Deep grey matter volumetry as a function of age using a semi-automatic qMRI algorithm

Yu, Hailong

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Thesis

DEEP GREY MATTER VOLUMETRY AS A FUNCTION OF AGE USING A
SEMI-AUTOMATIC QMRI ALGORITHM

by

HAILONG YU
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Approved by

First Reader
Hernán Jara, Ph.D.
Professor of Radiology
Adjunct Associate Professor of Biomedical Engineering

Second Reader
Osamu Sakai, M.D., Ph.D.
Professor of Radiology, Otolaryngology- Head and Neck, and Radiation Oncology
DEDICATION

I would like dedicate this work to my parents Congli Yu, Xinwen Zhang and Yanhe Bing. Thank you for always being there to support me through the whole process. I love you forever.
I would like extend my sincere gratitude to Dr. Hernán Jara for his guidance, support and patience. Without his help I would never have been able to complete this study. I would also like to show my appreciation to Dr. Osamu Sakai for all of his valuable time and advice.
DEEP GREY MATTER VOLUMETRY AS A FUNCTION OF AGE USING A SEMI-AUTOMATIC QMRI ALGORITHM

HAILONG YU

ABSTRACT

Quantitative Magnetic Resonance has become more and more accepted for clinical trial in many fields. This technique not only can generate qMRI maps (such as T1/T2/PD) but also can be used for further postprocessing including segmentation of brain and characterization of different brain tissue. Another main application of qMRI is to measure the volume of the brain tissue such as the deep Grey Matter (dGM). The deep grey matter serves as the brain’s “relay station” which receives and sends inputs between the cortical brain regions. An abnormal volume of the dGM is associated with certain diseases such as Fetal Alcohol Spectrum Disorders (FASD). The goal of this study is to investigate the effect of age on the volume change of the dGM using qMRI.

Thirteen patients (mean age= 26.7 years old and age range from 0.5 to 72.5 years old) underwent imaging at a 1.5T MR scanner. Axial images of the entire brain were acquired with the mixed Turbo Spin-echo (mixed -TSE) pulse sequence. The acquired mixed-TSE images were transferred in DICOM format image for further analysis using the MathCAD 2001i software (Mathsoft, Cambridge, MA). Quantitative T1 and T2-weighted MR images were generated. The image data sets were further segmented using the dual-space clustering segmentation. Then volume of the dGM matter was calculated using a pixel counting algorithm and the spectrum of the T1/T2/PD distribution were also generated. Afterwards, the dGM volume of each patient was calculated and plotted on
scatterplot. The mean volume of the dGM, standard deviation, and range were also calculated.

The result shows that volume of the dGM is $47.5 \pm 5.3$ml ($N=13$) which is consistent with former studies. The polynomial tendency line generated based on scatter plot shows that the volume of the dGM gradually increases with age at early age and reaches the maximum volume around the age of 20, and then it starts to decrease gradually in adulthood and drops much faster in elderly age. This result may help scientists to understand more about the aging of the brain and it can also be used to compare with the results from former studies using different techniques.
# TABLE OF CONTENTS

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>TITLE</td>
<td>i</td>
</tr>
<tr>
<td>COPYRIGHT PAGE</td>
<td>ii</td>
</tr>
<tr>
<td>READER APPROVAL PAGE</td>
<td>iii</td>
</tr>
<tr>
<td>DEDICATION</td>
<td>iv</td>
</tr>
<tr>
<td>ACKNOWLEDGMENTS</td>
<td>v</td>
</tr>
<tr>
<td>ABSTRACT</td>
<td>vi</td>
</tr>
<tr>
<td>TABLE OF CONTENTS</td>
<td>viii</td>
</tr>
<tr>
<td>LIST OF TABLES</td>
<td>x</td>
</tr>
<tr>
<td>LIST OF FIGURES</td>
<td>xi</td>
</tr>
<tr>
<td>LIST OF ABBREVIATIONS</td>
<td>xii</td>
</tr>
<tr>
<td>INTRODUCTION</td>
<td>1</td>
</tr>
<tr>
<td>METHODS</td>
<td>12</td>
</tr>
<tr>
<td>RESULTS</td>
<td>16</td>
</tr>
<tr>
<td>DISCUSSION</td>
<td>18</td>
</tr>
<tr>
<td>CONCLUSION</td>
<td>20</td>
</tr>
<tr>
<td>REFERENCES</td>
<td>21</td>
</tr>
</tbody>
</table>
LIST OF TABLES

