ASeTs: MAP-based Brain Tissue Segmentation using Manifold Learning and Hierarchical Max-Flow regularization

Martin Rajchl[1,2*], John S.H. Baxter[1,2], A. Jonathan McLeod[1,2], Jing Yuan[1,3], Wu Qiu[1], Terry M. Peters[1,2,3], and Ali R. Khan[1,3]

[1] Imaging Laboratories, Robarts Research Institute, London, ON
[2] Department of Biomedical Engineering, Western University, London, ON
[3] Department of Medical Biophysics, Western University, London, ON

Abstract. This document describes the methodology used for the team KSOM GHMF. The *Advanced Segmentation Tools (ASeTs)* include a maximum a-posteriori (MAP) segmentation method [1] to combine information from multi-atlas labeling with an intensity model. The intensity models for 7 structures (background, white matter, cortical gray matter, corticospinal fluid, ventricles, basal ganglia and white matter lesions) are learned from a training database ($N_{Training} = 5$) via manifold learning and subsequently combined and regularized using generalized hierarchical max-flow framework. The source code to the proposed framework will be made publically available on `http://sourceforge.net/projects/ASeTs/`

1 Introduction

We developed a fully-automatic multi-atlas initialized segmentation algorithm for tissue segmentation using multi-sequence MR images. The *Advanced Segmentation Tools (ASets)* introduce a *Generalized Hierarchical Max-Flow* (GHMF) [2] framework proposed in [3] to regularize a maximum a-posteriori data term with a custom label-ordering constraint [4–6]. The data term is derived from two probabilistic cost functions, i) an intensity model from learned Gaussian Mixture Models (GMM) via Kohonnen Self-organizing maps (KSOM) and ii) a spatial prior from multi-atlas labeling. These costs are combined and subsequently regularized using the GHMF framework. The algorithm is fully automated and major components of the image processing pipeline are implemented using General-Purpose Programming on Graphics Processing Units (GPGPU) to achieve a substantial increase in computation speed (see Figure 1 for an overview).

1.1 Pre-processing and Multi-Atlas initialization

Multi-atlas segmentation with the set of 10 training subjects was used to provide initial label estimates for the test data. For this purpose we left-right (LR) flipped

* M.Rajchl and J.S.H. Baxter contributed equally to this manuscript. Send correspondence to mrajchl@robarts.ca

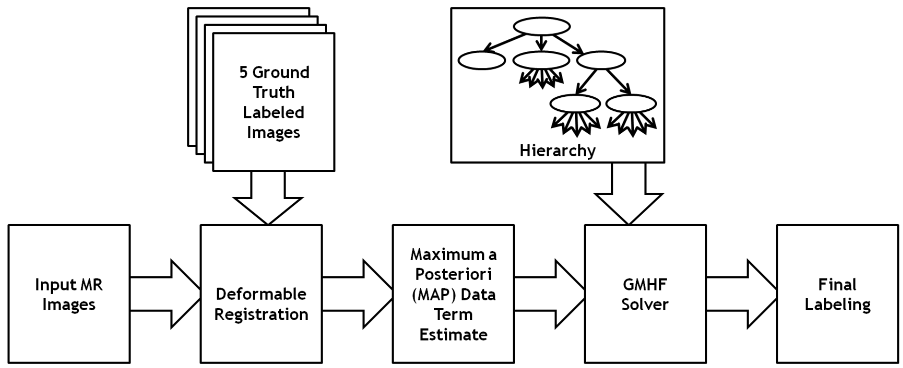

Fig. 1. Image processing pipeline for the proposed multi-atlas initialized HMF method

the available 5 training datasets to construct a better atlas prior. Registration of the training data to the test subjects was carried out with the T1 images (3mm slice thickness) using an initial affine block-matching approach [7] (default parameters) followed by a deformable registration with a Gauss-Newton gradient descent optimizer [8] with TV-L1 regularization [9]. The deformable registration method was implemented using Matlab 2013 (Mathworks, Natick, MA) and CUDA 5.5 (NVIDIA, Santa Clara, CA). All T1, T1 IR and T2 FLAIR images were bias corrected using the N3 algorithm [10] and subsequently brain masked via the deformably registered label maps. Posterior probabilies were computed using the label fusion technique in [11] to function as a shape prior.

