Histogram-based gravitational optimization algorithm on single MR modality for automatic brain lesion detection and segmentation

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ABSTRACT

Magnetic resonance imaging (MRI) is a very effective medical imaging technique for the clinical diagnosis and monitoring of neurological disorders. Because of intensity similarities between brain lesions and normal tissues, multispectral MRI modalities are usually applied for brain lesion detection. However, the time and cost restrictions for collecting multi-spectral MRI, and the issue of possible errors from registering multiple MR images necessitate developing an automatic lesion detection approach that can detect lesions using a single anatomical MRI modality. In this paper, an automatic algorithm for brain stroke and tumor lesion detection and segmentation using single-spectral MRI is presented. The proposed algorithm, called histogram-based gravitational optimization algorithm (HGOA), is a novel intensity-based segmentation technique, which applies enhanced gravitational optimization algorithm on histogram analysis results. The mathematical descriptions as well as the convergence criteria of the developed optimization algorithm are presented in detail. Using this algorithm, brain is segmented into different number of regions, which will be labeled as lesion or healthy. Here, the ischemic stroke lesions and tumor lesions are segmented with 91.5% and 88.1% accuracy, respectively.

1. Introduction

The detection and segmentation of brain tumor and stroke lesions in medical images have a great influence on clinical diagnosis, predicting prognosis, and treatment of these ailments (Shen, Sandham, Granat, & Sterr, 2005). Additionally, it is beneficial for general modeling of pathological brains and the anatomical construction of brain atlases (Toga, Thompson, Mega, Narr, & Blanton, 2001). The detailed information about the location and volume of brain lesions is essential to number of researches in this field, such as identifying chronic functional deficits, or sleep problem analysis of stroke patients (Shen et al., 2005).

Among the different medical imaging techniques, magnetic resonance image (MRI) is the most widely used because it is a non-invasive procedure, which unlike other medical imaging techniques enables the differentiation of soft tissues with high resolution. Another advantage of MRI is that it produces multiple images of the same tissue with different contrast visualization via the application of different image acquisition protocols and parameters (Mortazavi, Kouzani, & Soltanian-Zadeh, 2011). These multiple imaging modalities provide additional useful anatomical information for the same tissue. Complementary information from different modalities helps researchers study the brain pathology more precisely.

Brain lesion detection and segmentation can happen either manually or automatically. Manual segmentation is very expensive, time consuming, and generally suffers from the lack of permanent availability, reliability and reproducibility (Kabir, Dojat, Scherrer, Forbes, & Garbay, 2007; Shen et al., 2005). Therefore, an effective automatic brain lesion segmentation algorithm is clinically beneficial and desirable. Although there are several segmentation methods such as thresholding (Lemieux, Krakow, & Woermann, 1999), region growing (Tang et al., 2000), and clustering (Liew & Yan, 2003; Pham & Prince, 1999; Van Leemput, Maes, Vandermeulen, & Suetens, 1999; Zhang & Chen, 2004), they are not easily applicable on the brain lesion identification domain. The reason for this is the intensity similarities between brain lesions and some normal tissues, which can result in confusion within the algorithm. For example, in T1-weighted MR images, a stroke lesion has similar intensities to those of gray matter (GM) or cerebrospinal fluid (CSF) (Shen et al., 2005). In order to overcome this problem, many researchers use multi-spectral MR images for lesion identification (Achiron, Gicquel, Miron, & Faibel, 2002; Alfano et al., 2000; Anbeek, Vincken, Van Bochove, Van Osch, &
van der Grond, 2005; Clark et al., 1998; Datta et al., 2006; Mohamed et al., 2001; Sajja et al., 2006; Udupa et al., 1997; Van Leemput, Maes, Vandermeulen, Colchester, & Suetsens, 2001; Zijdenbos, Dawant, Margolin, & Palmer, 1994). However, applying multi-spectral MR images has three main difficulties (Kabir et al., 2007). Firstly, acquiring such data is not always feasible due to patient condition severity and time importance. Secondly, collection of multi-spectral MR images is expensive. And thirdly, multimodal MRI data suffers from inconsistency and misalignment, which requires image registration and bias correction prior to applying the segmentation algorithm (Lemieux et al., 1999). Note that, any inaccuracy in registration or bias correction stages will directly affect the precision of the lesion segmentation. Due to of these limitations, detection and segmentation of the brain lesion based on single anatomical MR modality is necessary and important.

In this paper, we propose a new algorithm called Histogram-based Gravitational Optimization Algorithm (HGOGA), which is based on brain histogram analysis and an enhanced gravitational optimization algorithm. The algorithm is implemented for brain tumor and stroke lesion detection and segmentation. Diffusion-weighted images (DWI) are used for stroke lesion analysis and T1-weighted (T1-w) images are used for tumor lesion investigation. It is important to consider that in previous studies, one method is applied for lesion detection and a different method is used for lesion segmentation, but in this paper, a single algorithm is used for lesion detection and segmentation at the same time.

The proposed algorithm begins with three main stages the result of which is the generation of several brain segments. These stages applied are: firstly, application of a weighted average technique on the brain histogram; secondly, convolution of a rectangular window with the histogram maximum bars; and thirdly, connection of the cutoff borders after thresholding. Once these are done, application of an enhanced optimization algorithm – N-dimensional Gravitational Optimization Algorithm (NGOA) – results in the desired number of brain segments is achieved. Intensity widths of the generated segments on the brain histogram are used for lesion detection and segmentation. Four criteria – sensitivity, specificity, accuracy, and similarity index – are applied to evaluate the algorithm performance.

