ESMRMB ’00
17th ANNUAL MEETING
EUROPEAN SOCIETY FOR
MAGNETIC RESONANCE IN
MEDICINE AND BIOLOGY
Paris, September 14-17, 2000

INDEX

Message from the President of ESMRMB II
Message from the Chairmen of the Meeting II
Message from the Scientific Programme Committee II
Local Organizing Committee III
Scientific Programme Committee III
Officers of ESMRMB III
Liaison Industry III
ESMRMB Council III
Corporate Members ESMRMB III
Reviewers III
Advisory Board IV
List of Exhibitors IV
Lunch Symposia IV
Debates V
General Information VI
Social Programme VII
Society Information VII
Opening of the Technical Exhibition VIII
Time Schedule VIII
Scientific Programme - Oral Presentations IX
Scientific Programme - Poster Presentations XXVI
Abstracts - Oral Presentations I
Abstracts - Poster Presentations 101
Authors' Index 290
**Image Processing and Quantification**

337

**3D-Bayesian reconstruction from arbitrary sampling**

S. F. Martinez, F. T. A. W. Wijay, R. Lethmate, J. A. C. van Osch, D. van Ormond, D. Gravenor-Demilly, D. Gravenor-Demilly, Spin Imaging Group, Department of Applied Physics, Delft University of Technology, Delft, The Netherlands. *Laboratoire de RMN, CNRS UMR 5012, Université Lyon I-CPE, France*

**Introduction:** In functional imaging, correction for patient motion is necessary. This correction invariably leads to pseudo-random sampling and undersampling [1]. The standard way of coping with non-uniform sampling positions — gridding [2] followed by FFT — is not well suited for sparse random sampling. We propose a 3D-Bayesian reconstruction method that uses general prior knowledge to alleviate the mentioned artefacts [3]; moreover it obviates density correction. To simulate motion during acquisition, a Cartesian data set has been resampled onto the known, but sampled positions.

**Method:** Our reconstruction algorithm aims at minimizing the following functional

\[
\min_{\{f(T)\}} L(\mathbf{y}) \equiv 2 \sigma^2 \log(2\pi) \sum_{k \in \mathbb{R}} \log(\sigma^2 + (\Delta k)^2 + (\Delta l)^2 + (\Delta r)^2)
\]

in which \(T\) is a matrix describing the 3D Fourier transform between the image and k-space. The first term represents the 'likelihood', the second term the general prior knowledge. The image matrix \(\mathbf{y}\) and k-space data matrix \(\mathbf{x}\) are written as vectors, stacking their elements on top of each other. \(\Delta k\), \(\Delta l\) and \(\Delta r\) are the differences between neighbouring image pixels in the \(x\), \(y\) and \(z\)-direction [4], \(\alpha\) is the Lorentzian parameter and \(\sigma^2\) is the Gaussian noise variance.

**Discussion:** If one assumes that the SNR scales as the 3/2 power of the magnetic field, the expected SNR gain is of about 4.6. This value is in good agreement with the SNR gain observed in imaging. The in vivo image performed with a thinner slice thickness exhibits an increased signal intensity on the epidermis, namely due to the smaller echo time (\(\sim T_2\)) [2]. To compare best images obtainable at 1.5 T and best images obtainable at 7 T further SNR comparison are underway involving the use of a high temperature superconducting coil at 1.5 T [3]. In this case, for both the 1.5 T and the 7 T experiments, the body-induced noise will significantly contribute to the SNR. This comparison should provide a starting point to discuss the advantage of a superconducting coil at moderate field strength over a conventional copper coil at high field strength.

**Acknowledgements:** The authors wish to thank people from the CIERM, CHU Bicêtre, directed by Jacques Bittoun, were the 1.5 T images were performed.

**References**


338

**Radial trajectories in MRI: uniform and Bessel non-uniform sampling**

N.E. Myridis, C. Chamzas. *Democritus University of Thrace. Xanthi, Thrace, Greece*

**Purpose/Introduction:** Amongst the variety of MR trajectories we refer to the radial trajectories order to discriminate those methods which acquire MR signal on radial lines and use line-oriented reconstruction methods. In the present paper we propose a new non-uniform sampling of radial trajectories based on Bessel functions and we develop the reconstruction solution of it.

**Subjects and Methods:** Projection reconstruction methods are based on the central slice theorem [1]. According to this theorem we can reconstruct unknown a-bandlimited images, if a sufficient number radial lines (trajectories) passing through the origin is obtained [2]. The samples on each line must be interpolated in order to reconstruct the image via 1D interpolation. Since-to-date we consider uniform 1D interpolation with equidistant samples [3]. The interpolation equation is given by

\[
f(r) = \sum_{k=-\infty}^{\infty} f(\alpha_0) \frac{\sin(\alpha r - \alpha_0 n)}{(r - \alpha_0)} \quad \text{for} \quad \alpha \leq \alpha_0 \leq \frac{2\pi}{r_0} - \alpha
\]

where \(\alpha\) is the maximum spectral content of the object under examination and usually \(\alpha = \sigma\).

We propose herein a new non-uniform sampling scheme of the radial lines. The location of the samples is prescribed by the roots of Bessel function of first kind zero order, \(J_0(\alpha)\). Each image slice can be reconstructed using the interpolation form [4]

\[
f(r) = \frac{2}{\alpha} \int_{\alpha_0}^{\alpha} \frac{\sin(\alpha_0 n)}{\alpha_0 - n} \quad \text{for} \quad \alpha_0 \leq \alpha \leq \frac{2\pi}{r_0}
\]

where \(\alpha_0\) are the roots of \(J_0\). We implement in this work Eq. (2) for medical purposes. Ad hoc, we use a modified Shepp and Logan prototype (see first figure).

