MODELING STRUCTURAL DISSIMILARITY BASED ON SHAPE EMBODIMENT FOR CELL SEGMENTATION

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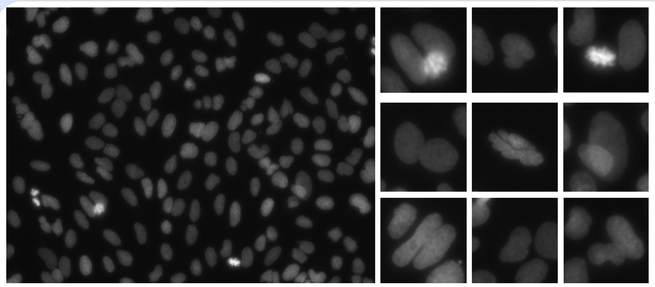
MOTIVATION

- Automatic methods of cell counting and tracking are important in cytometric analyses that classify cell types or analyze cell structure
- Accurate cell segmentation in microscopic images is one of the critical problems in the cell-based research

CHALLENGE

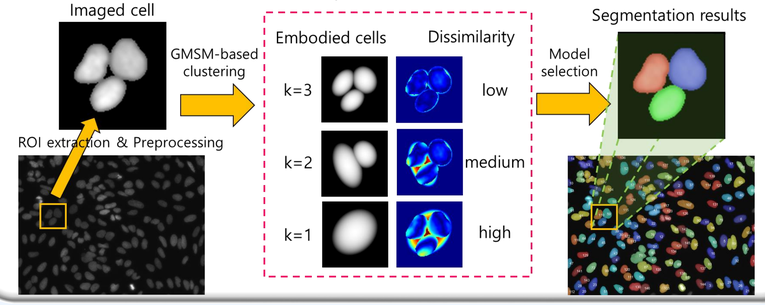


BBBC dataset:
- 696X520
- Ground truth
- 768 images

- Various cell brightnesses, sizes, and shapes
- Ambiguous boundaries between connected cells

WORK FLOW

- **Assumption:** the shape of adjoining cells follows a 2D Gaussian mixture model, and each component of the model relates to a cell
- **A key idea of our segmentation method:** to find the number of components of 2D Gaussian mixture model, which corresponds to the number of actual cells



METHOD

1. Combination of thresholding using seed detection based on MSER

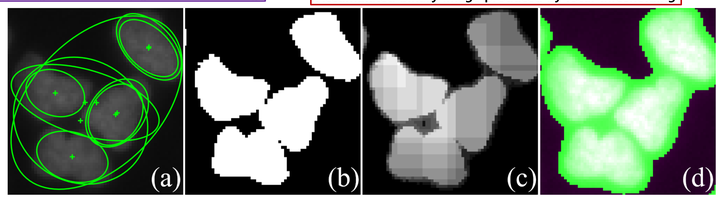
- To extract the reliable ROI under a large variation of intensities, we define an **Otsu-based ROI detector** combined with local and global thresholding, as follows:

$$\Psi(x,y)=\begin{cases}1, \text{if } \Psi_{\text{blur}}(x,y)>\delta\\ 0, \text{otherwise}\end{cases}, \qquad \Psi_{\text{blur}}=(\Psi_{\text{global}}+\frac{1}{\alpha}\Psi_{\text{local}})*g(\sigma)$$

Extracted ROI — Gaussian kernel

$$\Psi_{\text{global}}(x,y)=\begin{cases}1, \text{if } G(x,y,\sigma)>\delta_{\text{global}}\\ 0, \text{otherwise}\end{cases}, \quad \Psi_{\text{local}}(x,y)=\sum_{i=1}^{n}\begin{cases}1, \text{if } G(x,y,\sigma)>\delta_{\text{local}}^{(i)}\\ 0, \text{otherwise}\end{cases},$$

Binary image produced by global thresholding — Accumulated binary image produced by local thresholding



(a) a result of seed detection using MSER(Maximal Stable Extremal Regions), (b) a binary image by global thresholding
(c) an accumulated binary image by local thresholding, (d) final ROI (green area)

2. Cell division using structural dissimilarity

- According to the assumption associated with the shape of ROI and Gaussian mixture model, we estimate a **GMSM (Gaussian Mixture based Shape Model) using EM (Expectation-Maximization)**, and the classified cell consists of pixels that contribute to generate each component of the GMSM

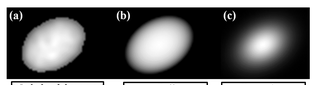
Embodied image consisted of several cells

