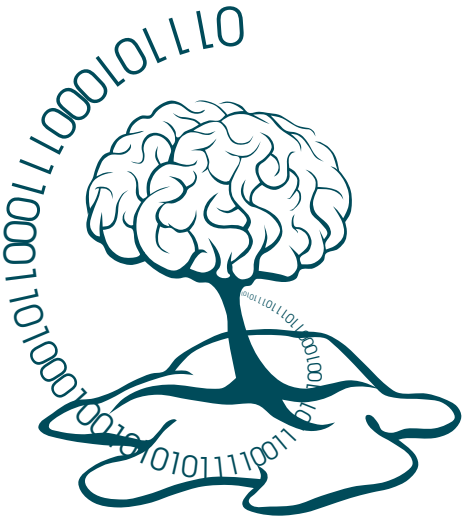

Ischemic Stroke Lesion Segmentation

www.isles-challenge.org

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Preface

Stroke is the second most frequent cause of death and a major cause of disability in industrial countries. In patients who survive, stroke is generally associated with high socioeconomic costs due to persistent disability. Its most frequent manifestation is the ischemic stroke, whose diagnosis often involves the acquisition of brain magnetic resonance (MR) scans to assess the stroke lesion's presence, location, extent, evolution and other factors. An automated method to locate, segment and quantify the lesion area would support clinicians and researchers alike, rendering their findings more robust and reproducible.

New methods for stroke segmentation are regularly proposed. But, more often than desirable, it is difficult to compare their fitness, as the reported results are obtained on private datasets. Challenges aim to overcome these shortcomings by providing (1) a public dataset that reflects the diversity of the problem and (2) a platform for a fair and direct comparison of methods with suitable evaluation measures. Thus, the scientific progress is promoted.

With ISLES, we provide such a challenge covering ischemic stroke lesion segmentation in multi-spectral MRI data. The task is backed by a well established clinical and research motivation and a large number of already existing methods. Each team may participate in either one or both of two sub-tasks:

SISS Automatic segmentation of ischemic stroke lesion volumes from multi-spectral MRI sequences acquired in the sub-acute stroke development stage.

SPES Automatic segmentation of acute ischemic stroke lesion volumes from multi-spectral MRI sequences for stroke outcome prediction.

The participants downloaded a set of training cases with associated expert segmentations of the stroke lesions to train and evaluate their approach, then submitted a short paper describing their method. After reviewing by the organizers, a total of 17 articles were accepted and compiled into this volume. At the day of the challenge, each teams' results as obtained on an independent test set of cases will be revealed and a ranking of methods established.

For the final ranking and more information, visit WWW.ISLES-CHALLENGE.ORG.

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August 2015

Version: 2015-09-30

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A Vascular Territory Prior for Bayesian Sub-Acute Ischemic Stroke Lesion Segmentation

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Abstract. The complex task of quantifying sub-acute stroke lesion volume is addressed by introducing prior information on the vascular territory in a Bayesian framework. Image data is described using a hidden Markov random field model, which accounts for spatial dependencies and allows for the inclusion of a priori spatial information. The algorithm is designed to perform without the need for a preliminary training phase by availing of this prior knowledge, and by imposing constraints on the estimation of MRF interaction parameters.

1 Introduction

Stroke is a global epidemic with levels of mortality and disability that entail a high societal cost. Approximately 70% of stroke survivors have significant sensorimotor, language and cognitive dysfunction requiring long-term special care and rehabilitation [3]. Ischemic stroke lesion quantification facilitates the development of new biomarkers for improved diagnosis, prognosis, and rehabilitation. Automatic methods are motivated by the demand for large-scale multi-center clinical research studies that require precise, consistent and cost-efficient analysis.

Existing methods frequently avail of complementary information from multiple sequences. For example, lesion voxels may appear atypical in one modality and normal in another. This is implicitly used by neurologists when examining data. In an automatic segmentation framework, multiple sequences increase the discriminative capacity of the model to identify different tissues and structures. The proposed statistical model is an implementation of a hidden Markov random field (HMRF) with a number of innovations to address the challenges posed by sub-acute ischemic stroke MR scans.

A general HMRF formulation is employed that encodes complex interactions between neighboring voxels. In particular, we encode the fact that certain tissue combinations in the neighborhood are penalized more than others, whereas the standard Potts model penalizes dissimilar neighboring classes equally, regardless of the tissues they represent.

Prior probabilistic spatial information is incorporated via the Markov prior to express our *a priori* knowledge on the location of tissues or lesion. The accurate segmentation of sub-acute stage ischemic stroke volume demands a more

comprehensive vascular understanding of the human brain. The statistical model includes *a priori* vascular information from a probabilistic vascular territory atlas derived from [2]. This atlas improves the classification by modeling the potential progression and delimitation of vascular accidents.

A solution to the model is found using the Expectation-Maximization (EM) framework [4] combined with a variational approximation for tractability in the presence of Markov dependencies. In particular, the mean field principle provides a deterministic way to deal with intractable MRF models[5].

