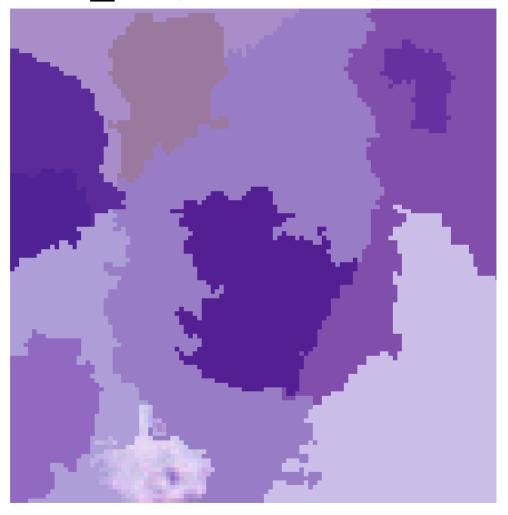
Yuli Wu Contour Refinement of Leukocyte Segmentations in Scans of Stained Bone Marrow



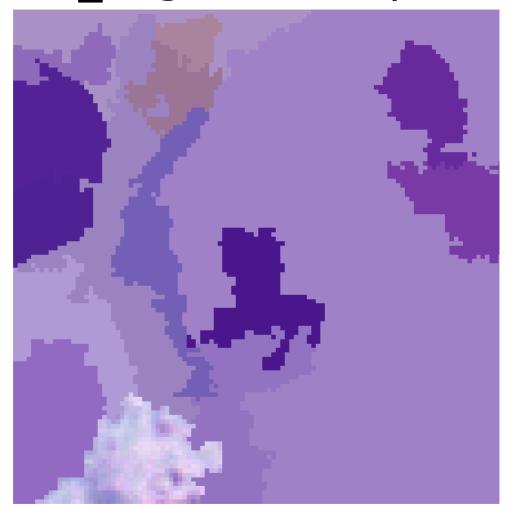
Lehrstuhl für Bildverarbeitung

RNTHAACHEN

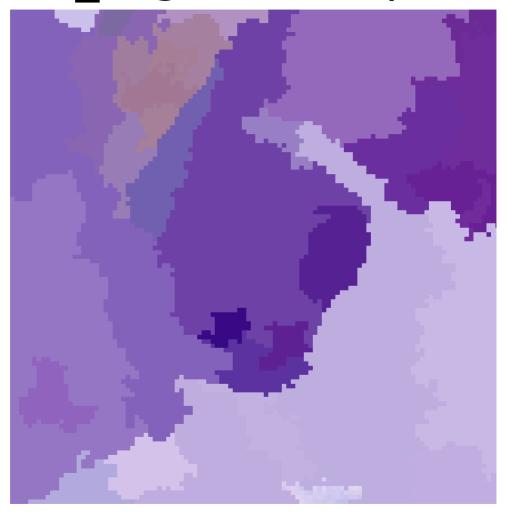
n_seg:50, cmp:1



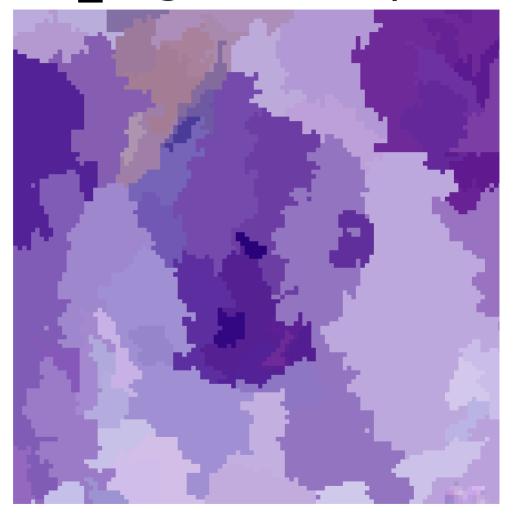
n_seg:100, cmp:1



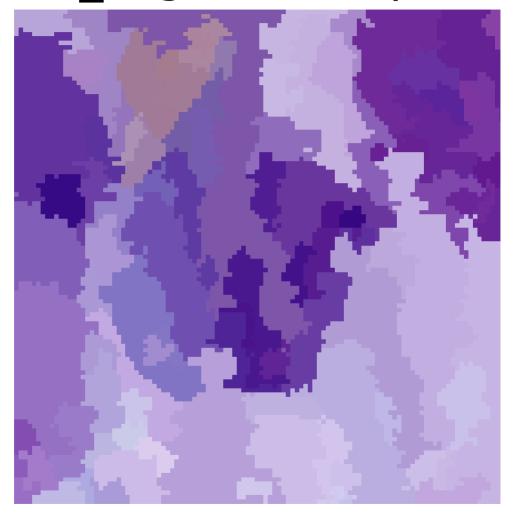
n_seg:200, cmp:1



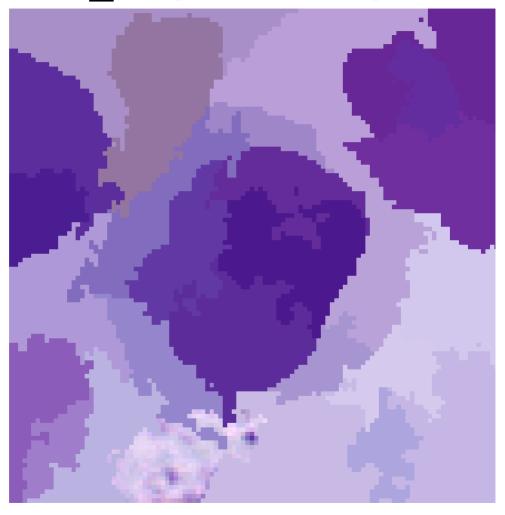
n_seg:350, cmp:1



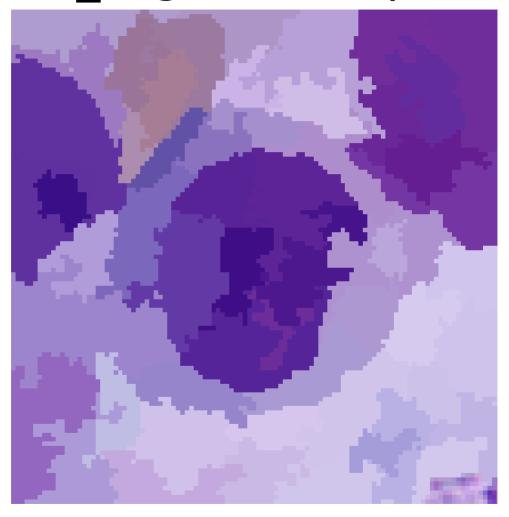
n_seg:500, cmp:1



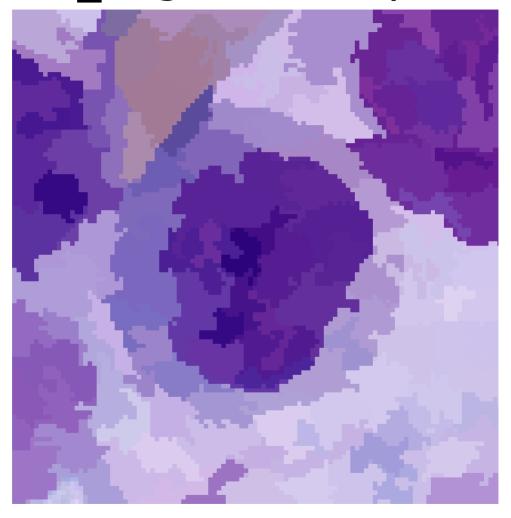