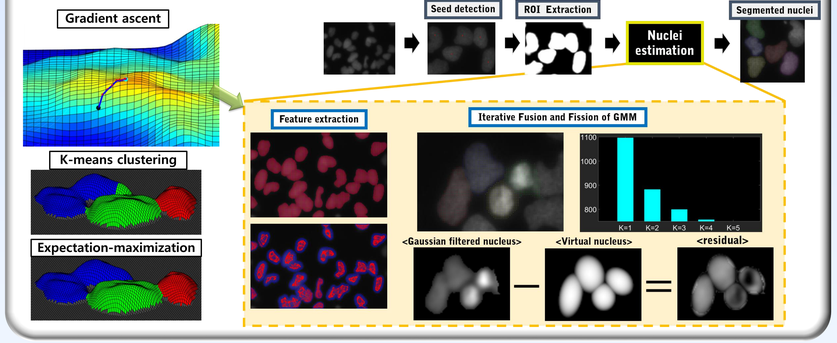
$$D(\mathbf{X},\Theta_K)=\sum_{i=1}^{}g(\mathbf{x}_i,\rho\Theta_1)|\mathbf{V}(\mathbf{x}_i,\Theta_K)-G(\mathbf{x}_i,\sigma)|, \quad \mathbf{V}(\mathbf{x}_i,\Theta_K)=\max_{\theta_k}(V(\mathbf{x}_i,\theta_k)), \mathbf{x}_i\in\mathbf{X},\theta_k\in\Theta_K$$

Structural dissimilarity — Parameter set of K components — Each embodied cell

$$V(\mathbf{x}_i,\theta_k)=\frac{\max_{\mathbf{x}_c}\left(e^{2\|\mathbf{x}_c\mathbf{W}\|}\right)-e^{2\|\mathbf{x}_c\mathbf{W}\|}}{\max_{\mathbf{x}_c}\left(e^{2\|\mathbf{x}_c\mathbf{W}\|}\right)-\min_{\mathbf{x}_c}\left(e^{2\|\mathbf{x}_c\mathbf{W}\|}\right)}+\delta_t$$

Intensity normalization term





EXPERIMENT

1. Evaluation metrics

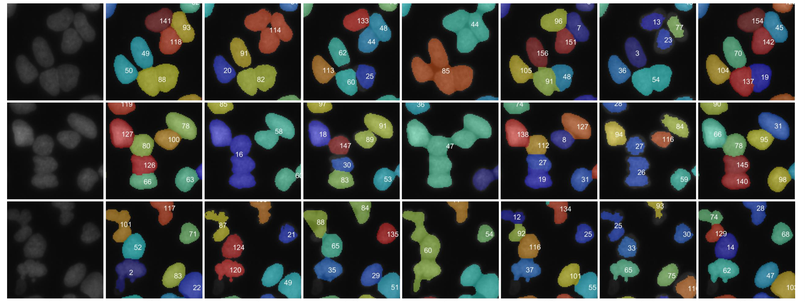
$$Sensitivity=\frac{|R\cap S|}{|R|}, \qquad J=\frac{|R\cap S|}{|R\cup S|}, \qquad DSC=\frac{2|R\cap S|}{|R|+|S|}$$

2. Quantitative analysis

Methods	*Sensitivity*	*J*	*DSC*
Otsu[1]	0.540	0.494	0.604
MINS[2]	0.592	0.568	0.634
Ilastik[3]	0.684	0.679	0.781
GC[4]	0.732	0.726	0.709
NOER[5]	0.767	0.758	0.829
Ours	**0.875**	**0.845**	**0.886**

[1] N. Otsu, A threshold selection method from gray-level histograms, *Automatica*, 1975
[2] X. Lou, M. Kang, P. Xenopoulos, S. Munoz-Descalzo, and A.-K. Hadjantonakis, A rapid and efficient 2d/3d nuclear segmentation method for analysis of early mouse embryo and stem cell image data, *Stem cell reports*, 2014
[3] C. Sommer, C. Straehle, U. Koethe, and F. A. Hamprecht, ilastik: Interactive learning and segmentation toolkit, *IEEE International Symposium on Biomedical Imaging*, 2011
[4] Y. Al-Kofahi, W. Lassoued, W. Lee, and B. Roysam, Improved automatic detection and segmentation of cell nuclei in histopathology images, *IEEE Transactions on Biomedical engineering*, 2010
[5] C. Arteta, V. Lempitsky, J. A. Noble, and A. Zisserman, Learning to detect cells using non-overlapping extremal regions, *MICCAI*, 2012

3. Qualitative analysis



(a) (b) (c) (d) (e) (f) (g) (h)

(a) Original image, (b) Ground truth, (c) OTSU, (d) MINS, (e) ilastik, (f) GC, (g) NOER, (h) **Ours**

CONTRIBUTIONS

- A high performance in quantification of cells can be obtained without accurate seed detection. This represents significant progress when compared to other cell segmentation methods, which require high accuracy of seed detection for accurate segmentation
- Boundaries estimated using the proposed method is similar to human perception of boundaries between aggregated cells