Re-Normalised Sinc Interpolation For Rapid Reslicing Of MRI Data

N. Thacker, E. Vokurka and A. Jackson
Clinical Radiology, Department of Medicine
University of Manchester, Manchester, England

Introduction

It has long been established that the appropriate way of reslicing volume MR images is to use the method of sinc interpolation [1, 3]. We have found, like other authors before us, that large convolution kernels are needed in order to produce accurate reslice data. However, we have found that the major component of the error introduced from interpolation with small kernels, is due to a first order normalisation problem introduced by truncation. We demonstrate the characteristics of this problem and show how it can be eliminated, so that accurate reslice data can be obtained with small kernels. The required changes in computation are simple and significantly reduce the processing requirement for any given interpolation accuracy.

Methods

The decomposable sinc interpolation algorithm from $X, Y, Z$ to $x, y, z$ co-ordinates with a cosine Hann (Hamming) window is defined as follows,

$$I(x, y, z) = \sum_{X} \sum_{Y} \sum_{Z} f(X, Y, Z) \cdot Hs(x, X) \cdot Hs(y, Y) \cdot Hs(z, Z)$$

with

$$Hs(a, A) = \frac{\sin(\pi(a - A))}{2\pi(a - A)}(1 + \cos(\pi(a - A)/(R + 1)))$$

The Hamming function eliminates problems with oscillatory effects at discontinuities and guarantees that the convolution coefficients fall off to zero at the edge of the sinc kernel (i.e. at $a = R + 1$). We also confirmed that this process was the same as used in our version of Woods’ reslice software [5]. We therefore believe that this reslice technique is equivalent to that being used by the vast majority of the research community [4]

Although this kernel would be optimal if it were the size of the image, computational aspects limit its size in practice. Truncation of the kernel makes the kernel sub-optimal and results in position dependant interpolation errors [Figure 1]. However, the first order effect of truncation can be eliminated by re-normalising the kernel. This can be accommodated within the standard algorithms for sinc interpolation or the framework of the so-called ‘fast-sine’ techniques [1]. On an NMR image this renormalisation will completely remove the first order error on the estimated grey-level leaving only error terms due to the inadequacy in the assumed Fourier model. The renormalised kernel is simply computed by replacing $Hs$ in the original equation with

$$Hs'(a, A) = Hs(a, A)/\sum_{A} Hs(a, A) = Hs(a, A)/|Hs(a)|$$

The effect of this is most quickly computed as a renormalisation of the final greylevel result.

$$I'(x, y, z) = I(x, y, z)/(|Hs(x)||Hs(y)||Hs(z)|)$$

Results

The standard sinc interpolation method was compared to the new renormalised technique on a typical MR brain image for a range of kernel sizes. The gold standard for sinc interpolation was defined using a large (15x15x15) kernel. On the basis of the relative percentage error, the interpolated image is found to be far more accurate and no longer display any of the systematic effects of the original technique. The performance ([Figure 2 a]) shows an immediate improvement over linear interpolation even for a 5x5x5 kernel, with a performance close to that obtained with the original 15x15x15 kernel. With the first order error eliminated, remaining errors should be proportional to image contrast (i.e. the dynamic range). The results seem to be comparable with those from the technique presented in [9], which is to appear in the latest version of the SPM package [6].

Conclusions

The time required for interpolation with the improved method is almost identical to equivalent sized kernels in the standard technique. Theoretically, for a normal sinc with pre-computed kernel coefficients, the convolution time would scale with the volume of the kernel (the straight line in [Figure 2 b]). For our implementation, without precomputation, this relationship becomes evident for large kernels, (a 206x206 slice on a multi-user 167 MHz SUN Ultra Sparc I and a Pentium II 300 PC). A comparison of using Wood's software gives a ratio of 4x4x4 to 14x14x14 reslice time of 30.6. The ability to use a 5x5x5 kernel in place of a 13x13x13 thus represents a computational saving factor of between 7 and 30.6. Using the timing for the linear interpolator as the minimum time for setting up a loop over a slice of data and the per voxel convolution rate, we can estimate the time curve for the 'fast sinc' (the second line in [Figure 2b]). The dominant contribution to this algorithm is expected to be the three loops over the data volume not the convolution stage. As a consequence this technique is not likely to be much faster than the standard techniques for small kernels. The renormalised kernel technique not only improves the computation efficiency of the algorithm, but also seems to make 'fast sinc' approaches less significant particularly when taking into account flexibility and memory requirements. Our software is available as open source as part of the TINA system from [7].

References


Fig. 1: Typical errors in a MR head image following reslicing.

Fig. 2: (a) Relative error and (b) Time curves.