n_seg:50, cmp:5



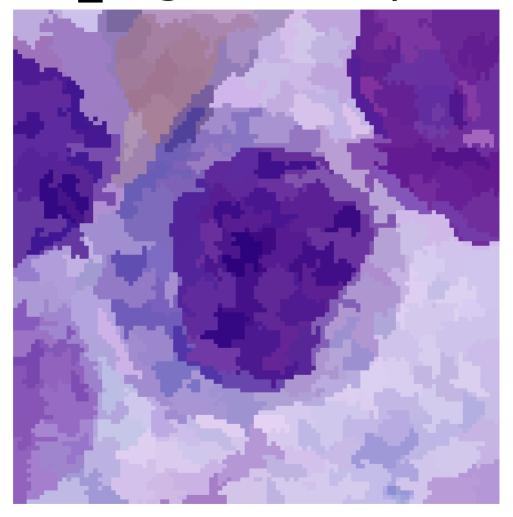
n_seg:100, cmp:5



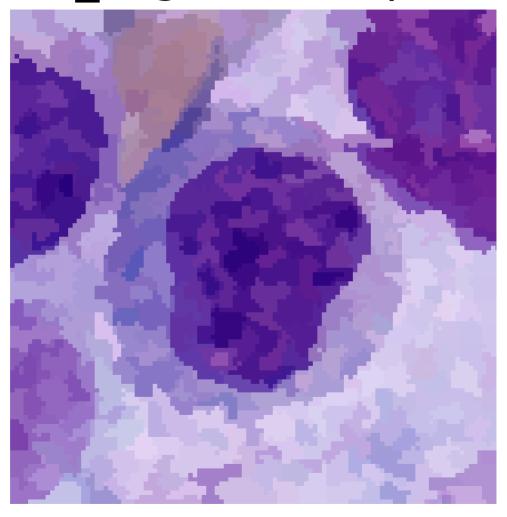
n_seg:200, cmp:5



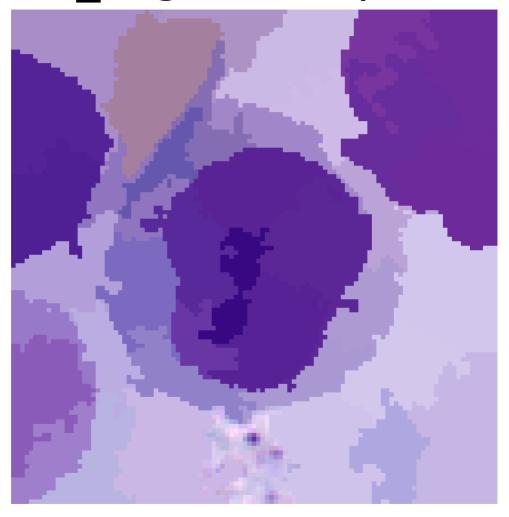
n_seg:350, cmp:5



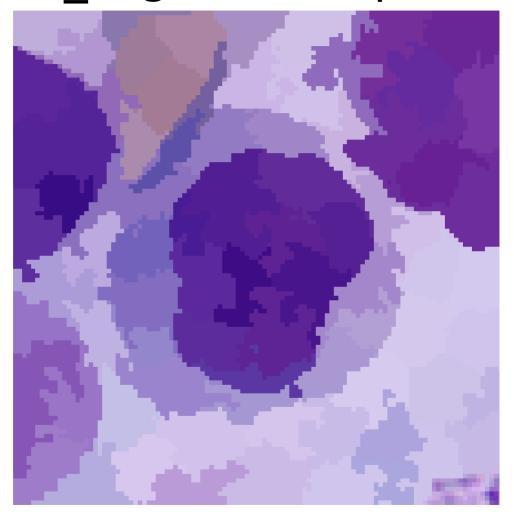
n_seg:500, cmp:5



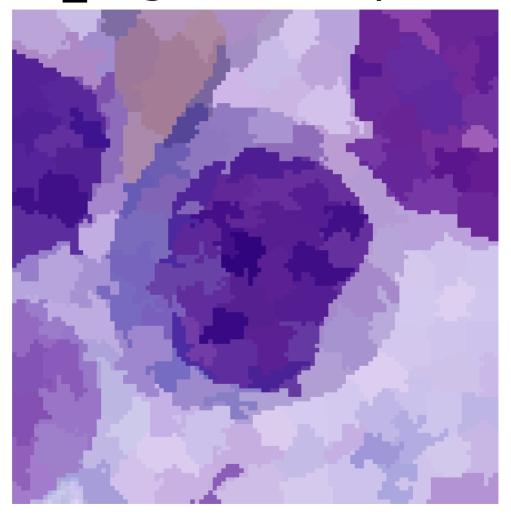
n_seg:50, cmp:10



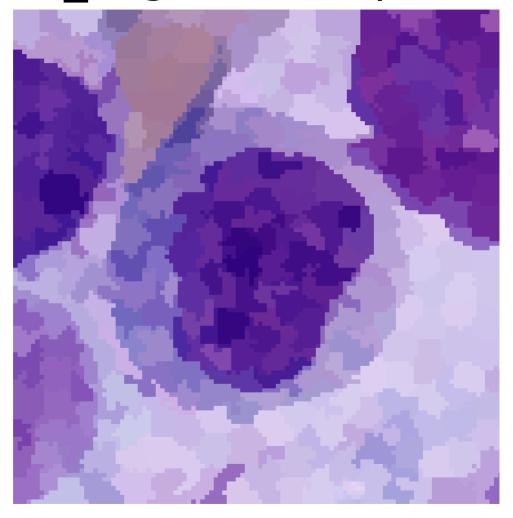
n_seg:100, cmp:10



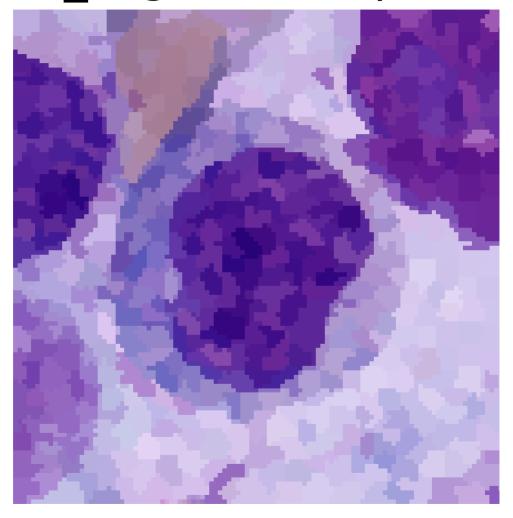
n_seg:200, cmp:10



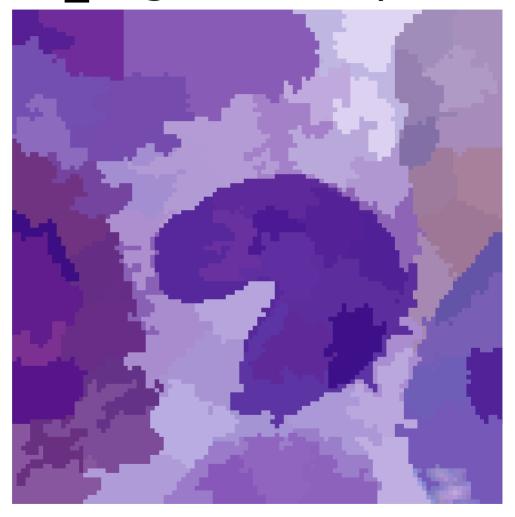
n_seg:350, cmp:10



n_seg:500, cmp:10



