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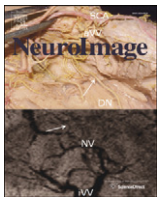

Segmentation priors from local image properties: Without using bias field correction, location-based templates, or registration

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ABSTRACT

We present a novel approach for generating information about a voxel's tissue class membership based on its signature—a collection of local image textures estimated over a range of neighborhood sizes. The approach produces a form of tissue class priors that can be used to initialize and regularize image segmentation. The signature-based approach is a departure from current location-based methods, which derive tissue class likelihoods based on a voxel's location in standard template space. To use location-based priors, one needs to register the volume in question to the template space, and estimate the image intensity bias field. Two optimizations, over more than a thousand parameters, are needed when high order nonlinear registration is employed. In contrast, the signature-based approach is independent of volume orientation, voxel position, and largely insensitive to bias fields. For these reasons, the approach does not require the use of population derived templates. The prior information is generated from variations in image texture statistics as a function of spatial scale, and an SVM approach is used to associate signatures with tissue types. With the signature-based approach, optimization is needed only during the training phase for the parameter estimation stages of the SVM hyperplanes, and associated PDFs; a training process separate from the segmentation step. We found that signature-based priors were superior to location-based ones aligned under favorable conditions, and that signature-based priors result in improved segmentation when replacing location-based ones in FAST (Zhang et al., 2001), a widely used segmentation program. The software implementation of this work is freely available as part of AFNI http://afni.nimh.nih.gov.

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Introduction

The tissue class segmentation of an MRI brain volume is a ubiquitous task in imaging (Dale et al., 1999; Fischl et al., 2002a,b; Ashburner and Friston, 2009; Shattuck et al., 2001; Van Leemput et al., 2003; Joshi et al., 1999; Davatzikos, 2005; Fischl et al., 2004; Pham and Prince, 1999; Prince et al., 1995; Warfield et al., 1995). It is central to morphometric studies and surface-based analyses (Ashburner, 2009; Ashburner and Friston, 2009; Hutton et al., 2008; Chiang et al., 2007; Tiemeier et al., 2009; Giedd et al., 2009; Lenroot et al., 2007; Van Essen et al., 2006; Hill et al., 2009; Lerch and Evans, 2005; Lerch et al., 2006, 2008; Kippenhan et al., 2005), and certain aspects of Blood Oxygenation Level Dependent brain imaging (Jo et al., 2010). In most instances, a T1-weighted MRI volume with spatial resolution of about 1 mm^3 is the target of segmentation. At its simplest, the process involves classifying voxels into three classes: White Matter (WM), Gray Matter (GM), and Cerebro-Spinal Fluid (CSF). A simple mixture of Gaussians would be an adequate model, if it weren't for the confounding effects of noise (ε), scan gain parameters g, and h, and more importantly the bias field (f). The bias field, generated by B1-field inhomogeneity, causes MR tissue intensity to vary as a function of spatial location (Vovk et al., 2007; Sled et al., 1998; Van Leemput et al., 1999), thus broadening the distribution of tissue intensities over the volume, and confounding voxel intensity based segmentations. In modern segmentation approaches, the bias field is often modeled as a smooth spatial field conjointly with the segmentation model (Zhang et al., 2001; Ashburner and Friston, 2005). To further improve the optimization's convergence, location-based tissue class prior probability maps are also employed. These priors are derived from tissue classifications of multiple subjects from a representative subject population that are registered to a common template space. The use of these location priors therefore requires a spatial registration of the observed image to the template image of the priors' space. The registration process requires optimization of between a dozen and hundreds of parameters in addition to the parameters needed for bias field estimation and segmentation.

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What we describe in this work is an approach for creating tissue prior maps that is insensitive to bias fields, and that does not require registration to a template space, or the use of location-based spatial priors. The priors we generate are not identical in meaning to the ones in current use, but can be used in their place, as we will show. They provide a means for initializing and regularizing the segmentation model without adding the complication associated with optimizing parameters for spatial registration, and bias field estimation.

The basic idea is quite simple. Typically a voxel's location in the priors' space is used to gain information about its tissue type. Instead, we propose to gain such information by examining the 3D texture of the image at that voxel location, and over multiple spatial scales. This collection of texture information over spatial scales is termed a voxel's signature $\vec{s}_{\Phi(y_i(r))}$, where Φ is a statistic computed over the voxels inside a sphere of radius r and centered on voxel i. Here, we hypothesize that voxels of different tissue types can be differentiated on the basis of their signatures, at least in as much as location-based spatial priors could.

