

# A Statistical Atlas-based Technique for Automatic Segmentation of the First Heschl's Gyrus in Human Auditory Cortex from MR Images

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**Abstract**—We present an automatic method for the segmentation of the first transverse temporal gyrus of Heschl (HG), the morphological marker for primary auditory cortex in humans. The proposed technique utilizes a statistical anatomical atlas of the gyrus, generated from a set of training samples using principal component analysis. The training set consists of MRI data from 12 subjects with the corresponding Heschl's gyri manually labeled in each hemisphere (separate atlases were generated for each hemisphere). We used a leave-one-out approach to automatically segment Heschl's gyri in both hemispheres from the MR image data using generated atlases. We assessed the accuracy of this atlas-based technique by using it to segment the HG region from several test cases and finding the overlap between the segmented and labeled HG regions. Results demonstrated more than 75% and 83% accuracy in the extraction of the HG volumes in the left and right hemispheres, respectively. It is expected that the proposed tool can be adapted to extract other anatomical regions in the brain.

## I. INTRODUCTION

Human primary auditory cortex (PAC) is located on the superior surface of the temporal lobe, buried in the Sylvian fissure. Anatomical and functional studies indicate that PAC is found on the middle portion of the transverse temporal gyrus of Heschl (HG) as shown in Fig. 1, on the anteriormost gyrus, if more than one is present [1], [2]. PAC is the first cortical processing area for sound, and its functional properties are therefore of great relevance to our understanding of communication and hearing. The morphology of HG has been described to be highly variable among individuals in terms of both geometry and topology, and it may appear as single, or with two or more folds [3]. Such complex inter-subject variability can make it hard to observe reliable functional/anatomical correspondence in neuroimaging studies. HG can be identified in MR scans through the use of a pre-labeled brain [4] or probabilistic atlases [5]. However, the best these atlases can do is to specify the likelihood of any voxel in a spatially standardized image being on HG - they do not actually segment the image into HG and non-HG voxels.

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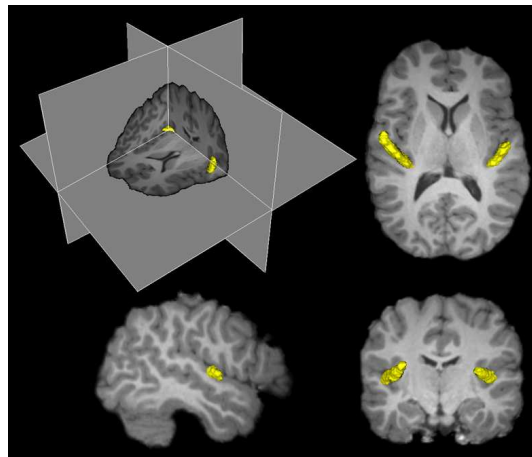


Fig. 1. Cross-sectional views of transverse temporal gyrus of Heschl.

Several techniques for statistical modeling of shape variability have been proposed [6], [7] and successfully applied for various image processing tasks such as segmentation [8], [9]. The construction of three-dimensional (3D) statistical shape models of different regions in human brain, however, is a challenging task due to the complexity of identifying the corresponding points on different training shapes. Most techniques rely on extracting common landmarks from every training set, which is a time consuming and tedious procedure. To overcome this problem, Rueckert *et al.* [10] proposed a new technique for the construction of a 3D statistical deformation model using human brain MR images. Their proposed technique inputs intensity image volumes as the training set for atlas construction. The correspondence is achieved using a non-rigid registration of intensity volumes. However, relying solely on intensity to find the correspondence is not sufficient for atlas construction of relatively small and anatomically variable structures such as Heschl's gyrus since adjacent structures have similar intensity characteristics. In such cases, the success of the intensity-based correspondence finding mainly depends on the accuracy of the non-rigid registration technique, and topological/geometrical constraints to further guide the atlas-based segmentation of the structure of interest.

We propose a fully automatic localization/segmentation tool for HG through the use of a statistical anatomical atlas. We adapt the methodology proposed by Rueckert to find the correspondence among training sets using a high-dimensional deformable registration technique known as Hierarchical Attribute Matching Mechanism for Elastic Registration (HAMMER) [11]. The achieved correspondence in deformation fields from template space to individual

subject frames is used to generate an atlas in the form of an average mean deformation plus the most dominant deformation directions captured from the training set using principal component analysis (PCA). Employing such an atlas, one can quantify the anatomical variation of a new subject’s HG structure along the dominant variation directions defined by the training set. Furthermore, the subject-specific atlas parameters are applied to the manually labeled HG region of the template to construct a specific model of Heschl’s gyrus for the new subject.

