MULTI-RESOLUTION SUPER-PIXELS AND THEIR APPLICATIONS ON FLUORESCENT MESENCHYMAL STEM CELLS IMAGES USING 1-D SIFT BASED MERGING

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Introduction

•The difficulty of visually scanning very large high resolution fluorescent microscopic images requires automated processing.
•It is necessary to implement a reliable algorithm that can follow the changes of each cell individually.
•A new super-pixel based algorithm is proposed to segment fluorescent microscopy images with varying super-pixel sizes.
•The goal is to represent a cell or a stem cell using a couple of super-pixels. 1-D SIFT concept is introduced to merge superpixels.

Literature & Our Model

•Super-pixel algorithms start by dividing the image into uniform segments.

•Iterative algorithms are used to modify the uniform segments into regions that try to cover similar pixels.

•Simple Linear Iterative Clustering [1] method is used as the underlying super-pixel method.

•Initial seed position are uniformly placed throughout the image.
•As a result initial super-pixel regions have honeycomb shapes.

•Let $x\,[n_1, n_2]$ be a 2-D microscopic image. It is processed by a wavelet high-pass filter both vertically and horizontally. $h[l]$ is a half-band wavelet high-pass filter with length L.

$$y_h[n_1, n_2\,] = \sum_{l=0}^{L-1} x[l - n_1, n_2].\,h[l] \quad (1)$$

$$y_v[n_1, n_2\,] = \sum_{l=0}^{L-1} x[n_1, l - n_2].\,h[l] \quad (2)$$

where $h[l]$=[-0.25 0.5 -0.25].

•An image y_e representing the edge information of the original image x is obtained by:

$$y_e = |y_{h,r}| + |y_{h,g}| + |y_{h,b}| + |y_{v,r}| + |y_{v,g}| + |y_{v,b}| \quad (3)$$

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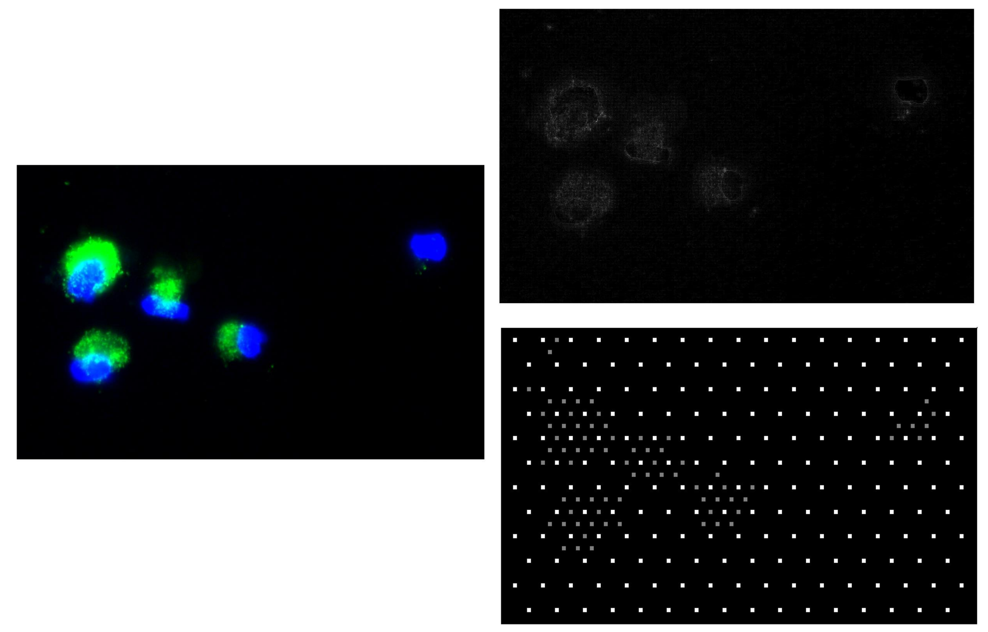
Seed Placement



• If a region between the two connected seeds on that pattern has high wavelet energy values, place an additional seed between them.

• A threshold is applied to $y_e[n_1,n_2]$ components to decide whether to place a new seed in the midpoint of two connected seeds.

• After this new seeding process, initial super-pixel groups are created by assigning pixels to the nearest cluster centers.