As a toy example, we create for each voxel i a vector $\vec{s}_{\tilde{y}_i(r)}$ of median values estimated in spherical neighborhoods centered on i and of radius r, with r taking on the successive values of 1,2,3,4,6,8, 10,13,16, and 19 mm. These signatures, computed for all voxels in the volume, form the signature dataset. Fig. 1 shows a slice of the anatomical volume. The graphs depict $\vec{s}_{\tilde{y}_i(r)}$ at four locations: White Matter in Corpus Callosum (CC), Gray Matter (GM), Deep White Matter (DWM), and thin white matter between gyral folds (gyWM). To illustrate how signatures can differentiate between tissue types or, more precisely, textures in the brain, we calculate the Pearson correlation coefficient of $\vec{s}_{\tilde{y}_i}(r)$ at CC with all other signatures in the dataset. The correlation map is arbitrarily thresholded to highlight voxels with signatures most similar to that at the cross hair. Red, and blue colors indicate positive and negative correlations, respectively. Correlations with the signature in the corpus callosum are highest in bands of white matter tissue that is surrounded by darker tissue. That would include white matter in the gyral folds and bright skull. The strongest negative correlations are in comparable bands of dark tissues. Note that a voxel's own intensity y_i contributes minimally to the similarity maps. At the smallest spatial scale (r) of 1 mm, 5 voxels contribute to the signature. In addition, the Pearson correlation removes the mean and normalizes the signatures before taking the dot product. It is the trend of the signatures as a function of scale that drives the match.

In this toy example, we used one statistic and a simple approach to illustrate the use of signature similarity. In the following sections, we detail how signatures are generated to be insensitive to scanner gain and bias field, and how to differentiate between physiologically relevant tissue types, namely GM, WM, and CSF, rather than textures. The aim is not to provide a final segmentation result, but rather to create a classification prior map from the same volume, using voxel signatures, that is comparable in accuracy to what can be obtained from population-based spatial priors.

To summarize, given an MRI anatomical volume, typically T1-weighted, we seek to determine the probability of each voxel belonging to one of a set of tissue classes. We propose to do so based on variations in local image statistics as a function of multiple neighborhood scales around that voxel. The collection of local statistics forms what we term a voxel's signature.

In what follows, we begin by describing the texture statistics making up a voxel's signature, then describe the multivariate approach for assigning class likelihood based on the signature. We also present comparisons between signature-based and the widely used location-based priors, and consider the effect of bias field on the results. Finally we compare segmentations using signature—in place of location-based priors in a segmentation implementation that is independent of the method developed here.

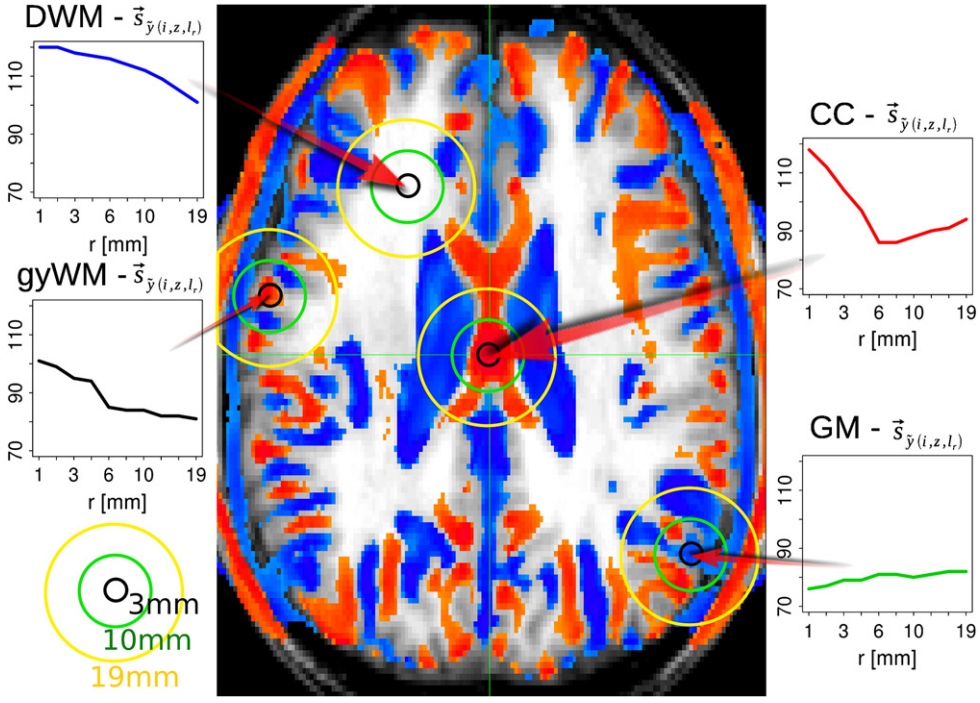

Fig. 1. An illustration of the use of voxel signature to differentiate between different textures. The image shows in gray scale an axial slice through a T1 weighted anatomical volume. Graphs depict the median statistic computed over spherical neighborhoods ranging in radius (r) from 1 to 19 mm. Concentric circles illustrate the intersection of spheres delimiting a voxel's neighborhood with the slice, at r of 3, 10, and 19 mm. The graphs show unscaled median-signatures at four locations: White matter in corpus callosum (CC), gray matter (GM), deep white matter (DWM), and thin white matter between gyral folds (gyWM). Color overlay shows Pearson correlation coefficients between the signature at CC and signatures at all other voxels, arbitrarily thresholded to highlight voxels with signatures most similar to that at CC. Positive and negative correlations are show in red, and blue colors, respectively.