<table>
<thead>
<tr>
<th>Table</th>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Relaxation time of different tissues at 1.5 T</td>
<td>4</td>
</tr>
<tr>
<td>2</td>
<td>Parameters of Mixed-TSE pulse sequence</td>
<td>13</td>
</tr>
<tr>
<td>3</td>
<td>Volumetry of the dGM in the function of age</td>
<td>16</td>
</tr>
</tbody>
</table>
## LIST OF FIGURES

<table>
<thead>
<tr>
<th>Figure</th>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Different weighted MRI images of the brain</td>
<td>6</td>
</tr>
<tr>
<td>2</td>
<td>Brain tissues segmentation using qMRI method</td>
<td>10</td>
</tr>
<tr>
<td>3</td>
<td>The principles of operation of dual-space clustering segmentation</td>
<td>15</td>
</tr>
<tr>
<td>4</td>
<td>Scatter Plot of the dGM volume changes in the function of age</td>
<td>17</td>
</tr>
<tr>
<td>5</td>
<td>Axial projection image of the dGM</td>
<td>17</td>
</tr>
<tr>
<td>6</td>
<td>Spectrum of PD/T1/T2 distributions</td>
<td>18</td>
</tr>
</tbody>
</table>
LIST OF ABBREVIATIONS

DGM ................................................................................................................ Deep Grey Matter
FASD ........................................................................................................ Fatal Alcohol Spectrum Disorders
FOV ............................................................................................................... Field of View
MRI ............................................................................................................ Magnetic Resonance Imaging
NMV .......................................................................................................... Net Magnetization Vector
PD .............................................................................................................. Proton Density
QMRI ............................................................... Quantitative Magnetic Resonance Imaging
RF ............................................................................................................. Radio Frequency
ROI ........................................................................................................... Region of Interest
TE ............................................................................................................. Time of Echo
TR ............................................................................................................. Time of Repetition
INTRODUCTION

Magnetic resonance imaging (MRI) is a nondestructive and noninvasive technique that can be used to acquire two-dimensional and three-dimensional images of human body. Unlike x-ray, computed tomography (CT), or positron emissions tomography all of which use ionizing radiation, MRI uses a strong magnetic field and radio frequencies instead. When an imaging subject is placed in a powerful static external magnetic field ($B_0$), all the spins of the protons starts to align with $B_0$. Then a series of time varying magnetic field (radio frequency pulse and gradient pulses) are applied which causes the spin of the protons to change. When returning to the equilibrium state caused by $B_0$, different protons will give up the absorbed RF energy and reach the equilibrium state at different rates. The echo signal, magnitude and phase of the energy released by a particular proton as it returns to equilibrium, is collected and mapped to produce an MR image.

In clinical MRI, the hydrogen nucleus is the MR active nucleus. The hydrogen nucleus contains a single proton which gives the hydrogen atom a relatively large magnetic moment. Besides, hydrogen is the most abundant atom in the body. It is most commonly found in the molecules of water (where two hydrogen atoms are arranged with on oxygen, $\text{H}_2\text{O}$) and fat (where hydrogen atoms are arranged with carbon and oxygen atoms). According to the laws of electromagnetism, the hydrogen nucleus contains one positively charged proton that spin, and when it moves, a magnetic field is induced around the hydrogen nucleus. Therefore, the hydrogen nucleus acts as a small magnet.
which has a north and a south pole of equal strength. The north/south pole axis of each nucleus is represented by a magnetic moment. In the absence of an applied magnetic field, the magnetic moments of the hydrogen nuclei are randomly orientated. When placed in a strong static external magnetic field (B₀), the magnetic moments of hydrogen nuclei align either parallel (spin-down) or anti-parallel (spin-up) with the magnetic field which were determined by the strength of the external magnetic field and the thermal energy level of the nuclei. The net magnetic moment of hydrogen produces a significant magnetic vector that is used in clinical MRI and it is called the net magnetization vector (NMV) which reflects the relative balance between spin-up and spin-down nuclei.

B₀ stands for the main strong static external magnetic field in which the imaging subject is placed in. After being exposed to the B₀, all the protons will spin with a specific angular momentum (ω₀) which is described by the Larmor Equation,

\[ \omega_0 = \gamma B_0 \]

Where \( \gamma \) is the gyromagnetic ratio unique to each element and it can express the relationship between the angular momentum and the magnetic moment of each MR active nucleus.

