A Fully Automated Approach to Segmentation of Irregularly Shaped Cellular Structures in EM Images

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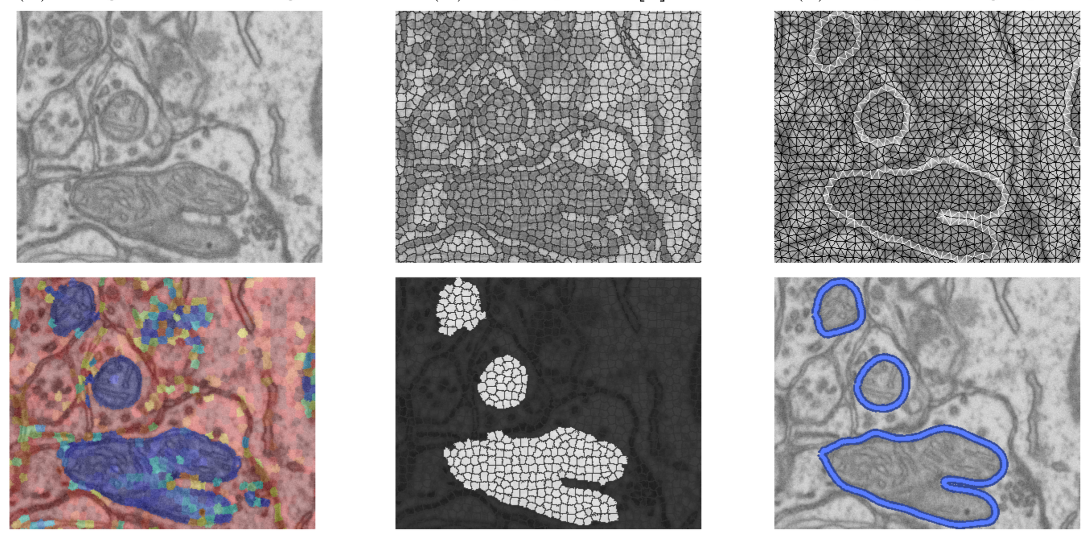
In EM imagery of neural tissue, numerous cells and subcellular structures appear within a single image, they exhibit irregular shapes that cannot be easily modeled by standard techniques, and confusing textures clutter the background. We propose a fully automated approach that handles these challenges by

1. **Using all available image cues simultaneously:** Texture and boundary cues are coupled with shape cues that do not require an explicit shape model.
2. **Learning the appearance of boundaries on a superpixel graph:** We train a classifier to predict where mitochondrial boundaries occur using these cues.

