



Hierarchical Markov Random Fields for Mast Cell Segmentation in Electron Microscopic Recordings

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Mast Cell Segmentation:



- Quantitatively analyze cell populations (e.g. receptor density)
- Distinguish 5 classes
- Ground truth labeling



EM Recording



Ground truth

background
 cytoplasm
 nucleus
 mitochondria
 vesicles

Motivation: Semantic Segmentation

- 1. Detection AND Segmentation of Regions
- 2. Semantic Information Needed (SVM + MRF)
- 3. Cues at different scales

Hierarchy in Semantic Segmentation





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Related Work







SVM: One vs. One MRF: remove some multiclass probabilities inconsistencies





[B. Mičušík and T. Pajdla, CVPR 2007]

Related Work







SVM:



MRF + Hierarchy high consistency



Our result

Markov Random Fields

MRF: Undirected Graphical Model Models Conditional Independence

Graph G = (V, E)Nodes $v \in V$ Edges $E \subseteq \binom{|V|}{2}$ Probability of a labeling: Labels $x_v \in X$

$$p(\mathbf{x}) = \frac{1}{Z} \prod_{C} \Psi_{C}(\mathbf{x}_{C})$$
potential functions

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Graph Construction

Hierarchical Graph Structure

- low level regions (fine contours)
- high level regions (coarser structures)



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Region Hierarchies

- Built with the Berkeley tool for hierarchical segmentation - Based on a Contour Detector and Watershed Transform [Arbelaéz et al.: CVPR , 2009.] BURG

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Region Hierarchies

- Oversegmentation at finest level
- All classes are separated





EM Recording with 0-level regions GT annotation



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Region Hierarchies

- Missing boundaries at coarser levels How can we merge the right regions?





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EM Recording with L/2 level regions

GT annotation

Training Labels

Hierarchical Graph Structure

- Labels at level 0: pixel labels inside the superpixels we assume there is only one label.
- Labels at level L/2: Generate new labels by the majority vote of the pixels inside the regions.

						high level regions
Label	1	2	3	4	5	
1'	98%	2%				superpixels
2'	8%	75%	1%	1%	15%	regions)
3'		3%	97%			
pixel-label distribution d				tion	d	

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MAX-SUM Problem

Find MAP of a given MRF Instance of a MAX-SUM problem:

 (G, X, \mathbf{g}) potentials

Find the set of optimal labelings:

[Werner, PAMI, 2007]

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$$\mathcal{L}_{G,X}(\mathbf{g}) = \underset{\mathbf{x}\in X^{|V|}}{\operatorname{argmax}} \sum_{v} g_v(x_v) + \sum_{v,v'} g_{vv'}(x_v, x_{v'})$$

$$\underbrace{}_{vertex}_{potentials} edge_{potentials}$$

Code for MAX-SUM solver from:

http://cmp.felk.cvut.cz/cmp/software/maxsum/.

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Vertex Potentials



Vertex Potentials

Features:

- Gabor Features
- Mean intensity inside a region
- Variance of the intensity inside a region

SVM:

- One vs one SVM for all classes
- Multiclass Probabilities from One vs. One SVM [Wu et al., JMLR, 2004]

SVM classification result





Edge Potentials



Intra-Level <u>Edge</u> Potentials pixel adjacency ratio AR:

average number of boundary pixels between label x_v and label $x_{v'}$ high le

 $g_{vv'}(x_v, x_{v'}) = \frac{2 \cdot \operatorname{AR}(x_v, x_{v'})}{\sum_{x_{v''}} \operatorname{AR}(x_v, x_{v''}) + \sum_{x_{v''}} \operatorname{AR}(x_{v''}, x_{v'})}$



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Edge Potentials



Inter-Level Edge Potentials Based on the High-level Region Label Distribution d:

Label	1	2	3	4	5
1'	98%	2%			
2'	8%	75%	1%	1%	15%
3'		3%	97%		

$$g_{\bar{v}v}(x_{\bar{v}}, x_v) = d_{x_{\bar{v}}, x_v}$$



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- Manually annotated with 5 labels:
 - Background
 - Cytoplasm
 - Nucleus
 - Mitochondria
 - Vesicles
- Compare: (threefold cross-validation)
 > SVM-only Classification
 - > MRF without Hierarchy
 - Hierarchical MRF

Results







SVM



SVM + MRF





Ground Truth

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Limitations

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SVM



SVM + MRF



SVM + HMRF



Ground Truth

Results

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Class-wise accuracy of the different methods.

	Back- ground	Cyt	Nucleus	Mito	Vesicles
HMRF	87.3%	61.7%	31.8%	8.1%	10.9%
MRF	83.5%	58.6%	21.9%	10.8%	14.9%
SVM	85.2%	57.3%	22.2%	9.5%	17.6%

 $\frac{\mathrm{tp}}{\mathrm{tp} + \mathrm{fp} + \mathrm{fn}}$ precision:

tp

tp + fp

accuracy:

Overall accuracy:

HMRF	65.42%
MRF	61.5%
SVM	60.5%

Precision and Recall of the HMRF-method.

recall:

tp + fn

	Back- ground	Cyt	Nucleus	Mito	Vesicles
precision	93.3%	67.4%	55.5%	22.7%	69.3%
recall	93.3%	89.1%	40.4%	18.2%	11.9%

Conclusion

- Hierarchical Graph structure leads to much higher consistency
- Convincing results for background, cytoplasm and nucleus



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Outlook

- Evaluation on a larger dataset
- Generate Benchmark from the data

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