When a radio frequency (RF) pulse at exactly the Larmor frequency of hydrogen is applied, the resonance of hydrogen occurs. During this process, termed excitation, the spin-up nuclei absorbs enough energy and becomes the spin-down nuclei. The result of resonance is that the NMV moves out of alignment away from B₀. The angle to which the NMV moves out of alignment is called the flip angle. The magnitude of the flip angle depends upon the amplitude and duration of the RF pulse. During resonance all the
magnetic moments move to the same position one the precessional path and are then in phase. When a receiver coil is placed in the magnetic field, a voltage is induced in this receiver coil. MR signal is produced when coherent (in phase) magnetization cuts across the coil.

When the RF pulse is switched off, the NMV starts to realign with $B_0$. To do so, the hydrogen nuclei must give release the energy given to them by the RF pulse. This process is then called relaxation.

$T_1$ relaxation time is a measure of the promptness of a tissue to return to its longitudinal state of magnetic equilibrium, after removal from equilibrium with an RF pulse. It is caused by the nuclei giving up their energy to the surrounding environment or lattice. Therefore, $T_1$ is also known as the spin-lattice relaxation time. The rate of the exponential recovery is measured by $T_1$ relaxation time, which is the time it takes 63% of the longitudinal magnetization to recover in the tissue.

$T_2$ relaxation time is a measure of the promptness of a tissue to return to its null transverse state of magnetic equilibrium, after removal from equilibrium with a radiofrequency excitation pulse sequence. This equilibration process is caused by nuclei exchanging energy with neighboring nuclei. Hence, $T_2$ is also known as the spin-spin relaxation time. The equilibration of the transverse magnetization is also an exponential decay process. The rate of this process is measured by $T_2$ relaxation time which is the time it takes 63% of the transverse magnetization to be lost.

$T_2^*$ decay is the decay of the free induction decay signal following the RF excitation. It is faster than $T_2$ decay because it is a combination of $T_2$ decay itself
and the dephasing due to magnetic field inhomogeneities. Inhomogeneities are areas within the magnetic field that do not exactly match the external magnetic field strength. The relative acceleration and deceleration of a nucleus, due to the magnetic field inhomogeneities and differences in the precessional frequency in certain tissues, cause immediate dephasing of the NMV and produces free induction decay. This dephasing is predominantly responsible for T2* decay.

<table>
<thead>
<tr>
<th>Tissue</th>
<th>T1 (ms)</th>
<th>T2 (ms)</th>
</tr>
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<tbody>
<tr>
<td>Fat</td>
<td>250-300</td>
<td>160</td>
</tr>
<tr>
<td>liver</td>
<td>500-600</td>
<td>50</td>
</tr>
<tr>
<td>White matter</td>
<td>600-700</td>
<td>72</td>
</tr>
<tr>
<td>muscle</td>
<td>800-1000</td>
<td>40</td>
</tr>
<tr>
<td>Grey matter</td>
<td>900-1100</td>
<td>95</td>
</tr>
<tr>
<td>Water</td>
<td>3000</td>
<td>2000</td>
</tr>
<tr>
<td>CSF</td>
<td>4000</td>
<td>2400</td>
</tr>
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</table>

A pulse sequence is a series of radio frequency pulses, gradient application and intervening time periods. The RF pulses are applied for excitation and rephase purposes. The gradient pulses are applied to spatially encode signal. The intervening time periods refer to the time intervals between these various function. A basic spin echo experiment will consist of a single 90° radiofrequency pulse, the echo signal will be detected at time
TE (Time of Echo) and the experiment will be repeated at time TR (Time of Repetition) after the previous excitation.

One of the main advantages of MRI compared with other imaging modalities is the excellent soft tissue discrimination of the images. In order to demonstrate contrast between normal anatomical features and any pathology, we need to weigh image contrast towards one of the parameters and away from the others that affect the contrast of the images.

A T1-weighted image is one where the contrast depends predominantly on the differences in the T1 times between fat and water. To achieve T1-weighting, the TR must be short enough so that neither fat nor water has enough time to fully return to $B_0$ so that the differences of T1 times between fat and water can be demonstrated on the image. T1 weighted images are characterized by bright fat and dark water.

