Continuously moving table acquisitions: Generalised Image Reconstruction Accounting For Field Effects (GIRAFFE)

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Introduction: MRI is often compromised by imperfections in the scanner. B_0, gradient and B_1 field distortions all limit the useful field of view (FOV). Multi station imaging is now widely used to scan regions of the body bigger than that which can be accommodated in a single acquisition but efficiency is improved by continuously moving the patient table (CMT) instead [1]. Unfortunately the latter method is much more sensitive to system imperfections which introduce inconsistencies in the data leading to image artefacts. These manifest themselves differently depending on the k-space sampling scheme used. A common strategy is to reduce the width of the excited slab, which diminishes scanning efficiency, and to use only linear sampling schemes to minimise inconsistency [2]. Being able to perform 3D segmented k-space acquisitions where different preparation schemes could be interlaced to obtain several images with different contrasts would be highly desirable. So far these have only been attainable using 2D transversal slices [3,4]. To remove these constraints and obtain time efficient artefact-free extended FOV images, there is a need to calibrate field distortions and construct a mathematical framework within which this knowledge can be incorporated into the reconstruction. Here we introduce a method: generalised image reconstruction accounting for field effects (GIRAFFE) which formulates the moving table reconstruction problem as a simple forward model where each element of the system (table motion, field distortion etc) is represented by a matrix multiplication summarised by a single system matrix. The approach is based upon the matrix formalism introduced by Batchelor et al [5]. Within GIRAFFE, any additional correction schemes can be included providing they can be described as part of the system matrix. In this example we include amplitude slab profile correction (caused by imperfect slab shape) and the moving table velocity correction.

Methods: We explored the method using simulated and real moving table data from a phantom. The simulated acquisitions were transverse 3D slabs with frequency encoding along the AP direction. Each sagittal plane (in k-space) was completely acquired before moving to the next plane, resulting in a "slow" or primary phase encode direction Right-Left, in patient co-ordinates (RL) and a "fast" or secondary phase encode direction Foot Head, (FH). To be consistent with other approaches we accounted only for motion between slow phase encodes, although this is not a required feature of the method. GIRAFFE considers the extended FOV uncorrupted object as an unknown vector $\boldsymbol{s_0}$ which is acted upon by a series of linear transformations. These can be summarised by a matrix g and lead to the measured k-space data $\boldsymbol{S} = g\,\boldsymbol{s_0}$ (1). Using GIRAFFE the matrix g is constructed from knowledge of the table motion u_t, the extent of the fixed sub-FOV which is extracted from the full FOV by applying m (an image domain rectangular sampling function corresponding to the maximum extent of the excitation slab), field effects, r, in this case a position dependent image domain amplitude modulation of signal (the slab profile which when combined with m produces the actual excitation) but could be extended to include other imperfections unrelated to B_1. F is the Fourier transform matrix for the sub-FOV and D_t is the k-space sampling strategy: $g = \sum_t D_t\, F\, r\, m\, u_t$ (2). Direct inversion of g would be too computationally onerous due to its size: $(N_xN_yN_{zst}N_{st} \times N_xN_yN_z)$, where N_{st} is the number of times the primary phase encode loop is repeated and N_{zst} the number of secondary phase encodes. Typically the size of g would be in the order of $10^7 \times 10^7$ for a whole body CMT acquisition. Therefore, in order to estimate the uncorrupted image, we invert g using an iterative solver (conjugate gradient method) which uses only the functional equivalents of the system matrix: *lsqr* routine implemented in Matlab (the Mathworks). The simulations included random Gaussian noise and multiple k-space sampling schemes to systematically test the method. The simulated and acquired MR images were reconstructed using both a standard reconstruction method [7] and GIRAFFE. The MR data was acquired on a 1.5T Philips Achieva using a 3D gradient echo pulse sequence with the following parameters: 270×32x50 (LR×APxFH) matrix size, $2\times8\times2$ mm^3 resolution, N_{st} equal to 16, 15° flip angle, TE/TR of 2.6/4.7 ms and table velocity of 13.3 mm/s. Table motion was controlled using a stepper motor and external PC. Frequency encoding was performed laterally as in [8], with symmetrical slab over-sampling along the FH direction (28% total). The body coil was used for both transmission and reception.