1.2 Learning GMMs via Kohonnen self organizing maps

The multi-dimensional image data (T1, T1 IR and T2 FLAIR) were robustly normalized by clipping all intensity values outside $\pm$ 2 standard deviations. Prior to training, the learned intensity features were normalized to zero mean and standard deviation units. The 2D KSOM was set to a size of 32x32 gaussians and binary masks for sampling generated. Manifolds were learned for gray matter (GM), external cerebro-spinal fluid (CSF), white matter (WM), white matter lesions (WML), ventricles (V), basal ganglia (B) and background (BG). To reduce the run time for the learning of the background label, a narrow band of 10 mm from the brain surface was computed as a region for sampling. The Gaussians to be learned were initialized by principal component analysis (PCA) for added robustness.

1.3 Energy formulation and HMF optimization

The MAP data term (1) is derived from that presented in [1] and the provided training labels used as shape prior in the energy functional (3): Given an image with training labels T, an energy $E(u)$ (3) is minimized such that hierarchical label ordering constraints (4). The parameters, β_L, weight the contribution from the intensity prior and the spatial prior for each label, L:

$$(1-\beta_L)\ \log P(L(x)),\quad \beta_L \in [0,1]; D_L(x) = -\log P(I(x)|L) - \beta_L\ \log(P(T_L(x))), \tag{1}$$

$$S_L(x) = e^{\lambda \,|\frac{\nabla I(x)}{\nabla I(x) * G(x)}|} \tag{2}$$

$$E(u) \;=\; \sum_{\forall L} \int_{\Omega} (D_L(x) u_L(x) + \alpha_{L.P} S_{L.P}(x) |\nabla u_L(x)|\, dx \tag{3}$$

s.t.

$$\forall L\ (u_L(x) \leq 0)\ \ \mathit{and}\ \ \exists! S\ (\nexists S.P \wedge u_S(x) = 1)\ \ \mathit{and}\ \ \forall L'\ (\sum_{L \in L | L.P = L'} u_L(x) = u_{L'}(x)) \tag{4}$$

The learned intensity GMMs were used to formulate intensity priors $P(I(x)|L)$ in the form of a log-likelihood data term for each label. The function $S_L(x)$ was designed to locally weight regularization by gradient information from the input (2). The linear label ordering is depicted in Figure 1.3 along with the corresponding datat term weighting (β) parameters.

A GPGPU-accelerated generalized hierarchical max-flow (GHMF) optimizer was used to minimize the provided energy equation given the hierarchy. The product of this optimizer is a probabilistic labeling which combines the effects of the data terms, discouraging edges in regions with higher $\alpha S_L(x)$ values identified as being less likely to include boundaries between labels due to having low gradient magnitude.

1.4 Post-processing

The resulting labels were fused to comply with the submission format. No other post-processing was employed.

1.5 Computing Specifications and Run Times

Computations were carried out on a Tesla C2070 GPU (NVIDIA, St. Clara, CA) with Ubuntu 12.04 machine and 144 GB RAM, where each registration and HMF computation took approximately 83 seconds and 39 seconds respectively. Miscellaneous and post-processing took approximately 5 seconds per image and the posterior probabilistic priors using [11] 11 minutes. Thus with 10 atlases (training data) a given test subject requires approximately 25:38 minutes to complete the entire pipeline.

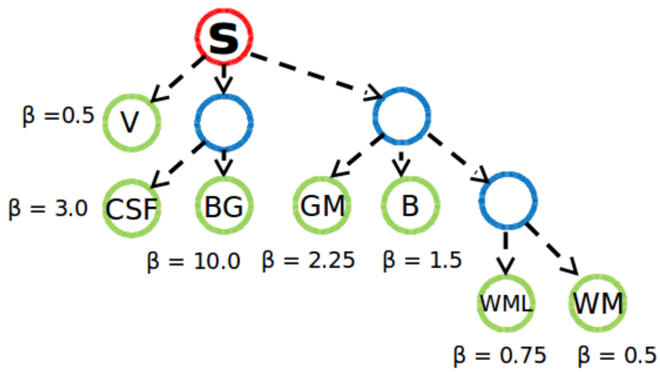

Fig. 2. Linearly ordered graph with source (S) terminal, parent nodes (light blue) and leaf nodes (green): Background (BG), corticospinal fluid (CSF), gray matter (GM), white matter (WM) and white matter lesions (WML). All source flows (dashed arrows) are of unconstrained capacity.

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