The N-dimensional gravitational optimization algorithm is based on the principle of gravitational fields. It is motivated by the idea of gravitational forces between several masses and Newtonian laws of motion (Hsiao, Chuang, Jiang, & Chien, 2005). The objective function is a non-linear function of variables, which are called masses and defined based on brain image histogram analysis. The value of the objective function determines the movements and new locations of the masses. The masses are the length of the averaging window, the length of a rectangular convolution window, and the threshold of cutoff borders. The algorithm is iterated until a predefined iteration number or convergence is met.

1.1. Related work

Most of the lesion segmentation techniques discussed and reported in the literature (Corso, Sharon, & Yuille, 2006; Cuadra et al., 2004; Dou, Ruan, Chen, Bloyet, & Constats, 2007; Han et al., 2006; Hevia Montiel et al., 2008; Hsiao et al., 2005; Jacobs et al., 2000; Kennedy et al., 2010; Khotanlou, Colliot, & Bloch, 2007; Lefohn, Cates, & Whitaker, 2003; Li & Tian, 2003; Li, Tian, Li, & Dai, 2004; Mah, Jager, Kennard, Husain, & Nachev, 2010; Martel, Allder, Delay, Morgan, & Moody, 1999; Moon, Bullitt, Van Leemput, & Gerig, 2002; Moonis, Liu, Udupa, & Hackney, 2002; Mujumdar, Varma, & Kishore, 2012; Prakash, Gupta, Jianbo, & Nowinski, 2008; Prastawa, Bullitt, Ho, & Gerig, 2004; Shen, Szameitat, & Sterr, 2007; Soltanian-Zadeh et al., 2003; Srivastava et al., 2005; Stamatakis & Tyler, 2005) have a few main limitations. These limitations can be concisely listed as: reliance on multi-spectral MRI (Jacobs et al., 2000; Soltanian-Zadeh et al., 2003), dependencies on preprocessing for bias-correction, or local or global registration of brain images to an anatomical atlas (Jacobs et al., 2000; Martel et al., 1999; Soltanian-Zadeh et al., 2003), requiring conformances to the initial assumption such as number of tissue classes (Han et al., 2006; Li et al., 2004), dependency on high resolution and low noise data (Hevia Montiel et al., 2008), and not being fully automatic (Kennedy et al., 2010; Li & Tian, 2003).

Several studies have addressed the brain lesion segmentation using single-spectral MR images (Corso et al., 2006; Cuadra et al., 2004; Dou et al., 2007; Hevia Montiel et al., 2008; Kennedy et al., 2010; Khotanlou et al., 2007; Li & Tian, 2003; Mah et al., 2010; Moon et al., 2002; Mujumdar et al., 2012; Prakash et al., 2008; Prastawa et al., 2004; Shen et al., 2007; Srivastava et al., 2005; Stamatakis & Tyler, 2005). Cuadra et al. (2004) used a priori lesion growth models in order to segment large brain tumors in T1-weighted images. The disadvantage of this method is that it is semi-automatic and requires a seed voxel within the tumor to be chosen manually. In addition, anatomical and biological knowledge of tumor growth is needed to select the seed appropriately.

Kennedy et al. (2010) presented a computational system called WebParc that measures the stroke lesion volume and provides the location information with respect to canonical forebrain neural systems using DWI modality. WebParc is implemented in the template registration style of localization analysis, and it is a data management system that segments the lesion manually with the clinician help. Afterward, it extracts the lesion information with respect to a set of co-registered anatomical templates of detailed brain structures. The setback of this system is that the lesion is segmented manually. Moreover, it depends on registration and anatomical templates.

Mah et al. (2010) introduced a simple unsupervised lesion segmentation algorithm based on Zeta using DWI images. Zeta is a recently proposed general measure of statistical abnormality, i.e., an abnormality score. The algorithm identifies the parameters of lesions within a brain image using a reference set of normal brain images. To determine the abnormality of a single image, it is compared to the k instances within the reference set that resembles it most closely. The drawback of this method is that the first step in Zeta segmentation relies on the image registration, which is the drawback of most voxel-wise algorithms. Moreover, Zeta requires a set of normal images to use as a standard reference. In addition, the Zeta abnormality score is a continuous variable with no a priori criterion on which one could discretize it.

Mujumdar et al. (2012) applied combined information from DWI-$b = 2000$, DWI-$b = 1000$ and the apparent diffusion coefficient (ADC) map to segment stroke lesions. Regarding the fact that DWI with higher $b$-values ($b = 2000$) provides improved sensitivity, higher conspicuity and reduced artifacts, it improves the detectability of smallest infarcts than conventional DWI-$b = 1000$. However, in most cases, DWI with higher $b$-values ($b = 2000$) is not available and it causes an impactful restriction.

Hevia Montiel et al. (2008) segmented the stroke lesions applying nonparametric density estimation based on mean shift algorithm and edge confidence map using DWI images. Briefly, the edge confidence map is computed from the data to be segmented. Afterward, filtering happens by applying a weighted mean shift procedure; and subsequently, region adjacency analysis, transitive closure operations, and pruning are used to segment stroke lesion. The drawback of this method is its inability to accurately handle low resolution and noisy data, particularly for the small-sized lesions.

Stamatakis and Tyler (2005) presented a statistical method to identify brain abnormalities using T1-weighted images. Every
image is compared to a normal control group and the detected structure differences between the image and the control group is identified as an abnormality. Srivastava et al. (2005) used a similar statistical approach to detect focal cortical dysplastic lesions from a lesion-specific feature map using T1-weighted images. However, the disadvantage of the above-mentioned methods is that the choice of a control group (e.g., group size) can affect segmentation results (Shen et al., 2007). In addition, the test data and the control group should be prepared using the same scanner machine, same parameters and coils, otherwise it causes further bias.