A T2-weighted imaging is one where the contrast mainly depends on the differences in the T2 times between fat and water. To achieve T2 weighting the TE must be long enough to give both fat and water time to decay otherwise the differences of T2 times between fat and water will not be demonstrated in the image. T2 weighted images are characterized by bright fat and dark water.

A proton density (PD) image is one where the difference in the numbers of protons per unit volume in the patient is the main determining factor in forming image contrast. When TR is very long and TE is very short, the effects of T1 and T2 contrast are minimized, therefore, the MR signal is directly proportional to the number of protons
present in each volume. Proton density weighted images are characterized by areas with high proton density (bright) and areas with low proton density (dark).

![Figure 1. Different weighted MRI images of the brain [2]](image)

For T1 weighted image, water is dark and fat is dark. For T2 weighted image, fat is bright and water is dark. For PD weighted image high proton density areas are bright and areas with low proton density are dark.

The qualities of the image are mainly determined by four main factors. The first factor is signal to noise ratio (SNR). Signal is the voltage induced in the receiver coil by the precession of the NMV in the transverse plane while the noise represents frequencies that exist randomly in space and time. Increasing the signal increase the SNR, while decreasing the signal decreases the SNR. The second factor determines the image quality is contrast to noise ratio (CNR). CNR is defined as the difference in the SNR between two adjacent areas. It is probably the most critical factor affecting image quality as it
directly determines the eye’s ability to distinguish areas of high signal from areas of low
signal. The third factor determines the image quality is spatial resolution. The spatial
resolution is the ability to distinguish between two points as separate and distinct and is
controlled by the voxel size. The voxel size is affected by slice thickness, FOV, and
number of pixels or matrix. Small voxels result in good spatial resolution, as small
structures can be easily differentiated. On the other hand, large voxels result in low
spatial resolution, as small structures are not resolved so well. The last factor is scan time.
The scan time is the time to complete data acquisition. It is very important in maintaining
image quality, as long scan time gives the patient more chance to remove during the
acquisition. Any movement of the patient will probably degrade the images. Ideally an
image should have high SNR, good spatial resolution and is acquired in a very short scan
time. However, this is rarely achievable as increasing one factor inevitably reduces one or
both of the other two. Therefore, it is very important that the users has full
understandings of all the parameters that affect the image quality and make trade-offs
when selecting parameters within a pulse sequence.

Conventionally acquired MR images are qualitative and contrast weighted. T1
and T2 weighted sequences form the core of most clinical protocol. Pathological
processes are therefore most often described in terms of T1 and T2 signal behavior, in
addition to contrast enhancement, anatomical location and morphological
characteristics.[3] In other words, conventional qualitative MRI focuses on qualitative
visual assessment of anatomy and disease processes rather than quantitative analysis. The
method to interpret the conventional MR images is to define gross extent of disease when
anatomic changes manifest as visibly detectable differences in signal intensity. However, if scan parameters and timings are not set optimally prior to scanning or if the patient is unable to cooperate throughout the entire length of a study, qualitative interpretation of the resulting directly acquired images suffers dramatically.

Quantitative Magnetic Resonance Imaging (qMRI) is a novel technique that follows the same physical principles and uses the same hardware equipment as conventional qualitative MRI. However, unlike conventional qualitative MRI, the goal of qMRI is the quantitative measurement of selected MR parameters, and the results are displayed in parameter maps (such as T1 mapping, T2 mapping and proton density mapping), where the local image intensity represents only the proton density and the relaxation times without bias from other parameters like field in homogeneities or variations of the receive coil sensitivity.[4] QMRI portrays information that is intrinsically more tissue-specific and in this way it can offer complementary medical information to conventional qualitative MRI. Besides, since qMRI are theoretically independent of experimental settings such as magnetic and radiofrequency field, inhomogeneity, receiver gain, and coil sensitivity, therefore the image data acquired from qMRI are comparable between different scanners, different institutions, and over differing points in time. [5]

Quantitative maps of T1, T2, and PD are products of qMRI. These data maps may be further processed using a wide variety of approaches for different clinical trial. Computer postprocessing of qMRI data is a natural next step in data interpretation and
may involve techniques such as segmentation, volumetry, structural analysis, and the generation of distribution histograms of T1/T2/PD.

