

Boundary Based Movement Correction of Functional MR Data Using a Genetic Algorithm

Guojun Bao, Jagath C. Rajapakse

School of Applied Science, Nanyang Technological University,
Singapore 639798

Abstract. This paper describes a novel image registration method for movement correction of fMR time-series. It is important to align the fMR images in the time-series before time-dependent analyses. This registration method aligns the boundaries of brains extracted from the functional images. It uses a genetic algorithm to minimize the distance function obtained from the chamfer distance transform. The global search nature of genetic algorithm makes this method robust to the presence of local minima.

1. Introduction

Movement correction of brain images obtained at different time instances of an fMR head time-series of scans is essential for the analyses of time-dependent changes. Despite the restraints to inhibit head movement, subjects could still show slight displacement in the scanner. If these motion artifacts are not corrected in the time-series analysis, the detected activities may be artifactual and important activities may be missed.

Although many techniques have been proposed for movement correction [2, 3, 4, 6, 11], most of these techniques use local hill-climbing optimization approaches. In general, movement correction of fMR time-series is a multidimensional optimization problem which may contain local minima. Therefore, these approaches are not appropriate. In this paper, we propose a novel method which uses boundary based genetic algorithm for movement correction of fMR data. We register a series of fMR images to a reference MR image. It conquers the local minimum problem using the global search nature of genetic algorithm.

Consider two images $f : \Omega_f \rightarrow Q_f \subset \mathbf{R}$ and $g : \Omega_g \rightarrow Q_g \subset \mathbf{R}$ where Ω_f and Ω_g are the domains of images f and g , respectively. Registration of images f and g is the process of performing spatial transformation on the images so that the voxel positions of images correspond to the same points in the imaging space. Without losing generality, let us consider one image, say g , as the *reference image* and that the spatial transformation is performed on the other image f to match g . Let S denote the spatial transformation and

f' denote the image f after transformation. We are interested in registering the boundaries of a prominent object. Let $\mathcal{C}_{f'}$ and \mathcal{C}_f be the boundaries of the object in f' and f respectively. When $\mathbf{p} \in \Omega_f$ and $\mathbf{q} \in \Omega_g$, one can write

$$\mathcal{C}_{f'}(\mathbf{q}) = \mathcal{C}_f(\mathcal{S}(\mathbf{p}, \boldsymbol{\alpha}))$$

where $\mathbf{q} = \mathcal{S}(\mathbf{p}, \boldsymbol{\alpha})$, and $\boldsymbol{\alpha}$ indicates the set of parameters for spatial transformation.

We assume that the spatial transformation \mathcal{S} is an affine transformation. That is when $\mathbf{p} \in \Omega_f$, $\mathcal{S}(\mathbf{p}, \boldsymbol{\alpha}) = \mathbf{M}\mathbf{p}$ where the linear transformation matrix \mathbf{M} is a combined matrix of the translation matrix \mathbf{T} , center translation matrix \mathbf{C} , rotation matrices \mathbf{R}_x , \mathbf{R}_y , and \mathbf{R}_z , and scaling matrix \mathbf{S} . \mathbf{M} can be written as $\mathbf{M} = \mathbf{T}\mathbf{R}_x\mathbf{R}_y\mathbf{R}_z\mathbf{S}\mathbf{C}$ which contains nine parameters [9].

2. Boundary Based Distance Transform

In our approach, image registration is to minimize a *distance function* that measures mismatch of corresponding boundary positions of the object in f' and g . Let \mathcal{C}_g be the boundary of the object in image g , $\mathcal{D}(\cdot, \cdot)$ be the distance function between the boundaries of two images and g'' be the reference distance image obtained from distance transform of g . Then

$$\mathcal{D}(\mathcal{C}_{f'}, \mathcal{C}_g) = \sum_{\mathbf{p}' \in \mathcal{C}_{f'}} g''(\mathbf{q}'')$$

where \mathbf{p}' is a voxel in f' , \mathbf{q}'' is the equivalent voxel of \mathbf{p}' in g'' and $g''(\mathbf{q}'')$ is the value of that particular voxel. The perfect alignment is achieved when \mathcal{D} is minimized.