Li and Tian (2003) presented a multi-stage process for stroke lesion segmentation on DWI images. The process consists of image preprocessing, global and local registration between the anatomical brain atlas and the patient, and finally segmenting stroke lesion based on region splitting and merging and multi-scale adaptive statistical classification. The drawback of this method is that it relies on the registration, and also is computationally expensive.

1.2. Contributions

Most of the methods discussed and reported in brain lesion segmentation suffer from dependencies on multi-spectral MRI data (Jacobs et al., 2000; Soltanian-Zadeh et al., 2003), multi-scale classification (Han et al., 2006; Li et al., 2004), local or global registration (Han et al., 2006), and high-resolution and non-noisy data (Li et al., 2004; Martel et al., 1999; Mujumdar et al., 2012; Soltanian-Zadeh et al., 2003). Other limitations are high computational complexity and not being fully automated (Kennedy et al., 2010; Li & Tian, 2003). Likewise, applying a single method for lesion detection and segmentation is missed. To address the above-mentioned shortcomings, in this paper, we propose HGOA, which is based on applying enhanced gravitational optimization algorithm on brain histogram analysis results. One of the contributions of our proposed algorithm is that it is independent of atlas registration, control groups, and prior anatomical knowledge. The other contribution is its computational efficiency. It applies the same algorithm for lesion detection and segmentation. Furthermore, it uses single modality MRI. Since collection of multi-spectral MR images is time and cost consuming, acquisition of just one MR modality is much more practical. As another noteworthy contribution, our method is fully automatic, no need for any help of a clinician or initialization. We also enhanced the gravitational optimization algorithm to extend it for N-dimension and decreased the possibility of masses being drawn into a local optimal solution.

Organization of the paper: Section 2 presents the system overview and evaluation criteria. The histogram-based gravitational optimization algorithm is explained in Section 3. In Section 4, data acquisition and experimental results are discussed. And finally, Section 5 concludes the paper.

2. System overview and system evaluation

In this study, stroke and tumor lesions are detected and segmented by applying a novel algorithm called “Histogram-based Gravitational Optimization Algorithm (HGOA)” using single modality MR images. This algorithm can be divided into two sections as “histogram-based brain segmentation algorithm” and “n-dimensional gravitational optimization algorithm”. The HGOA is summarized as follows:

- Select the desired number of brain segments.
- Select the number of initial generation and the iteration.
- Run n-dimensional gravitational optimization algorithm. The fitness value is defined as the squared difference between the desired number of segments and the achieved number of segments. There are three variables that influence the fitness value. These are the length of averaging window in step two, the length of convolution window in step four, and the threshold value in step five, which will be explained in the following section. The objective function of the optimization algorithm with respect to each single set of variables is calculated using result of histogram-based brain segmentation algorithm, which includes seven steps as following:

  Step 1: Calculate the image intensity histogram.
  Step 2: Apply a weighted averaging technique on the image histogram.
  Step 3: Extract the local maximum from the averaged image histogram.
  Step 4: Convolve a rectangular window with the intensity histogram peaks obtained from step 3.
  Step 5: Obtain the lower and the upper cutoff borders for all segments using a threshold value.
  Step 6: Connect the upper cutoff border of nth segment to the lower cutoff border of (n + 1)th segment proportionally to the distribution value of the calculated intensity histogram from step 4. (In this step the number of achieved segments is equal to the total number of low or up cutoff borders.)
  Step 7: Allocate a specific intensity value to each generated segment.

To evaluate the performance of the lesion segmentation algorithm, we require a standard to assess it with. Here the standard is the manual tracing of each lesion by a trained operator: this is considered the “gold standard” in the field (Han et al., 2006). What we have to determine is therefore the correspondence between two binary volume images. In line with established practices (Zijdenbos et al., 1994; Anbeek, Vincken, van Osch, Bisschops, & van der Grond, 2004), the following summary measures are used, where True Positives (TP) are voxels correctly identified as part of a lesion, True Negatives (TN) are voxels correctly identified as healthy, False Positives (FP) are voxels incorrectly identified as part of a lesion, and False Negatives (FN) are voxels incorrectly identified as healthy.

\[
\text{Sensitivity} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}} \times 100\% \\
\text{Specificity} = \frac{\text{True Negatives}}{\text{True Negatives} + \text{False Positives}} \times 100\% \\
\text{Accuracy} = \frac{\text{True Positives} + \text{True Negatives}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \times 100\% \\
\text{Similarity Index} = \frac{2(\text{True Positives})}{2(\text{True Positives}) + \text{False Positives} + \text{False Negatives}} \times 100\%
\]

3. Histogram-based gravitational optimization algorithm (HGOA)

As mentioned earlier, HGOA is separated into two parts as “histogram-based brain segmentation algorithm” and “n-dimensional gravitational optimization algorithm”. The histogram-based brain segmentation algorithm starts by building the image intensity histogram. It is assumed that the local maximums of the histogram are potentially representatives of various segments in the brain. Therefore, the number and the intensity value of the histogram local maximums can be related to the number and the center value of
of segments, respectively. Even though in MRI each pixel is actually a voxel, we will treat each pixel as belonging to one segment. The reasons for this assumption are computational simplicity as well as its practical medical use. Therefore, the distance from one local maximum to another one should be equally or proportionally divided between the two local maximums to cover the whole intensity range. If it is divided proportionally, then the local maximum value affects the width of each segment. Doing so, the brain can be segmented to the same number of segments as its histogram’s local maximums. However, if the desired number of brain segments is different from the total number of brain histogram’s local maximums, a modified optimization algorithm called \textit{n-dimensional gravitational optimization algorithm} helps to dynamically segment the brain into the desired number of segments. For this purpose, it is necessary to define an optimization process in which the objective function is created from the intensity histogram analysis. An optimization process is defined to minimize the difference between the achieved number of segments and the desired number of segments. The optimization process works based upon an iterative calculation of an objective function, which is created from histogram-based brain segmentation algorithm.

