

Brain Image Analysis: The RAVENS way

Rama Krishna K

Department of Computer Science and Engineering,
Presidency University, Bangalore

Abstract

This paper presents brain image analysis of magnetic resonance images (MRIs) to detect the defected regions (atrophy) in the brain via Hammer image registration methodology. To start with, MR brain images can be registered via HAMMER (Hierarchical Attribute Matching Mechanism for Elastic Registration) methodology. The registered images are then used to create RAVENS (regional analysis of volumes examined in normalized space) maps. Finally, RAVENS maps hold the volumes of various tissues both at the interior and at the globalized level. Ravens maps for of brain tissues namely GM (Grey Matter), WM (White Matter) and CSF (cerebrospinal fluid) are investigated by using statistical parametric mapping tool (SPM) using MATLAB platform. The proposed strategy precisely identified the atrophy regions in brain scan. The identified atrophy regions are useful for further investigation to diagnose the brain related disorders diseases.

Keywords: MRIs, Image registration, Atrophy, HAMMER, RAVENS MAPS, SPM

INTRODUCTION

Aligning of two or more images of the same scenery clicked at dissimilar instances, from dissimilar views & by various sensors [1]. Image registration maps couple of images- the target and source ones, also called as referenced and sensed pictures, respectively as shown in Fig.1. The reference image is called template image and the sensed image is the input brain subject image, which is to be registered/normalized. Image registration, an important phase in many

image analysis functionalities in which the resultant information is obtained from the composition of many data sources like in segmentation of images, v detection of variance, and restoration of images. Typically, the applications of Image registration are related to medicine such as detecting growth of tumour. In remote sensing, change detection, forecasting of weather, creating High-resolution images, combining information into geographic information systems, [2, 3].

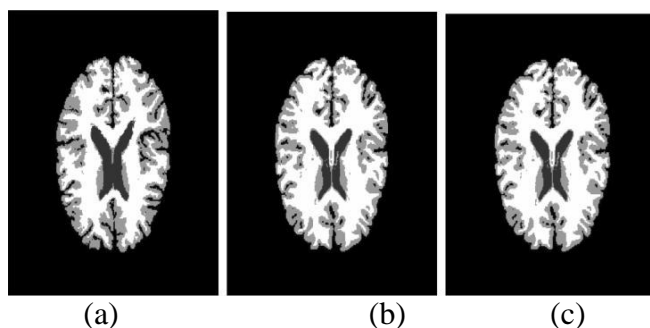


Fig. 1: Image registration process (a) Input MRI Scan, (b) Template image and (c) Target image

Magnetic resonance (MR) imaging has been applied extensively in many studies

of brain. MR brain images termed as inputs/subjects can be explored to detect the atrophy, i.e. which is nothing but affected region in the brain. Many studies were based on an initial description of relative quantity of ROIs (regions of interest), which then followed by volumes measurement of tissues with in an individual ROI. The above strategy is very inefficient, since it needs the manual description of many ROIs on many subjects. Also, the crucial constraint of ROI-based investigation is, ROIs should be described initially, to reserve a volumetric quantity. In general, ROIs cannot be described at an initial stages brain image analysis i.e, which regions of brain might have been affected due to disorders.

In proposed strategy, the MR (magnetic resonance) brain images registration is carried out with HAMMER methodology. The obtained regional analysis of volumes examined in normalized space (RAVENS) maps for three brain tissues namely Grey Matter, White Matter and cerebrospinal fluid are further investigated using MATLAB's statistical parametric mapping (SPM) tool .

METHODOLOGY

About Hammer

In proposed strategy, image registration is carried out via an automated Image registration methodology termed as HAMMER. The two crucial aspects of major HAMMER method are, Firstly, it makes use of attribute vector [4], which is nothing but a geometric moment invariants (GMIs) set that are described on every voxel in image to replicate the core structure at various levels. An attribute vector, if informative, will differentiate between disparate aspects of image, which aids in creating structural correspondences in the deformation methodology; reduction of local minima is also beneficial. This is a

vital deviancy in HAMMER methodology, compared to other volumetric deformation methods, which are generally based on exploiting image resemblance. Secondly, to elude being stuck by local minima, HAMMER practices a successive approximation of the energy function being enhanced by lower dimensional smooth energy functions, which are constructed to have considerably fewer local minima. This is accomplished by hierarchically selecting the driving characteristics that have dissimilar attribute vectors, thus significantly decreasing ambiguity in discovering correspondence. On the other hand, the HAMMER registration methodology stringently involves pre-segmentation of brain tissues GM (Grey Matter), WM (White Matter) and CSF (cerebrospinal fluid), subsequently the attribute vectors are then applied to hierarchically map the respective sets of sections whose detail description are provided by segmented images. HAMMER also needs both the input and template images to be compatible.

