

Efficient solving for arbitrary susceptibility distributions using residual difference fields

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INTRODUCTION. Magnetic susceptibility is important in MRI, since it is a source of contrast [1,2] and quantitative measurements are desired for certain diagnoses [3]. To date, no numerically tractable methods exist for calculating arbitrary susceptibility distributions. An important contribution was made by Leigh and Li [4] in 2004 regarding the formulation of a solvable inverse problem. The authors admit however that the method is numerically intractable even for small MRI data sets. Proposed here is a means of sidestepping the numerical difficulties by recasting the inverse problem as an iterative model fitting problem which does not require massive matrix manipulation.

METHOD. The inverse problem is defined exactly as in [4]. Varying susceptibility χ will create small changes in the magnetic field that can be measured [5]. The magnetic field and the susceptibility over the whole object K are related via

$$\frac{1}{4\pi} \int_{K \neq \vec{r}} \chi(\vec{\rho}) \frac{3 \cos^2(\theta) - 1}{|\vec{r} - \vec{\rho}|^3} d\vec{\rho} = \frac{B_z(\vec{r}) - B_0}{B_0(\vec{r})} = RDF(\vec{r})$$

where B_z is the measured magnetic field map, B_e is the background field, B_0 is the main field and θ is the angle between the points \vec{r} and $\vec{\rho}$. RDF is the unitless residual difference field. This can be written discretely: given the discrete position (i,j,k) and susceptibility χ_q of every voxel q , the RDF_p produced for every voxel p at discrete position (x,y,z) can be calculated as

$$RDF_p = \sum_q \eta_{pq} \chi_q \quad \text{with} \quad \eta_{pq} = \frac{2(k-z)^2 - (j-y)^2 - (i-x)^2}{4\pi((i-x)^2 + (j-y)^2 + (k-z)^2)^{3/2}} \quad \text{for } p \neq q \quad \text{and} \quad \eta_{pq} = 0 \quad \text{for } p = q.$$

The authors of [4] recommend calculating all the single voxel demagnetization factors η_{pq} to create the transform matrix \mathbf{A} . The vector of all RDF_p values \mathbf{b} and all χ_q values \mathbf{x} are related by the matrix equation $\mathbf{Ax}=\mathbf{b}$ which can be solved using inverse methods. This is the computationally impossible step since \mathbf{A} is huge: for a 256^3 voxel volumetric image the matrix would occupy 512 terabytes, and even for 64^3 voxel images the matrix is 128 gigabytes. We propose that instead of calculating the transform matrix \mathbf{A} we need only replicate its action. From the definition of the single voxel demagnetization factor, $\eta_{pq}=\eta_{pq}(i-x,j-y,k-z)$, it can be seen that the above sum is in fact a 3-dimensional convolution.

$$RDF(x, y, z) = (\eta(i, j, k) * \chi(i, j, k))(x, y, z)$$

Here we have dropped the pq subscripts. The convolution kernel is the field of single voxel demagnetization factors calculated with respect to the origin. Calculating this convolution is not computationally expensive even for large data sets and it opens the door for iterative solving techniques.

An experiment was conducted on a 0.5-T Phillips Gyroscan system using a water phantom containing five test tubes with gadolinium solutions of known susceptibilities. A 64^3 voxel field of view contained the whole phantom. The background field B_e was measured by imaging the phantom without the test tubes present and B_z measured once the tubes were in place. After subtraction and division to produce the RDF , any remaining linear terms in the field were removed so that only dipole fields remained. The susceptibility was then solved for iteratively using $LSQR$ in $MATLAB$.

RESULTS. The iterative technique quickly converged to reasonable values of χ . Each convolution took 3 seconds on a Pentium IV and the results converged after 1000 iterations. The fast field echo imaging technique used is particularly prone to susceptibility artefacts and as a result, there was no signal available in the immediate vicinity of the test tubes. The RDF is shown in figure 1 with the voids evident. These signal voids caused the solver to err in calculating the absolute values of χ because a larger diameter tube with a lower susceptibility is indistinguishable from a small tube with higher susceptibility in the RDF produced outside the voids. Figure 2 shows the solved susceptibility values. The mean values of χ within each tube from the solver were adjusted to correct for the erroneously large tube sizes by calculating the susceptibility that would produce the same far field if confined to the actual test tubes. The adjusted values of χ correlated linearly with the actual values as shown in figure 3.

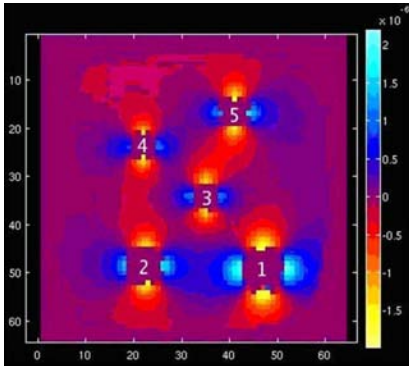


Figure 1. Residual difference field map (unitless) for a cross sectional slice through five tubes with different susceptibilities. Signal voids are evident. 64 by 64 pixels, 208 mm by 208 mm. χ relative to water are #1: 34, #2: 17, #3: 8.5, #4: 3.4, #5: 9.1 (all $\times 10^{-6}$).

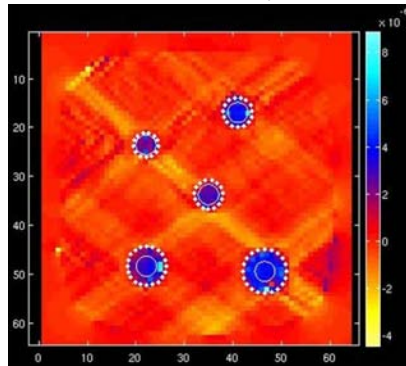


Figure 2. The same slice as Fig.1 through the iteratively calculated susceptibilities (unitless). The diameters of the real tubes are drawn with solid lines, the incorrect larger diameters from the solution are shown with the dotted lines.

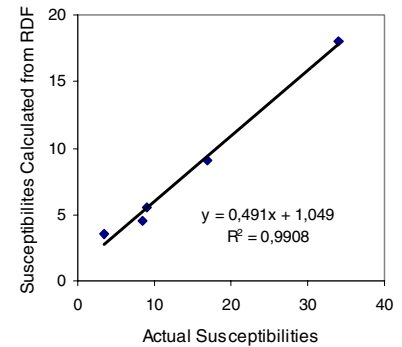


Figure 3. Susceptibilities $\times 10^{-6}$. Actual χ relative to water ($\chi_{\text{water}} = -9.05 \times 10^{-6}$) plotted versus the value of χ calculated from the RDF using the iterative technique and adjusted to correct for the misjudged diameter.

CONCLUSION. The realization that the transform matrix containing the single voxel demagnetization factors need never be formed is important. For 256^3 images the matrix would occupy 512 terabytes of memory, the convolution kernel for such a case occupies a mere 32 megabytes and its application is trivial. The problem of solving for susceptibility given the RDF becomes possible. The RDF was easily computed in this case because the background field was so easily removed, this is not the case in general, especially when parts of the object extend outside the field of view. But other methods exist to remove B_e for more complicated cases [4] and once the background field is removed, solving for the susceptibility is possible.

REFERENCES. [1] Haacke et al. MRM, 52:612–618, 2004. [2] Sehgal et al. JMRI 22:439–450, 2005. [3] Chu et al. MRM, 52:1818–1327, 2004. [4] Li & Leigh. MRM, 51:1077–1082, 2004. [5] Irrazaval et al. MRM, 35:278–282,1996.