3D geometric split–merge segmentation of brain MRI datasets

Ioannis Marras*,1, Nikolaos Nikolaidis, Ioannis Pitas

Aristotle University of Thessaloniki, Department of Informatics, Box 451, 54124 Thessaloniki, Greece

**A R T I C L E   I N F O**

**A B S T R A C T**

In this paper, a novel method for MRI volume segmentation based on region adaptive splitting and merging is proposed. The method, called Adaptive Geometric Split Merge (AGSM) segmentation, aims at finding complex geometrical shapes that consist of homogeneous geometrical 3D regions. In each volume splitting step, several splitting strategies are examined and the most appropriate is activated. A way to find the maximal homogeneity axis of the volume is also introduced. Along this axis, the volume splitting technique divides the entire volume in a number of large homogeneous 3D regions, while at the same time, it defines more clearly small homogeneous regions within the volume in such a way that they have greater probabilities of survival at the subsequent merging step. Region merging criteria are proposed to this end. The presented segmentation method has been applied to brain MRI medical datasets to provide segmentation results when each voxel is composed of one tissue type (hard segmentation). The volume splitting procedure does not require training data, while it demonstrates improved segmentation performance in noisy brain MRI datasets, when compared to the state of the art methods.

© 2014 Elsevier Ltd. All rights reserved.

1. Introduction

Imaging modalities like Magnetic Resonance Imaging (MRI) view in a non-invasive way the 3D human anatomy. Although modern volume visualization techniques produce extremely accurate and high quality 3D views of anatomical structures, their utilization for accurate and efficient analysis is still limited. One of the main reasons for this limitation is the highly complex internal human anatomy, hindering data visualization in various ways. To overcome this problem, volume segmentation has to be performed. The process of representing meaningful physical entities by partitioning the voxels of a volume into 3D regions is taking place during the volume segmentation procedure. These entities are more comprehensible and easier to analyze and use in future applications. Various approaches regarding segmentation have been proposed in the literature. Generally speaking, the existing volume segmentation techniques can be classified into three classes: structural, stochastic and hybrid.

The structural 3D segmentation techniques utilize some information about the structure of the region when segmenting it. They include graph-searching algorithms, 3D edge detection techniques [1], morphological techniques, deformable models, isosurfaces and level sets. Mathematical morphology uses a set of transformations for image analysis [2]. It encodes the primitive 3D geometrical shapes via the concept of 3D structuring elements (basic morphological set transformations). In graph-searching algorithms [3], the edges and surfaces that exist in a volume are represented as graphs while the algorithm tries to find the lowest-cost path between two nodes using a search algorithm [4]. Energy minimization approaches have had a renaissance, primarily due to powerful new optimization algorithms such as graph cuts [5]. An optimal surface detection method capable of simultaneously detecting multiple interacting surfaces was developed in [6]. Deformable models [7,8] are curves, surfaces or solids defined within a volume that deform under the influence of external and internal forces. Iso-surfaces are collections of locations that form a dividing or bounding surface. Level sets, introduced in [9], are, in short, moving fronts (curves).

Stochastic 3D segmentation techniques perform segmentation by statistical analysis and are applied at discrete voxels without any consideration of the 3D region structure. Thresholding approaches, classification techniques, clustering algorithms and Markov Random fields are some methods contained in this category [10,11]. Thresholding is probably the simplest of the segmentation techniques used for scalar volumes. Feature classifiers belong to the supervised category as they require pre-segmented training data (either manually or using other methods). Such classifiers are the Artificial Neural Networks (ANNs) [12], the k-nearest neighbor (kNN) classifier [13], the Parzen Window classifier [14] and the Maximum Likelihood (ML) or Bayes classifiers [15]. ANNs [16,17] are parallel networks of processing nodes or elements for simulating...
biological learning [18]. To estimate the tissue fractions and tissue model parameters simultaneously, the Expectation–Maximization (EM) algorithm [15,19,20] is used. Markov Random Field (MRF) modelling is not a segmentation method itself but a statistical model, using local voxel correlations for 3D region segmentation [21]. In many cases, it is difficult to select the proper parameters in MRF models that control the strength of spatial interactions that define the number of produced regions [21].

The last segmentation category includes the hybrid methods, which combine characteristics of both structural and stochastic techniques. Hybrid methods include techniques like region growing [22] and, splitting and merging [23,24]. The region growing technique usually needs manual interaction, while it extracts a connected region from a volume based on some predefined region homogeneity criterion [25,26]. The split–merge segmentation algorithm requires the input data to be organized in a region graph [1]. The segmentation procedure can be treated as a registration problem [27] or as a template to perform segmentation when a standard atlas approach is used, like in the case of atlas-guided approaches. A pre-segmented atlas image is mapped to the target image to be segmented based on the one-to-one transformation provided by the anatomical atlas. In [28], a framework to address the consequent problems of scale in multi-atlas segmentation is presented. Only appropriately implemented atlas selection improves the accuracy of multi-atlas segmentation.

The proposed hybrid method, called Adaptive Geometric Split Merge (AGSM) segmentation algorithm, exploits both region shape and data value characteristics. The main novelty lies in the complex feature extraction approach for image volume splitting by selecting one or more optimal splitting strategies according to certain criteria. Features such as region data value and connectivity are used to this end. Another novelty of the segmentation algorithm is that it exploits the spatial volume connectivity and homogeneity by finding the maximal homogeneity axis, in order to perform the splitting procedure. After the splitting step, a 3D region merging procedure is applied. This region merging procedure comprises two different merging steps. The first one exploits the statistical region data value similarity, using a Minimum Spanning Tree (MST) approach, while the second one exploits the degree of intersection between the regions. The flowchart in Fig. 1 demonstrates the method’s individual steps and their interconnections. The proposed method can be used in morphometric brain analysis, in the planning of brain surgery or in brain tumor segmentation.

This paper is structured as follows. The definition of the maximal homogeneity axis of a 3D image volume is described in Section 2. The 3D spatial region splitting according to the maximal homogeneity axis is introduced in Section 3. The multistage region splitting step is illustrated in Section 4. The experimental results are presented in Section 5. A discussion regarding the proposed method is included in Section 6. Finally, conclusions are drawn in Section 7.

### 2. Maximal homogeneity axis definition

In the existing 3D split–merge techniques, volume splitting is performed along the axis $Z$ in which the volume cross sections reside, using planes parallel to the original volume coordinates $(X, Y, Z)$. However, this is not the optimal choice since an inappropriate original axis $Z$ may lead to over-segmentation during the splitting process. One of the novelties of AGSM algorithm is that it takes a volume as input and scans it, in order to find the appropriate axis for splitting. In MRI datasets, within the same cross section there is a correlation between an element and its spatial neighbours. Furthermore, there is a correlation between an element of a cross section and its spatially adjacent neighbours in

![Flowchart](image-url)
nearby cross sections. AGSM algorithm exploits this spatial volume connectivity and homogeneity, as it is described below.