2 Sub-Acute Stroke Lesion Model

The classification task is performed using a multi-sequence hierarchical Bayesian model that allows us to identify, not only the total lesion volume, but also sub-regions such as necrotic regions, that may be of clinical relevance.

We consider a finite set V of N voxels on a regular 3D grid. The intensity values observed at each voxel are denoted by $\mathbf{y} = \{\mathbf{y}_1, \ldots, \mathbf{y}_N\}$. Each $\mathbf{y}_i = \{y_{i1}, \ldots, y_{iM}\}$ is itself a vector of M intensity values corresponding to M different MR sequences. The classification task is to assign each voxel i to one of K classes. The latent data, denoted by $\mathbf{z} = \{\mathbf{z}_1, \ldots, \mathbf{z}_N\}$, better describes the observed data in the context of the statistical model. The $\mathbf{z}_i$'s correspond to class memberships, and assume values in $\{e_1, \ldots, e_K\}$, where e_k is a K-dimensional binary vector whose k^{th} component is 1, all other components being 0. We will denote by $\mathcal{Z} = \{e_1, \ldots, e_K\}^N$ the set in which $\mathbf{z}$ takes its values. The set of voxels V has an associated neighborhood system. Spatial dependencies between voxels are modeled by assuming a Markov random field (MRF) prior. Denoting $\psi = \{\beta, \phi\}$ additional parameters, we assume that the joint distribution $p(\mathbf{y}, \mathbf{z}; \psi)$ is a MRF with the following energy function:

$$H(\mathbf{y}, \mathbf{z}; \psi) = H_{\mathbf{Z}}(\mathbf{z}; \beta) + \sum_{i \in V} \log g(\mathbf{y}_i | \mathbf{z}_i; \phi) \ , \tag{1}$$

where the $g(\mathbf{y}_i|\mathbf{z}_i;\phi)$'s are probability density functions of $\mathbf{y}_i$. For brain data, the data term $\sum_{i \in V} \log g(\mathbf{y}_i|\mathbf{z}_i;\phi)$in (1) corresponds to the modeling of tissue dependent intensity distributions. For our multi-dimensional observations, we consider M-dimensional Gaussian distributions with diagonal covariance matrices. For each class k, $(\mu_{k1}, \ldots, \mu_{kM})$ is the mean vector and $\{s_{k1}, \ldots, s_{kM}\}$ the covariance matrix components. We will use the notation $\mu_m = {}^t(\mu_{km}, k = 1 \ldots K)$ and $s_m = {}^t(s_{km}, k = 1 \ldots K)$.When $\mathbf{z}_i = e_k$ then $\mathcal{G}(y_{im}; \langle \mathbf{z}_i, \phi_m \rangle)$ and $\mathcal{G}(y_{im}; \langle \mathbf{z}_i, \mu_m \rangle, \langle \mathbf{z}_i, s_m \rangle)$ both represent the Gaussian distribution with mean μ_{km} and variance s_{km}. The whole set of Gaussian parameters is denoted by $\phi = \{\phi_{km}, k = 1, \ldots K, m = 1, \ldots, M\}$. Our data term is then defined by setting $g(\mathbf{y}_i|\mathbf{z}_i;\phi) \propto \prod_{m=1}^{M} \mathcal{G}(y_{im}; \langle \mathbf{z}_i, \phi_m \rangle)$.
The missing data term $H_{\mathbf{Z}}(\mathbf{z}; \beta)$ in (1) describes the dependencies between neighboring Z_i's, and is specified by further assuming that the joint distribution on $\{Z_1, \ldots, Z_N\}$ is a discrete MRF:

$$P(\mathbf{z};\beta) = W(\beta)^{-1} \exp\left(-H_{\mathbf{Z}}(\mathbf{z};\beta)\right) \tag{2}$$

where β is a set of parameters, $W(\beta)$ is a normalizing constant and $H_{\mathbf{Z}}$ is a function restricted to pair-wise interactions,

$$H_{\mathbf{Z}}(\mathbf{z};\beta) = -\sum_{i\in S} z_i^t \alpha - \sum_{\substack{i,j \\ i\sim j}} z_i^t \mathbb{B} z_j,$$

where we write z_i^t for the transpose of vector z_i and $i \sim j$ when i and j are neighbors. The set of parameters β is decomposed into $\beta = (\alpha, \mathbb{B})$. Parameter α is a $K-$dimensional vector which acts as weights for the different values of z_i. $\mathbb{B}$ is a $K \times K$ matrix that encodes interactions between the different classes. If in addition to a null α, $\mathbb{B} = b \times I_K$ where b is a real scalar and I_K is the $K \times K$ identity matrix, parameters β reduce to a single scalar interaction parameter b and we get the Potts model traditionally used for image segmentation.

Note that the standard Potts model is often appropriate for classification since it tends to favor neighbors that are in the same class. However, this model penalizes pairs that have different classes with the same penalty, regardless of the tissues they represent. In practice, it may be more appropriate, to encode higher penalties when the tissues are known to be unlikely neighbors. For example, the penalty for a white matter and extraventricular CSF pair is expected to be greater than that of a grey matter and extraventricular CSF pair, as these two classes are more likely to form neighborhoods.

