

Alphabet SOUP: A Framework for Approximate Energy Minimization



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Overview

- Alphabet SOUP provides a general purpose framework for approximate energy minimization of arbitrary energies that scales to accommodate available resources and problem complexity.
- Many problems in computer vision can be modeled using conditional Markov random fields.

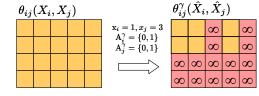
$$\begin{array}{ll} \text{minimize} & E(\mathbf{x}) = \sum_c \theta_c(\mathbf{x}_c) \\ \text{subject to} & x_i \in \mathbf{dom}(X_i) & \forall X_i \in \mathcal{X} \\ \end{array}$$

- Finding the MAP solution is NP-hard, so people resort to approximate techniques.
- Very efficient methods exist for problems with certain structure (e.g., α -expansion (Veksler, 1999) for submodular energies).
- Message passing algorithms (e.g., max-product or its convex) variants) are the only general purpose approach (for problems with arbitrary energies and non-homogeneous domains).
- · Static and dynamic theoretical guarantees when the inner loop of our method is exact.

γ-Expansion Moves

- For each i, let A_i^{γ} be a subset of the domain for variable X_i . Then a γ -expansion move maps each X_i from its current value x_i to a value in $\{x_i\} \cup A^{\gamma}$. This generalizes other approaches:
 - α -expansion: set $A_i = \{\alpha\}$ for all i.
 - α - β swap: set $A_i = \{\alpha\}$ for all $x_i = \beta$, $A_i = \{\beta\}$ for all $x_i = \alpha$, and empty
 - ICM: set $A_i = dom(X_i)$ for i = k and empty otherwise.
 - Fusion move: set $x_i = x_i^0$ and $A_i = \{x_i^1\}$.
- We can find the γ -expansion move with minimum energy by minimizing $\mathbf{E}^{\gamma}(\hat{x};x) = \sum_{c} \theta_{c}^{\gamma}(\hat{x}_{c})$ where

$$\theta_c^{\gamma}(\hat{x}_c) = \left\{ \begin{array}{ll} \theta_c(\hat{x}_c) & \text{if } \forall X_i \in \mathbf{X}_c : \hat{x}_i \in A_i^{\gamma} \cup x_i \\ \infty & \text{otherwise} \end{array} \right.$$



Alphabet SOUP Algorithm

start with arbitrary assignment x repeat

for $k = 1, \ldots, K$ find $\hat{\mathbf{x}}$ one γ_k -expansion-move away from \mathbf{x} if $E(\hat{\mathbf{x}}) < E(\mathbf{x})$ then $\mathbf{x} \leftarrow \hat{\mathbf{x}}$

Theoretical Guarantees

- **Definition (covering set):** A set of moves $\gamma_1, ..., \gamma_K$ is covering if for every $x_i \in \text{dom}(X_i)$, there exists a γ_k such that $x_i \in A_i^k$.
- Theorem (static): Let γ₁, ..., γ_K be a covering set of moves.* If x is a local optimum relative to $\gamma_1, ..., \gamma_K$, then $E(\mathbf{x})$ is within a constant factor of the optimal energy.
- Theorem (dynamic): By using the LP-dual message passing methods for the inner loop we can provide a global bound on the optimality gap. E.g., for the method of Globerson et al. (2007) the current assignment is within

$$\Delta = E(\mathbf{x}) - \sum_{s} \min_{x_s} \sum_{c \in N(s)} \delta_c^s(x_s)$$

of the optimal, where $\delta_c^s(x_s) = \min_{x_{c \setminus s}} \left\{ \{\beta_c^s(x_c)\}_{x_c \in \gamma}, \left\{ \frac{1}{|S(c)|} \theta_c(x_c) \right\} \right\}$

*
Assume θ (x) > 0 for all cliques c, with equality only if there exists some γ, such that x ∈ A for all variables X in the clique

Choosing the γ-expansion Moves

• Our method allows the selection of γ -expansion moves to be tailored to the problem at hand, e.g., (static) overlapping ordinal ranges, grouped low-energy configurations, or (dynamic) coordinate descent on vector-valued variables

Object Detection and Outlining

- Task: Detect object and localize using landmark based outline.
- Model: LOOPS (Heitz et al. (2008)).
- γ-Expansion Moves: Overlapping candidate landmark locations, sorted by unary potential (highest to lowest).







Image Completion and In-painting

- · Task: Fill in missing part of image using image patches.
- Model: Pairwise MRF of Komodakis and Tziritas (2006).
- γ-Expansion Moves: Non-overlapping sets of 250 patches. Patches for adjacent variables taken from adjacent locations in the image. This provides low energy pairs.



Cell Membrane Surface Reconstruction

- Task: Reconstruct surface of bacteria from tomography scans.
- Model: Discretized mesh: 3D orientation and 1D radial offset. Here the energy is regular, but α -expansion does not scale.
- γ-Expansion Moves: (θ_x, θ_y, θ_z, R) coordinates.

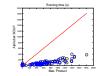
	Energy per pixel			Running time (s)		
Problem	(i)	(ii)	(iii)	(i)	(ii)	(iii)
40x43	0.507	0.509	0.521	39	1	<1
112x116	n/a	0.527	0.555	00	23	5



- (i) simultaneous optimization of all coordinates
- (ii) Alphabet SOUP over coordinate pairs (iii) Alphabet SOUP over individual coordinates ∞ indicates that problem could not fit into memory

Rosetta Protein Design

- Task: Find most stable configuration of amino-acids that give rise to a given 3D structure.
- Model: Protein design dataset from Yanover et al. (2007).
- γ-Expansion Moves: Subset of 50 values (modulo domain size)





Conclusion

- Alphabet SOUP is a flexible method for finding approximate solutions to the MAP inference problem for arbitrary energy functions. Our method is faster than standard max-product belief propagation, requires significantly less memory, and often produces lower energy solutions.
- Most interesting direction for further study is in providing more formal foundations for the choice of subsets used for the different variables.