Let the volume be of size $L_x \times L_y \times L_z$ voxels along the axes $X, Y$ and $Z$, respectively. The goal is to find a new coordinate system $(X', Y', Z')$, so that the volume has maximal homogeneity along axis $Z'$. Consequently, the volume coordinate system $X, Y, Z$ is rotated around its mass center in steps. After the $s$-th rotation, a new orthogonal coordinate system $x_i', y_i', z_i'$ defines new volume cross sections with varying dimensions. The axis $z_i'$ is examined whether it is the $Z'$ axis or not. During the process of finding the $s$-th possible maximal homogeneity axis $z_s'$, the volume is enclosed in a parallelepiped of dimensions $L_x'$ (width), $L_y'$ (height) and $L_z'$ (depth), respectively, as shown in Fig. 2(a). The $Z'$ axis aims firstly at the volume splitting procedure primarily to produce as much as possible large homogeneous 3D regions and secondly to unveil regions with higher disparity. The number of potential very small homogeneous regions during the splitting step becomes smaller. The volume splitting along $X'$ and $Y'$ axes is much more elaborate than in the case of $Z'$. Along the $Z'$ axis, the volume is split into half in the case of non-homogeneous 3D regions. Usually, very homogeneous regions are split into homogeneous regions after the implementation of a quite big number of splitting steps. This is essential for the merging step that follows. Therefore, the ensuing segmentation step will preserve and clearly define even small homogeneous regions by avoiding assigning them at larger regions, since this involves a loss of detail that cannot be recovered by the merging step.

In our experiments on MRI datasets, the kurtosis criterion was used as a homogeneity criterion. The rationale behind this approach is the following: the ensuing volume splitting step is based on a region homogeneity criterion which postulates that the difference of the minimum and maximum volume intensities should not exceed a predefined threshold. By considering the volume in which the kurtosis value is low (indicating short-tailed voxel data value distributions) along the axes that are parallel to the $Z'$ axis, the splitting step will produce larger homogeneous regions, as the voxel intensities are expected to be more concentrated around their mean value. The kurtosis of voxel intensities is calculated to produce a vector of kurtosis values $\mathbf{D}_s = [K_{s1}', K_{s2}', \ldots, K_{sl}', \ldots]$. $K_i'$ refers to the kurtosis value of all voxels that are located at an axis parallel to $z_i'$ corresponding to the $i$-th column and the $j$-th row along the $x_i', y_i'$ directions. From $\mathbf{D}_s$, one can find which volume parts in the 3D space have low kurtosis value. However, it is difficult to compare two candidate maximal homogeneity axes. A region compactness measure is needed for this purpose. In order to have such a measure for each tested axis and reach a decision regarding the maximal homogeneity axis $Z'$, the mean value $m_s$ and the total kurtosis $K_s$ of each vector $\mathbf{D}_s$ are evaluated. The use of the appropriate $Z'$ axis should boost the splitting step to produce as large homogeneous regions as possible within the entire volume area (Fig. 2(b)) and not only within a part of it. Consequently, this axis should possess the minimum mean value $m_s$, while at the same time, the kurtosis values in its vector $\mathbf{D}_s$ should be very concentrated around their mean value $m_s$ resulting in a small value of $K_s$. Finally, the axis $z_s'$ with the largest $K_s/m_s$ value is selected to be the $Z'$ axis. Let $l_{ij}$ be the data value of the $(i,j,h)$ voxel in the coordinate system $(x_i', y_i', z_i')$. $\overline{l}_{ij}$ is the sample mean of an axis passing from the $i$-th column and $j$-th row and parallel to the $z_i'$ direction. The value of the total kurtosis $K_s$ for this direction is given by

$$K_s = \left( \frac{L_x L_z}{2} \sum_{l=0}^{L_y-1} \sum_{i=0}^{L_x-1} \sum_{j=0}^{L_z-1} \frac{(l_{i,j} - \overline{l}_{ij})^4}{\left( \sum_{i=0}^{L_x-1} (l_{i,j} - \overline{l}_{ij})^2 \right)^2} \right) - 3,$$

$$K_{ij} = \frac{L_x L_z}{2} \sum_{l=0}^{L_y-1} \sum_{i=0}^{L_x-1} \frac{(l_{i,j} - \overline{l}_{ij})^4}{\left( \sum_{i=0}^{L_x-1} (l_{i,j} - \overline{l}_{ij})^2 \right)^2} - 3,$$

$$\overline{l}_{ij} = \frac{1}{L_x L_z} \sum_{i=0}^{L_x-1} \sum_{j=0}^{L_z-1} l_{i,j}.$$

This definition ensures that the kurtosis of a Gaussian distribution is normalized to zero. The analysis for finding the maximal homogeneity axis is applied only once for a volume. Regardless of the initial volume coordinate system, the maximal homogeneity axis is always the same, so the splitting procedure will always provide the same results.

3. 3D geometric region splitting procedure

Volume splitting divides the entire volume $V_o$ into $N_i$ sub-regions, $R_i$, $i = 1, \ldots, N_i$ ($V_o = \bigcup_{i=1}^{N_i} R_i$), so that two sub-regions, $R_m$ and $R_l$, are disjoint ($R_m \cap R_l = \emptyset$) when $m \neq l$. The adaptive 3D region splitting procedure is a top-down approach that begins by making the assumption that the entire volume is homogeneous. If

---

**Fig. 2.** (a) Choice of the maximal homogeneity axis of an image volume, (b) large homogeneous regions are unveiled using the maximal homogeneity axis.
this is not the case, the volume is recursively split into polyhedra, until only 3D homogeneous regions are encountered. Initially, the maximal homogeneity axis \( Z \) is determined, as described in Section 2. Afterwards, the volume is always split by a plane perpendicular to this axis at its midpoint, while several splitting strategies are applied only to the \( X' \) and \( Y' \) axes. Fig. 3 exemplifies each one of the twelve strategies used in the simple case of a parallelepiped region. For each strategy, the separation of the sub-regions requires the determination of a certain number of 2D planes which represent their boundaries and indicate the voxels that belong to segregation bounds. The AGSM method can extract 3D regions without limitations on their boundary size. Due to hard segmentation, a voxel on the oblique cutting planes (Fig. 3) is assigned to the region which includes the largest area of it. The volume splitting procedure can be terminated at a voxel level. In general, the strategies involve the following:

- all cases that are created by connecting the midpoints of two consecutive edges of a polygon (we refer to a polygon since the different splitting strategies are applied only to the \( X' \) and \( Y' \) axes) (8th, 9th, 10th, 11th and 12th strategies in the case of a parallelepiped region);
- all cases that are created by taking two consecutive edges of the polygon and connecting the two non-common vertices (5th, 6th and 7th strategies in the case of a parallelepiped region);
- all cases that are created by taking three consecutive edges of the polygon and connecting the midpoints of the first and the third edge (1th, 2th and 4th strategies in the case of a parallelepiped region);
- the case of splitting along \( Z' \) axis at its midpoint (3th strategy in the case of a parallelepiped region).

