Markov Random Fields for Segmentation of Biological Images

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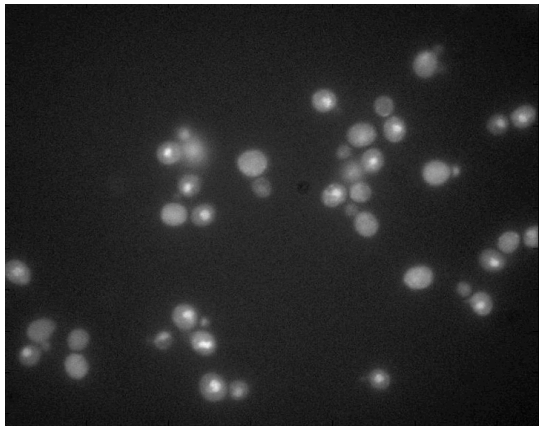
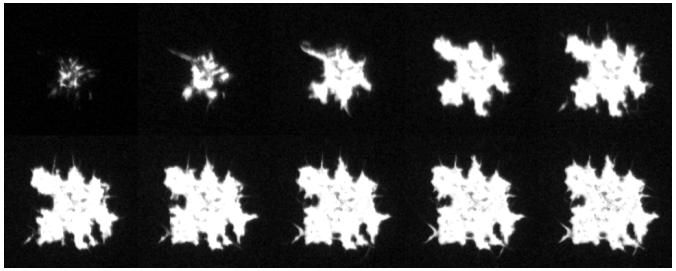
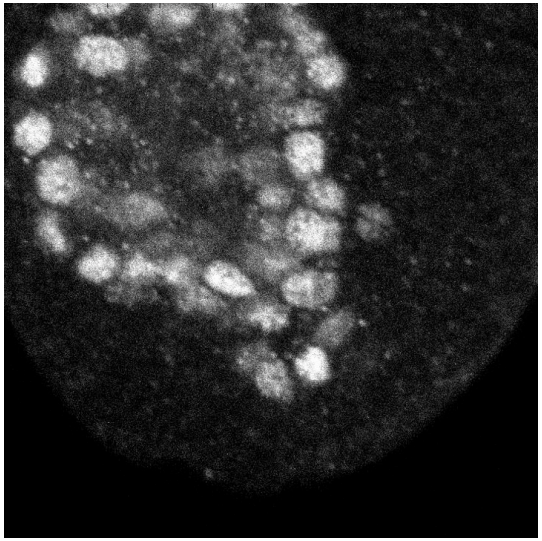
Problem Statement



Cell Classification



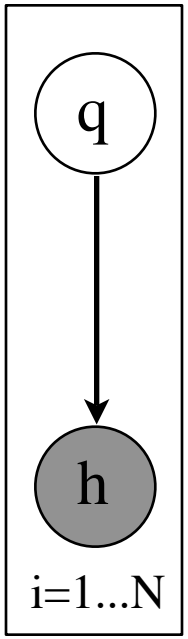
Spreading Dynamics

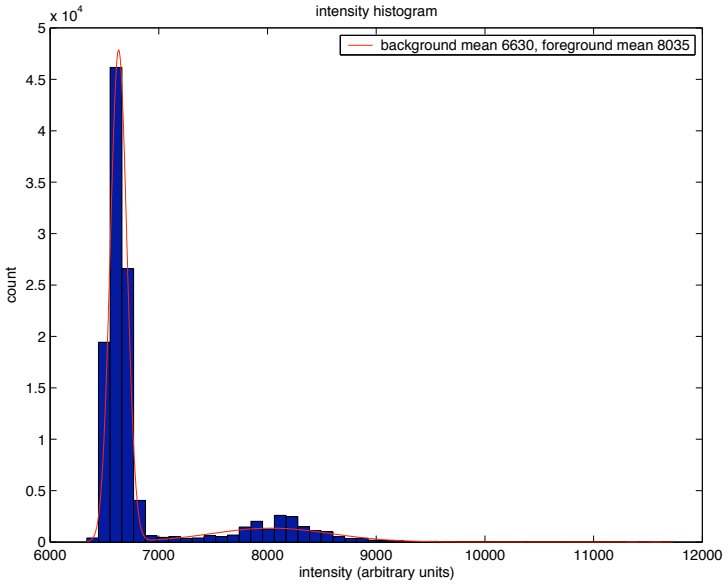


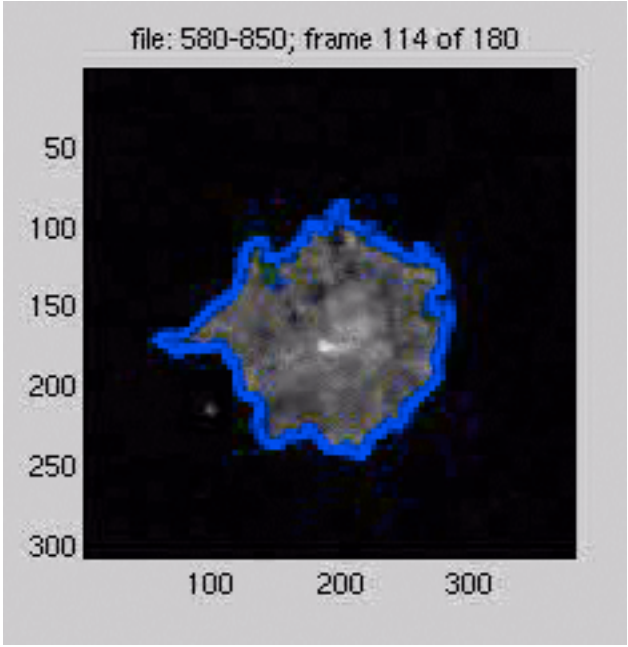
Protein Expression

- Implement automatic segmentation scheme for biological images (for arbitrary number of scene classes)