We demonstrate, using a leave-one-out approach on 12 segmented high-resolution MR whole-brain images, that HAMMER can accurately identify corresponding regions within the HG. In each iteration, every labeled subject volume was considered once as a test case, while the remaining datasets were used as the training samples for the construction of the atlas. To assess the performance of the constructed atlas, the overlap region was calculated between the HG region automatically extracted using the 11-dataset constructed atlas, and the manually painted HG region. A separate atlas was generated for each hemisphere.

## II. METHOD

The proposed segmentation tool utilizes the a-priori knowledge of the desired structure available through a set of training samples together with high-dimensional image warping (HAMMER) in order to construct a 3D statistical atlas using principal component analysis.

### A. Data Acquisition

T1-weighted anatomical images were acquired from 12 volunteer subjects (ages 18–26, right-handed). Whole-brain, T1-weighted MPRAGE images were acquired using a 3.0 Tesla Siemens Trio MRI scanner (TE 2.99 ms, Flip angle 9 degrees, TR 2250 ms; resolution 1 mm isotropic). Images were stripped to remove skull and scalp using the Brain Extraction Tool (BET) of the FSL software <sup>1</sup>. All subjects gave informed consent and the procedure was approved by Queen’s University Health Sciences Research Ethics Board.

### B. Heschl’s Gyrus Boundaries

Three raters labeled left and right Heschl’s gyrus volumes according to the criteria proposed by Penhune [12]. MRICron [13] was used to display the images as well as to label and save the regions of interest. For cases with two or multiple Heschl’s gyri, only the most anterior one was painted. Final volumes of left and right HG were created by identifying voxels labeled as HG by at least two out of three raters. The inter-rater reliability measure, defined as the average of the Dice’s similarity coefficient [14] for all combinations of two out of three, was  $72.0 \pm 7.8\%$  (mean $\pm$ std).

### C. Data Pre-processing

The structural MR volume data were rigidly registered to a common reference frame (i.e., Colin27 or CJH27 [15]) using

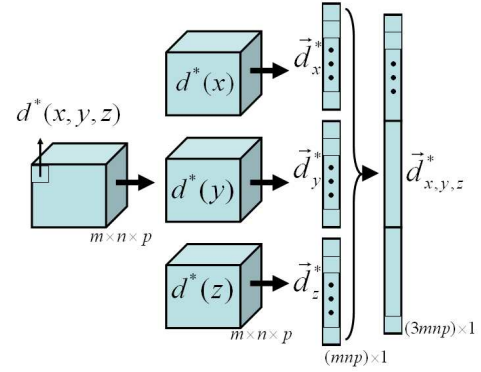


Fig. 2. Vectorization procedure of the 3D deformation field.

the SPM5 toolbox (Statistical Parametric Mapping: Wellcome Department of Cognitive Neurology, London, UK). The rigid transformation guarantees the alignment of the volume centers among all the brains. The resulting transformation parameters were also applied to the painted HG volumes of the corresponding subject. The rigidly registered HG volumes were thresholded to generate binary masks  $M_{S_i}$ , assigning value 1 to voxels ( $p$ ) corresponding to HG and 0 to the background:

$$\forall p \in S_i, M_{S_i}(p) = \begin{cases} 1 & \text{if } S_i(p) \in \text{HG volume;} \\ 0 & \text{else,} \end{cases} \quad (1)$$

where  $S_i$  refers to subject  $i$ ’s volume data.

### D. Non-rigid Registration

Rigid-body transformation only compensates for translational and rotational differences among different datasets. Non-rigid deformable registration is required to capture the geometrical/topological inter-subject variabilities. For this study, we chose to use HAMMER [11]: an elastic registration technique which utilizes an attribute vector for every voxel of the image. The attribute vector expresses the geometric features that are calculated from the tissue maps to reflect underlying anatomy at different scales. Our application of the HAMMER algorithm proceeded in two steps: First, in order to generate the tissue map, the brain data is segmented into gray matter, white matter and cerebrospinal fluid using FMRIB’s Automated Segmentation Tool (FAST) of the FSL software package. Second, HAMMER registration is applied to warp the brain images to a selected template. HAMMER provides a 3D deformation field from the subject space to the template frame ( $d_i : S_i \mapsto S_T$ , where  $S_i$  and  $S_T$  refer to the subject and template volumes, respectively).