A splitting along the \( Z' \) axis in the same manner as with the other two axes was tested, but the obtained segmentation results were always inferior. Although, a special kind of volume splitting along the \( Z' \) axis is described in Section 3.2. The splitting technique does not split the volume using only parallelepipeds, as the classical splitting approaches do [23,24]. A region to be split is the result of the application of one or more consecutive splitting strategies in previous regions, thus polyhedra of various shapes can be produced. One of our motivations for using this technique for producing irregular polyhedra is that the volume division by using one of the five finite convex regular polyhedra (tetrahedron, cube, octahedron, dodecahedron and icosahedron), known as the Platonic solids, could not describe the region boundaries well. This is because of the splitting restrictions related to their shape. The reason for using the proposed iterative volume splitting procedure is that for a 3D region, among the other polyhedra, these convex regular polyhedra could be produced during our splitting procedure but only after a certain number of splitting steps and not in just one splitting step. This enables us to define the region boundaries more accurately and unveil regions with higher disparity.

The proposed splitting strategies have been produced by using the general line equation:

\[
x' = \begin{cases} \alpha y' + \beta, & \alpha, \beta \in \mathbb{R}, \lim_{r \to \infty} \frac{\alpha}{r} \neq 1 \\ c_2, & c_2 \in \mathbb{R}^+ \end{cases}
\]

where \( c_2 \) is a constant. The parametric line equation meets some obstacles when representing vertical straight lines due to the fact that the parameter \( \alpha \) must tend to infinity, so the expression \( x' = c_2 \) is used separately. If a volume part having dimensions \((x_{\max} - x_{\min} + 1) \times (y_{\max} - y_{\min} + 1) \times (z_{\max} - z_{\min} + 1)\) is to be split, we determine the midpoints \( x_m, y_m \) and \( z_m \) along the corresponding \( X' \), \( Y' \) and \( Z' \) axes, then any of the possible splitting strategies could be generated by changing the factor \( \alpha \). By applying the appropriate line equations on each cross section belonging to a region that is to be split, several parametric planes are created.

Fig. 3. The twelve 3D region splitting strategies in the simple case of a parallelepiped region.
which divide this region into several sub-regions. In the simple case of a parallelepiped region, the cutting lines for each strategy are detailed in Table 1.

The volume splitting method selects one or more optimal splitting strategies according to certain criteria described in detail below. For each inhomogeneous 3D region to be split, the smallest parallelepiped that encloses the 3D region is evaluated. The splitting procedure is applied at this parallelepiped region. The parts of the region that remain outside this smallest parallelepiped are taken into consideration when the neighbouring sub-regions are to be split. Due to the region’s geometrical shape, in some cases, it is possible that some of the strategies produce varying number of valid sub-regions. Fig. 4 depicts a parallelepiped region during the recursive splitting procedure. For visualization purposes, only the half of the initial parallelepiped region’s volume is split (shaded volume part), while the rest of the volume will be split in a different splitting sub-step. An application of the 4th splitting strategy on this parallelepiped region will produce only 6, instead of 8, valid regions (children). For each non-homogeneous region, the splitting strategy selection procedure consists of the following steps:

- First, the splitting strategy that produces the maximum ratio of the total number of voxels that belong to homogeneous sub-regions over the total number of voxels belonging to the region to be split is selected.

- If two or more strategies provide the same number of voxels included in homogeneous sub-regions, the strategy that produces the smaller number of valid sub-regions is chosen.

- If two or more strategies provide the same number of voxels included in homogeneous sub-regions and the same number of valid sub-regions, then the strategy that produces the most homogeneous region is chosen.

- If two or more strategies provide the same number of voxels included in homogeneous sub-regions, the same number of valid sub-regions and the same value of homogeneity, then the strategy with the lower id number is chosen (given in Fig. 3). This enables us to avoid when possible, increased shape complexity for the polyhedra produced during the splitting procedure. It can be seen that the smaller id a splitting strategy has, the smaller shape complexity it introduces at the produced polyhedra.

Regarding the region homogeneity check method, the one based on the data value range \(|I_{\text{max}} - I_{\text{min}}|\) was chosen, where \(I_{\text{max}}\) and \(I_{\text{min}}\) are the maximum and minimum data values of the region. If the data value range is larger than a certain user-defined threshold \(1_{\text{max}} - 1_{\text{min}}| \geq T_s\), the newly created region to be split is selected.

\[
T_s \geq \frac{1}{C_0} \frac{I_{\text{max}} - I_{\text{min}}}{|1_{\text{max}} - 1_{\text{min}}|} \;
\]

\[
T_s \geq \frac{1}{C_0} \frac{I_{\text{max}} - I_{\text{min}}}{|1_{\text{max}} - 1_{\text{min}}|} \;
\]

The table below details each splitting strategy as follows:

<table>
<thead>
<tr>
<th>ID</th>
<th>Sr</th>
<th>Cutting lines</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4</td>
<td>(X = X_{\text{old}}, \ X' = Z_{\text{old}})</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>(Y = Y_{\text{old}}, \ Y' = Z_{\text{old}})</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>(Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>4</td>
<td>8</td>
<td>(X = X_{\text{old}}, \ Y = Y_{\text{old}}, \ Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>5</td>
<td>4</td>
<td>(X_{\text{old}} - X_{\text{max}} + 1 \ (Y_{\text{max}} - Y_{\text{min}}) + X_{\text{min}}, \ Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>6</td>
<td>4</td>
<td>(X_{\text{old}} - X_{\text{max}} + 1 \ (Y_{\text{max}} - Y_{\text{min}}) + X_{\text{min}}, \ Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>7</td>
<td>8</td>
<td>(X_{\text{old}} - X_{\text{max}} + 1 \ (Y_{\text{max}} - Y_{\text{min}}) + X_{\text{min}}, \ Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>8</td>
<td>4</td>
<td>(X_{\text{old}} - X_{\text{max}} + 1 \ (Y_{\text{max}} - Y_{\text{min}}) + X_{\text{min}}, \ Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>9</td>
<td>4</td>
<td>(X_{\text{old}} - X_{\text{max}} + 1 \ (Y_{\text{max}} - Y_{\text{min}}) + X_{\text{min}}, \ Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>10</td>
<td>4</td>
<td>(X_{\text{old}} - X_{\text{max}} + 1 \ (Y_{\text{max}} - Y_{\text{min}}) + X_{\text{min}}, \ Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>11</td>
<td>4</td>
<td>(X_{\text{old}} - X_{\text{max}} + 1 \ (Y_{\text{max}} - Y_{\text{min}}) + X_{\text{min}}, \ Z = Z_{\text{old}})</td>
</tr>
<tr>
<td>12</td>
<td>10</td>
<td>(X_{\text{old}} - X_{\text{max}} + 1 \ (Y_{\text{max}} - Y_{\text{min}}) + X_{\text{min}}, \ Z = Z_{\text{old}})</td>
</tr>
</tbody>
</table>

\[
I_{\text{max}} - I_{\text{min}}| \geq T_s,
\]

\[
I_{\text{max}} - I_{\text{min}}| \geq T_s,
\]