Naive Approach: IID Pixels



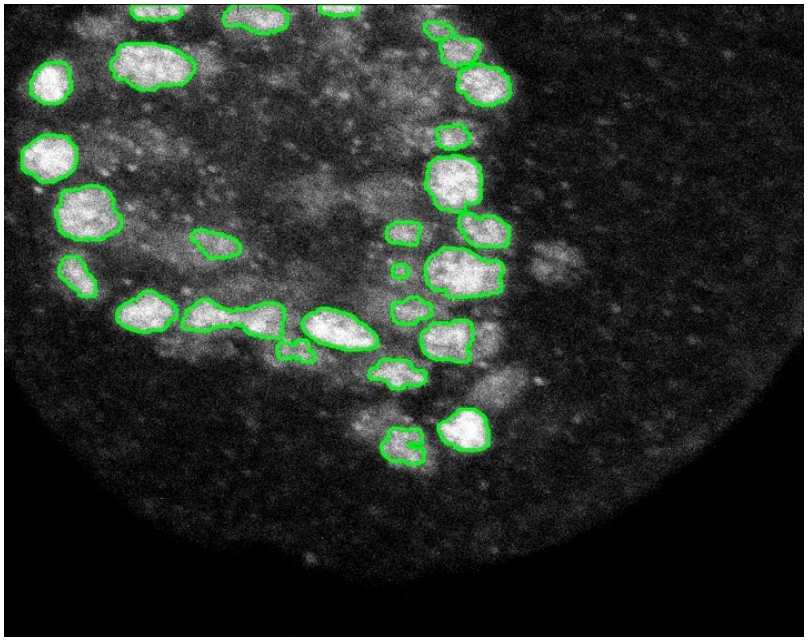




- Examine intensity histogram, ignoring spatial information
- Gaussian mixture model; Infer q's using EM

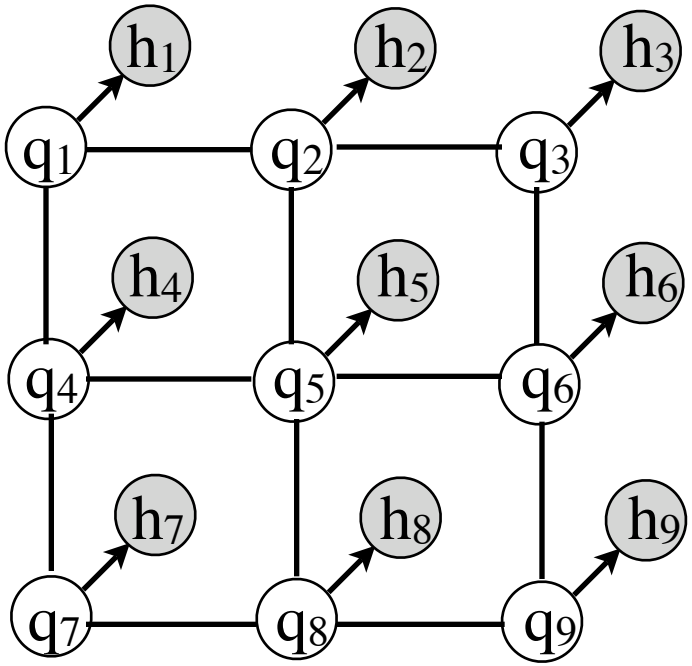
$$p(h) = \sum_{q=\pm} p(q)p(h|q) = \pi N(h;\mu_+,\sigma_+) + (1-\pi)N(h;\mu_-,\sigma_-)$$

Multi-Cell Images: Local information needed



- IID model makes assumption about *global* intensity distribution
- Instead, need model that captures *local* information

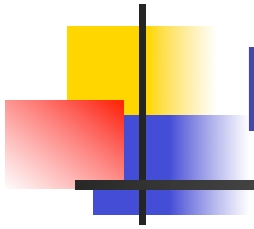
Adding Spatial Information: Markov Random Fields



- Undirected grid with Gaussian emissions; Infer q's using EM

$$p(\{q\},\{h\}) = \frac{1}{Z}\prod_{\{i,j\}}\psi(q_i,q_j)\prod_k p(h_k|q_k) \quad \text{where} \quad p(h_k|q_k) = N(h_k;\mu_{q_k},\sigma_{q_k})$$

E-Step: Loopy Belief Propagation



- Exact inference on this model via JTA becomes intractable (because of large clique sizes in J-tree)
- Instead, pass messages on graph itself (which is not tree and has loops)
- Has been shown to converge to global minimum of Bethe approximation to free energy

M-Step: Iterative Proportional Fitting

$$l(D|\theta) = \sum_c \sum_{x_c} n(x_c) \log \psi_c(x_c) - N \log Z$$

$$\frac{\partial l}{\partial \psi_c(x_c)} = \frac{n(x_c)}{\psi_c(x_c)} - N \frac{p(x_c)}{\psi_c(x_c)} \longrightarrow p_{ML}(x_c) = \frac{n(x_c)}{N} \equiv q(x_c)$$

- Model marginals equal empirical marginals (necessary but not sufficient condition)
- Instead, iterate set of fixed point equations (converges to local maximum)

$$\psi_c^{(t+1)}(x_c) = \psi_c^{(t)}(x_c) \frac{q(x_c)}{p^{(t)}(x_c)}$$

Acknowledgments

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