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Step Interpolation of MR Images with Inter-Slice Gap Correction

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abstract

This report describes the design of an algorithm for the binary up-interpolation of normal structural MR data in the through slice direction. The method is intended as a pre-processing stage for the measurement of cortical thickness, where data has already been acquired at lower resolution than would have been ideal. More work is still needed to quantify performance, though a theoretical evaluation is provided here in order to put the method in the context of other interpolation methods.

Introduction

Many MR data sets are often acquired with anisotropic voxels, in that one dimension (referred to here as the z ordinate) is acquired with much poorer resolution than the other two. This degradation in image quality is generally not immediately obvious if images are presented in the perpendicular (x y) plane. However, quantitative spatial analysis of MR volume data can be severely affected by such data, which precludes the calculation of meaningful 3D spatial derivatives. In addition the data is often acquired with a significant “slice-gap” in that adjacent slices do not quite meet, leaving unseen regions in the data. These problems invariably lead to the need to reslice data into a more convenient sampling interval in order to perform 3D analysis or graphical rendering [1, 2].

It is generally accepted that for MR images the optimal way of performing interpolation is the use of Sinc based methods [3]. Here the functional model used is consistent with interpolation using the underlying Fourier description of the data. Resulting interpolated images are therefore at least consistent with the information content of the original data. Inevitably however, this process cannot recover the high spatial frequency information which was not measured, and although the process may result in more data values each is still at the same intrinsic resolution as the original data. It is not possible to perform genuine up-interpolation without a functional model of the data with which to synthesise high resolution voxel data (corresponding to filling in the missing frequencies in the Fourier domain). Consequently, the main conclusion might well be that if a particular approach to 3D data processing required high spatial definition in the through plane direction then this should be done not by attempting to up-interpolate an image but by a better designed acquisition.

However, for the specific case of brain segmentation from MR images it has been shown that it is a good assumption imaged tissues will be composed of homogenous regions of uniform grey level value, bounded by partial volume voxels [4]. If this is the case then we should be able to model local regions of data either as pure tissue or as partial volume voxel boundaries. This suggests the use of an explicit boundary interpolation model. The purpose of this work was therefore to investigate the possibility of using a simple step edge interpolation model for the interpolation of partial volume voxels in the through slice (z) direction. If this model is correct then we would expect to see improved spatial resolution of up-interpolated images, in comparison with conventional Sinc interpolation approaches. We also show how the problem of interslice gaps can also be accommodated within this framework.

Step Interpolation

Conventional partial volume grey level analysis will yield an estimate of the fractional contributions from two pure tissue values to a voxel’s contents. This information provides a constraint on the possible boundaries which could pass through this voxel. In addition, it is possible to construct an estimate of the orientation of the boundary from spatial differentiation of the local grey level structure. The combination of these constraints is enough to determine a linear boundary model for the voxel grey level up to a directionality ambiguity (ie: up or down). However, this ambiguity can then be resolved by the simple expedient of selecting the orientation of the voxel according to the best agreement with adjacent slices of data.

If we consider a voxel as a 3D rectangular region we find that there are many special cases which must be considered for intersection with an arbitrary plane. In addition, a 3D rectangular region is not entirely an accurate description of the true voxel geometry (in terms of spatial sensitivity) due to details of the MR acquisition process. For reasons of simplicity we have therefore made the assumption that the boundary can be analysed as a 2D model in the direction w perpendicular to the plane between the two tissues along the between slice (z) direction. The partial volume estimate, the local slope, and the directional orientation provide enough information from which to synthesise (ie: interpolate) new grey level values for any subdivision of the voxel. Knowledge of the inter-slice gap also allows this to be done in a way which recovers the missing data region.

We define m as the slope of the image, I :
$$m = \frac{2(\nabla_z I)^2}{\sqrt{(\nabla_x I)^2 + (\nabla_y I)^2}}$$

In the following model we will always assume that m is negative, the sign of this slope will be determined later in the boundary orientation step.

f is the partial volume fraction of the voxel under investigation, which can be computed using Bayesian segmentation approaches [4] if they are available. Otherwise, assuming a linear image formation process we can compute this value using knowledge of expected pure tissues values for the particular combination of partial volume components within this voxel g_1 and g_2 .

$$f = \frac{g_2 - g(x, y, z)}{g_2 - g_1}$$

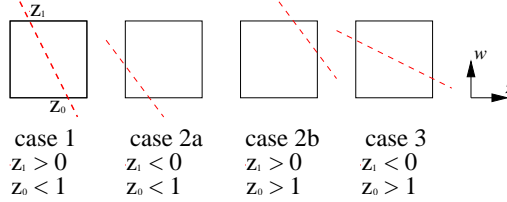


Figure 1: Selection of area calculation.