The splitting procedure is as follows:

1. First, the splitting strategy that produces the maximum ratio of the total number of voxels that belong to homogeneous sub-regions over the total number of voxels belonging to the region to be split is selected.

2. If two or more strategies provide the same number of voxels included in homogeneous sub-regions, the strategy that produces the smaller number of valid sub-regions is chosen.

3. If two or more strategies provide the same number of voxels included in homogeneous sub-regions and the same number of valid sub-regions, then the strategy that produces the most homogeneous region is chosen.

4. If two or more strategies provide the same number of voxels included in homogeneous sub-regions, the same number of valid sub-regions and the same value of homogeneity, then the strategy with the lower id number is chosen (given in Fig. 3). This enables us to avoid when possible, increased shape complexity for the polyhedra produced during the splitting procedure. It can be seen that the smaller id a splitting strategy has, the smaller shape complexity it introduces at the produced polyhedra.

Fig. 4. Example of a region where a strategy produces six, instead of eight, valid sub-regions because of the recursive region splitting procedure. Only half of the initial parallelepiped region's volume needs to be split (shaded volume part). The rest of the region's volume will be split in a different splitting sub-step.
levels (contrast). In the threshold estimation method, we exploit the fact that the statistical energy of cross sections is mainly located in the low spatial frequencies. Firstly, volume histogram equalization filtering is performed. The fact that histogram equalization allows regions of lower local contrast to gain a higher contrast without affecting the global contrast tends to amplify noise. This results in a threshold which will not eliminate small critical regions during the volume splitting procedure. Instead, it will eliminate only a small part of noise without deforming the edges noticeably. Subsequently, the locations of the histogram peaks (excluding the ones corresponding to the background) \( n_1, \ldots, n_k \) are identified. The threshold \( T_s \) is selected as the distance of the pair of the closest peaks separated by deep valleys
\[
T_s = \min_j |n_i - n_j|.
\]

Valleys in the histogram represent less common values. The histogram peaks correspond to homogeneous and uniform regions. Thus, a selection of \( T_s \) ensures that the two most similar sub-regions (in terms of data values) will not be considered as one region. Let us assume that the desired number of tissue regions after the segmentation procedure \( N_{SM} \) is known. The threshold \( T_s \) should be smaller than the distance of the two closest peaks if we take into consideration the most distinct \( N_{SM} \) peaks. The background color is excluded. When \( N_{SM} \) is unknown, a good and fast estimation of the discriminant peaks (\( N_{SM} \) tissue regions) in the image volume histogram could be found by using relaxation labelling techniques [30]. The superiority of such a threshold value has been verified experimentally, providing very good results. At each voxel a data value equal to the mean data value of the region it belongs to is assigned. Thus, a volume with less noise is produced. This can be seen in Fig. 5. Experiments have shown that the volume splitting procedure is fairly insensitive to small threshold \( T_s \) variations.

3.1. Representation of the splitting results

We use two different approaches for representing the \( N_t \) 3D regions, \( R_1, \ldots, R_{N_t} \), derived from the volume splitting procedure. Both approaches provide a compact volume representation. In the first one, a Newton polynomial interpolation form, \( C(v) \), which is used by the AGSM algorithm returns the region label \( R_{CV} \) when fed with the voxel index \( v \). The second approach produces a volume representation that can be described as a tree (that will be referred to as the single AGSM Tree from now onwards), as shown in Fig. 6. Each internal node in this tree corresponds to a non-homogeneous region, whereas leaves correspond to homogeneous regions. As can be seen in the graphical representation, the connections between adjacent regions (father-child) denote the strategies’ connection as well. The children of each internal node correspond to regions that were generated by splitting the region indicated by this node. For each region only two values consisting of the strategy id that has been used for generating the current region and its id (Fig. 3) have to be stored. If the selected splitting strategy and the equivalent child id are assigned to every node (region), then it constitutes enough information in order to define the geometrical characteristics of every node. This can be done by

![Fig. 5. Noise decreasing after the volume splitting procedure. (a) Initial brain cross section, (b) its data value histogram, (c) the brain cross section after voxel value reassignment and (d) its data value histogram.](image)

![Fig. 6. The single tree representation of the volume splitting procedure. Each internal node corresponds to a non-homogeneous region, whereas leaves correspond to homogeneous regions.](image)
applying the splitting procedure to the regions (nodes) that are included in the path from the root (initial volume) until this node, or by applying the splitting strategy directly on his father node. Such a path indicates the consecutive strategies that should be applied in the initial volume in order to obtain a region. As experimentally verified in noisy MRI datasets, AGSM algorithm’s volume splitting procedure produces up to 30–40% less 3D regions in comparison with the octrees technique [24,23] given the same threshold $T_i$.

3.2. Development of complex AGSM Tree

The use of $\lambda > 1$ (usually $\lambda = 3$) candidate maximal homogeneity axes, and not only of the best one as mentioned above, constitutes a very useful tool when it is desired to change the volume splitting procedure along the $Z$ axis. For each such axis, a different single AGSM Tree is produced. One can combine/merge, as explained below, those single AGSM Trees, creating one complex AGSM Tree. Additional regions with different homogeneity are created, while the connectivity and the number of the regions are increased. There is not a major division of the large homogeneous regions produced during the $\lambda$ independent splitting steps. In this way, volume over-splitting (which cancels out the benefit of the use of maximal homogeneity axis) is avoided. Let us consider a reference partition $R_1, ..., R_N$ of the volume $V$, after the volume splitting procedure. For each region $R_i$, we can define a logical map which indicates the existence of a voxel index $v$ related to the surface $\partial R_i$ of region $R_i$. Let $q(R_i, C(v))$, $q : R \rightarrow \{0, 1\}$ be the logical map of the $v$–th voxel:

$$q(R_i, C(v))= \begin{cases} 0, & C(v) \neq i, \\ 1, & C(v) = i. \end{cases}$$ (5)