Overview

(a) Original EM image (b) Superpixels [3] (c) Superpixel graph



(d) SVM prediction (e) Graph-cut segmentation (f) Final segmentation

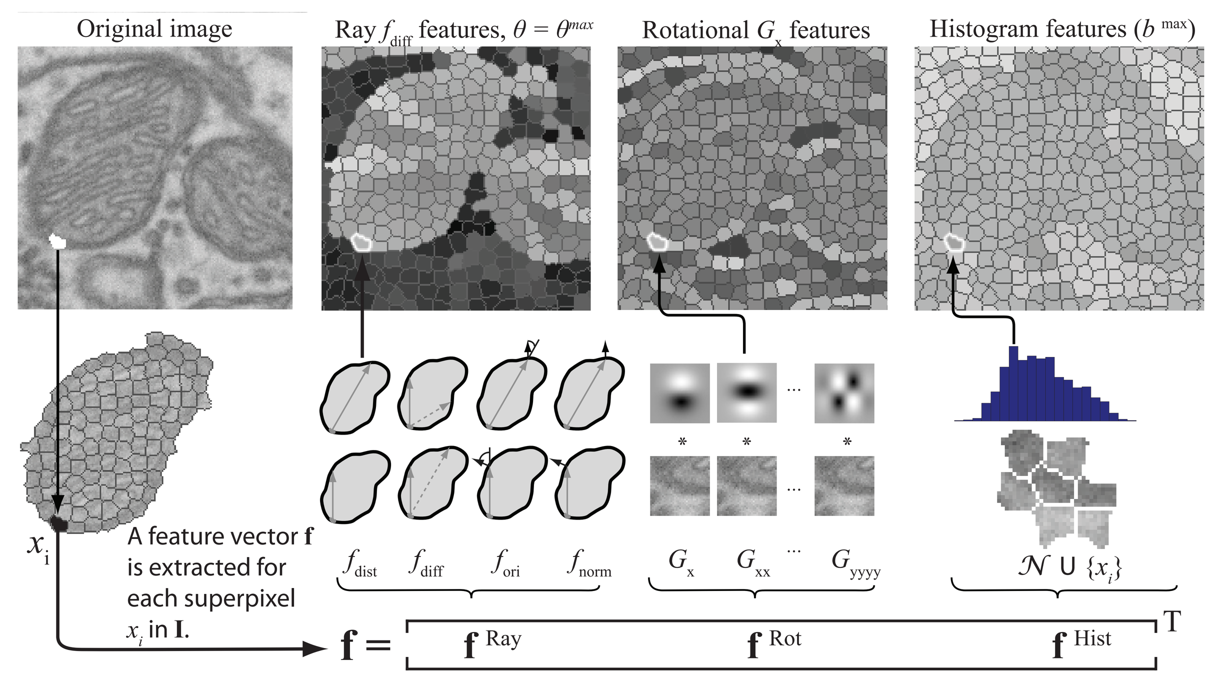
Notations The graph nodes $\mathcal{V}$ correspond to superpixels x_i. Edges $\mathcal{E}$ connect neighboring superpixels. The following objective function is minimized using a mincut-maxflow algorithm.

$$E(c|x,w) = \sum_i \underbrace{\psi(c_i|x_i)}_{\text{unary term}} + w \sum_{(i,j)\in\mathcal{E}} \underbrace{\phi(c_i,c_j|x_i,x_j)}_{\text{pairwise term}} , \quad (1)$$

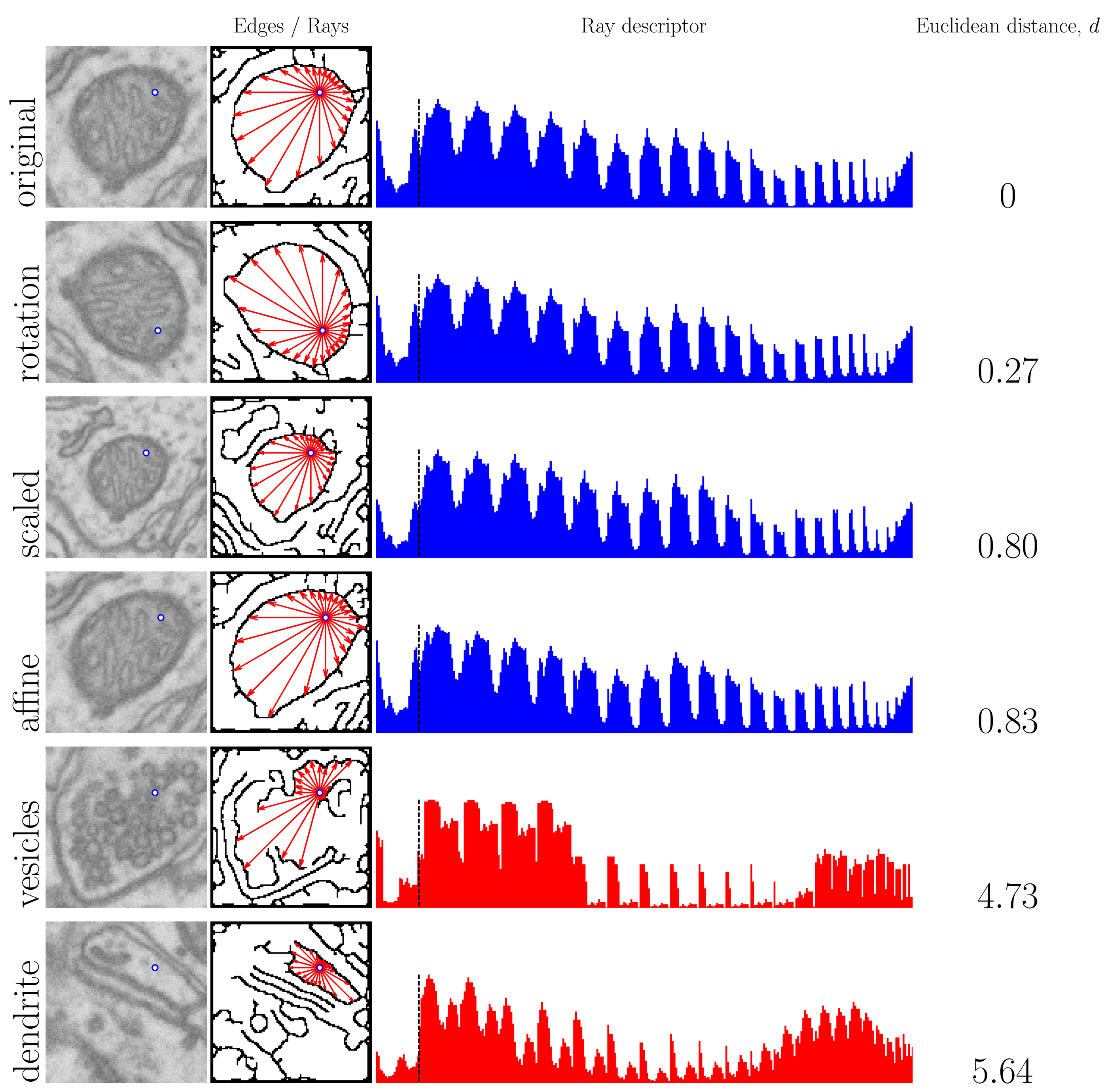
where $c_i \in \{foreground, background\}$. $\psi(c_i|x_i) = \frac{1}{1+P(c_i|\mathbf{f}(x_i))}$ is based on a probability $P(c_i|\mathbf{f}(x_i))$ computed from the output of an SVM classifier.