Several distance transform techniques exist to obtain the reference distance image, and the chamfer distance transform [1] is the most popular one because of its speed and simplicity. For image g with boundary \mathcal{C}_g , chamfer distance transform converts g into a binary image g' consisting of boundary elements and non-boundary elements, and then converts g' into a chamfer distance image g'' where each element has a value that approximates the distance to the nearest boundary element $q \in \mathcal{C}_g$.

3. Genetic Algorithm

Local hill climbing algorithms are not suitable for optimization of distance function due to local minima. Though some stochastic global search procedures like simulated annealing [7] are available, they are time-consuming and not strongly reliable. In this section, we introduce genetic algorithms (GA) [5, 8, 10] for optimization of the distance function in our study.

3.1. Genetic Optimization

GA is a class of global optimization techniques that model some natural phenomena, namely genetic inheritance and Darwin's strife for natural survival. It attempts to maximize a parametric function $\mathcal{E}(\boldsymbol{\alpha})$ referred to as the *evaluation function* where $\boldsymbol{\alpha} = \{\alpha_1, \alpha_2 \dots \alpha_n\}$ is the set of parameters and n is the number of parameters. GA finds the optimal set $\boldsymbol{\alpha}^*$ of parameters such that

$$\boldsymbol{\alpha}^* = \arg \max_{\boldsymbol{\alpha}} \mathcal{E}(\boldsymbol{\alpha})$$

In our application, the evaluation function is

$$\mathcal{E}(\boldsymbol{\alpha}) = -\mathcal{D}(\mathcal{C}_f, \mathcal{C}_g) + A$$

where constant A is added to make $\mathcal{E}(\boldsymbol{\alpha})$ positive for all parameter sets. The algorithm evolves efficiently in the whole parameter space in a probabilistic manner to realize the global optimal parameters.

To formulate GA, all parameters $\alpha_i \in \boldsymbol{\alpha}$ are represented with binary strings called *genes*. A *chromosome* is formed by concatenating genes representing different parameters of the evaluation function. If γ_i denotes the gene representing parameter α_i , the chromosome \mathbf{c} can be written as $\mathbf{c} = \gamma_1 \gamma_2 \dots \gamma_n$. A *population* \mathcal{P} consists of a set of chromosomes representing the same parameter set

$$\mathcal{P} = \{\mathbf{c}_1, \mathbf{c}_2 \dots \mathbf{c}_K\}$$

where K denotes the population size.

GA performs multidirectional search by maintaining a population of chromosomes encoding potential solutions. Optimization begins by relating the distance function to an evaluation function, and defining a population of chromosomes representing parameters of the evaluation function. The population is randomly initialized and iteratively updated by performing genetic operations until the evaluation function is maximized. Genetic operations namely, selection, crossover, mutation, and exchange are performed to update the population in each generation. This can be formulated as follows:

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Randomly initialize  $\mathcal{P}$  of size  $K$ 
While not end
     $\mathcal{P} = \text{selection}(\mathcal{P})$ 
     $\mathcal{P} = \text{crossover}(\mathcal{P})$ 
     $\mathcal{P} = \text{mutation}(\mathcal{P})$ 
     $\mathcal{P} = \text{exchange}(\mathcal{P})$ 
Repeat
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3.2. Genetic Operations

A population evolves from each generation by incorporating and exchanging new information in every direction of the multidimensional parameter space.

In every generation, GA tries to get rid of inferior members and encourages reproduction and exchange between superior members in an optimal way towards the optimum solution.

3.2.1. Selection

Selection is performed based on the fitness of chromosomes calculated from the evaluation function. The fitness of a chromosome indicates the closeness of the chromosome to optimal solution. Those chromosomes with higher fitness values have a better chance and more copies to appear in the next generation. Before the selection process, a simulated biased roulette wheel with slots sized according to chromosome fitness is constructed. The selection process is then carried out by spinning the roulette wheel K times. Each time, we select a single chromosome for a new population. The population size is thus held constant from one generation to the next.

