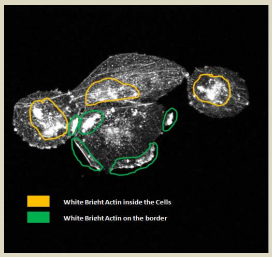


Fig 4. *The figure on the left shows the appearance of cortical actin and punctuate dots inside the cell*

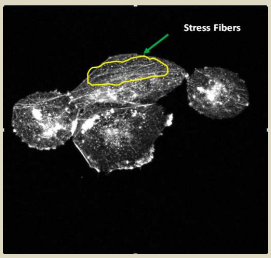


Fig 5. *The figure on the right shows the appearance of stress fibers inside the cell.*

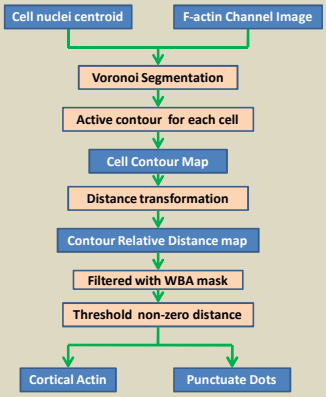


**Fig 6.** *This figure shows the sub-classification of WBA*

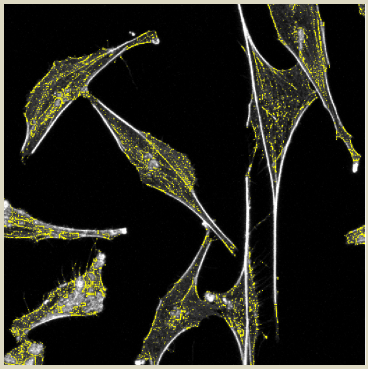

**Fig 8.** *This figure shows an example of the stress fiber extraction in the F-actin Channel Image. The yellow color highlighted parts are stress fibers*

## •Results

We extracted 5 feature regions from each F-actin channel Image: white bright actin, cytoplasm, cortical actin, punctuate dots and stress fibers. The quantification descriptors to profile the drug dependant cellular changes are built by computing the pair-wise ratios of the area or the integrated intensity of these featured regions and showing how these ratios for one drug changes with the concentration increase. We also did this for the cytoplasm texture analysis results. Fig 9. shows one of the profile graphs for a drug.

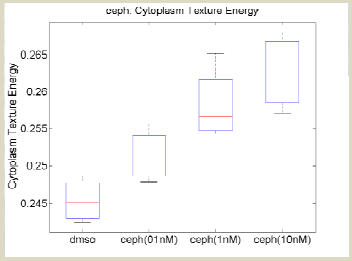


**Fig 9.** *This figure shows how the profile of cytoplasm texture energy for a drug named "ceph"*

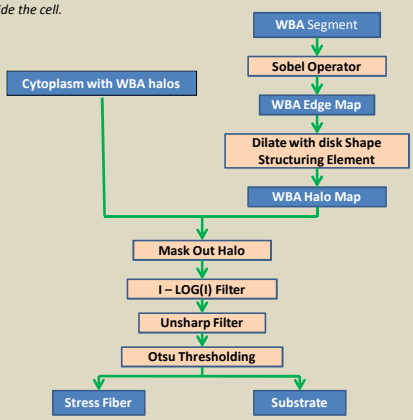


**Fig 7.** *This figure shows the sub-classification of cytoplasm*

### 4. Cytoplasm Texture Analysis

Cytoplasm is a region full of textures. Quantifying the texture properties of these region will help profile the changes of F-actin patterns. We did this as the procedures shown in Fig. 10, for details about Weighted Multiscale Gray Level Co-ocurrence Matrix WMGLCM , please refer our paper [3] submitted to EMBS 2009 for details

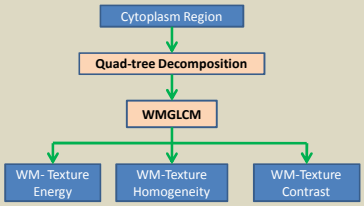


**Fig 10.** *This figure shows the flow chart for cytoplasm texture analysis*

## •Reference:

[1] Ting Zhao and Soto, S. and Murphy, R.F. (2006) Improved comparison of protein subcellular location patterns.Biomedical Imaging: Nano to Macro, 2006. 3rd IEEE International Symposium on, 562-565
[2] Jones TR, Kang IH, Wheeler DB, Lindquist RA, Papallo A, Sabatini DM, Golland P, Carpenter AE (2008) CellProfiler Analyst: data exploration and analysis software for complex image-based screens. BMC Bioinformatics 9 (1):482, /doi: 10.1186/1471-2105-9-482. PMID: 19014601 PMCID: PMC261443
[3] F-ACTIN image analysis for quantifying the astrocytoma cell response to candidate pharmaceutical, Chi Cui, Joseph JaJa, Thomas Turbyville, John Beutler and Stephen Lockett, Submitted to EMBS 2009