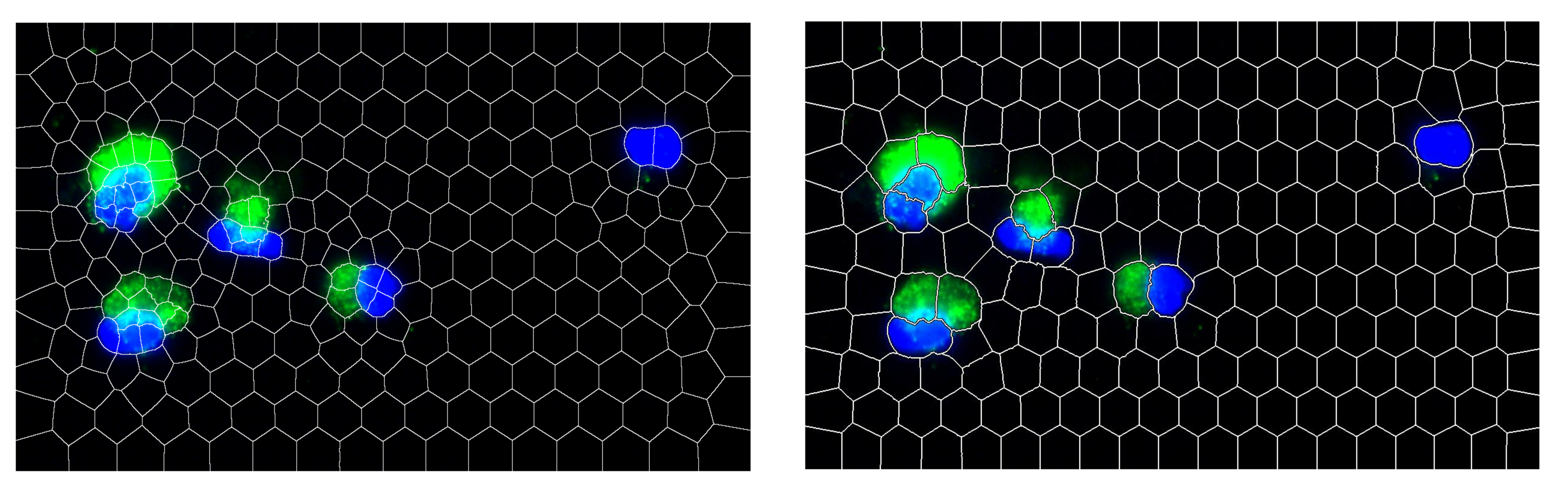
$$\bullet t = \frac{1}{4}(\max(y_e[n_1, n_2\,]) + min(y_e[n_1, n_2\,])) + \frac{1}{2N}(\textstyle\sum_{n_1 n_2}(y_e[n_1, n_2])) \quad (4)$$

• As in SLIC algorithm two distance measures are defined as d_c and d_l.

$$d_l = \sqrt{(p_x - m_x)^2 + (p_y - m_y)^2} \quad (5) \qquad d_c = \sqrt{(p_1 - m_1)^2 + (p_2 - m_2)^2 + (p_3 - m_3)^2} \quad (6)$$

• A weighted sum of d_c and d_l are used as a distance.

$$d = \sqrt{{d_c}^2 + k{d_l}^2}\,c \quad (7) \qquad c = \frac{1}{Area} \quad (8)$$



