Automatic construction of 3D statistical deformation models: Application to patients with schizophrenia

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Abstract. In this paper we introduce the concept of statistical deformation models (SDM) which allow the construction of average models of the anatomy and their variability. SDMs are built by performing a statistical analysis of the deformations required to map anatomical features in one subject into the corresponding features of another subject. We demonstrate the applicability of this new framework to MR images of the brain and show results for the construction of anatomical models from 25 different subjects.

1 Introduction

The significant inter-subject variability of anatomy and function makes the interpretation of medical images a very challenging task. Atlas-based approaches address this problem by defining a common reference space to compare anatomy and function over time, between subjects, between groups of subjects and across sites. Consequently, a number of different elastic and fluid warping techniques have been developed for this purpose [1]. However, traditional medical atlases contain only information about anatomy and function from a single individual focusing primarily on the human brain. Even though the individuals selected for these atlases may be considered normal, they may represent an extremum of a normal distribution. One approach to overcome this problem is based on statistical models of shape variability [2]. In building those statistical models, a set of segmentations of the shape of interest is required as well as a set of landmarks that can be unambiguously defined in each sample shape. A fundamental problem when building these models is the fact that it requires the determination of point correspondences between the different shapes. The manual identification of such correspondences is a time consuming and tedious task. This is particularly true in 3D where the amount of landmarks required to describe the shape accurately increases dramatically compared to 2D applications.

In this paper we present an automated way in which correspondences between the surfaces of different shapes are established via a non-rigid registration algorithm [3]. In addition we perform a statistical analysis directly on the deformation fields required to match different anatomies. We use the term statistical deformation models (SDM) to describe this framework since it allows the construction of average models of the anatomy and their statistical variability across a population of subjects.

2 Method

Traditionally, landmarks are anatomically characteristic points which can be uniquely identified across a set of individuals. In our approach we are first using a non-rigid registration algorithm which has been previously successfully applied to a number of different registration tasks [3] to calculate a dense set of so-called *pseudo-landmarks* between subjects. This algorithm uses a free-form deformation (FFD) model based on B-splines. The basic idea of FFDs is to deform an object by manipulating an underlying mesh of control points. The resulting deformation controls the shape of the 3D object and can be written as the 3D tensor product of the familiar 1D cubic B-splines,

$$\mathbf{T}_{local}(\mathbf{x}) = \sum_{l=0}^{3}\sum_{m=0}^{3}\sum_{n=0}^{3} B_l(u)B_m(v)B_n(w)\mathbf{c}_{i+l,j+m,k+n} \tag{1}$$

where $\mathbf{c}$ denotes a $n_x \times n_y \times n_z$ lattice of control points which parameterise the free-form deformation, i, j, k denote the indices of the control points and u, v, w correspond to the relative positions of $\mathbf{x}$ in lattice coordinates. The optimal transformation is found by maximising the normalised mutual information between images [4].

After calculating the registration we apply a principal component analysis (PCA) to the deformation fields required to map one anatomy to another anatomy: Suppose that we have n deformation fields described as vectors $\mathbf{d}_i$. Each deformation field is the result of the non-rigid registration algorithm described in the previous section and maps the anatomy of the reference subject $\mathcal{S}_r$ into the anatomy of the other individuals $\mathcal{S}_i$ in the population class under investigation. Using the fact that each deformation field $\mathbf{d}_i$ is represented as a linear combination of the control points $\mathbf{c}_i$ of the FFD, we perform the PCA directly on the control points rather than the deformation field defined by the control points. Our goal to approximate the distribution of $\mathbf{c}$ using a parameterised linear model of the form

$$\mathbf{c} = \hat{\mathbf{c}} + \mathbf{\Phi}\mathbf{b} \tag{2}$$

where $\hat{\mathbf{c}}$ is the average control point vector (or average deformation field) for all n subjects and $\mathbf{b}$ is the model parameter vector. The columns of the matrix $\mathbf{\Phi}$ are formed by the principal components of the covariance matrix $\mathbf{S}$:

$$\mathbf{S} = \frac{1}{n-1}\sum_{i=1}^{n}(\mathbf{c}_i - \hat{\mathbf{c}})(\mathbf{c}_i - \hat{\mathbf{c}})^T \tag{3}$$

From this, we can calculate the principal modes of variation of the control points (or deformation fields) as the eigenvectors ϕ_i and corresponding eigenvalues λ_i of $\mathbf{S}$.

3 Results

To demonstrate our approach we have used 25 brain MR images from different subjects with schizophrenia to construct a statistical deformation model of the brain. All images were acquired at the Department of Psychiatry of the University Medical Center Utrecht using a 3D FFE sequence (TE = 4.6 ms, TR = 30 ms, flip angle = 30°) on a 1.5 T