Eq. (5) associates a voxel of label $v$ with the region it belongs to. Let us define that, generally, the $e$–th, $e \in [1, \lambda]$, candidate maximal homogeneity axis produces a set $L_e$ of $N_e$ regions, $L_e = \{R_{e,1}, ..., R_{e,N_e}\}$. We define as $I^e$ the set of all the 3D regions represented in the complex AGSM Tree. If we set at the beginning $I^0 = \{\emptyset\}$, then by using Eq. (5) the combination formula in order for the method to produce the complex AGSM Tree is given by

$$I^e = R^* \cup R^0 \cup R^e,$$

where

$$\begin{align*}
\forall e \in [1, \lambda], & \quad \forall v \in [1, \lambda], \\
R^e & \in \left( \bigcap_{\rho \neq e} R_{\rho} \right) \cap \left( \bigcup_{\rho \neq e, \rho \neq e} R_{\rho} \right), \\
|p^{\min}_{\rho} - p^{\min}_{\mu}| & \leq T_i, \\
|p^{\max}_{\rho} - p^{\max}_{\mu}| & \leq T_i, \\
R^* & \in (R^0 / (R^0 \cup R^e)).
\end{align*}$$ (6)

The first inequality represents the 3D regions that are common for all the $\lambda$ single AGSM Trees, while the second inequality represents the 3D regions that are common at least for two and not for all AGSM Trees. In order for a intersection to be taken, the method checks its homogeneity using Eq. (3). Finally, the third inequality expresses the remaining parts of regions that have been produced after the splitting step along each one of the $\lambda$ best candidate maximal homogeneity axes. In the last inequality, it is not necessary to check the homogeneity of the produced 3D regions because each 3D region remains homogeneous as a consequence of the splitting procedure.

The new 3D cross regions, produced during the above tree combination formula, represent critical regions during the merging procedure. Each one of them is placed as the only child under a new parent in the complex AGSM Tree. The remaining parts of initial regions are considered as independent 3D regions.

4. Multistage region merging

The opposite procedure to region splitting is region merging. Many region merging approaches were proposed in the literature [22,31,32]. The merging step is of great importance for the AGSM method, since at this step the final region classification is performed. The volume splitting method is followed by a two-stage merging procedure that aims at reducing the number of regions bringing them down to the desired number $N_{SM}$. In the first merging stage, the 3D regions represented in the complex AGSM Tree are merged by taking into consideration their statistical data value similarity. A Minimum Spanning Tree (MST) approach based on Kruskal’s algorithm [33] is used for this purpose. The second region merging stage includes geometrical proximity criteria for merging regions in three dimensions. The criteria used are the relative homogeneity of two or more adjacent regions, as well as their geometrical cohesiveness which depends on the size of the 3D regions and their common border area. The second region merging stage is only activated when the number of regions after the first merging step is bigger than $N_{SM}$. In the next subsections each merging stage will be presented in detail.

4.1. Region classification using a minimum spanning tree approach

During this merging step, only the leaves of the complex AGSM Tree are involved for merging. Before describing the first stage of the merging procedure, the relationship of the volume $V$ with the 3D homogeneous regions (leaves) represented in the complex AGSM Tree, must be constructed. MST is a connected acyclic sub-graph $G = (V, E) : |V| = N_v, V = \{1, ..., N_v\}$ that spans all the tree leaf nodes, $R_1, ..., R_{N_v}$.

Let us assume that the gray-level values $f_i$ in a 3D region $R_i$ are drawn from Gaussian distributions

$$p(f_i) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(f_i - \mu)^2}{2\sigma^2}},$$ (7)

where $\mu_i$ and $\sigma^2_i$ denote the mean value and variance of region $R_i$. We can estimate the parameters of the Gaussian distribution as follows:

$$\hat{\mu_i} = \frac{1}{n_i} \sum_{f_{ni}} f_i, \quad \sigma^2_i = \frac{1}{n_i} \sum_{f_{ni}} (f_i - \hat{\mu_i})^2,$$

where $n_i$ is the number of voxels of the region $R_i$. In this way, in two given regions $R_1$ and $R_2$, there are two possible hypotheses:

- **$H_0$:** The two regions should be merged. The voxel intensities are all drawn by a single Gaussian distribution $N(\mu_i, \sigma^2_i)$. Assuming that the voxel gray-level values from both regions $R_1$ and $R_2$ are independently drawn, the joint probability density, $P(f_1, ..., f_{n_1+n_2} | H_0)$, is a multidimensional Gaussian distribution with the same variance for every variable.

- **$H_1$:** The two regions should not be merged. In that case, the voxel gray-level values of each region are drawn by separate Gaussian distributions $N(\mu_i, \sigma^2_i)$ and $N(\mu_j, \sigma^2_j)$. The joint probability density, $P(f_1, ..., f_{n_1+n_2} | H_1)$, is a multidimensional Gaussian with two different variances.

The likelihood ratio from regions $R_1$ and $R_2$ is defined as the ratio of the probability densities under the two hypotheses:

$$r_{R_1,R_2} = \frac{P(f_1, ..., f_{n_1+n_2} | H_0)}{P(f_1, ..., f_{n_1+n_2} | H_1)} = \frac{\sigma^2_{\mu_j}^{n_2} \sigma^2_{\mu_i}^{n_1}}{\sigma^2_{\mu_i}^{n_1+n_2} \sigma^2_{\mu_j}^{n_2}}.$$ (9)

The lower the value of the $r_{R_1,R_2}$ is, the stronger the evidence that the two regions $R_1$ and $R_2$ should be merged is.

The leaf regions whose distances from the root are characterized by big values (measured by the number of intermediate
nodes) have been produced from consecutive splitting steps of a very inhomogeneous region. For two regions \( R_i \) and \( R_j \), the distances of those regions from the tree root are defined as \( d_{R_i} \) and \( d_{R_j} \), respectively. Thus, the distance between those two regions is equal to \( d_{R_i,R_j} = \| d_{R_i} - d_{R_j} \| \). The most probable regions for merging are those that have similar data value statistics and are characterized by a smallized distance \( D_{R_i,R_j} \).