Brain tissue segmentation and volume estimation of white matter, grey matter, and cerebrospinal fluid are very important in many neurological applications. For instance, it can be used to assess local and global brain atrophy that is present in diseases such as multiple sclerosis [6] and Alzheimer’s disease [7]. Most brain tissue segmentation methods are based on conventional contrast-weighted MR images. Although these images provide high anatomical detail, segmentation is complicated by contrast inhomogeneities and the arbitrary grey scale of the images. Besides, a variety of experimental parameters affect conventional MRI.[8] On the contrast, qMRI allows the measurements of physical tissue parameters such as the relaxation rates R1 (inverse relaxation time T1, 1/T) and R2 (1/T2) and the proton density. By using qMRI for tissue segmentation, the dependence on MR scanner hardware and setting is largely removed and it allows for segmentation based on physical tissue characteristics. [9]
Due to the advantage mentioned above, qMRI techniques are becoming more popular and acceptable for both clinical trial and experiment research. One of the main applications of qMRI is the segmentation of brain to characterize different types of tissue such as grey matter, white matter and cerebrospinal fluid (CSF) based on physical tissue properties.[9, 10] The second main application of qMRI is the volumetry of different tissues such as the volume of GM, WM, CSF, and cerebral blood in the brain [11, 12] as well as volume of the specific region of the brain, such as hippocampus and amygdala in severe depression.[13] Besides the brain tissues, qMRI is also applied to measure other organs, such as the liver and spleen.[14] Research on the analysis of craniofacial bone marrow volume [15] and the neovasculature volume in carotid atherosclerotic plaque[16]
using qMRI has already been studied. Some other application of qMRI includes the evaluation of structural changes and the assessment of cartilages status in patients with osteoarthritis patients.[17-19]

Grey matter is a major component of the central nervous system and it contains most of the brain’s neuronal cell bodies. It can also be divided into cortical grey matter distributed on the surface of the cerebrum and the deep grey matter (dGM) which is in the depths of the cerebrum. The dGM usually contains thalamus, hypothalamus, basal ganglia (caudate nucleus, putamen and globus pallidus) and claustrum. The dGM serves as the brain’s “relay station” which receives and sends inputs between cortical brain regions and the efficient communication of between different regions of the brain is essential for proper cognitive function.[20] The malfunction of the dGM could be associated with many diseases such multiple sclerosis (MS).[21-23] Studies suggested that the dGM involvement is associated with clinical progression in MS.[22] Significant volume reduction of the dGM can also be found in children with fetal alcohol spectrum disorders (FASD) which may be the key factor to understand alcohol-related brain injuries.[20]
METHODS

Subjects and MR imaging

This study included 13 patients who were referred to MRI for different clinical reasons. The mean age of the subjects was 35 with the age range from 0.5 to 72.5 years. The gender composition was 6 females and 7 males. All the 13 patients were examined under the protocol approved by the internal review board.

All the subjects underwent imaging at a 1.5T with a clinical MR scanner (Philips Intera; Philips Medical Systems of North America, Andover, MA). Standard quadrature body and head coil were used. Axial images of the entire brain were acquired with the mixed Turbo Spin-echo (Mixed TSE) pulse sequence.

Mixed Turbo Spin-echo (Mixed TSE) pulse sequence is a fast multislice quadruple time point qMRI pulse sequence that combines the principles of T1 weighting by inversion recovery and of T2 weighting by dual-echo sampling in a single acquisition. The mixed-TSE pulse sequence begins with a slice selective inversion pulse and has two inversion times (TI1 and TI2) and two effective echo times (TE1_{eff} and TE2_{eff}), thus generating four self-co-registered images per slice, each with different levels of T1 and T2 weighting. Hence four directly acquired images are generated for each slice. The directly acquired images can be processed to generate qMRI maps portraying the T1, T2 and secular-T2 distributions with the native spatial resolution and anatomic coverage of the directly acquired mixed-TSE scan. The pulse sequence interrogates two interleaved packages of slices sequentially in the same acquisition. The interslice gap of each
package is equal to the slice thickness, thus interslice cross talk artifacts are negligible.

The parameters of the mixed- TSE pulse sequence are listed in Table 2[24, 25].