$$\phi(c_i,c_j|x_i,x_j) = \begin{cases} \frac{1}{1+P(c_i,c_j|\mathbf{f}(x_i),\mathbf{f}(x_j))} & \text{if } c_i \neq c_j, \\ 0 & \text{otherwise.} \end{cases} \quad (2)$$

Extraction of global and local cues

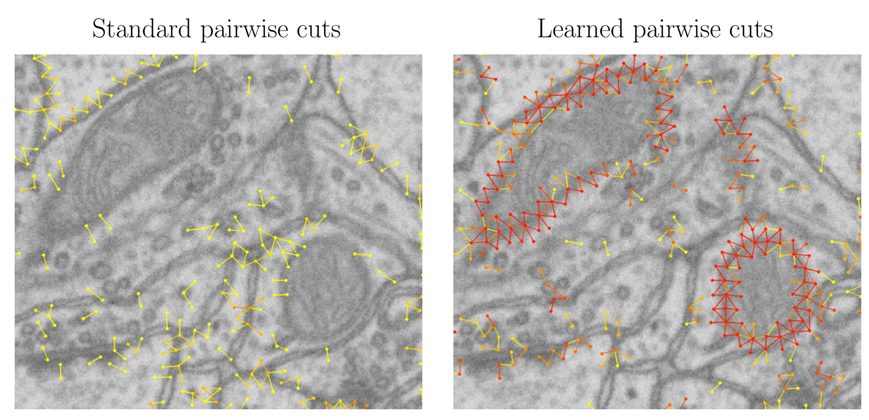


Ray features



- Ray descriptors built from features in [2] provide a compact representation of local shape for each point in an image.
- The descriptors are stable when subjected to rotation, scale, and affine transformations but change dramatically for different images.

Edge classifier



Red lines indicate strong probable boundaries, yellow lines indicate weaker boundaries.