We define the active region of the voxel between a z value of 0 and 1, and then z_1 is the z -intercept of the linear boundary at $w = 1$, and z_0 is the z -intercept of the linear boundary at $w = 0$.

There are multiple ways in which the linear boundary can pass through the voxel and in order to find the correct one given only f and m it is necessary to compute all possible boundary models and then check that the intersection points are consistent with the definitions of each (Figure 1). The three possible computational cases are described below.

Case 1

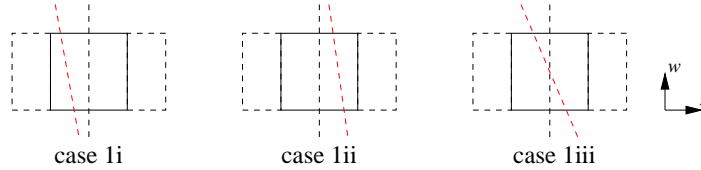


Figure 2: The boundary passes entirely within the imaged voxel.

For this case (Figure 2) the locations of the intersections are given by;

$$z_1 = f - \frac{1}{2m}$$

$$z_0 = f + \frac{1}{2m}$$

Case 2a

For the Case 2a when $f \leq 0.5$ (Figure 3) we have

$$z_0 = \sqrt{\frac{2f}{m}}$$

$$z_1 = z_0 - \frac{1}{m}$$

For the Case 2b when $f > 0.5$, (from symmetry arguments):

$$z_0 = 1 - \sqrt{\frac{2(1-f)}{m}} + \frac{1}{m}$$

$$z_1 = z_0 - \frac{1}{m}$$

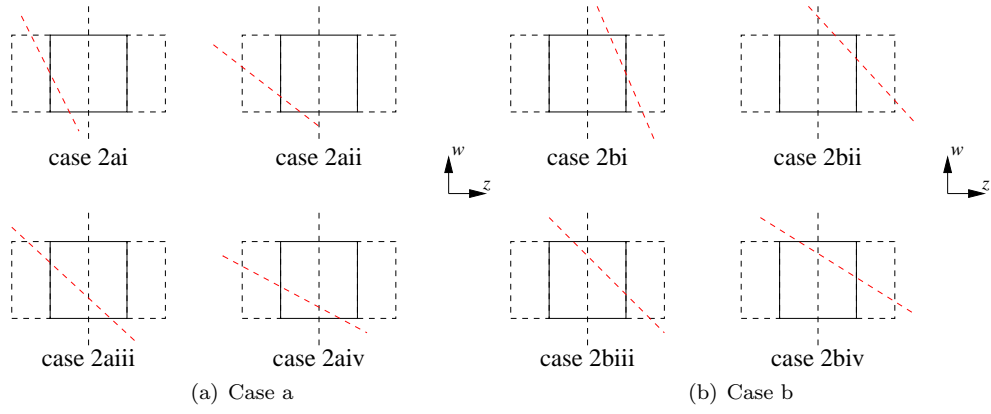


Figure 3: The boundary passes into the slice gap region on one side.

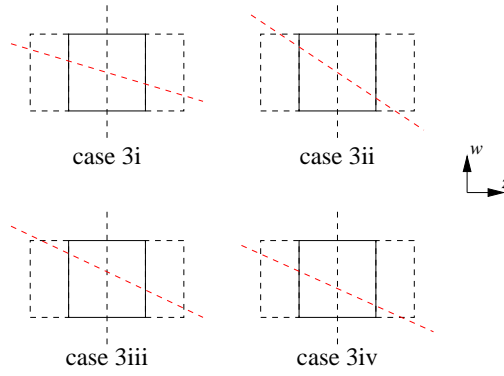


Figure 4: The boundary passed into the slice gap on both sides.