Table 2. Parameters of Mixed-TSE pulse sequence[24]

<table>
<thead>
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<th>Parameter</th>
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<tr>
<td>Acquisition matrix</td>
<td>256×192</td>
</tr>
<tr>
<td>Voxel dimensions</td>
<td>0.94× 0.94 × 3.00</td>
</tr>
<tr>
<td>Interstice gap</td>
<td>Null</td>
</tr>
<tr>
<td>Number of slices</td>
<td>80</td>
</tr>
<tr>
<td>Effective echo time (ms)</td>
<td>TE1eff = 7.142 and TE2eff= 100</td>
</tr>
<tr>
<td>Repetition time (ms)</td>
<td>TR= 14,8882.18</td>
</tr>
<tr>
<td>Inversion times (ms)</td>
<td>TI1= 700 and TI2= 7441</td>
</tr>
<tr>
<td>Echo train lengths</td>
<td>1ETL= 18 (9 per echo)</td>
</tr>
<tr>
<td>Fat suppression</td>
<td>NO</td>
</tr>
<tr>
<td>Slice Thickness</td>
<td>SLTH= 3mm</td>
</tr>
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</table>

**Image processing and statistical analysis**

The acquired mixed-TSE images were transferred in DICOM format image for further analysis using the MathCad 2001i software (Mathsoft, Cambridge, MA). The identifying information of patients was removed. Then the quantitative T1 and T2-weighted MR images were generated. The image data sets were further segmented by the computer program that was designed by Dr. Jara using MathCad 2001i. During this process, windows of ROI were first chosen manually with a rectangular mask for each slide and then all the intracranial soft tissues were segmented using the dual-space clustering segmentation.[14]
Dual-space clustering segmentation (Figure 3) operates by interrogating each voxel in the data set to determine whether the voxel is contained within both a user predefined quantitative MR images space subvolume and a predefined anatomic space volume. This determination is made by using a graphic user interface in which the operator draws and ROI on a desired organ in a single section. The program then evaluates the entire set of quantitative MR imaging data and uses there data to segment the specified organ. [25]

In addition to the ROI specifications, there are three adjustable segmentation parameters that allow the operator to tailor the dual-space clustering segmentation and thus improve segmentation fidelity and volumetric assessment. The first parameter is the number of standard deviations relative to the mean T1, mean T2, and mean normalized proton density of the pixels in the graphic user interface-selected ROI. This single parameter effectively specifies the sizes of the nominal acceptance subvolumes in the quantitative MR imaging space in the T1, T2, and normalized proton density direction. The second adjustable parameter is the nominal cluster size in the anatomic space. The third parameter is the percentage acceptance cluster size in the anatomic space.[9]

After segmentation, the volume of dGM matter was calculated using a pixel-counting algorithm and histograms of the T1/T2/PD distribution were also generated. Afterwards, the dGM volume of each patient was calculated and plotted on scatterplot. The mean volume of dGM, standard deviation, and range were also calculated.
Figure 3. Principles of operation of dual-space clustering segmentation[14]

With dual-space segmentation, voxel are classified according to their clustering properties in both quantitative MR imaging space (left) and anatomic space (right). Left diagram illustrates the quantitative MR imaging space, in which each point corresponds to a voxel in the anatomic space. Voxels in the data set are interrogated for determination of whether they are contained both in a user predefined quantitative MR imaging space subvolume and within a predefined anatomic volume. This determination is made by using a graphic interface in which the operator draws an ROI on a desired organ in a single section and then the program evaluates the entire set of qMRI data and uses the data to segment the specified organ.
RESULTS

The volume of dGM of all the 13 subjects covering the age span of 0.5 to 72.5 years was calculated and the results were shown in Table 3. In addition, the tendency of the volumetry of the dGM in the function of age was also studied based on the scatter plot as shown in Figure 4. The axial projection images of one patient (age=27 years) is shown in Figure 5 and the spectrum of T1/T2/PD distributions of the same patient is shown in figure 6.