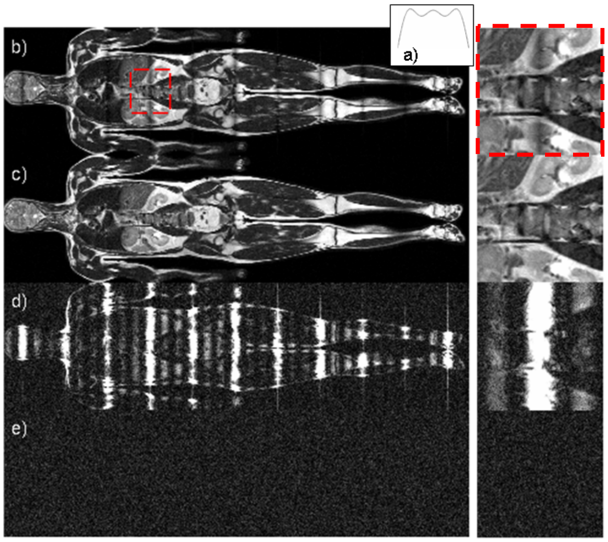

Figure 1 –Simulated CMT acquisition with imperfect slab profile and linear k-space sampling: *a)* slab profile; *b)* image reconstructed with the standard method; *c)* using GIRAFFE with knowledge of *a)*; *d)* and *e)* show the result of subtracting the gold standard image from b) and c), respectively (different scaling from b) and c)). On the right of each image is a zoomed version showing the area indicated with the red square.

Results: Reconstructions of the simulated data using only the standard approach yielded artefacted images. The artefacts varied with sampling strategy in the same way as previously reported in [2]. When GIRAFFE was applied with correct forward model informed by knowledge of the source of these artefacts they were removed in all cases. Figure 1 shows a 2D sagittal plane of the 3D images simulated with an imperfect slab profile (shown in *a)*) and a linear k-space filling order. The image in *b)* was reconstructed using the Krugger approach [7] and is clearly corrupted as seen in the difference image *d)*. An accurate image could be recovered using GIRAFFE by including knowledge of the slab profile – image *c)* and difference image *e)*. The real data from a phantom also showed improvement using GIRAFFE but was not fully corrected as effects due to gradient and B_0 in-homogeneities were not included in the reconstruction.

Discussion and Conclusions: We present a framework within which known system perturbations can be included to allow accurate reconstruction of CMT data. Such knowledge can either come from prior calibrations or be obtained during the actual scan as in [9]. Within this framework it is possible to use previously developed correction methods for fixed FOV acquisitions as for example in [10], providing their forward counterpart (for instance, warping due to gradient non-linearities) is included in r. Although more computationally intensive than simpler approaches, GIRAFFE enables the use of arbitrary k-space sampling schemes whilst avoiding increasing the level of image artefacts. Such flexibility is essential to interleave acquisition of images with different contrasts, allowing truly flexible imaging with moving table whilst removing the currently accepted hardware limits.

Acknowledgements: EPSRC for funding, Ingmar Graesslin and Peter Boernert from Philips Hamburg for help with the equipment required to control table motion.
References: [1] O Dietrich et al, ISMRM 1653 (1999); [2] B Aldefeld et al, ISMRM, 102 (2004); [3] NA Ghanem et al, ISMRM 796 (2005); [4] G Sommer et al, ISMRM 1966 (2005); [5] P.G. Batchelor et al, MRM 54:1273 (2005); [6] http://www.medical.philips.com; [7] DG Kruger et al, MRM 47:224 (2002); [8] B Aldefeld et al, ISMRM 2367 (2005); [9] A Shankaranarayanan et al, ISMRM 103 (2004); [10] JA Polzin et al, MRM 52:181 (2004).