### 3.1. Histogram-based brain segmentation algorithm

The histogram-based brain segmentation algorithm can be described in seven steps as shown in Fig. 6 and detailed as follows:

\textit{Step 1:} The image intensity histogram is calculated. Let \(f\) be a given image represented as a matrix of integer pixel intensities ranging from 0 to \(L - 1\). \(L\) is the number of possible intensity values, often 256. Let \(H[n]\) denote the normalized histogram of \(f\) with a bin for each possible intensity (Gonzalez & Woods, 2008). So

\[
H[n] = \frac{\text{number of pixels with intensity } n}{\text{total number of pixels}} \quad n = 0, 1, \ldots, L - 1
\]

(5)

Noise reduction is an important step to increase image quality and to improve the performance of quantitative imaging analysis tasks. A low pass Gaussian filter is applied for noise removal. Fig. 1 shows one example of histogram of a normalized and denoised DWI image.

\textit{Step 2:} In order to smooth the histogram \(H[n]\), local weighted averaging technique is applied over the histogram using Eq. (6).

\[
\overline{H}[n] = \frac{\sum_{i \in G} w_i \cdot H[n_i]}{\sum_{i \in G} w_i}, \quad H[n_i] = H[n] / \text{bin width}
\]

(6)

where \(H[n_i]\) is the histogram distribution value of \(i\)th bin, \(w_i\) is the weight corresponding to the \(i\)th bin, and \(G\) is the length of averaging window. \(w_i\) is a window centered at the \(i\)th pixel intensity for the \(i\)th element, and \(H[n_i]\) is local average value of the histogram. It is obvious the greater the \(G\), the smoother the averaged histogram will be. Fig. 2 shows the average image histogram of Fig. 1 for different values of \(G\). This part helps to control the number of local maximums and local minimums of the intensity histogram.

\textit{Step 3:} The local maximums of smoothed histogram are simply calculated by:

\[
H_{\max-\text{local}}[n] = \overline{H}[n] \cap \left( \overline{H}[n_{i+1}] < \overline{H}[n_i] < \overline{H}[n_{i-1}] \right)
\]

(7)

By applying Eq. (7) on Fig. 2 with \(G = 1\), the local maximums are derived as represented in Fig. 3.

\textit{Step 4:} A rectangular window is convolved with the histogram local maxima calculated from step 3. It is assumed that the number and intensity location of the local maxima of the histogram can be an indication of different segments in the brain image. Therefore, the key idea for brain image segmentation is to automatically grow a local maximum of the smoothed histogram toward its neighbor local maximum with respect to its amplitude, location, and anticipated number of brain segments. To do this, the convolution of \(H_{\max-\text{local}}[n]\) and a rectangular window is employed to connect the local maximums that are in each others neighborhood. Let \(W\) be the length of a rectangular window called \(Win\), and \(M\) be the length of \(H_{\max-\text{local}}[n]\), then \(Y[n]\) is the vector of length \(M + W - 1\) whose element is calculated by:

\[
Y[n] = Win[n] \cdot H_{\max-\text{local}}[n] = \sum_{j} Win[j] H_{\max-\text{local}}[n-j]
\]

(8)

The function \(Y[n]\) potentially has several discriminative segments. A narrower convolved window obviously produces higher number of segments, and vice versa, a wider convolved window results in lower number of segments. The application of Eq. (8) on Fig. 3 for a narrow and a wide window is depicted in Fig. 4. A narrower window obviously yields higher numbers of segments.

\textit{Step 5:} The lower and upper cutoff boundaries for all segments are obtained using a threshold value. In order to create continuous and discriminative segments, convolution of \(H_{\max-\text{local}}[n]\) and a rectangular window, \(Win\), was calculated, which result in \(Y[n]\). A threshold value as \(Thr\) controls the cutoff boundaries and removes the values smaller than the specified threshold value in the distribution. Also it helps to increase the flexibility of optimization method because changing the threshold level would change the number of remained segments. The cutoff boundaries of \(Y[n]\) are calculated as:

\[
\mathcal{x}_{\text{low}}[n] = \{n \cdot Y[n_{i+1}] > Thr \cap Y[n_{i-1}] < Thr\}
\]

(9)

\[
\mathcal{x}_{\text{high}}[n] = \{n \cdot Y[n_{i+1}] > Thr \cap Y[n_{i-1}] < Thr\}
\]

(10)

The number of the segments which are visible in histogram data is the same as the total number of lower or upper cutoff boundaries of the function \(Y[n]\). The value of the selected threshold has a great influence on the final number of created segments. The application of Eqs. (9) and (10) on the results illustrated in Fig. 4(a) is depicted.
in Fig. 5. Significant impact of specified threshold value on the number of generated segments is clearly seen. For example, \( Thr_2 \) only results in one segment, however, \( Thr_1 \) leads to four segments.

Step 6: The upper cutoff border of \( n \)th segment is connected to the lower cutoff border of \( (n+1) \)th segment based on Eq. (11). The reason is to cover all intensity bins and fill up the gaps between \( X_{\text{low}}(n) \) and \( X_{\text{low}}(n+1) \). Moreover, every pixel needs to be assigned to a single segment. In this step, upper cutoff border of one segment reaches to the lower cutoff border of the next one based on the following rule:

\[
X_{\text{up,new}}(sn) = X_{\text{low,new}}(sn-1) = X_{\text{up}}(sn) + \frac{(X_{\text{low,new}}(sn+1) - X_{\text{up,new}}(sn)) \times LM(sn)}{LM(sn) + LM(sn+1)}
\] (11)

where the \( sn \) is the index of the \( n \)th segment, \( LM(sn) \) is the local maximum amplitude of the segment \( sn \) and \( LM(sn+1) \) is the local maximum amplitude of the segment \( sn+1 \).