- Boundaries predicted by a standard pairwise term (Eq. 3) correspond to strong gradients, but not necessarily to mitochondrial boundaries.

$$\phi(c_i,c_j|x_i,x_j) = \begin{cases} \exp\left(-\frac{\|I(x_i)-I(x_j)\|^2}{2\sigma^2}\right) & \text{, if } c_i \neq c_j \\ 0 & \text{, otherwise,} \end{cases} \quad (3)$$

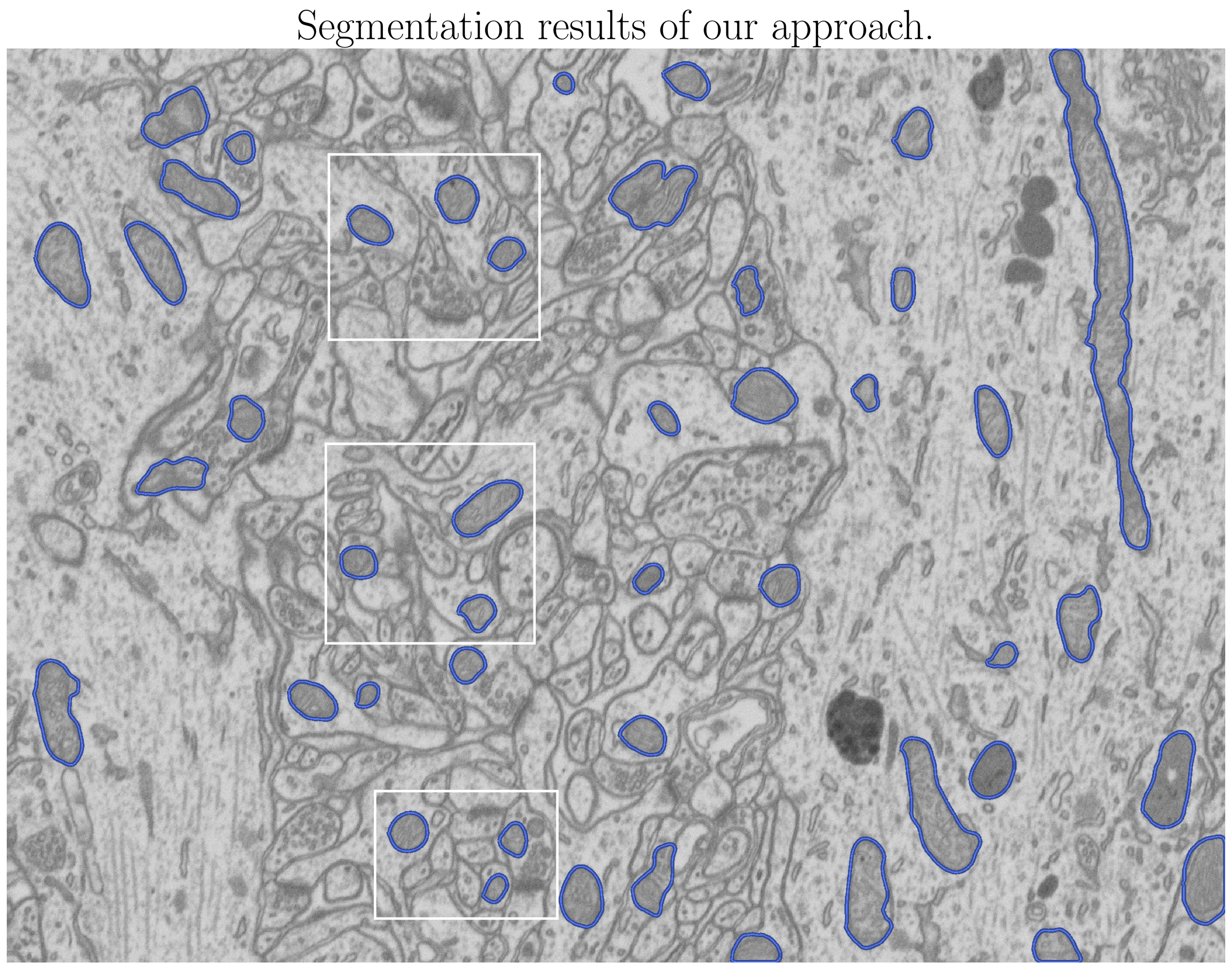
- A learned pairwise term (Eq. 2) using more sophisticated cues $[\mathbf{f}_i^\top,\ \mathbf{f}_j^\top]^\top$ results in better boundary predictions.