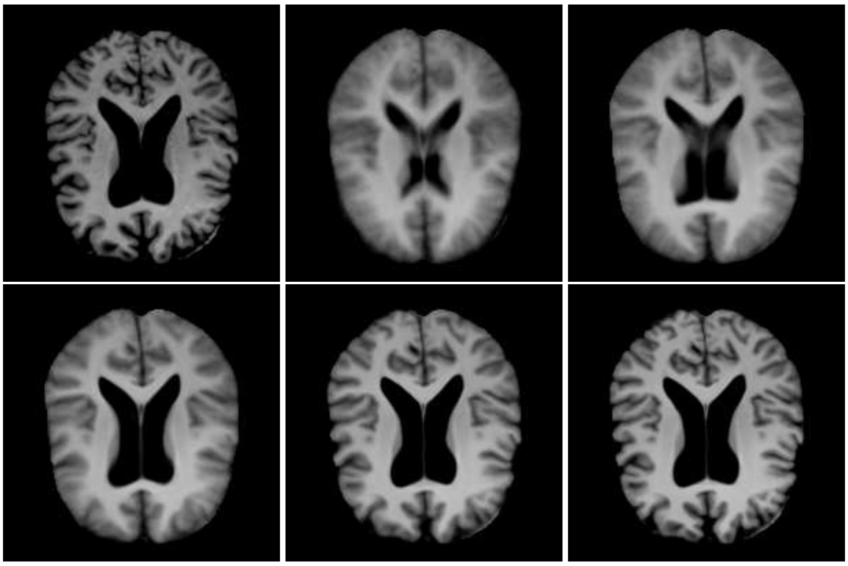

Fig. 1. Construction of an average intensity atlas: reference subject (top row, left), atlas after affine registration (top row, middle) and (c)-(f) the atlas after non-rigid registration using control point spacings of 20mm, 10mm, 5mm and finally 2.5mm (top row, right and bottom row).

MR imaging system (Philips Gyroscan ACS-NT). These images have a voxel size of $1 \times 1 \times 1.2\,\text{mm}^3$ and $200 \times 200 \times 160$ voxels. For the inter-subject registration we have first performed a global registration using an affine transformation with nine degrees of freedom followed by a local registration at multiple resolutions of control point spacing of 20 mm, 10 mm, 5 mm and finally 2.5mm [3].

The first step of the construction of statistical deformation models is to build a model of the average anatomy of all subjects after non-rigid registration to a reference subject. The resulting *atlas* shown in form of an average intensity image calculated from all 25 subjects without any intensity normalisation is shown in Figure 1. The next step involves generating the principal modes of variation of the deformation field to give an indication of the anatomical variability across the population under investigation. An example of the first three modes of variation focusing on the corpus callosum is shown in Figure 2. In this example the first mode of variation corresponds to a horizontal expansion and contraction while the second and third modes of variation correspond to a lifting and sinking in the vertical direction. When interpreting the modes of variation it is important to bear in mind that the modes of variation are not only the result of the variability of a single anatomical structure but the result of the variability of a large number of different anatomical structures as well as their inter-relationship.

4 Discussion and Conclusions

In this paper we have presented a new method for the automatic construction of statistical deformation models (SDM). These models can be used to build an atlas of the

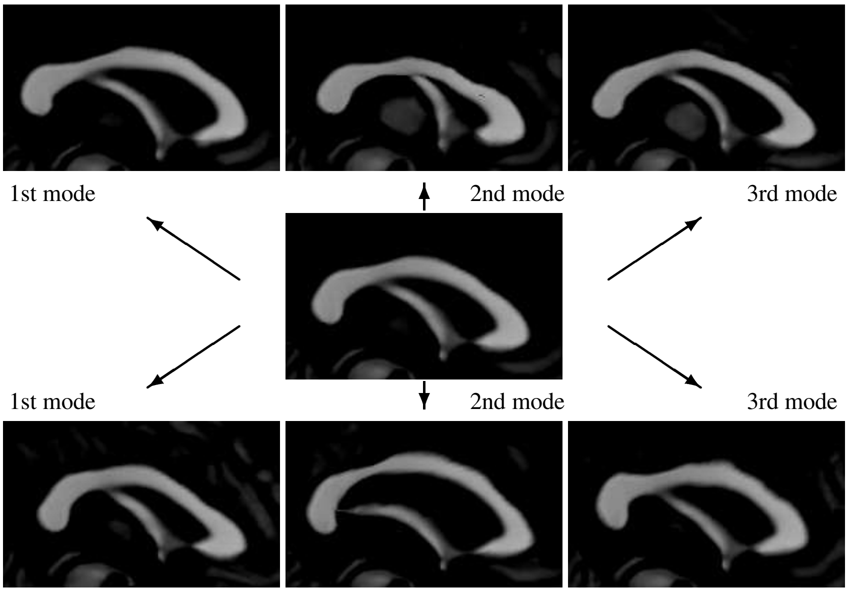

Fig. 2. Instances of the statistical deformation model showing the corpus callosum: Each image has been generated by varying the first three modes of variation between $-3\sqrt{\lambda_i}$ (top row) and $+3\sqrt{\lambda_i}$ (bottom row) and the average model (middle row).

average anatomy as well as its variability. This is achieved by performing a principal component analysis of the deformations required to map the anatomy of a reference subject to all other subjects in the population. In contrast to other approaches [5] we are exploiting the compact parameterisation of the deformation fields by the B-spline representation. In addition the proposed method can also be used for the construction of "stable" anatomical models which are not dependent on the choice of the reference subject. We are currently investigating whether statistical deformation models may be used as a morphometric tool to characterise shape differences between groups of normals and schizophrenic subjects.

References

1. D. Rueckert. Non-rigid registration: Techniques and applications. In J. V. Hajnal, D. L. G. Hill, and D. J. Hawkes, editors, *Medical Image Registration*. CRC Press, 2001.
2. T. F. Cootes, C. J. Taylor, D. H. Cooper, and J. Graham. Active Shape Models - their training and application. *Computer Vision and Image Understanding*, 61(1):38–59, 1995.
3. D. Rueckert, L. I. Sonoda, C. Hayes, D. L. G. Hill, M. O. Leach, and D. J. Hawkes. Non-rigid registration using free-form deformations: Application to breast MR images. *IEEE Transactions on Medical Imaging*, 18(8):712–721, 1999.
4. C. Studholme, D. L. G. Hill, and D. J. Hawkes. An overlap invariant entropy measure of 3D medical image alignment. *Pattern Recognition*, 32(1):71–86, 1998.
5. J. C. Gee and R. K. Bajcsy. Elastic matching: Continuum mechnanical and probabilistic analysis. In A. W. Toga, editor, *Brain Warping*, pages 183–197. Academic Press, 1999.