### E. Point Correspondence

HAMMER’s optimization requires consistent transformations that give identical mapping between two registering images, regardless of which of the two images is treated as the template. Therefore, there exists a one-to-one mapping between every subject and the template. The inverse of the deformation field from subject space to the template frame guarantees point correspondence among all datasets. The inverse of the deformation field between each set and the template (represented as  $d_i^*(x, y, z) : S_T \mapsto S_i$ ) was

<sup>1</sup>FSL: Oxford Centre for Functional MRI, Oxford University, UK.

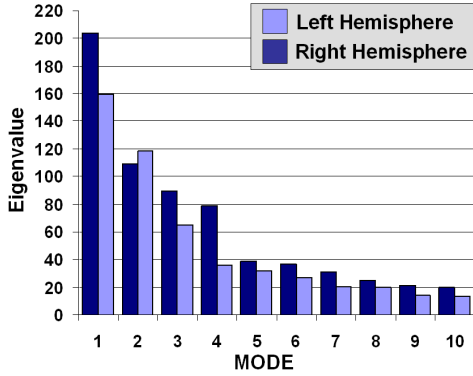


Fig. 3. Eigenvalues corresponding to different principal modes of variation for right, and left hemispheres.

masked with the template’s HG binary mask to include only those voxels that correspond to Heschl’s gyrus. The resulting masked deformation fields (from the template space to the subject space) were then used as the training samples for statistical atlas generation as described next.

#### F. Statistical Atlas Construction

HAMMER provides a deformation vector per voxel and, therefore, the number of degrees of freedom for the deformable registration is equal to the number of voxels within the image volume. Each deformation field  $d_i^*(x, y, z)$  can be expressed as a concatenation of 3D vectors, which describe the deformation in three orthogonal directions of X, Y, and Z at each voxel in the reference frame. Figure 2 depicts the procedure for the vectorization of the 3D deformation field.

Next, PCA is applied to the vectorized deformation fields to approximate the distribution of  $d_i^*$  using a parameterized linear model:

$$\vec{d}^* = \hat{d}^* + \sum_i \alpha_i \vec{\phi}_i, \quad (2)$$

where  $\hat{d}^*$ ,  $\alpha_i$  refer to average deformation vector, and model parameter coefficients, respectively.  $\vec{\phi}_i$ s are formed by the principal components of the covariance matrix  $\Sigma$ :

$$\Sigma = \frac{1}{n-1} \sum_{i=1}^n (\vec{d}_i^* - \hat{d}^*)(\vec{d}_i^* - \hat{d}^*)^T \quad (3)$$

Assuming a multi-dimensional Gaussian distribution for every voxel, we can parameterize any deformation field in the form of the principal modes of variation generated using the training set. Principal modes were calculated for the left and right hemispheres separately.

#### G. Segmenting Heschl’s Gyrus from a New Subject Volume

The constructed atlas, in the form of a mean deformation and several variation modes, can be used to automatically extract HG structure from any new test case using the following procedure:

- (1) Using HAMMER, the new subject data is registered to the selected template.
- (2) The inverse of the deformation field is calculated, masked using template’s HG binary region, and vectorized using the procedure described in the previous section.

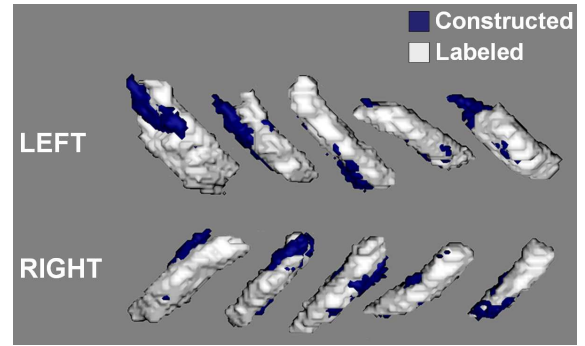


Fig. 4. Atlas-based constructed HG shape models overlaid on the labeled regions for several test cases.

- (3) The vectorized deformation field is then decomposed along the eigenvectors of the constructed atlas to find the coefficients for different variation modes. Coefficients are calculated by solving the following equation:

$$\vec{d}_{new}^* = \hat{d}^* + \Phi \vec{\alpha}^T, \quad (4)$$

where  $\vec{d}_{new}^*$ ,  $\hat{d}^*$ ,  $\Phi$ , and  $\vec{\alpha}$  refer to the inverse of the new subject’s deformation field (size:  $3mnp \times 1$ ), mean inverse deformation (size:  $3mnp \times 1$ ), and eigenvectors (size:  $3mnp \times k$ ) generated by atlas and eigen coefficients (size:  $1 \times k$ ), respectively.  $m \times n \times p$  and  $k$  represent the volume size and the number of training samples.