**Results:** The gradients necessary for the radial trajectories are similar to those of projection reconstruction techniques, although a variable step is imposed. Initially we reconstruct a 64 × 64 phantom via the non-uniform sampling (Eq. (2)) (second figure). A number of 1480 radial lines depending on the grid, with 128 samples on each slice, suffices for a 64 × 64 grid. We also reconstruct the prototype via uniform sampling Eq. (1) with the same number of samples (third figure). Although the same attributes were
used for both the methods, we observe from the second and third figures that non-uniform sampling produces images of higher quality than the reconstruction is ripple-free and the individual objects of the head are sharper, in comparison to the uniform sampling. This improvement results from the better approximation of non-uniform interpolation near the tails of 1D functions, producing a better description of the head skull in the second figure.

Discussion/Conclusion: In this presentation we developed a new reconstruction technique for MRI using radial trajectories. This technique uses non-uniform sampling ordered by Bessel functions and produces images of higher quality compared to those of uniform sampling.

References

Improving the time resolution of dynamic MIR using partial k-space reconstruction
A. Degenhard, J. Wolber, C. Hayes, M.O. Leach. CRC Clinical Magnetic Resonance Research Group, The Institute of Cancer Research and The Royal Marsden NHS Trust, Sutton, Surrey SM2 5PT, UK

Introduction: Dynamic T₁-weighted MRI imaging during Gd contrast agent uptake has become a widespread technique for the evaluation and characterization of benign and malignant lesions [1,2]. However, especially when full 3D volume coverage of the tissue of interest is required, there is a tradeoff between the spatial and the temporal resolution of the dynamic images. Here, we propose to apply a half-Fourier (HF) reconstruction method to overcome this problem and hence improve the time resolution of 3D MRI enhancement curves.

Methods: In this abstract we apply the Cuppen-POCS method [3], which is a commonly used algorithm for HF reconstruction techniques to reduce MRI acquisition time. Our approach is different from the usual HF MRI in that fully sampled k-space data are acquired, but the first (or second) halves of each data set are used to reconstruct additional images. To overlap the HF reconstructed uptake curve with the original one to a sufficient accuracy, we used the calculated values in the uptake curves as base points for computing the derivatives of the curves which then automatically overlap, and numerically integrated this result. This approach is universally applicable, provided the full complex k-space data is available.

Results: We applied the method to dynamic Gd-enhanced T₁-weighted 3D MR images of the breast. The sequence implemented on a 1.5 T Siemens Vision MR system (3D FLASH, TE/TR = 5 ms/12 ms) acquired two pre- and five post-contrast MRI data sets (matrix size 256 x 128 x 64) in 90 s each. Although HF reconstruction algorithms are well established [3], it is crucial that phase propagation in post-contrast images is not disrupted by intensity redistribution. Before reconstructing the HF MR images, it was therefore verified that the phase of the complex raw data only varies with low frequencies, as required for application of the algorithm. In the figure we display a post-contrast enhancement uptake curve for a suspicious enhancing breast lesion. (⊥) Conventional 3D images, (C) HF images (2nd half). The plot illustrates how efficient our reconstruction method interpolates between conventionally reconstructed 3D MR images.

Discussion and Conclusion: The time-course of contrast agent uptake and wash-out in suspicious lesions is considered to be a marker for malignancy [1-4] and can also serve to assess treatment response. With the proposed method we therefore contribute to more accurate post-processing and analysis of the enhancement kinetics, which is required for the interpretation of dynamic MRI data using pharmacokinetic models [1].

References

Co-registration of serial 3D MR breast data sets
J.R. Reichenbach, J. Hopf, M.E. Bellermann, W.A. Kaiser, Institute of Diagnostic and Interventional Radiology, Friedrich-Schiller University Jena, Germany, 2Department of Biomedical Engineering, University of Applied Sciences Jena, Germany

Purpose/Introduction: Precise registration of MR breast images may be essential for evaluation of dynamic MR mammography studies for detecting breast cancer or for quantitative assessment of potential parenchyma breast tissue changes induced by hormonal therapy. Such an assessment requires serial scanning of patients with time intervals of several weeks or even months. Unlike the brain, the breast cannot be considered a rigid body with well defined internal landmarks which complicates the matching problem. The aim of this study was to develop and to implement an algorithm which improves the coregistration between serial 3D MR breast images by applying combined translation and rotation operations with locally varying parameters.

Subjects and Methods: Three female volunteers were imaged in prone position with a 1.5 T MR scanner (Magneton Vision plus, Siemens, Erlangen, Germany) and a two element phased-array double breast coil. A 3D, r.f.-spoiled gradient-echo sequence (TR/TE/a = 14/5/35) was used to acquire 60 and 96 partitions with a thickness of 2 mm in transverse orientation with a FOV of 350 mm and a matrix of 256 x 256. Data were acquired threec within the same session while the subjects were allowed to take a break between the scans followed by repositioning.

Images were processed off-line using DL 5.2 (Research Systems, Boulder, USA) and consisted of the following steps: (i) Creation of separate sub-images for the left and right breast. (ii) Application of a rigid pre-matching algorithm to correct for gross translation in all three directions between the data sets. The first set was taken as the reference set. Optimum in-plane translation parameters and slice shift were determined by maximizing the mutual information (MI) between the images. (iii) Determination of local rotation parameters. Selected slices of the first set were chosen as reference points. Corresponding slices of the serial data set were rotated alternately around a horizontal (ϕ) and a vertical axis (θ) in small steps and interpolated to new images, respectively. Optimum rotation parameters were obtained by maximizing the MI. The rotation parameters for the remaining slices were determined by linear interpolation between the optimized values of the two nearest reference slices or by linear extrapolation for the slices outside the optimization range. For extrapolation the slope of the linear regression analysis of the support points was taken.