Hammer Procedure

There are two key phases in the brain warping/normalizing algorithm. Phase-1 deals with removal of skull of the brain and tissues will be labelled to Grey Matter (GM), White Matter (WM) and cerebrospinal fluid (CSF), as mentioned in [5]. Phase-II deals with the usage of the fully automatic HAMMER algorithm to register and normalize/warp the input brain image scans.

Step 1: Convert the input subject to the space of the model by the usage of a global affine transformation that is given by a matrix of the regular moments of the subject [6].

Step 2: Calculate an attribute vector for every voxel in the input and model images.

Step 3: Define driving boundary voxels set $\{ Y_i \mid 1 \leq i \leq N_s \}$ in the input image, built on their attribute vectors.

Step 4: Hierarchically choose boundary voxels set in the model image, $\{ X_i \mid 1 \leq i \leq NT \}$ for driving the deformation of the model image.

Step 5: For every input subject, driving voxel Y_i , examine in its neighborhood for an exiled template driving voxel $h(X_j)$ with the most alike attribute vector. If the amount of resemblance between the input subject driving voxel Y_i and the model driving voxel X_j is beyond a threshold t_{Voxels} , then a power is created on the deformed model driving voxel $h(X_j)$, in the direction from $h(X_j)$, to Y_i .

Step 6: For every model/template driving voxel X_i , examine in its neighborhood for every input subject voxels with same attribute vectors. Then, cautiously deform the sub-volume of the voxel X_i to every alike subject voxel that has been established, and join the resemblance degrees of all voxels in the sub-volume. Lastly, this sub-volume deformed to a subject voxel with the leading resemblance degree, if this biggest resemblance degree is beyond a definite threshold (t_{Volume}). In addition, if there exists powers created on the model/template driving voxel X_i from the input subject driving voxels, which are found in step 5, then this sub-volume will also be deformed under these powers.

Step 7: Hierarchically improve the displacement fields using internal and external affine transformations that are computed from the deformations in the model/template driving voxels.

Step 8: Enhance the displacement fields

using the levelness constraint.

Step 9: If the registering methodology is merged, then stop. Otherwise, go to step 4.

RAVENS MAPS GENERATION

Statistical analysis of anatomical maps in a stereotaxic space has been revealed as a beneficial tool in population-based researches for quantifying local anatomical variances or variations, without the need of earlier guessing regarding ROIs' position and range. One such strategy to perform above mentioned analysis is called as regional analysis of volumes examined in normalized space (RAVENS) [7, 8]. RAVENS strategy precisely determines the atrophy regions or locations, regardless of their localized characteristic and the inter-individual changeability of cortical structures. In this work, high density RAVENS maps for input brain images are produced initially by carrying out the segmentation job on the input brain subject images, the segmented images will visibly display the three dissimilar tissues of the brain i.e. GM (Grey Matter), WM (White Matter) and CSF (cerebrospinal fluid). This is a mandatory pre-processing task which is vital for the automated Image registration method HAMMER. The segmented brain images are now the inputs for HAMMER, which makes use of them for carrying out standardisation/normalisation on segmented brain subjects by mapping them with a suitable template. After getting the normalised/warped images, RAVENS maps are created for three dissimilar tissues GM (Grey Matter), WM (White Matter) and CSF (cerebrospinal fluid). The normalised/registered brain image along with three associated RAVENS maps as shown in Fig.2