Step 7: One specific intensity value is specified for each generated segment. All intensity values between lower and upper cutoff borders of one segment would be represented by one intensity value named \( X_{\text{center}}(sn) \). The intensity of the \( sn \)th segment is defined as:

\[
X_{\text{center}}(sn) = \frac{X_{\text{low,new}}(sn) + X_{\text{up,new}}(sn)}{2}
\] (12)

The brain is segmented according to the number of generated segments, the intensity of center of the generated segment, and the cutoff borders of the generated segments. In order to automate this process, an optimization process is applied to minimize the difference between the achieved number of brain segments and the desired number of brain segments. The objective function is described as squared difference between the desired number of brain segments and the achieved number of brain segments. That is, if we need to segment the brain to four segments, the desired number of brain segments would be four. There are three variables that influence the objective function. These are the length of averaging window described in step two (\( G \)), the length of convolution window described in step four (\( W \)), and the threshold value described in step five (\( Thr \)). In next section, the \( n \)-dimensional gravitational optimization algorithm is explained.

3.2. \( N \)-dimensional Gravitational Optimization Algorithm (NGOA)

The second part of our proposed algorithm is an enhanced optimization algorithm called \( N \)-dimensional Gravitational Optimization Algorithm (NGOA). In order to achieve the desired number of brain segments, NGOA is applied on the results of histogram-based brain segmentation algorithm, which produce the objective function value. As it was explained before, if we need to segment the brain to four segments, the desired number of brain segments would be four.

NGOA utilizes the principles of gravitational field. Similar to the space gravitational algorithm (Hsiao et al., 2005), this algorithm is motivated by a simulation of several space masses to search for the heaviest mass. In this paper, we expand the search over the \( N \)-dimensional search space while in Hsiao et al. (2005) masses are modeled in 2-D. Some formula modifications are also considered. According to the Newton’s law of gravity, the strength of gravity existing between particles depends on the mass of particles and the gravitational acceleration rate and the inverse squared distance of the particle masses. Moreover, Einstein’s general theory of relativity confirms that the particle will be able to accelerate toward the heavy mass around it by the changes in the geometry of space–time. It means that if \( K \) particles with different masses are left in a free space, the particles have a tendency to move toward each other. While the heavy particles have slight movements, the movement of lighter particles is more than that of the heavier ones. So, the particles with lower mass move towards heavy ones and then keep exploring for other heavy particles around. This is very desirable in development of optimization algorithms.

The NGOA is initialized by random selection of \( K \) sets of \( N \)-dimensional masses and the iteration number. In other words, for the \( N \)-dimensional search space, the \( i \)th mass, can be represented by an \( N \)-dimensional vector \( x_i = [x_{1i}, x_{2i}, \ldots, x_{Ni}]^T \), the velocity by \( v_i = [v_{1i}, v_{2i}, \ldots, v_{Ni}]^T \), and acceleration vector by \( a_i = [a_{1i}, a_{2i}, \ldots, a_{Ni}]^T \). Therefore the total size of population is a \((K \times N)\) matrix.

In NGOA, the gravitational force on the \( i \)th object is calculated as:

\[
F_i = \frac{\prod_{j \neq i} m_j \cdot m_i \cdot (K \times x_{i}(t) - \sum_{j \neq i} x_{j}(t))}{\sum_{j \neq i} (x_{i} - x_{j})^2 + \cdots + (x_{Ni} - x_{Nj})^2} + \frac{1}{I_c}
\] (13)

where \( m_i \) is defined by the value of the inverse objective function value in a minimization problem, Eq. (14). In a maximization objective function, there is no need to invert the objective function value. In Eq. (14), \( I_c \) is added to denominator to prevent dividing by zero when the distance between masses becomes zero.

\[
m_i = \frac{1}{\text{ObjectiveFunctionValue}_{i} + I_c}
\] (14)

Following the calculation of the gravitational force on the \( i \)th mass, assuming a unit time length, the new speed of the object is:
The function \( \frac{\bar{F}_i/m_i}{\min \left( \frac{F_j}{m_j} \right)} \) represent the acceleration of mass \( X_i \), and the function \( \min \left( \frac{F_j}{m_j} \right) \) finds the minimum acceleration between all masses. Here, \( g \) is the gravity constant. Having the speed of the system at \( t+1 \) and the previous location of the \( i \)th mass at \( X_i(t) \), the position in the next iteration is adjusted by:

\[
X_i(t+1) = V(t+1) + X_i(t)
\]

It is worthy to mention that adding a random movement of the particles up to a specific iteration number adds a randomization factor and speeds up the convergence rate. This is done by adding a random vector to some of the worst variables. In addition, replacing the worst variables of each iteration with the best of all past generations moves the average of all point toward the optimal points.

In this application \( N = 3 \), which corresponds to the three variables derived from the histogram-based brain segmentation algorithm. These three variables are “\( G \)”, i.e., the length of the averaging window, “\( W \)”, i.e., the length of a rectangular convolution window \( (W_{\text{in}}) \), and \( \text{Thr} \), i.e., the threshold of cutoff borders as explained in Section 2. The Eqs. (13)-(16) are iteratively calculated until the objective function or the iteration number is met or the \( V_i(t+1) \) becomes lower than a threshold value.