Case 3

Finally, for this case (Figure 4) we have

$$z_0 = 0.5 + \frac{f}{m}$$

$$z_1 = z_0 - \frac{1}{m}$$

Intersection at the Interslice Gap.

Now we have consistent values of z_1 and z_0 we have an unambiguous linear parametrization of the boundary. Next we need to take into account the inter slice interval, s (defined as half the interslice gap) and calculate the areas, a_1 from $z = -s$ to $z = \frac{1}{2}$ and a_2 from $z = \frac{1}{2}$ to $z = 1 + s$, that the voxel should be split into in the z -direction.

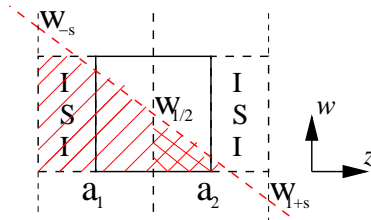


Figure 5: Inter slice gap.

w_{-s} is the w -intercept of slope at $z = -s$:

$$w_{-s} = m(z_0 - \frac{1}{2})$$

$w_{\frac{1}{2}}$ is the w -intercept of slope at $z = \frac{1}{2}$:
 $w_{\frac{1}{2}} = m(z_0 + s)$

w_{1+s} is the w -intercept of slope at $z = 1 + s$:
 $w_{1+s} = m(z_0 - (1 + s))$

Step interpolation for Binary Division of a Voxel

The computed step boundary can now be used to construct the grey level values expected for two equal sized active regions which extend into the inter-slice gap across the entire region from $z = -s$ to $z = 1 + s$.

There are 10 equations needed to calculate the areas under and over the linear boundary curve (a_1 and a_2) and their selection depends upon the geometry of the specific areas:

$$\begin{aligned}
 a_1 &= s + z_1 + \frac{z_0 - z_1}{2} \text{ for cases 1i and 2ai.} \\
 a_1 &= s + \frac{1}{2} \text{ for cases 1ii, 2bi and 2bii.} \\
 a_1 &= s + \frac{1}{2} - \frac{(\frac{1}{2} - z_1)(1 - w_{\frac{1}{2}})}{2} \text{ for cases 1iii, 2aiii, 2biii, 2biv, 3ii and 3iii.} \\
 a_1 &= w_{\frac{1}{2}}(s + \frac{1}{2}) + \frac{(w_{-s} - w_{\frac{1}{2}})(s + \frac{1}{2})}{2} \text{ for cases 2aiv, 3i and 3iv.} \\
 a_1 &= \frac{w_{-s}(s + z_0)}{2} \text{ for case 2aii.} \\
 a_2 &= z_1 - \frac{1}{2} + \frac{z_0 + z_1}{2} \text{ for cases 1ii and 2bi.} \\
 a_2 &= 0 \text{ for cases 1i, 2ai and 2aii.} \\
 a_2 &= \frac{w_{\frac{1}{2}}(z_0 - \frac{1}{2})}{2} \text{ for cases 1iii, 2aiii, 2aiv, 2biii, 3ii and 3iv.} \\
 a_2 &= w_{-s}(s + \frac{1}{2}) + \frac{(w_{\frac{1}{2}} - w_{-s})(s + \frac{1}{2})}{2} \text{ for cases 2biv, 3i and 3iii.} \\
 a_2 &= s + \frac{1}{2} - \frac{(1 + s - z_1)(1 - w_{1+s})}{2} \text{ for 2bii.}
 \end{aligned}$$

Finally, using these areas, g_2 and g_1 the values of each half of the voxel are calculated.

$$\begin{aligned}
 g_{a_1} &= a_1 g_1 + (1 - a_1) g_2 \\
 g_{a_2} &= a_2 g_1 + (1 - a_2) g_2
 \end{aligned}$$

However, we still do not know the orientation of these values, due to the ambiguity mentioned earlier. We also need to decide if a step interpolation model is suitable for the voxel under consideration. Both of these issues can be settled using local context.