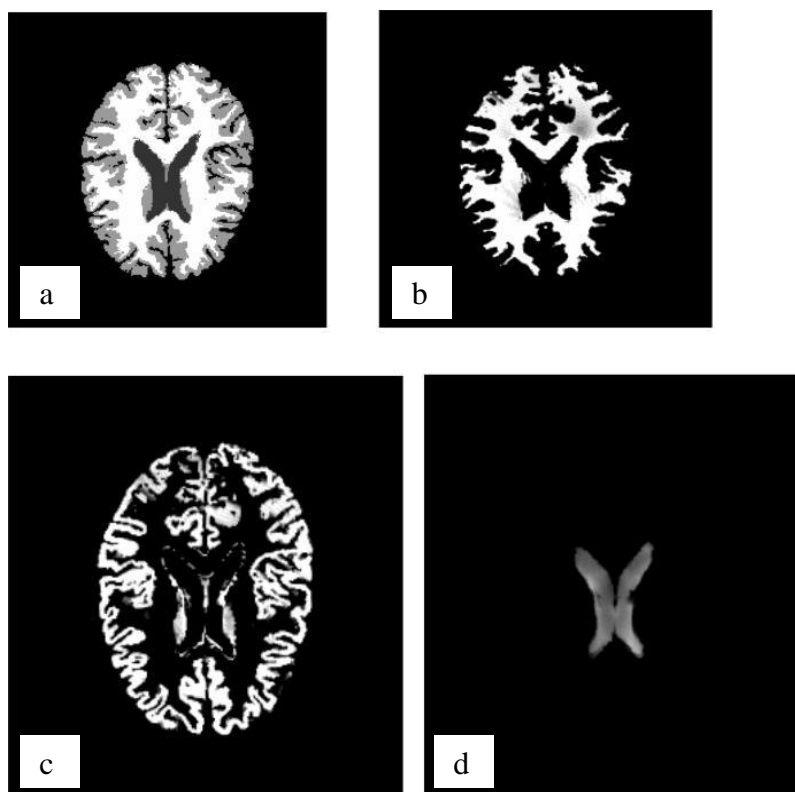


Fig 2: The figure depicts the Registered subject brain (a) and the three tissue density maps; Grey matter (b), White matter (c) and cerebrospinal fluid (d).

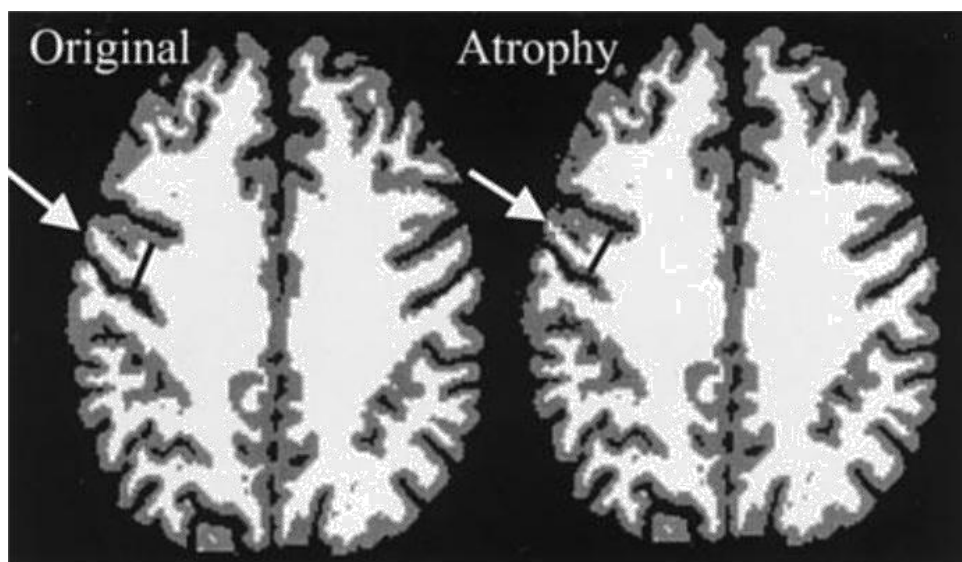


Fig 3: Simulated atrophy in Precentral gyrus part of brain image

Fig 3: Simulated atrophy in Precentral gyrus part of brain image. The purpose of RAVENS analysis to spot the locally precise simulated atrophy by inspecting by voxel-wise paired t tests applied on the corresponding RAVENS maps.

Outcomes are depicted in Fig. 4. It is obvious that the paired t -test analysis detected substantial variances in volumes for the two regions in which atrophy was simulated.

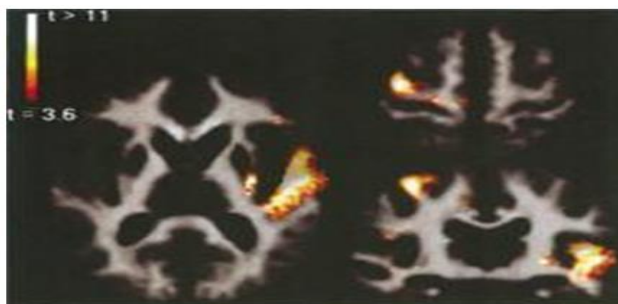


Fig 4: Atrophy in PCG and STG parts of brain.