### 3.3 Convergence of N-dimensional gravitational optimization algorithm

The initial population and the number of iterations are two factors that affect the convergence rate in the evolutionary optimization algorithms. In gravitational optimization algorithm the gravity constant, \( g \), controls the acceleration rate of the optimization. The higher value of \( g \), the higher the acceleration rate will be.

In spite of all of these considerations, one may not see the objective value satisfaction since the convergence rate is also dependent to the nature of the objective function. For example, strictly speaking, a second order function has only one local and global maximum. However, summing this function with a low value random function increases the number of local maximums or minimums. This idea is employed here to increase the chance of convergence. In other words, the convergence of the optimization algorithm is not guaranteed but adding a low value random function \( I_i \), with a growing rate \( g_r \), to the preprocessed function \( I_0 \), during the optimization process increases the convergence chance. The size of \( I_i \) will be the same as function \( I_0 \). The initial amplitude of the \( I_i \) is about one percent of \( I_0 \) values. This leads to a random but slight movement of local maximums along the intensity vector. These movements increase the chance of optimization convergence immensely. Fig. 7 illustrates convergence of n-dimensional gravitational optimization algorithm for several different runs. The whole procedure for brain lesion segmentation is summarized in Fig. 8.

### 4. Experimental results

#### 4.1 Image acquisition

For stroke lesion analysis, 12 subjects (6 with stroke and 6 healthy, female 5, mean age of 57.23, and age standard deviation of 10.9, less than one months after stroke) were scanned in this study. All MR images were attained on a 3T Siemens Avanto scanner (Germany). High-resolution 3-D T1-weighted brain MRI images were acquired, with the following characteristics: repetition time (TR) = 6000 ms, echo time (TE) = 128 ms, inversion time = 2200 ms, one acquisition, flip angle = 90°, field of view (FOV) = 71 mm, 46 slices, voxel size = 1 × 1 × 1 mm, and in-plane matrix = 256 × 256. Prior to scanning, all participants gave written informed consent according to the guidelines of the University of Miami Institutional Review Board. Participants were not paid for participation.

For tumor lesion analysis, 25 simulated data of brain T1 weighted-MRI images were acquired from neuroimaging tools and resources (NITRC) (Prastawa, Bullitt, & Gerig, 2009; http://www.Nitrc.Org/Projects/Tumorsim). The data was generated using cross-platform simulation software called TumorSim. Each subject’s MRI modality includes 181 slices.

The ground truth is prepared by labeling the ischemic stroke lesion by an expert. In this study the DWI sequences are used for this purpose. Cerebral ischemia pathophysiology involves variation of brain water volume even in its earliest steps, and DWI’s sensitivity to changes in tissue water content allows the detection of ischemic damage to the brain even within one hour after onset (David et al., 1999).

Here, sequences with stroke lesion and tumor lesion are called SL and TL, respectively. The sequences without lesion, which are healthy, are called HD for DWI and HT for T1-w.
4.2. Pre-processing

Preprocessing includes three parts: noise reduction using low pass filter (Gaussian filter), background segmentation, and normalization.

Noise Reduction: Gaussian Filter is a low-pass spatial frequency filter where all elements in this filter are weighted according to a Gaussian (Normal) distribution. Depending on the mean and the variance value \((\mu, \sigma)\), in the Gaussian distribution, the convolution of this kernel with the image results in a smooth image (Gonzalez et al., 2014).
Results of applying Gaussian filters with different variance values are represented in Figs. 9 and 15. $SL1$ and $TL1$ images are filtered out using the Gaussian filter using two different $\sigma$ that are depicted in Figs. 9(b, c) and 15(b, c), respectively. It is seen that higher value for sigma (such as $\sigma = 4$) blurs the image more; therefore, the low value for $\sigma$ is preferred.

Background Segmentation: Due to the prior knowledge of the background intensity values, which is zero here, it is necessary to exclude the background from the calculations wherever the histogram of the image is evaluated. The reason for doing this is that the background normally has much higher number of pixels than the brain. Using Gaussian filter in previous step helps to remove zero
Fig. 16. Tumor lesion TL1: dividing into two (a), three (b), and four (c) segments.

(a) (b) (c)

Fig. 17. Tumor lesion TL1: dividing into five (a), six (b), and twelve (c) segments.

(a) (b) (c)

Fig. 18. Tumor lesion TL2: original image (a), its dividing into four (b), and five (c) segments.

(a) (b) (c)

Fig. 19. Healthy HT1: original image (a), its dividing into four (b), and five (c) segments.

(a) (b) (c)

Fig. 20. Stroke lesion SL1: original image (a), extracted stroke lesion manually (b), extracted stroke lesion after three levels of segmentation (c), extracted stroke lesion after consistency verification (d).

(a) (b) (c) (d)
Fig. 21. Stroke lesion SL2: original image (a), extracted stroke lesion manually (b), extracted stroke lesion after three levels of segmentation (c), extracted stroke lesion after consistency verification (d).

Fig. 22. Tumor lesion TL1: original image (a), extracted tumor lesion manually (b), extracted tumor lesion after four levels of segmentation (c), extracted tumor lesion after consistency verification (d).

Fig. 23. Tumor lesion TL2: original image (a), extracted tumor lesion manually (b), extracted tumor lesion after four levels of segmentation (c), extracted tumor lesion after consistency verification (d).

Fig. 24. 3 level segmentation of SL1 (with stroke lesion): (a) intensity histogram after step 2, (b) the local maximums of the histogram in step 3, (c) results of step 4, (d) results of step 5 and 6.
intensity values inside the brain part. Therefore, background separation is done excluding pixels with zero intensity from intensity histogram.