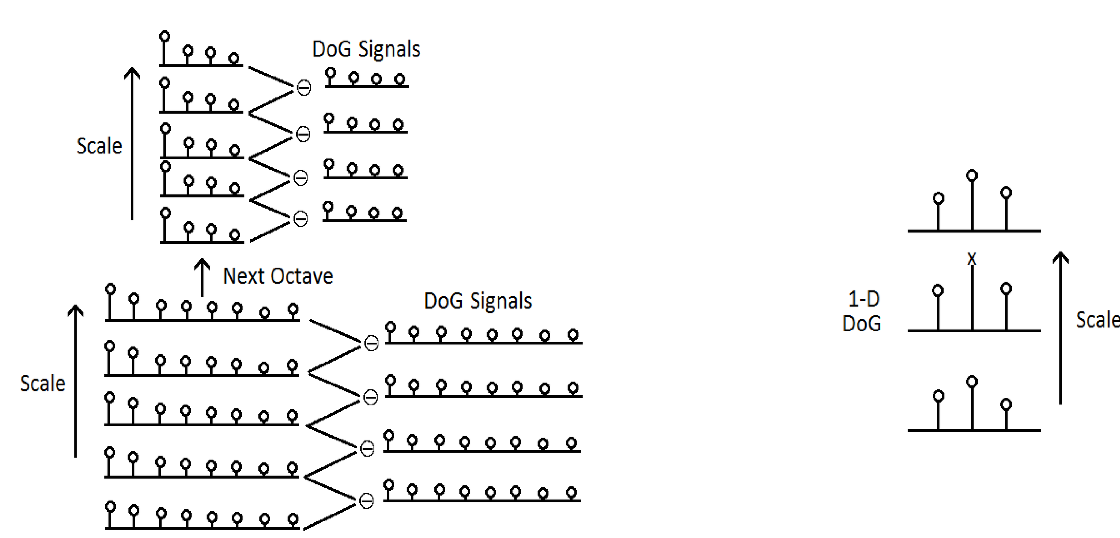
Multiresolution vs SLIC

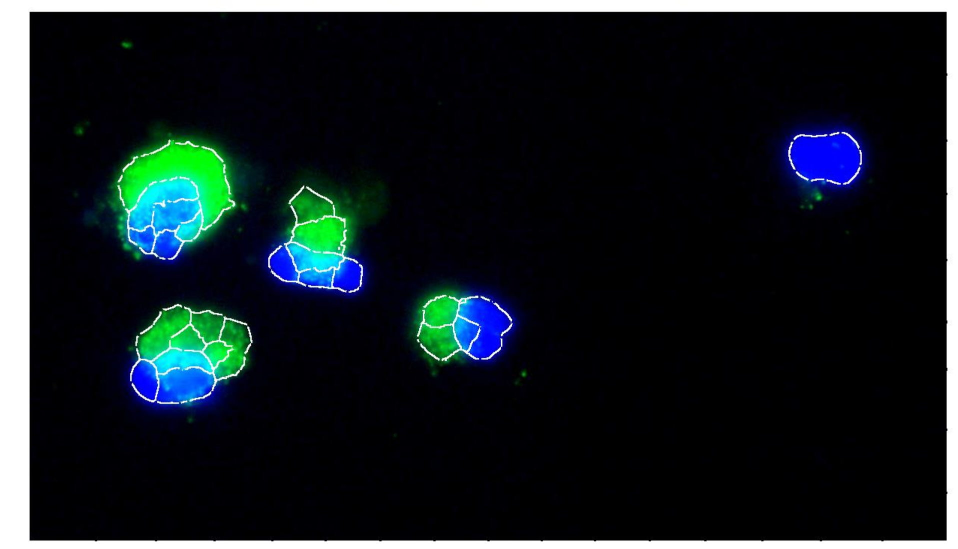
1-D SIFT Algorithm

• SIFT is a well known algorithm used in many computer vision applications. In 1-D SIFT histograms are filtered with 1-D DoG filters and local extrema locations are determined.

• A point on DoG scale is an extrema if it is greater than the surrounding 8 points.

• Two super-pixels are considered to be similar as long as indices of DoG extrema points are similar to each other.





• Two super-pixels are considered to be similar as long as indices of DoG extrema points are similar to each other.

Results

	Multi-resolution SP	SLIC
MSCs Image	Detection rate (%)/ False Alarm rate (%)	Detection rate (%)/ False Alarm rate (%)
Image 1	90.51 / 2.06	93.23 / 3.01
Image 2	94.31 / 8.39	83.90 / 3.60
Image 3	81.39 / 1.30	81.16 / 3.00
Image 4	87.89 / 7.42	87.84 / 5.78
Image 5	83.84 / 10.01	82.46 / 13.73
Image 6	85.90 / 8.89	79.46 / 10.40
Image 7	85.58 / 0.11	87.34 / 4.89
Image 8	84.32 / 8.99	92.30 / 21.88
Image 9	82.53 / 0.38	63.06 / 6.23
Image 10	86.72 / 0.96	72.58 / 19.92
Image 11	92.66 / 6.50	74.60 / 8.08
Image 12	80.64 / 8.26	78.99 / 26.84
Image 13	93.58 / 15.45	66.69 / 18.26
Average	80.33 / 6.05	80.20 / 11.20

Table 1. Comparison of cell detection in MSCs images using proposed super-pixels and SLIC.

	Multi-resolution SP	SLIC
MSCs Image	Detection rate (%)/ False Alarm rate (%)	Detection rate (%)/ False Alarm rate (%)
Image 1	91.10 / 1.23	51.29 / 0.81
Image 2	81.63 / 0.32	91.15 / 1.97
Image 3	92.10 / 1.75	28.26 / 0.96
Image 4	95.30 / 1.13	80.30 / 3.71
Image 5	62.84 / 0.27	68.24 / 43.67
Image 6	69.56 / 16.02	59.65 / 16.89
Image 7	77.75 / 1.43	83.23 / 8.76
Image 8	88.12 / 11.28	90.71/19.84
Image 9	61.21 / 3.83	46.31 / 6.73
Image 10	64.06 / 0.01	61.06 / 19.08
Image 11	90.05 / 7.52	72.51 / 7.54
Image 12	79.23 / 20.99	81.55 / 51.61
Image 13	89.90 / 23.57	62.72 / 26.33
Average	80.21 / 6.87	67.46 / 15.99

Table 2. Nucleus region detection accuracy of the proposed method compared to the SLIC method.

• Detection and false alarm rates for each cell nucleus and cytoplasm are calculated by comparing the results of the proposed algorithm and SLIC in [1] with manually marked regions of MSCs images as ground-truth.

•Super-pixels are classified as cell-type or background-type depending on the region they cover in the ground-truth image.

•The cell region detection accuracy of the proposed method is compared to the SLIC method [1] in Table 1.

Conclusion

•A multi-resolution super-pixel method for MSCs images is proposed.
•Initial seed locations are determined according to local wavelet energy.
•A threshold-free superpixel similarity method becomes possible with 1-D SIFT algorithm.

References

[1] Radhakrishna Achanta, Appu Shaji, Kevin Smith, Aurelien Lucchi, Pascal Fua, and Sabine Susstrunk, "Slic superpixels compared to state-of-the-art superpixel methods,"Pattern Analysis and Machine Intelligence, IEEE Transactions on, vol. 34, no. 11, pp. 2274–2282, 2012.
[2] David G Lowe, "Distinctive image features from scaleinvariant keypoints," International journal of computer vision, vol. 60, no. 2, pp. 91–110, 2004.