For two regions \( R_i, R_j \in V \), the function \( w(R_i, R_j) \in E \) used for the MST construction, which denotes the weight of the edge between two regions, is given by

\[
w(R_i, R_j) = \begin{cases} 
\max(e_i, e_j) / \min(e_i, e_j) \, D_{R_i,R_j}, & \mu_i - \mu_j \leq 1 - \frac{\sigma_i}{\mu_i} \#T_m \\
\infty, & \text{otherwise}, 
\end{cases}
\]

(10)

where \( e_i \) is the number of adjacent regions the region \( R_i \) has. \( MST \) has the lowest total weight of its edges measured as the sum of the weights of the edges in the spanning tree. The merging of two regions depends on the threshold parameter \( T_m \) which is provided by the user. Since the samples are all positive, the quantity \( (1 - \sigma_i / \mu_i^2) \) varies between 0 (low uniformity) and 1 (high uniformity) and denotes the expected uniformity of the merged region. If the quantity \( (1 - \sigma_i / \mu_i^2) T_m \) is small, the merging is difficult, thus many small regions are created. If it is large, it may create regions that have less homogeneity and large standard intensities are sufficient. As explained below, such a constraint, \( \mu_i - \mu_j \leq 1 - \frac{\sigma_i}{\mu_i} \#T_m \), is the number of adjacent regions the region \( R_i \) has. \( MST \) is placed in the tree as a new child under a new parent with depth \( d_{R_i} \), which is computed automatically as the minimum mean data value difference between all region pairs at each iteration. At each iteration the mean data volume and variance of the merged region are re-estimated.

- This stage constitutes a variation of the above criterion used for further formation of larger regions. It is only used if the previous criterion \( 11 \) cannot produce the predefined number of final segmented tissues \( N_{SM} \). Firstly, the size factor \( N_{SM} / N_k \) and the second inequality in Eq. (11) are disregarded and we focus on the size of the term \( \partial R_i / C_{ij} \) to remove regions that are almost fully covered by the large regions (almost contained into the larger regions).

5. Experimental results

The AGSM algorithm was compared for brain MRI segmentation with other MRI segmentation techniques such as the classical split–merge algorithm (SM) [24,23], the GHMRF algorithm proposed in [18] and reviewed by Bach-Cuadra et al. [34] and Cardenes et al. [35] and the PV–MAP algorithm for hard image volume segmentation [36,37]. The brain MRI datasets used in our experiments are presented in the following sub-section, while the results are presented in detail in Section 5.2.

5.1. Used datasets

In general, the AGSM volume segmentation algorithm was build for MRI datasets. For the evaluation of the AGSM segmentation algorithm a large number of simulated brain MRI data volumes, created by McConnell Brain Imaging Center [38], were used in our segmentation experiments. In this pre-computed simulated brain database (SBD), the parameter settings are fixed to 3 modalities (\( T_1, T_2 \) and proton density weighted \( P_0 \)), 5 slice thicknesses (1 mm, 3 mm, 5 mm, 7 mm and 9 mm), 5 levels of noise (0% 1% 3% 5%, 7% and 9%), and 3 levels of intensity non-uniformity (0%, 20% and 40%). In our experiments, 24 \( T_1 \) weighted volumes with 3%, 5%, 7%, 9% noise and 0%, 20%, 40% intensity non-uniformity were used for the evaluation of the performance of the AGSM segmentation algorithm. The noise in these simulated images has Rayleigh statistics in the background and Rician statistics in the signal regions [38]. The percentage noise number represents the percentage ratio of the standard deviation of the white Gaussian noise versus the signal for a reference tissue. More specifically, the standard deviation of the Gaussian noise that is to be added to the real and imaginary channels is given by the noise percentage multiplied by the reference tissue intensity range. The volumes taken into consideration have been preprocessed to remove non-brain tissues, so that only the intracranial cavity has been used. In the brain, \( T_1 \)-weighting causes the nerve connections of white matter (WM) to appear white, and the congregations of neurons of gray matter (GM) to appear gray, while cerebral–spinal fluid (CSF) appears dark. The volumes were of size 161 × 161 × 161 voxels, with isotropic 1 mm voxel size. Each volume was classified into three \( N_{SM}=3 \) classes: white matter (WM), gray matter (GM) and cerebral–spinal fluid (CSF). Since the ground truth for brain MRI data volumes is valid only for hard segmentation (non-mixture), the AGSM segmentation algorithm labels each voxel with one tissue label only, which corresponds to the highest class probability.
5.2. Brain MRI segmentation

To study the method’s performance, two metrics were even used to further perform a quantitative comparison using the confusion matrices: True Positive Fraction (TPF) and False Positive Fraction (FPF), which are defined as follows:

\[
\text{TPF} = \frac{\text{Volume}_{\text{seg}} \cap \text{Volume}_{\text{groundtruth}}}{\text{Volume}_{\text{groundtruth}}} \times 100\% \]

\[
\text{FPF} = \frac{\text{Volume}_{\text{seg}} \cap \text{Volume}^c_{\text{groundtruth}}}{\text{Volume}^c_{\text{groundtruth}}} \times 100\% \]

where the operators + and − are used whether a voxel belongs to a specific tissue or not. Obviously, an ideal segmentation has a TPF value equal to one and a FPF value equal to zero. A confusion matrix has been used to display the information about the confusion of real class labels with the labels obtained through classification. The diagonal entries of the confusion matrix are the rates of voxels that are correctly classified, while the off-diagonal entries are the rates corresponding to misclassification rates.

In general, the use of the complex AGSM Tree significantly improves the performance of the AGSM volume segmentation algorithm especially in very noisy datasets. The reason is that in very noisy datasets, in contrary to robust statistic criteria used in bibliography [40,41], the border tissues are described much better when complex AGSM Tree is used. Since the merging procedure depends on the size (in voxels) of the 3D regions and the size of their mutual border, the use of AGSM algorithm with complex AGSM Tree is very important. Since the volume lies in the 3D space, \( \lambda = 3 \) candidate maximal homogeneity axes is a reasonable number for the creation of the complex AGSM Tree. In some cases, these three maximal homogeneity axes were close to the three main axes of the initial volume coordinate system. Moreover, based on our experiments, this fixed choice of \( \lambda \) value produces the best segmentation results on average. Because of that, we shall focus our attention on the volume splitting procedure and the use of the complex AGSM Tree created by the three best candidate maximal homogeneity axes.

Fig. 7 shows how the volume segmentation algorithm affects a MR T1 volume section of a noisy (5% noise) brain MRI dataset. For the brain MRI dataset with 5% noise, the estimated value for the splitting threshold \( T_s \) (depending on the histogram of the volume to be split as it was mentioned in Section 3) was 16. This means that the distance of the pair of the closest peaks (excluding the ones corresponding to the background) separated by deep valleys was equal to 16. For the same dataset, the 3D region merging procedure depends on the threshold parameter \( T_m \), which is provided by the user, and was set equal to 14. For a noisy brain MRI dataset (7% noise), the achieved segmentation results for several volume cross sections are depicted in Fig. 8. The table in Fig. 9 shows how often each one of the twelve investigated splitting strategies has been applied on the noisy brain MRI dataset (7% noise). In addition, for each splitting strategy this is also expressed as a percentage ratio over the total number of splitting steps performed. Suggestively, Tables 2–6 show the confusion matrices between the ground truth and the classification results obtained by the AGSM algorithm when it was applied.