Normalization: In order to achieve dynamic range consistency, we normalize the image using Eq. (17) Shapiro & Stockman, 2001.

\[
I_N = \frac{(I - \text{Min})}{(\text{Max} - \text{Min})}
\]

in which Max and Min are maximum and minimum of image intensity.

4.3. Brain MRI segmentation

Original image of SL1 (with stroke lesion) and TL1 (with tumor lesion) are represented in Figs. 9 and 15(a), respectively. The segmentation of SL1 and TL1 into two, three and four segments is depicted in Figs. 10 and 16, respectively. Correspondingly, Figs. 11 and 17 display the segmentation of SL1 and TL1 into five, six and twelve segments. It is seen that after two levels of segmentation the stroke lesion appears in the segmented image. In addition, after three levels of segmentation the tumor lesion appears in the segmented image. It is also met that in high levels of segmentation some of the segments are visually indiscriminative; however, there is still a clear appearance of the lesion in the segmented image.

Fig. 25. 4 level segmentation of SL1 (with stroke lesion): (a) intensity histogram after step 2, (b) the local maximums of the histogram in step 3, (c) results of step 4, (d) results of step 5 and 6.

Fig. 26. 5 level segmentation of SL1 (with stroke lesion): (a) intensity histogram after step 2, (b) the local maximums of the histogram in step 3, (c) results of step 4, (d) results of step 5 and 6.
Figs. 24–27 show the results of five steps of histogram-based brain segmentation algorithm for segmentation of DWI image of SL1 (with stroke lesion) into three, four, five, and twelve segments, correspondingly. In these diagrams, part (a) corresponds to image histogram after step 2. Part (b) shows the local maximums of the histogram in step 3. Part (c) illustrates the results of step 4. Part (d) displays the results of step 5 and 6. In all these figures, red dots are initial lower and upper cutoff borders, which are the results of step 5, and black dots are final lower and upper cutoff borders, which are the results of step 6.

4.4. Lesion detection

Comparing the positions of cutoff borders in part (d) of Figs. 24, 25, 28 and 29, it is clear that the last segment’s intensity width differs for healthy and lesion slices. The brain images, which include lesions are called lesion slices in this paper. After

Figs. 28 and 29 show the similar results for segmentation of DWI image of HD1 (healthy) into three and four segments. Parts (a–d) illustrate the same steps as mentioned above. Likewise, red dots are initial lower and upper cutoff borders, which are results of step 5, and black dots are final lower and upper cutoff borders, which are results of step 6.

Figs. 30 and 31 show the results of five steps of histogram-based brain segmentation algorithm for T1-w image of TL1 (with tumor lesion) for four and five levels of segmentation, respectively. Figs. 32 and 33 show the similar results for segmentation of T1-w image of HT1 (healthy) for four and five levels of segmentation, respectively. Parts (a–d) illustrate the results of the same steps as mentioned above. Likewise, red dots are initial lower and upper cutoff borders, which are results of step 5, and black dots are final lower and upper cutoff borders, which are results of step 6.
segmentation of the brain into $L$ segments, $L$th segment’s intensity width for lesion slices is much smaller than the healthy ones. The following criterion is defined as the first condition for stroke lesion slice detection:

$$X_{up\text{final}}(L)/C_0 X_{low\text{final}}(L) > q_{(18)}$$

Eq. (18) is interpreted as if $L$th segment’s width is less than $q$, the slice is considered as lesion slice and vice versa as healthy one. Here, $q$ is selected as 1.8.

Comparing Fig. 24(d) with 28(d), and also Fig. 25(d) with 29(d), one can see the obvious difference in movements of $(L/C_0)$th segment’s initial and final lower and upper cutoff borders in healthy and lesion slices. Initial and final cutoff borders are shown with red dots and black dots, respectively. After segmentation of the brain into $L$ segments, following criterion is defined as the second condition for stroke lesion slice detection:

$$[X_{up\text{final}}(L) - X_{low\text{final}}(L)] > P \times [X_{up\text{final}}(L-1) - X_{low\text{final}}(L-1)]_{(19)}$$

Eq. (19) is interpreted as if the intensity width of final segment is larger than $P$ times of the initial segment’s intensity width. Here, $P$ is selected as 1.2. The results show that for higher number of segments the movement of cut-off borders at segment $(L-1)$ is more discriminative than that of the lower number of segmentation. Therefore, for detection of the stroke lesion slice the high number (>5) of segmentation is preferred. For example, the brain can be

Fig. 29. 4 level segmentation of HD1 (healthy): (a) intensity histogram after step 2, (b) the local maximums of the histogram in step 3, (c) results of step 4, (d) results of step 5 and 6.

![Segmentation of HD1](image1)

Fig. 30. 4 level segmentation of TL1 (with tumor lesion): (a) intensity histogram after step 2, (b) the local maximums of the histogram in step 3, (c) results of step 4, (d) results of step 5 and 6.
segmented into eight or twelve segments. However, for lesion extraction from a detected lesion slice, the lower number (<5) of segmentation is more preferable since it covers wider intensity range around the stroke with a distributed intensity. Our experiments show that for stroke lesion extraction, $L = 3$ is satisfactory. All in all, for a complete stroke lesion detection and segmentation two separate segmentations are needed. Initially, the brain image is segmented into a high number of segments (here 12) and the slice including stroke lesion is detected. After stroke lesion detection, the brain image is segmented into three segments and the last segment is chosen to be the stroke lesion. Here, considering logical OR between condition one and condition two, slices including stroke lesion are detected with 94.7% accuracy.