Use of the Step Model within an Interpolation Algorithm

We first determine the grey level values above (g_{z+1}) and below (g_{z-1}) the current voxel g . Selection of the appropriate interpolation model requires some knowledge of the expected noise in the interpolated image. If the three grey levels are consistent with a straight line within the limits expected by noise σ , ie:

$$(g + g_{z+1} + g_{z-1})/3 - g < k * \sigma$$

where k is determined empirically, we can linearly interpolate the binary division of the voxel. We may also linearly interpolate if the grey level value is outside of the range of values permitted by linear combination of known pure tissue values. Otherwise, we can compute a pair of values using the above geometrical model. Ordering of the two values along the z direction is achieved by choosing the pairing which gives the minimum test statistic t based upon a summed difference between adjacent values

$$t_1 = |g_{a_1} - g_{z+1}| + |g_{a_2} - g_{z-1}|$$

or

$$t_2 = |g_{a_2} - g_{z+1}| + |g_{a_1} - g_{z-1}|$$

The results of applying the above interpolation procedure are shown in figure 6. The method made use of four pure tissue grey levels (CSF, grey Matter, white matter, air and fat) estimated from the histogram of grey levels

within the head and with a value of $k = 2$. The data was up-interpolated by a factor of 4, first with simple linear interpolation and then with one binary step interpolation followed by a linear. The data illustrates the blurring inherent in pure linear interpolation and the apparent improvement in image sharpness when using a step model. A more quantitative evaluation is needed to establish the best parameters and to identify possible artefactual structures.

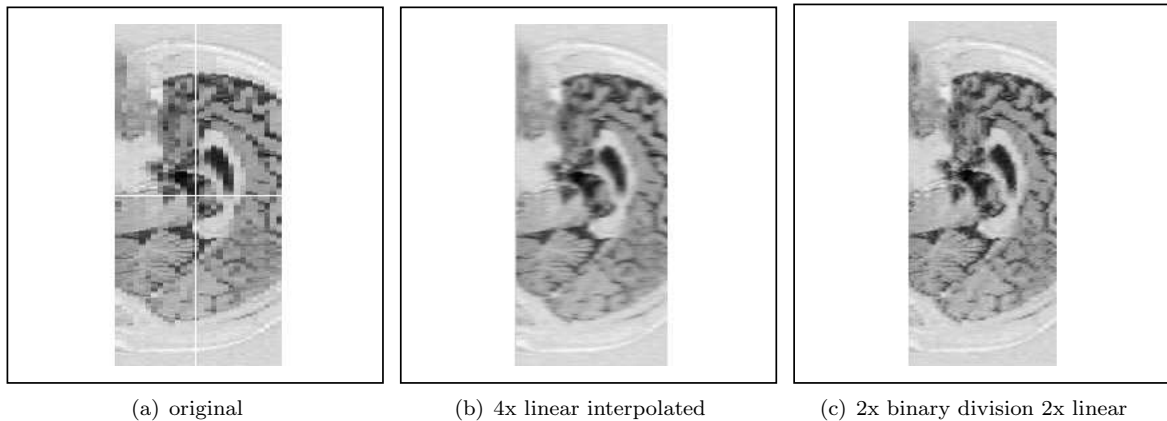


Figure 6: Up-sampling using linear and step interpolation in the zy plane.

Discussion

The interpolated grey-level values generated by this approach are those which should have resulted if the image were composed of a local linear boundary and had been imaged at twice the resolution in z and without an interslice gap. Moreover, the use of a linear model ensures that if there is no interslice gap ($s = 0$) then the sum of the two grey level values (g_{a_1} and g_{a_2}) will equal the original grey level. In the case of an interslice gap the sum of the grey levels is an estimate of the value which would have been obtained if the voxel had extended into the gap.

The above technique requires estimates of parameters for tissues and one control parameter k for the selection of the interpolation scheme. The pure tissue values can be obtained from segmentation schemes, but in addition it should be possible to determine all free parameters by optimising over the error on the ability to regenerate the original image after down-sampling in either the x or y direction, before finally upsampling in the z direction. Thus in principle this interpolation scheme could be optimised directly for the data it is intended to be used on. The performance of this algorithm is expected to vary with the grey level contrast between tissues and the extent of inter-slice gap it is required to deal with. Large interslice gaps (ie: $s > 0.5$) are almost certain to generate poor results. The results from this interpolation approach need to be quantitatively compared with other approaches, such as Sinc and Tri-Linear interpolation.