We adopt a data model comprising of five normal tissue classes; *white matter*, *grey matter*, *ventricular CSF*, *extraventricular CSF*, and *other*. The lesion is modeled by a further two classes representing abnormal tissue state; sub-necrotic and necrotic. In the absence of sufficient data to robustly and accurately estimate a full free $\mathbb{B}$ with $K = 7$, further constraints are imposed on the MRF interaction matrix. The two lesion classes are considered sub-classes of a single *structure*, whose interaction with the normal tissue classes is not dependent on the specific lesion sub-class. Letting τ be the set of classes comprising the lesion structure, $\mathbb{B}$ is a matrix defined by:

$$\begin{aligned} &\mathbb{B}(k,k') = b_t \quad \forall k,k' \in \tau \\ &\mathbb{B}(k,k') = b_{\{k,k'\}} \quad \text{otherwise.} \end{aligned} \tag{3}$$

Prior knowledge on the expected neighborhoods can be encoded in $\mathbb{B}$. For example, given two classes that are likely to be adjacent, the matrix entries for this pair can be initialized at, or even fixed to, a higher value. Conversely, when there is enough information in the data, a full free $\mathbb{B}$ matrix can be estimated and will reflect the class structure (*i.e.* which class is next to which as indicated by the data) and will then mainly serve as a regularizing term to encode additional spatial information.

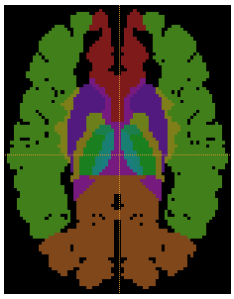
For the distribution of the observed variables $\mathbf{y}$ given the classification $\mathbf{z}$, the usual conditional independence assumption is made. It follows that the conditional probability of the hidden field $\mathbf{z}$ given the observed field $\mathbf{y}$ is

$$P(\mathbf{z}|\mathbf{y};\psi,\beta) = W(\beta)^{-1} \exp\left(-H_{\mathbf{Z}}(\mathbf{z};\beta) + \sum_{i\in S} \log g(y_i|z_i,\phi)\right).$$

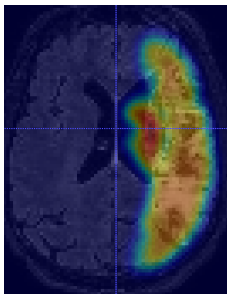
Parameters are estimated using the variational EM algorithm, which provides a tractable solution for non trivial Markov models.

3 Vascular Territory Atlas

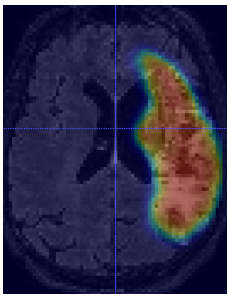
We introduce a novel probabilistic vascular territory atlas to model the potential progression and delimitation of vascular accidents, and therefore overcome misclassification due to artefacts. The vascular territory atlas was derived from [2] and refined by a neurologist. The atlas is discrete, and so Gaussian blur is applied to express uncertainty inherent to patient-specific analysis. In effect, the territory prior does not forbid the realization of lesion labels at any location in the image, but expresses the lower probability of solutions that contain lesions in multiple vascular territories. The vascular territory structure is subject to an affine transformation as the iterative segmentation-registration framework executes. This also helps to overcome patient-specific bias. The discrete vascular territory atlas is shown in Figure 1a alongside an example of the Gaussian blurred territory for use in the joint segmentation & registration step (Fig.1b). The final territory (Fig.1c) is produced by the transformation of the initial territory in the joint model, and shows how the territory is adapted to the individual patient data.



(a) Discrete Vascular Territory Atlas



(b) Initial MCA Territory



(c) MCA Territory Post-Analysis

Fig. 1: Prior Vascular Territory Construction and Transformation

4 Method

The MR images are first preprocessed. The images are corrected for intensity inhomogeneities using the N4 algorithm [1]. The deformable transform that describes the mapping between the International Consortium for Brain Mapping (ICBM) template and the data space is found using tools provided by the Insight Segmentation and Registration Toolkit (ITK). The transform is used to register both the probabilistic tissue atlases, and the vascular territory atlas, to the MR sequences.

An initial preprocessing step identifies the vascular territory to be used in the subsequent segmentation step. Outlier intensities are quantified in each vascular territory grouping based on the DWI and Flair images, and the maximum is chosen.

Adopting Bayesian principles, the algorithm performs joint segmentation and registration of the a priori probabilistic vascular territory structure, as described in [6]. Bias caused by commitment to the initial registration is thus alleviated by refining the registration as the algorithm executes.

5 Discussion & Conclusion

We proposed an adaptive scheme of multiple MR sequences for sub-acute stroke lesion segmentation. Our approach is fully automatic and requires no training. The model parameters are instead estimated using a variational EM algorithm with MRF constraints and the inclusion of a priori probabilistic maps to provide a stable parameter trajectory during optimization. Vascular information is included by way of a prior vascular territory atlas that is modified in a joint segmentation & registration framework to adapt to patient-specific data.

6 The References Section

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