For tumor slice detection, positions of cutoff borders in the second segment differ for healthy and lesion slices when brain is divided into four segments. The following criterion is defined as the condition for tumor lesion detection:

$$T = \{X_{\text{low}}(2) < q_1 \land X_{\text{up}}(2) < q_2\}$$

where $X_{\text{low}}(2)$ refers to the lower cutoff boundary of second segment, and $X_{\text{up}}(2)$ refers to the upper cutoff boundary of second segment. $q_1$ is specified as 2.25, and $q_2$ is specified as 4.85. The slices including tumor lesion are detected with 89.3% accuracy.

4.5. Lesion segmentation

After detection of slices including stroke lesion, the brain image is segmented into three segments or four segments. Because of high intensity of stroke lesion, the stroke normally is positioned in the last segment and therefore with extracting the last segment,
the stroke lesion can be extracted. The results show that the stroke lesion extracted with segmenting the brain into four segments has smaller area than the labeled lesion, and includes less false positives. However, lesions extracted with brain segmentation into three segments are closer to the labeled lesion but include more false positives. Performance of histogram-based gravitational optimization algorithm is quantified using four commonly used performance criteria: sensitivity, specificity, accuracy, and similarity index (as explained in Section 3), which is presented in Table 1.

For tumor lesion segmentation, the brain is segmented into four segments or five segments. Here, the tumor is positioned in the second segment. Therefore, tumor lesion can be segmented with extracting the second segment. Performance of the proposed algorithm in tumor lesion segmentation is presented in Table 1. Table 1 shows it is indicated that segmenting the brain into three segments for stroke lesion segmentation and four segments for tumor lesion segmentation provides us with higher accuracy. Results of the segmentation for two different stroke lesion samples and two different tumor lesion samples are shown in Figs. 20–23, correspondingly.

A consistency verification (CV) algorithm is used to remove the false positives (Haghighat, Aghagolzadeh, & Seyedarabi, 2011; Li, Manjunath, & Mitra, 1995). That is, we use a majority filter to alter the pixel labels that are not consistent with their neighbor labels in a certain neighborhood. For instance, if the center pixel of a window is labeled as tumor while the majority of the surrounding pixels are labeled as healthy, the center pixel’s label is simply switched to healthy. On the other hand, if a pixel inside the tumor area is mistakenly labeled as healthy, since the majority of the surrounding labels are tumor, it will switch to tumor. Here, consistency verification is applied in a 5 × 5 neighborhood window. The results of applying consistency verification algorithm are depicted in part (d) of Figs. 20–23. Furthermore, lesion segmentation accuracy after using consistency verification algorithm is presented in Table 1. Despite using consistency verification algorithm, we still have false positives, which reduce the recognition rate in the tumor lesion segmentation. As another limitation, our method cannot detect very small lesions (<1 cm³). Further algorithm refinement to address those drawbacks comes at the expense of computational cost. However, higher recognition rate can outweigh the additional computational burden in non-online procedures, which can be considered in future research.

5. Conclusion and future work

In this work, we present a novel method for stroke and tumor lesion detection and segmentation in the brain MR images. The method is called the histogram-based gravitational optimization algorithm (HGOA), which is based on applying enhanced gravitational optimization algorithm on histogram analysis results using single modality MR images. This algorithm uses histogram-based techniques to determine the initial set of brain segments, then applies a gravitational optimization based algorithm to reduce the number of segments, and finally uses thresholding to detect the tumor or stroke lesion. One of the main advantages of the proposed method is that it is independent of atlas registration, prior anatomical knowledge, or bias corrections that restrict the general application of many state-of-the-art methods. Reliance on atlas registration in other algorithms implies that their accuracy is
dependent on how well the atlas is constructed and how well the registration algorithm can register the test data to the atlas. Prior anatomical knowledge dependence implies that such algorithms must be trained to incorporate such information, which can lead to error. The need for bias correction in many other algorithms also introduces errors into the data to be analyzed, and thus adds inaccuracy and difficulties with consistency of the final results. As this algorithm has no reliance on any of these, it does not suffer from inherent errors.

The other contribution is in the use of single-spectral MRI. While using multi-spectral MR images address the intensity similarities between lesion and healthy tissues, in majority of practical clinical situations only one type of anatomical MR image is collected due to time and cost and patient situation limitations. In addition, use of multi-spectral data implies the need to ensure that each of the spectra must be properly registered. Failure to do the registration can result in misalignment of suspected lesions in the different spectra.

Our algorithm is also fully automatic and computationally light as it involves the application of a single algorithm for both lesion detection and segmentation. Additionally, despite some other methods’ need to have the initial assumptions, such as a given number of tissue classes or a multi-scale classification, our algorithm does not require any such information. This makes the proposed algorithm much more robust and more general than other methods.

The experimental results on both synthetic and real MR images show that the proposed algorithm, when applied by itself, provides an accuracy of almost 90% for stroke lesion and 85% for tumors. With the application of a consistency verification algorithm to reduce the false-positives, the accuracy rates climb to 91% and 88%, respectively. This compares well with other algorithms without suffering from some of the drawbacks as stated earlier. The accuracy and computational simplicity of our method make it suitable as an additional tool for the clinician. Moreover, the automated segmentation can be used to more consistently calculate the lesion volumes and track them in the treatment progress.

The major shortcoming of the proposed method is that it is incapable of detection of hardly visible lesions (<1 cm³). Another shortcoming is the presence of false positives, which affects the recognition rate, especially in the tumor lesion segmentation. As future work, we will focus on enhancing the performance of the method in case of very small lesions. Moreover, we will work on reduction of false positives, beyond the use of the consistency verification algorithm. The capability of the proposed method in detection of other type of brain lesion such as lesions caused by injury and dementia will also be evaluated. Other MRI modalities, like FLAIR (fluid attenuated inversion recovery) or T2-weighted images, can be examined for the lesion detection purpose.

References


