Ultra fast registration of multiple MR volumes using MOPED

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Introduction

A critical step in the calculation of imaging biomarkers derived from functional, diffusion, perfusion and permeability MRI is the registration of the component volumes that constitute these datasets. This step, which in its simplest form provides a rigid (6 d.o.f.) or full affine (12 d.o.f.) transformation of each volume to a predefined reference volume, is required to remove bulk patient motion and/or artifacts such as eddy current induced distortions so that each voxel represents spatially consistent tissue information across the acquisition. Such MR datasets typically comprise many tens of volumes, and contain up to 100 individual images, registration of which leads to a significant computational overhead in the processing pipeline; one which needs to be reduced if results are to be presented to clinicians in an acceptable time.

In this abstract we present initial results from the application of a novel registration method based on the 'Massively Optimized Parameter Estimation and Data compression' (MOPED) algorithm, developed in the field of astronomy [1], which has the potential to reduce significantly the time taken to align high dimensional MRI data. The MOPED approach works by enabling very fast calculations of the likelihood of a given dataset. The speed-up is attained by a carefully designed data compression step, via construction of a set of optimized weighting vectors (y-vectors), which are designed to retain as much information as possible. Given a small set of constraints, well met in the case of medical image registration, this compression step allows results of the same accuracy as would be obtained using the full dataset, but with several million times fewer calculations. The core algorithm also has the remarkable property that the calculation time is proportional to the number of parameters, for example 12 for a full 3D affine transformation, rather than the number of voxels, thereby allowing easy scaling from low to high resolution. To show the potential of this method, we present timings and χ^2 maps obtained for MOPED, and for comparison FLIRT (FMRIB, Oxford, UK; http://www.fmrib.ox.ac.uk), when registering brain volumes acquired with different contrasts and acquisition matrices.

Methods

Three healthy volunteers underwent a range of standard structural (T_2-, T_2*- and FLAIR-weighted), 3D T_1-weighted (3D T_1W) volume and single shot (echo planar imaging (EPI) and fast spin echo (FSE)) clinical acquisitions on a GE Signa LX 1.5T clinical scanner. All scans shared the same field-of-view (256 × 256 mm), with acquisition parameters indicated in Table 1. To investigate the effects of inter-scan patient motion on the accuracy of image registration, each sequence was repeated four times with the volunteer moving in a random fashion after each scan was completed. The time taken by MOPED and FLIRT to register each volume was determined using the Linux 'time' function and averaged for each volunteer. The accuracy of registration was assessed using the χ^2 metric (see Fig. 1). Finally, to investigate the effects of differing acquisition matrix size on registration time, the T_2W single shot FSE (ssFSE) sequence was acquired with 128, 256 and 512 square matrices. All calculations were performed on a Dell Precision 690 workstation (Dell Computers, Round Rock, TX, USA).

Modality	Matrix	Slices	Slice thickness (mm)
	Single shot acquisitions		
SE-EPI	128 × 128	72	2
T_2W ssFSE	128 × 128	75	2
	Standard structural acquisitions		
3D T_1W	192 × 192	124	1.3
T_2W FSE	256 × 256	72	2
T_2*W	256 × 192	72	2
FLAIR	256 × 192	36	4

Table 1: Acquisition parameters for the different sequences used to assess the MOPED algorithm. All standard structural volumes were zero filled to 256 × 256.

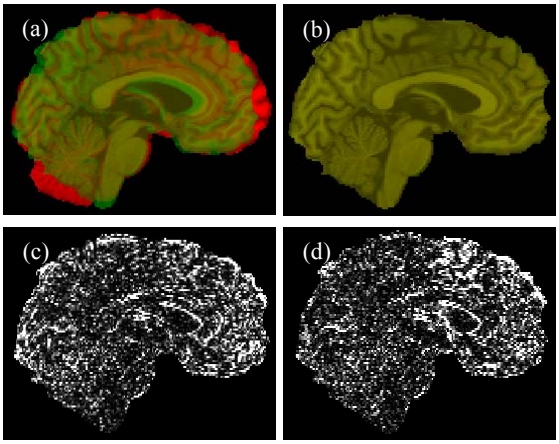

Figure 1: (a, b) Color sagittal maps showing overlaid acquired (red) and reference (green) 3D T_1W volumes before (a) and after (b) registration with MOPED. Near perfect alignment results in a yellow map in (b). (c, d) χ^2 maps generated from registered and reference 3D T_1W volumes for the MOPED (c) and FLIRT (d) algorithms. Note the similarity in these maps.

Results

Figure 1 displays example sagittal images obtained from the registration analysis. The first row shows color maps before (a) and after (b) registration of two 3D T_1W volumes using MOPED. After registration, the acquired (red) and reference (green) volumes are well aligned. The second row shows χ^2 maps generated from registered and reference 3D T_1W volumes for MOPED (c) and FLIRT (d). This example shows that MOPED performs similarly to FLIRT in terms of accuracy. Table 2 shows timings for MOPED and FLIRT obtained when registering a range of structural and single shot acquisitions. The MOPED timings include both the time to perform the initial weighting vector (y-vector) calculations and the time to register subsequent volumes. Table 3 shows the same data for ssFSE sequences acquired with three different matrix sizes.

Modality	y-vectors	MOPED	FLIRT
	Single shot acquisitions (matrix 128 × 128)		
SE-EPI	330 (3)	2 (0)	35 (0)
T_2W ssFSE	332 (2)	2 (0)	42 (1)
	Standard structural acquisitions (matrix 256 × 256)		
3D T_1W	284 (4)	4 (0)	165 (14)
T_2W FSE	330 (2)	4 (0)	118 (2)
T_2*W	331 (2)	3 (0)	118 (2)
FLAIR	331 (2)	2 (0)	99 (6)

Table 2: Mean (SD) values of timings for MOPED and FLIRT obtained when registering a range of structural and single shot clinical acquisitions.

Discussion

These data show that the MOPED algorithm is capable of registering MR volumes acquired with different contrast both accurately and rapidly. Calculation of the weighting vectors is a computational overhead that is performed once for each reference volume. Once this step is complete further volumes can be registered in the order of a few seconds. Such an approach is optimal when registering a large number of high-resolution volumes. This is clearly shown in Table 3 where MOPED provides a significant time saving compared with FLIRT when registering one 512 × 512 volume, and more than three 256 × 256 volumes and eight 128 × 128 volumes. For example, to register 20 128 × 128 ssFSE volumes would take 840 s with FLIRT and 372 s with MOPED. Given that a diffusion or functional MRI exam may contain tens of volumes, the time savings provided by MOPED can be significant. Work is ongoing to reduce the time required for the weighting vector calculation to optimize further this approach.

Matrix	y-vectors	MOPED	FLIRT
128 × 128	332 (2)	2 (0)	42 (1)
256 × 256	330 (2)	4 (0)	123 (6)
512 × 512	334 (3)	12 (0)	1078 (106)

Table 3: Mean (SD) values of timings for MOPED and FLIRT obtained when registering ssFSE volumes acquired with different matrix sizes.

References

[1.] Heavens, A. F., Jimenez, R., Lahav, O. Mon.Not.Roy.Astron.Soc. 2000;317:965-972.