Fig 4 clearly shows, the regions of major atrophy spread into areas of gray matter. Still, the most noteworthy peaks, predominantly after spatial cleaning of the data, are in the middle of the gyri. For better visualization of results Fig. 5 depicts volume renderings of the t statistic

overlapped on the regular brain RAVENS map. The renderings noticeably depicts noteworthy changes confined to the two regions of atrophy, the right gyrus and left gyrus which are pre-central and superior temporal in nature.

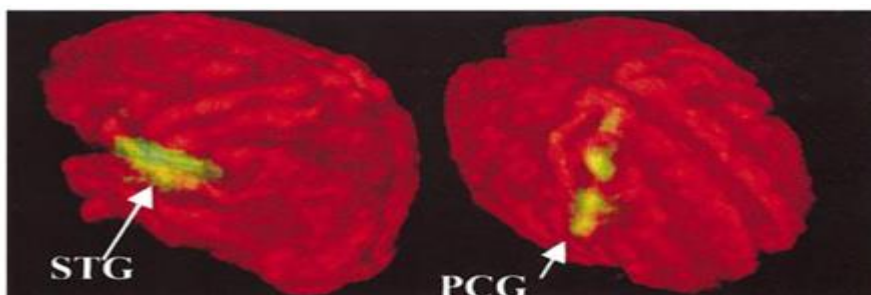


Fig. 5: depiction of PCG (precentral gyrus) and the left STG (superior temporal gyrus) by overlaying brain images

RESULTS

Image registration achieved via Hammer methodology will provide with a registered brain image consisting with the three tissues namely, GM (Grey Matter), WM (White Matter) and CSF (cerebrospinal fluid). In order to detect the presence of Atropy in exact tissue, RAVENS MAPS are generated and provided as input for Statistical Parameter Matching (SPM) component in MATLAB. Fig.6 shows various brain image scans in brain image analysis. The first image represents an input brain image (under analysis) with skull, second image shows input image without skull achieved via Brainsuite tool. The third image shows the standard brain image

template. Performing image registration on it with input image gives the resultant registered image I.e. fourth image in figure. Images five, six and seven are RAVENS MAPS representing GM (Grey Matter), WM (White Matter) and CSF (cerebrospinal fluid). Finally, careful investigation of these MAPS via Statistical Parameter Matching (SPM) component in MATLAB is performed for Brain image analysis process complete. For the given Input brain image, our strategy successfully detected the defected regions in it at cerebrospinal fluid (CSF) tissue of brain. The last three images in the figure represent cerebrospinal fluid (CSF) with defected part highlighted in red colour.

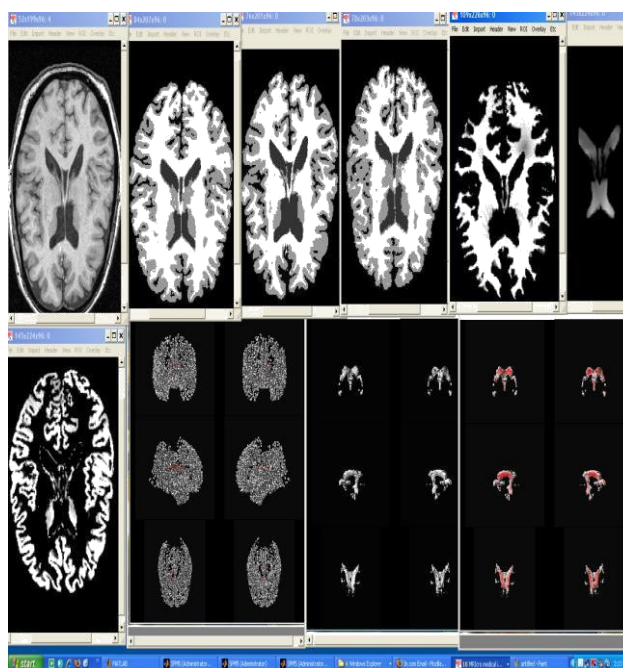


Fig.6 : various brain image scans in brain image analysis

CONCLUSION

Magnetic resonance brain image analysis centred on automated image registration and generation of RAVENS maps was performed. After thorough investigation, it is observed that RAVENS analysis is found to precisely discover and display the extremely localised atrophy in the input brain subjects. This approach not only aids in finding atrophy in brain but also conserves the complete brain size after carrying out registration on it. The proposed strategy for finding the atrophy regions in the brain avoids the need to put forth the regions of interest in advance which is tedious and impossible in some cases and this approach will also find out the disorders in brain if the atrophy region flows from one tissue to another.

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