n_seg:100, cmp:10



k = 50, m = 10

k = 100, m = 10

k = 200, m = 10

k = 350, m = 10

k = 500, m = 10

k = 50, m = 5

k = 100, m = 5

k = 200, m = 5

k = 350, m = 5

k = 500, m = 5

k = 50, m = 1

k = 100, m = 1

k = 200, m = 1

k = 350, m = 1

k = 500, m = 1

SLIC Superpixel

$$d_c = \sqrt{(l_c - l_i)^2 + (a_c - a_i)^2 + (b_c - b_i)^2},$$

$$d_s = \sqrt{(x_c - x_i)^2 + (y_c - y_i)^2},$$

 $D = \sqrt{{d_c}^2 + \left(\frac{d_s}{r}\right)^2} m^2,$

Pixel as 5D vector:

L T /

 $[l,a,b,x,y]^T$

Distance:

Methodology

Normalisation





Preprocessing

Segmentation

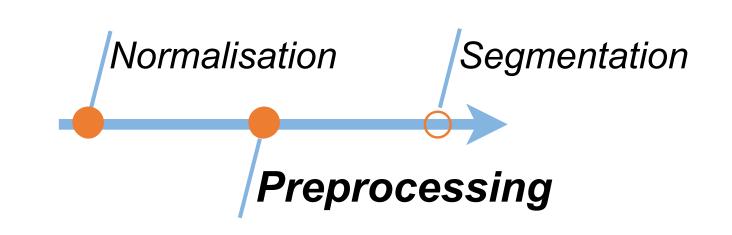








SLIC Superpixel



Methodology

- Pixel as 5D vector: $[l, a, b, x, y]^T$
- Distance:

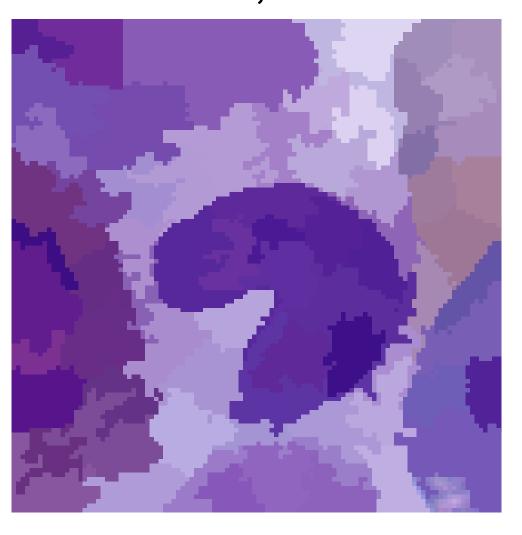
$$d_{c} = \sqrt{(l_{c} - l_{i})^{2} + (a_{c} - a_{i})^{2} + (b_{c} - b_{i})^{2}},$$

$$d_{s} = \sqrt{(x_{c} - x_{i})^{2} + (y_{c} - y_{i})^{2}},$$

$$D = \sqrt{d_{c}^{2} + \left(\frac{d_{s}}{r}\right)^{2} m^{2}},$$

$$r = \sqrt{n_{I}/k}$$

$$k = 100, m = 10$$







RAG

Normalisation Segmentation

Preprocessing

Methodology

Region Adjacency Graphs