- (4) The atlas parameters (eigenvectors and eigen coefficients) together with the mean deformation are used to construct a new mapping that deforms the template’s HG volume towards the anatomy of the new subject.

### III. RESULTS AND DISCUSSION

From the 12-MRI dataset with labeled HG volumes, one dataset was randomly selected as the template for the registration. Using a leave-one-out technique, the 11 remaining labeled datasets were divided into a set of 10 training samples and a testing set (11 different cases). The 10 training sets were registered to the selected template using HAMMER. The inverse of the resulting deformation fields were used to construct a statistical deformation model for Heschl’s gyrus following the procedure described in Section II. The constructed atlas consisted of a mean deformation field and 10 principal modes of variation.

For a new test case, the difference between the deformation field (from the template frame to the test set) and the mean deformation resulting from the atlas was mapped along the eigenvectors to find the corresponding coefficients. This procedure was performed for left and right hemispheres separately. Figure 3 shows the sorted eigenvalues corresponding to left and right hemispheres for one of 11 test cases. The exponential drop of the eigenvalues confirms that the constructed atlas was able to considerably capture the variability of Heschl’s gyrus among individuals, even with a limited number of training samples. Figure 4 shows the atlas-based constructed HG volume overlaid on the corresponding manually labeled region for several test cases.

We quantified the overlap between the manually labeled and the segmented HG volumes by calculating the ratio of the voxels in the intersection of the two volumes to the total number of voxels within the constructed HG volume. This was done separately for each hemisphere. Results of the overlap measure are summarized in Table I, and indicate that at least 75% of the automatically segmented voxels were also identified as HG by the human labelers. Although the right hemisphere showed somewhat greater overlap, this difference was not significant (paired t-test,  $\alpha = 0.05$ ).

Hemisphere	Overlap (mean $\pm$ std) %
Left Hemisphere	75.3 $\pm$ 11.4%
Right Hemisphere	83.6 $\pm$ 7.8%

TABLE I

OVERLAP BETWEEN THE CONSTRUCTED AND LABELED HG REGIONS FOR 11 TESTING CASES (MEAN $\pm$ STD).

The technique as implemented here has at least three limitations: (a) the small number of available labeled datasets limits the amount of variability captured by the training sets in the construction of the atlas, (b) the pair-wise registration using a specific template introduces a bias towards the anatomy of the selected template, which affects the registration results, and (c) finally, individual training samples might have highly asymmetric topologies that makes it even more complex to find the correspondence among datasets. An example of such topological variability is the existence of multiple Heschl's gyri in one hemisphere and a single gyrus in the other hemisphere.

#### IV. CONCLUSIONS AND FUTURE WORK

We present an automatic tool for the localization and extraction of first Heschl's gyrus, the morphological location of primary auditory cortex, in human brains. We constructed statistical anatomical atlases using principal component analysis from 12 high-resolution MR images from normal human participants. HG was manually labeled in these brains by three independent observers, who were not informed of the purpose of the study. We used HAMMER, a high-dimensional deformable registration technique, to identify corresponding points on different training sets. Since HAMMER performs a consistent registration (meaning that there exists a one-to-one mapping between the two images), point correspondence among registered data is guaranteed. The resulting deformation fields (from the template space to the subject frame) were used to construct a 3D statistical atlas for the HG region in the form of a mean deformation and several principal modes of variation. To assess the performance of the constructed atlas, the overlap region was calculated between the manually labeled and extracted HG region using the constructed atlases. The method demonstrated accuracy over 75% in segmenting HG over the subject set.

The performance of the proposed technique can be further enhanced in a few different ways. Currently, a pair-wise registration (HAMMER) is used to find the correspondence among training samples. This introduces a bias toward the

specific anatomy of the selected template image. We are in the early stages of developing a template-free group-wise registration that replaces the current pair-wise registration framework to avoid such bias. Second, this study included only 12 labeled subject volume sets, and we plan to extend this work to a larger sample. Third, it would be interesting to know whether one could incorporate the constructed subject model as an initialization of another segmentation method such as active contours, level sets, region growing, etc. for the extraction of the desired anatomy from intensity image volumes. The automatically segmented regions could be easily segmented into grey and white matter, and the grey-matter segments used to conduct anatomically informed, region-of-interest analysis on functional MRI data. This may significantly increase the accuracy of functional analysis. The proposed method could also be adapted for the extraction of other anatomical regions in the brain, as long as they are morphologically defined enough that they can be manually segmented (labeled) by skilled observers.

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