3.2.2. Crossover

Crossover operation occurs among the chromosomes selected from the current population with a probability of p_c . This gives us an expected number $p_c \cdot K$ of chromosomes undergoing crossover operation. The selected chromosomes are paired randomly and the crossover operation takes place in each pair where the bit patterns beyond a randomly selected bit position of the two chromosomes are interchanged.

3.2.3. Mutation

Mutation introduces new information to the current population at bit level. Every bit of each chromosome in a population has a probability p_m for mutation by simply reversing its value. The expected number of mutated bits is given by $p_m \cdot N \cdot K$, where N is the length of a chromosome. Mutation should be used sparingly as in nature because it is a random search operator; otherwise the algorithm will become little more than a random search.

3.2.4. Exchange

Exchange occurs between pairs of chromosomes in a subset of the population where each chromosome was selected with a probability of p_e from the current population. The genes at a randomly selected position of a randomly selected pair of chromosomes from the subset are interchanged. $p_e \cdot K$ number of chromosomes are expected to undergo exchange operation. The exchange operator forces the population to increase its diversity and thus prevents premature convergence during optimization process.

4. Motion Correction

We demonstrate our techniques for analysis of a fMRI time-series using images obtained in a visual experiment. All images were acquired on 3T Bruker Med-spec 30/100 system at the Max-Planck-Institute of Cognitive Neuroscience, Leipzig, Germany.

4.1. Visual Experiment

While a subject was performing the experiment, 2D T_2^* -weighted images, each with 64 scans, were acquired using a gradient-echo FLASH sequence. An 8Hz alternating checkerboard pattern with a central fixation point was projected on a LCD system and subjects were asked to fixate on the point during stimulations. Four successive ON and OFF stimuli were presented each at a rate of 5.162 s/sample. The stimulations were repeated for eight cycles. Extensive experiments showed $K = 40$, $N = 32$, 30 iterations for GA, $p_c = 0.5$, $p_m = 0.005$ and $p_e = 0.1$ gave satisfactory results.

The chamfer distances before and after movement correction of the image series are shown in Figure 1(a). The convergence of the algorithm is illustrated by showing a particular slice in Figure 1(b).

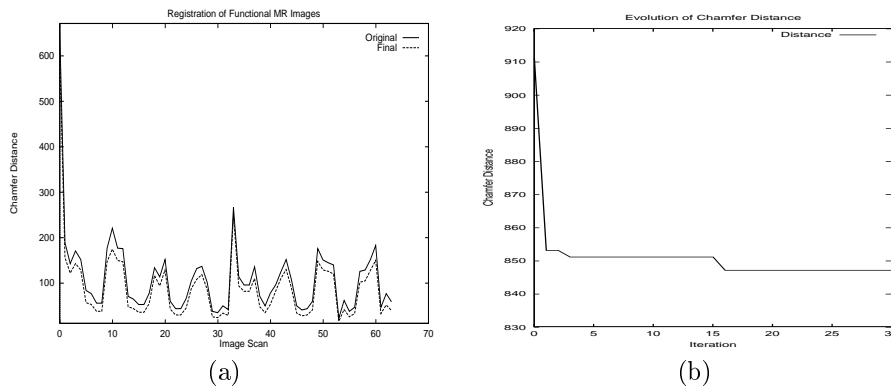


Figure 1: (a) Chamfer distances between boundaries of fMR slices and a reference image obtained before and after registration (b) Illustration of convergence of chamfer distance between boundaries of an fMR slice and a reference image.

4.2. Conclusion

The experiment results show significant improvement in the chamfer distance of the image slices by applying our novel algorithm. The genetic algorithm also shows rapid convergence of the distance function. Because only the boundary voxels are involved in computation, our technique is more efficient than those

volume based techniques where all brain voxels are involved in computation. Due to the global search nature of genetic algorithm, this novel technique does not have local minimum problem. We tried gradient descent technique and genetic algorithm showed superior performance. As a conclusion, our boundary based genetic algorithm gives great efficiency and effectiveness in movement correction of functional MR images.

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