This method is specifically designed to work with normal tissues and we would not expect it to be of great benefit in diseases which alter the signal characteristics of the tissues. However, there are many tasks, particularly involving analysis of normal brain structure (for example ageing) for which this technique would provide a useful way of up-sampling data prior to quantitative analysis of boundaries. It is our intention to use it as a pre-processing stage in a cortical thickness analysis. As the technique makes explicit use of a boundary model, the output data is also consistent for use in graphical rendering packages which assume iso-greylevel contours. In fact the idea of using an assumption of a continuous linear boundary between two tissues is exactly the principle behind the marching cubes algorithm for the rendering of 3D surfaces [5], which has been shown to provide substantial subjective improvement in the rendering of structure on the scale of the data quantization.

The method described here attempts genuine up-interpolation, rather than padding with extra values of the same intrinsic frequency content. As such even a factor of two expansion might be seen as significant. Although we have only described binary division of the input voxel here, we could also imagine extending the technique to 3 or more sub-divisions. However, we might expect that this would soon lead to problems with accuracy and loss of structure. If the performance of the marching cubes algorithm is to be used as a guide, up-sampling by a factor of three might be expected to be a reasonable limit for this approach. The technique is also expected to be limited by the scale of the structures it is interpolating. It can only reconstruct a single boundary within a voxel accurately. If a structure is so thin as to begin and end entirely within the voxel (Figure 7) then this partial volume contribution

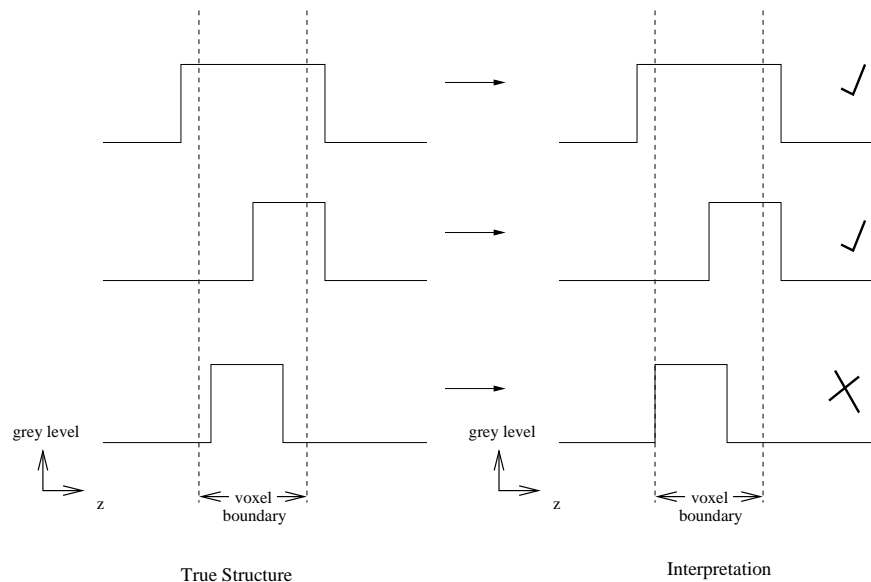


Figure 7: Limiting Resolution.

will be moved from its true location towards one end of the up-interpolated voxels. This problem will be at its most extreme when the tissue is oriented perpendicular to the z direction. In this case, a structure of half the thickness of the voxel size will have an incorrect interpretation 50 % of the time, with an r.m.s. error in assumed position of $0.25/\sqrt{12}$ voxels for these data. This will be at a maximum value of 0.25 voxels when the structure is central to the voxel (assuming that voxel ordering is always correct). This is not a large error in structure and may even be considered tolerable, particularly when considered in comparison to the effects of image noise. The frequency and scale of this problem will grow for smaller structures, reinforcing our previous comment on the likely limits on up-interpolation using this technique. For the particular case of interpolating brain tissues we would not expect a problem with grey matter, in that it is expected to be 3-5mm thick, which is above this scale limit for conventional imaging protocols. There may however be problems with narrow sulci, but at least these errors are not expected to be systematic over regional structures, meaning that summary variables such as mean vector length should not have bias. Thus it is expected to be a safe process as a precursor to cortical thickness measurement.

One final point, the step interpolation method is also a valid means of interpolating partial volume probabilities. However, for this case there are effectively only two pure tissue values with grey level values defined as 0 and 1. Thus, the problem of calibrating several pure tissue parameters and computing appropriate partial volume values (f) could be completely eliminated if the results of a partial volume segmentation were to be step interpolated rather than the raw grey level image.

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