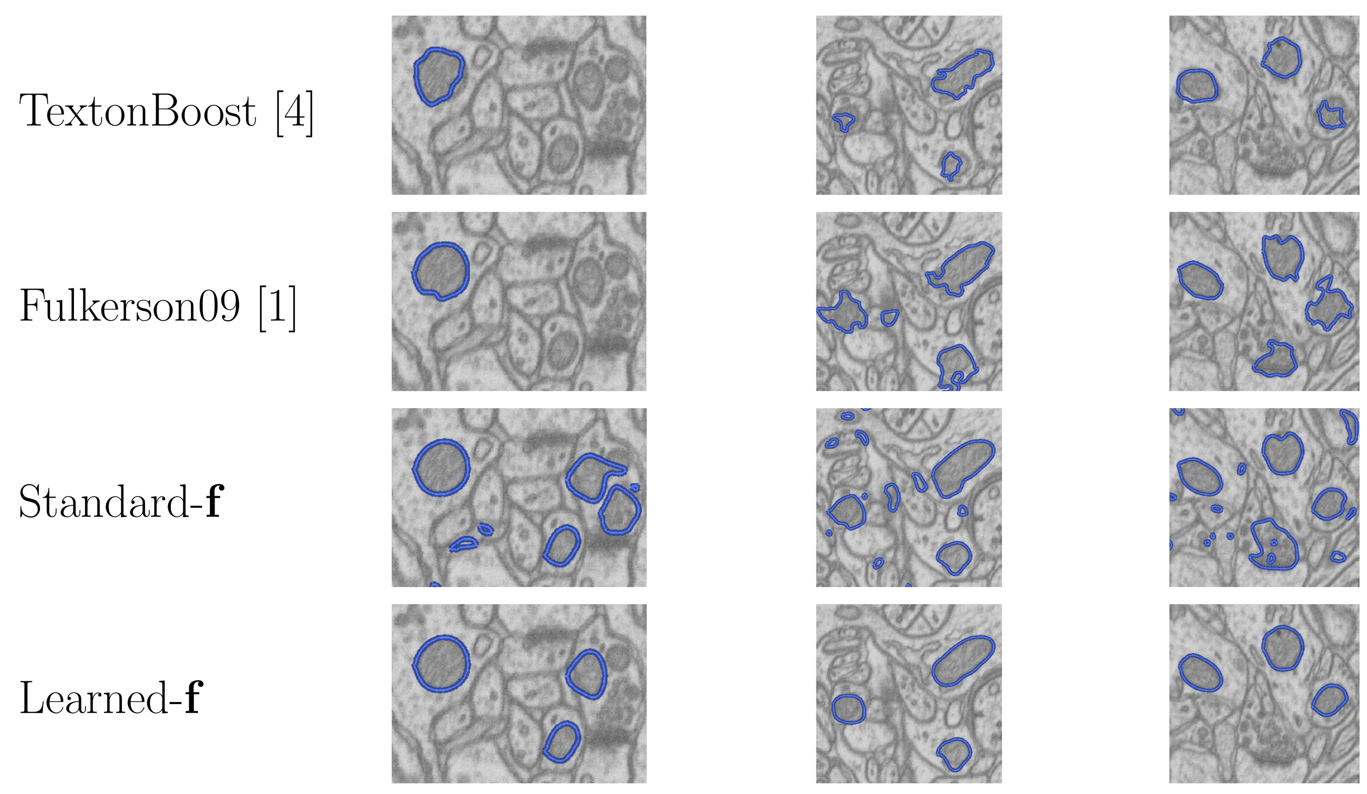
Performance evaluation

	TextonBoost [4]	Fulkerson09 [1]	Standard-$\mathbf{f}^*$	Standard-$\mathbf{f}$	Learned-$\mathbf{f}$
Accuracy	95%	96%	94%	96%	**98%**
VOC score	61%	69%	60%	68%	**82%**

Results

Segmentation results of our approach.





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References

[1] B. Fulkerson, A. Vedaldi, and S. Soatto. Class Segmentation and Object Localization With Superpixel Neighborhoods. In *ICCV*, 2009.

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[3] A. Radhakrishna, A. Shaji, K. Smith, A. Lucchi, P. Fua, and S. Susstrunk. SLIC Superpixels. Technical Report 149300, EPFL, June 2010.

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