Fig. 7. (a) An MR T1 volume section with 5% noise, (b) its non-mixture ground truth, (c) the segmentation results of the proposed algorithm using the complex AGSM Tree created by the three best candidate maximal homogeneity axes, (d) three different cross sections of the same volume (left) and volume view renderings (right) indicated by the three best candidate maximal homogeneity axes. Inside the black boxes are a volume cross section example (left) and the volume view rendering (right) indicated by the maximal homogeneity axis.
on noisy brain MRI datasets with 3%, 5%, 7% and 9% noise. The results obtained by the classical split-merge (SM), the GHMRF and the PV–MAP algorithms for the same datasets are also in the same tables for comparison purposes. The results correspond to the optimal parameters of these algorithms as proposed by their authors. The execution time of AGSM for the above brain MRI datasets with 3%, 5%, 7% and 9% noise is 2.3 min, 2.7 min, 3.4 min and 4.4 min, respectively on a Pentium III computer with 1.0 GB RAM. The analysis for finding the best three candidate maximal homogeneity axes is applied only once for the same volume, while its computation requires an additional 1.2 min.

Based on the previous discussion on experiments, the AGSM algorithm performs very well in noisy brain MRI segmentation by segmenting it into three main classes (WM, GM and CSF). In order to assess AGSM algorithm's performance on real pathological cases, we have used real $T_1$ brain MRI data volumes that contain compact tumors [42]. The goal was to verify that tumors can also be delineated very well by the AGSM algorithm, since in these datasets, only tumors have been manually delineated, while for WM, GM and CSF tissues the database creators do not provide the respective annotations. Fig. 11 shows a characteristic real pathological case of a compact brain tumor, where 93% of the tumor voxels were correctly classified by the AGSM algorithm.

The number of thresholds used in the AGSM method ($T_s$ and $T_m$) is not greater than the ones employed in other techniques, e.g. the GHMRF algorithm uses two, while $k$NN [13] uses three thresholds. Also, a method for the semi-automatic evaluation of threshold $T_s$ is provided (Eq. (3)). For a brain MRI dataset with 5% noise, the values of modified Jaccard ($JC$) distance based similarity measure $JC_d$ and the intensity based similarity measure $JC_i$ proposed in [35], for all algorithms, are shown in Fig. 10(a) and (b), respectively. The measure $JC_d$ is used in order to penalize more severely the voxels that are further away from their corresponding class in the gold standard, i.e. to weight every misclassified voxel by its Euclidean distance.

Fig. 8. Left: a MR T1 volume section with 7% noise, Middle: its non-mixture ground truth, Right: the segmentation results obtained by the AGSM algorithm.

Fig. 9. Usage of splitting strategies of AGSM algorithm for a noisy (7% noise) brain MRI dataset.
distance to the nearest voxel of the class it should belong to. To compute those Euclidean distances, it is enough to simply compute the Distance Transformation (DT) from a given class in the gold standard to the rest of the image, and look at the voxels of the DT at the positions of the misclassified voxels. The measure \( JCi \) uses the intensity values of the image instead of the Euclidean distances. In that way, the misclassified voxels that should belong to a given class are penalized more severely, when they are close to the theoretic mean of that class, as the voxels that are near the theoretic mean should be easy to classify. Therefore, a weighting function is defined, depending on the theoretic mean and variance of each class. Those parameters are easy to obtain from the gold standard and the original data, by computing the mean and variance values of the original voxels indexed by each class in the gold standard segmentation.

6. Discussion

The AGSM algorithm, in the majority of cases, outperforms other state of the art unsupervised volume segmentation techniques especially on very noisy datasets. This is due to the fact that the geometrical shape information of the various regions is best exploited during both the volume splitting and merging steps. A major advantage of the AGSM algorithm is that it achieves the best segmentation accuracy for all tissue types, as seen in Fig. 10. In the literature, several segmentation techniques exist that increase the segmentation accuracy of only a few tissue types. For the case of 3% noise, the mean segmentation error for AGSM algorithm is 3.63%, while for the second best method, namely the GHMRF, is 4.53%.

The execution time of the AGSM algorithm is longer than that of the classical split–merge segmentation algorithm and comparable to that of the other techniques. When we consider to use region size restrictions in order to stop the splitting procedure, less time is needed for the execution of the AGSM algorithm. However, no region size restrictions to stop the splitting procedure were used in the AGSM algorithm for the reasons described below:

- As already mentioned, the maximal homogeneity axis is used in order for the splitting method to produce a smaller number of very small homogeneous regions. In order to highlight the importance and the effectiveness of this sub-procedure, very small regions (even consisting of one voxel) can be produced during the splitting step. Based on our experiments, indeed a small number of very small homogeneous regions is produced during the volume splitting procedure.
- When region size restrictions are considered, the resulted complex AGSM Tree produces bigger 3D homogeneous regions. During the creation of complex AGSM Tree smaller regions (even consisting of one voxel), especially around the regions’

### Table 2
Confusion matrices between the ground truth and the classification results obtained by the AGSM algorithm and the three other algorithms for a noisy (3% noise) brain MRI dataset with 0% of in-homogeneity (3N0RF).

<table>
<thead>
<tr>
<th>l_{sc}</th>
<th>l_{sd}</th>
<th>l_{sd}</th>
<th>l_{sd}</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>AGSM</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CSF</td>
<td>0.965</td>
<td>0.008</td>
<td>0.017</td>
</tr>
<tr>
<td>GM</td>
<td>0.016</td>
<td>0.965</td>
<td>0.015</td>
</tr>
<tr>
<td>WM</td>
<td>0.013</td>
<td>0.020</td>
<td>0.961</td>
</tr>
<tr>
<td><strong>SM</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CSF</td>
<td>0.954</td>
<td>0.023</td>
<td>0.012</td>
</tr>
<tr>
<td>GM</td>
<td>0.020</td>
<td>0.958</td>
<td>0.028</td>
</tr>
<tr>
<td>WM</td>
<td>0.019</td>
<td>0.013</td>
<td>0.952</td>
</tr>
</tbody>
</table>

### Table 3
Confusion matrices between the ground truth and the classification results obtained by the AGSM algorithm and the three other algorithms for a noisy (5% noise) brain MRI dataset with 0% of in-homogeneity (5N0RF).

