Perfect MCMC Sampling in Bayesian MRFs for Uncertainty Estimation in Segmentation Saurabh Garg, Suyash P. Awate

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- Accounting for uncertainty in automated segmentation results can improve risk analysis in clinical procedures and reliability in clinical diagnosis and studies.
- Typical segmentation methods, e.g., using graph cuts or using expectation maximization (EM) and hidden Markov random fields (MRFs), typically produce a single optimal solution, and don't provide information about (i) object-boundary uncertainty or (ii) alternate close-to-optimal solutions.
- To estimate uncertainty, some methods intend to sample segmentations from label-image posterior models using Markov chain Monte Carlo (MCMC) sampling or perturbation models. However, they cannot guarantee sampling from the true posterior, deviating significantly in practice.
- □ We propose methods that guarantee exact sampling, in finite

Validation on Simulated Data

□ Mean and standard deviation (SD) per voxel (for multi-category case, we generalize SD by square-root of unalikeability) Difference between ideal Gumbel (γ) and its tractable approximation aGPM [Alberts et. al. 2016 ISBI] ($\hat{\gamma}$): Approx. histogram Closest Gumbel fit ²robability (-20 $\widehat{\gamma}^l \overset{0}{\operatorname{value}} \overset{20}{\operatorname{40}} \overset{40}{\operatorname{40}}$ value value 50 128-voxel 1D image, 2 labels (average over multiple images): True image Sam SD Noisy image -aGPM



time, from generic Bayesian MRFs to estimate uncertainty.

Our Approach for Uncertainty Estimation

- We introduce a new framework for uncertainty estimation in segmentation by relying on perfect MCMC sampling, in finite time, from generic Bayesian MRF models.
- Perfect MCMC tracks *parallel coupled* chains (one chain started at each point in state space, each chain using the same random number generator) and then checks *coalescence*.
- We propose perfect sampling of label images in two ways:
 (i) by combining coupling-from-the-past (CFTP) [Propp-Wilson 1996 Rand. Struct. Algo.] with the bounding-chain (BC) [Huber 2004 Ann. Appl. Prob.] scheme, which we call CFTP-BC.
 (ii) by theoretically extending Fill's algorithm (FA) [Fill 1998 Ann. Appl. Prob.] using the BC scheme, which we call FA-BC.

CFTP-BC Algorithm for Perfect Sampling

□ Consider Markov chain $\mathring{\mathcal{M}}$ with state space $(2^{\mathcal{L}})^V$, where $2^{\mathcal{L}}$ is the set of subsets of label set $\mathcal{L} := \{1, \ldots, L\}$ □ For $\mathring{\mathcal{M}}$, each state, say, \mathring{X} , contains a set of states $X \in \mathcal{L}^V$



Results on Classic Segmentation Problems

Multiatlas Segmentation of Subcortical structures:



- \Box Initialize X_v to the label set \mathcal{L} , for all voxels v.
- \Box At voxel v, let $P^{\min}(X_v = l | x_{-v})$ and $P^{\max}(X_v = l | x_{-v})$ be the max and min conditional probabilities over all possible chains.
- \Box At each voxel *v*, do the following:

(1) In the bounding chain $\hat{\mathcal{M}}$, initialize the set of labels $X_v = \phi$ (2) Draw l uniformly from the label set \mathcal{L} . Draw $u \sim U(0,1)$ (3) If $u > P^{\max}(X_v = l | x_{-v})$, then do nothing. (4) If $u \in [P^{\min}(X_v = l | x_{-v}), P^{\max}(X_v = l | x_{-v})]$, insert l into \mathring{X}_v (5) If $u < P^{\min}(X_v = l | x_{-v})$, then insert l into set \mathring{X}_v and exit. (6) Repeat from Step 2.

 \Box When $\forall v$, X_v is a singleton, say $\{\hat{x}_v\}$, then all Markov chains \mathcal{M} have coalesced to the label image \hat{x}

Our FA-BC Algorithm for Perfect Sampling

 Based on acceptance-rejection sampling. Generate proposal: pick randomly, a state z and integer T > 0; run (reverse) Markov chain for T steps to take z -> x. Accept proposal x by simulating parallel coupled chains, constrained so that x -> z, and checking for coalescence after T steps.

□ Let l* be label at voxel v for time t + 1 along Markov chain path x → z and let P*(X^t_v = l*|x^t_{-v}) be conditional probability conditioned on the neighbor-pixels' labels for the path x → z
 □ Initialize t := 0, x⁰ := x

1. At time t, do the following at each voxel v: a) In the bounding chain $\mathring{\mathcal{M}}$, initialize set of labels $\mathring{X}_v = \phi$ b) Draw l uniformly from label set \mathcal{L} c) If $l \neq l^*$, draw $u \sim U(P^*(X_v^t = l^* | x_{-v}^t), 1)$; otherwise draw $u \sim U(0, 1)$ d) If $u > P^{\max}(X_v^t = l | x_{-v}^t)$, then do nothing. e) If $u \in [P^{\min}(X_v^t = l | x_{-v}^t), P^{\max}(X_v^t = l | x_{-v}^t)]$, then insert label l into the set \mathring{X}_v f) If $u < P^{\min}(X_v^t = l | x_{-v}^t)$, then insert label l into \mathring{X}_v . Exit 2. Increment t by 1. If t < T, repeat step 1. If t = T and coalescence has occurred then accept x as a draw.

Ours aGPM Gibbs aGPM Gibbs Ours Simulated Mild Lesion, Tissue Segmentation: Mean Mean 3 SD 0.3 aGPM Gibbs Gibbs Ours aGPM Gibbs's convergence time varies severely with the MRF model and the data, making it very difficult to predict burn-in. \Box For a safe-side Gibbs burn-in of 5000, FA-BC is 10-20x faster.