Table 3. Volumetry of dGM in the function of age

This table shows the volume of the dGM of 13 patients (average age = 26.68 years) which is 47.5 ± 5.3ml (minimum=37.36ml, maximum=55.36ml)

<table>
<thead>
<tr>
<th>case #</th>
<th>Age (years)</th>
<th>Volume (ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.5</td>
<td>37.36</td>
</tr>
<tr>
<td>2</td>
<td>0.6</td>
<td>44.63</td>
</tr>
<tr>
<td>3</td>
<td>4.2</td>
<td>44.05</td>
</tr>
<tr>
<td>4</td>
<td>9.1</td>
<td>53.5</td>
</tr>
<tr>
<td>5</td>
<td>11.4</td>
<td>49.4</td>
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<td>48.6</td>
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</tr>
<tr>
<td>12</td>
<td>56</td>
<td>43.94</td>
</tr>
<tr>
<td>13</td>
<td>72.5</td>
<td>43.21</td>
</tr>
</tbody>
</table>
Figure 4. Scatter Plot of dGM volume changes in the function of age

This figure shows the volume of the dGM changes in a polynomial tendency as the function of age with $R^2 = 0.3661$.

$$y = -0.0067x^2 + 0.4391x + 43.766$$

$R^2 = 0.3661$

Figure 5. Axial projection image of the dGM

Figure 5 on the left shows the axial projection image of a patient (age 27) with the dGM volume of 49.1 ml and total pixel number of 16625.
Figure 6. Spectrum of PD/T1/T2 distributions
This figure shows the spectrum of the PD/T1/T2/ADC distributions of the same patient as Figure 5.

DISCUSSION

The result shows the volume of dGM of 13 patients (average age = 26.68 years) the mean of which is 47.5 ± 5.3ml (Table 3) which is consistent with prior studies.[20] Further analysis reveals that the volumes of the dGM are well represented by a polynomial function (Figure 4). Volume of the dGM gradually increase with age in early ages and reach the maximum volume around the age of 20s then it starts to decrease
gradually in adulthood and reduces much faster in elderly age. It shows a weak correlation between the age and volume of the dGM ($R^2 = 0.3661$).

Former studies have shown that in early ages especially the first two years after birth, the volume of the GM increases dramatically in the early ages (149% volume increase for GM in the first year after birth), while the caudate increases 19% and the hippocampus increases 13% in the second year after birth.[26] Another study shows that throughout the adult life, volume loss of the GM appears to be a linear function, whereas the volume loss of WM most likely to be delayed until the middle adult life. [27] When it comes to the dGM, different structures in the dGM show different tendency and rate of changes. For instance, volume losses of thalamus, amygdala and caudate start to be seen around the ages of 20, however the volume loss of the hippocampus is not seen until the age around 40.[28] These prior studies may explain the reasons for the polynomial tendency of the dGM volume changes.

The main limitation for this study relates to the small number of subjects studied. Secondly, the process of semi-automated segmentation using the MathCad 2001i software is also a limitation to this study. This process required manual operation, which heavily depended on the operator’s knowledge and visual assessment. These manual steps included selection of the ROI and adjustments of the segmentation parameters based on inspection of the segmented images during the dual-space clustering segmentation.
CONCLUSION

This study has shown volume of the dGM in different subjects (47.5 ± 5.3ml) which are consistent with former studies. The changes of volume of the dGM show in a polynomial tendency in the function of age and it suggests a weak correlation between the age and volume of the dGM. This study may help scientists understand more about aging of the brain and it can also be used to compare with the results from prior studies using different techniques other than quantitative MRI.
REFERENCES


CURRICULUM VITAE

HAILONG YU

Year of Birth: 1986
Nationality: People’s Republic of China
Local address: NO.16 Clifton ST. Malden MA 02148
Phone number: 857-207-8685
Email: yuhl2011@bu.edu

Education

Sept.2011—Sept.2014 Master of Science in Bioimaging, Graduate School of Medicine Science, Boston University, USA
Sept. 2004—July 2010 Bachelor’s Degree of Medicine in Radiology, Bethune Medical School, Jilin University, China
Sept. 2001--July 2004 No.1 Senior High School, China

Research:

June. 2010 Bachelor’s Thesis: Cloning of smac gene and its overexpression effects on radiosensitivity of MCF-7 cells to X-rays

Oct.2010 – Jun 2011 Research Assistant & Internship at the Department of Radiation Oncology of Haigang Hospital in Qinhuangdao, China.

Experience:

2005--2009 Chairman of Hebei Clansmen Association in Jilin University.
Responsibility: Leading club monthly social activities and weekly academic coaching programs for 30 members.

Nov.2009 --Jan. 2010 Internship at the Department of Radiotherapy of the Second Hospital affiliated to Jilin University.
Responsibility: Assist the oncologists and medical physicists to prepare patient data and perform physical measurement and calibration.

Oct. 2008 Volunteer
Responsibility: Promote the knowledge of AIDS and the programs to stop dangers of drugs.