<table>
<thead>
<tr>
<th>l_{sc}</th>
<th>l_{sd}</th>
<th>l_{sd}</th>
<th>l_{sd}</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>AGSM</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CSF</td>
<td>0.947</td>
<td>0.022</td>
<td>0.013</td>
</tr>
<tr>
<td>GM</td>
<td>0.022</td>
<td>0.951</td>
<td>0.032</td>
</tr>
<tr>
<td>WM</td>
<td>0.025</td>
<td>0.020</td>
<td>0.948</td>
</tr>
<tr>
<td><strong>GHMRF</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CSF</td>
<td>0.930</td>
<td>0.017</td>
<td>0.048</td>
</tr>
<tr>
<td>GM</td>
<td>0.044</td>
<td>0.940</td>
<td>0.011</td>
</tr>
<tr>
<td>WM</td>
<td>0.019</td>
<td>0.017</td>
<td>0.935</td>
</tr>
</tbody>
</table>
Table 4
Confusion matrices between the ground truth and the classification results obtained by the AGSM algorithm and the three other algorithms for a noisy (7% noise) brain MRI dataset with 0% of in-homogeneity (7N0RF).

<table>
<thead>
<tr>
<th></th>
<th>$l_{cf}$</th>
<th>$l_{li}$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>AGSM</td>
<td>SM</td>
</tr>
<tr>
<td></td>
<td>CSF</td>
<td>GM</td>
</tr>
<tr>
<td>CSF</td>
<td>0.918</td>
<td>0.060</td>
</tr>
<tr>
<td>GM</td>
<td>0.052</td>
<td>0.930</td>
</tr>
<tr>
<td>WM</td>
<td>0.023</td>
<td>0.003</td>
</tr>
<tr>
<td></td>
<td>GHMBRF</td>
<td>PV–MAP</td>
</tr>
<tr>
<td></td>
<td>CSF</td>
<td>GM</td>
</tr>
<tr>
<td>CSF</td>
<td>0.906</td>
<td>0.035</td>
</tr>
<tr>
<td>GM</td>
<td>0.043</td>
<td>0.920</td>
</tr>
<tr>
<td>WM</td>
<td>0.044</td>
<td>0.037</td>
</tr>
</tbody>
</table>

Table 5
Confusion matrices between the ground truth and the classification results obtained by the AGSM algorithm and the three other algorithms for a noisy (7% noise) brain MRI dataset with 20% of in-homogeneity (7N20RF).

<table>
<thead>
<tr>
<th></th>
<th>$l_{cf}$</th>
<th>$l_{li}$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>AGSM</td>
<td>SM</td>
</tr>
<tr>
<td></td>
<td>CSF</td>
<td>GM</td>
</tr>
<tr>
<td>CSF</td>
<td>0.909</td>
<td>0.059</td>
</tr>
<tr>
<td>GM</td>
<td>0.004</td>
<td>0.912</td>
</tr>
<tr>
<td>WM</td>
<td>0.080</td>
<td>0.022</td>
</tr>
<tr>
<td></td>
<td>GHMBRF</td>
<td>PV–MAP</td>
</tr>
<tr>
<td></td>
<td>CSF</td>
<td>GM</td>
</tr>
<tr>
<td>CSF</td>
<td>0.899</td>
<td>0.044</td>
</tr>
<tr>
<td>GM</td>
<td>0.012</td>
<td>0.889</td>
</tr>
<tr>
<td>WM</td>
<td>0.082</td>
<td>0.060</td>
</tr>
</tbody>
</table>

Table 6
Confusion matrices between the ground truth and the classification results obtained by the AGSM algorithm and the three other algorithms for a noisy (9% noise) brain MRI dataset with 0% of in-homogeneity (9N0RF).

<table>
<thead>
<tr>
<th></th>
<th>$l_{cf}$</th>
<th>$l_{li}$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>AGSM</td>
<td>SM</td>
</tr>
<tr>
<td></td>
<td>CSF</td>
<td>GM</td>
</tr>
<tr>
<td>CSF</td>
<td>0.889</td>
<td>0.070</td>
</tr>
<tr>
<td>GM</td>
<td>0.054</td>
<td>0.909</td>
</tr>
<tr>
<td>WM</td>
<td>0.050</td>
<td>0.014</td>
</tr>
<tr>
<td></td>
<td>GHMBRF</td>
<td>PV–MAP</td>
</tr>
<tr>
<td></td>
<td>CSF</td>
<td>GM</td>
</tr>
<tr>
<td>CSF</td>
<td>0.881</td>
<td>0.066</td>
</tr>
<tr>
<td>GM</td>
<td>0.086</td>
<td>0.899</td>
</tr>
<tr>
<td>WM</td>
<td>0.027</td>
<td>0.028</td>
</tr>
</tbody>
</table>
boundaries, should be produced. The splitting step should preserve these small homogeneous regions by avoiding assigning them to larger regions, since this involves a loss of detail that cannot be recovered by the merging step.

In order to ensure that the above two explanations are reasonable, experiments by using region size restrictions in order to stop the splitting procedure were conducted.

The proposed method can be used in morphometric analysis by extracting informative characteristics like volumes and shapes from cortical and sub-cortical structures in large datasets. In the clinic, these features have the potential to be used to evaluate the condition of a subject or in the planning of brain surgery. In neuroscience research, statistics derived from the segmentations of control and experimental groups can be used to identify structural differences between them. In the context of disease studies, such differences can lead to the identification of new pathological biomarkers. In clinical applications, the segmentation of brains with anatomical deviations from those commonly observed within a homogeneous population is of particular interest. One example is provided by brain tumors, since delineation of

---

**Fig. 10.** Distance based similarity measures for a brain MRI dataset with 5% noise: (a) $J_{Cd}$, computed for all algorithms, (b) intensity based similarity measure $J_{Ci}$ computed for all algorithms.

**Fig. 11.** A characteristic real pathological case of a compact brain tumor. (a) Examples of volume cross sections along the three main axes, (b) 3D visualization of the $T_1$ brain MRI dataset, (c) 3D visualization of the brain tumor ground truth and (d) 3D visualization of the tumor segmentation result obtained by the AGSM algorithm.
the tumor and of any surrounding edema is often critical for treatment planning.

7. Conclusions

A hybrid split–merge method (AGSM) for volume segmentation is proposed in this paper. The method uses both the data value similarity and the geometrical characteristics in order to segment the entire volume. During the splitting step, several splitting strategies are examined and the most appropriate is activated. The choice of the maximal homogeneity axis allows the implementation of the optimal region splitting procedure which is complemented by a region merging procedure based on statistical region data value similarity and geometrical proximity. This, together with the use of rich splitting strategies, enables good region segmentation that fits well to the rich geometry of the MRI dataset regions. AGSM has been tested using simulated clinical brain MRI volume datasets. The segmentation results on MRI volumes indicate that AGSM provides better segmentation accuracy when compared to the state of the art 3D segmentation techniques.

Conflict of interest statement

None declared.

References