Edge Detection at Low Resolution using Padé Approximants

M. F. Callaghan[1], D. J. Larkman[1], M. C. Wiltshire[1], J. V. Hajnal[1]

[1]Robert Steiner MRI Unit, Imaging Sciences Department, Clinical Sciences Centre, Hammersmith Hospital, Imperial College London, London, United Kingdom

Introduction: Many applications of MRI involve image segmentation for quantitation and other purposes. Extraction of salient structures in images often relies on use of image thresholds or direct edge detection both of which benefit from high-resolution data to achieve reliable and accurate results. Threshold based measurements are also often highly dependant on the threshold level chosen and this dependence is accentuated at lower resolution. In conventional MRI, acquiring higher resolution data increases the scan time due to the serial nature of the phase encoding process. This reduces the achievable temporal resolution and increases the risk of motion artefact. Here we present a method for automatic edge detection based on Padé approximants, which does not require any thresholding and, more importantly, can be preformed with reduced data sets. This method was tested using cardiac data since delineation of the boundary between the myocardium and the blood pool is often required in the assessment of cardiovascular function and since cardiac MR has added time constraints that can constitute a critical limiting factor.

Methods: Padé approximants are rational polynomials, P(z)/Q(z), of a specified order (N) in z, whose power series expansion agrees with a given power series to the highest possible order[1]. These approximants are known to accelerate the convergence of partial Fourier series and can therefore be applied to MR data[2]. This is done by using the substitution $z=e^{i\Delta k.x}$ where Δk is the sampling interval in k-space and x is the corresponding spatial variable (all points in the image domain are represented on the circumference of the unit circle in the complex z plane). This substitution allows the explicit Fourier transform of acquired k-space data to be represented as a simple power series in z for which Padé approximants can be calculated. For a given order N, N+1 phase encode lines are required from the centre of k-space in one direction ($k_0 - k_N$). Discontinuities in the image domain are captured by the denominator polynomial, Q(z), which goes to zero at locations corresponding to these discontinuities. The location of image domain discontinuities, or edges, can be found by determining the roots of Q(z). This is done in both the frequency and phase-encoded directions and the results are combined. Although there is no time constraint in the frequency encode direction, this step is necessary in order to determine the location of edges that are tangential to the phase encode direction. The acceleration properties of the Padé method should allow edge locations that would only be precisely defined in high resolution MR images to be determined using a small fraction of the data, so allowing reduced phase encoded acquisition. To test this hypothesis high-resolution (512x512 Matrix, 33cm FoV, TE/TR=25/1714ms) cardiac images were acquired using a PDw/BB sequence on a 3T Philips Intera scanner. These were used as reference images and their k-space data sets were then progressively truncated to qualitatively evaluate the performance of the edge detection at lower resolution. To quantitatively assess edge location high resolution (512x512 matrix) images of a phantom consisting of concentric cylinders (6.3mm and 10.8mm in dia.) designed to mimic the ventricular geometry of a short axis view of the heart were used.

Results: Table 1 shows errors in the area measurements determined by thresholds at 10%, 50% and 90% contrast as a function of phase encoded resolution for the phantom images compared to the Padé method. Note that the Padé estimate remains within 1% down to N=32 (using 15% of the data). Below this it fails because there are too few Fourier terms to distinguish the inner and outer boundaries of the phantom. By contrast the Fourier reconstruction shows an error of 3.63% for the correct threshold with a range of (-10.29 to 2.70)%. In the *in vivo* images, edge locations were correctly identified down to N=23+/-8. The precise point of failure depends on the details of the anatomy in each case. Figure 1 shows an example.

Table 1: % Deviation of Area Measurement relative to Mean Threshold result from a high-resolution reconstruction

Terms	50% Threshold	90% Threshold	10% Threshold	Padé
128	-2.96	-8.84	4.06	-0.14
64	-2.90	-10.29	2.70	-0.29
32	-5.02	-13.18	7.40	8.98

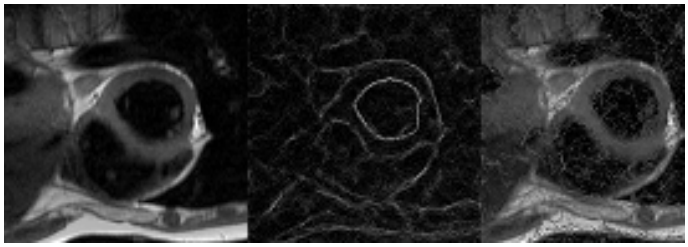

Fig. 1: High Resolution Cardiac image, right; Edges found using N=32, centre; Overlaid edges with insufficient data

Discussion: The use of Padé approximants in edge detection offers the possibility for threshold independent structure delineation at low resolution. The use of fewer data means that greater temporal resolution can be achieved and this may be of particular value in time-critical applications such as in cardiac MR as illustrated. It may also allow quantitative measurements to be made with reduced sensitivity to motion artefact and be helpful for single shot images where the number of data lines is limited. The degree of reduction in acquired data that can be achieved depends on the structures being imaged. The distinguishing benefit of this technique is that edges are detected by taking full advantage of the intrinsic Fourier nature of raw MR data.

References:

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