A MULTiresolution APPROACH TO FLOW
FEATURE EXTRACTION
FROM PHASE CONTRAST MRA

Abhir H. BHALERAO 1, Paul E. SUMMERS 2
Department of Medical Physics, St. Thomas’ Hospital, London, UK 1
Department of Radiological Sciences, UMDS, Guy’s Hospital, London, UK 2
a.bhalerao@umds.ac.uk p.summers@umds.ac.uk

Abstract

Phase contrast magnetic resonance angiography provides a uniquely rich information content in a relatively short imaging time. In effect, not one, but four image data sets are obtained – a T1 weighted anatomical image, and three images of orthogonal velocity components. This information is only crudely communicated in traditional maximum intensity projection views which are based on a (vector) sum of components of the velocity images. Similarly, surface rendered views of the vessels represent only a thresholding of the new velocity and are not uniquely conveyed to the viewer.

A model based segmentation method to determine the vascular network is described in detail. The algorithm employs a multi-resolution image model where the centre lines of blood vessels are modelled as interconnected, piece-wise linear, 3D curves. Parameters of the model, and hence the segmentation, are obtained by first expanding the image data into an oct-tree representation. Curve segments are identified across a number of voxel resolutions, which represent the current best fit of the data to the model. Probable curves are then inferred through these “trace” points by means of an adjacency graph, which forms the basis of the symbolic description. The method’s computational complexity is shown to be low (equivalent to less than a filter kernel of size 3) and its robustness and accuracy is demonstrated for real data. The paper concludes with a discussion of the possible ways to exploit the potential of such general purpose approach for both visualisation and flow modelling.

Keywords: 3D Image Processing, Multiresolution Image Segmentation, Magnetic Resonance Angiography, Phase Contrast Angiography

1 Introduction

Magnetic resonance imaging (MRI) is used to map the distribution and dynamics of nuclei such as hydrogen. MR image data generally consists of two parts (the intensity and phase of the signal) related to the magnitude and orientation of the magnetisation vector which generated the signal. Typically only the intensity information is displayed in clinical images. Imaging can be adapted to show blood in contrast to the surrounding stationary tissues. This application of MRI referred to as MR angiography (MRA) has become widely used in the demonstration of vascular morphology. The two main classes of MRA techniques use blood’s motion to modify the intensity (Time of Flight techniques) or phase (Phase Contrast techniques) of the blood signal relative to that of static tissues. The spatial localisation and resolution of the imaging procedure provide a depiction of vessel position and patency. Because blood vessels are sparsely distributed in the tomographic images, alternative visualisation tools are used to provide a coherent view of the vascular network. The most common approach is to use a maximum intensity projection (MIP).

The reliance on velocity to establish contrast enables MRA to provide a quantitative description of blood flow. Time of Flight techniques are most widely available, but have severe limitations in terms of robustness of the quantifiable relationship. Phase contrast angiography (PCA) produces a vector image i.e. estimates are formed of three orthogonal components of the velocity field. In
effect, not one, but four images are obtained - a T1-weighted anatomical image, and three images of orthogonal velocity components. Phase-contrast magnetic resonance angiography provides a uniquely rich information content in a relatively short imaging time. The information is only crudely communicated in MIP views which are based on the square root of the sum of squares of the velocity component images. Similarly, surface rendered views on the vessels represent only a thresholding of the net velocity. In particular, directionality and magnitude of velocity are not conveyed to the viewer. To incorporate the function information into an image which also portrays the spatial arrangement of vessels, is a difficult task with the large volumes of data which may be present. Attempts have been made to superimpose the velocity field information on MIP or tomographic views by the use of colour, or the display of moving points which “flow” along the velocity field. Whilst the colour approaches works well with Doppler ultrasound, volumetric MR scans tend to overload the viewer with ambiguous direction, depth and connectivity. Bubble tracking on the other hand is very susceptible to noise in the velocity field and the limited spatial resolution relative to vessel size in many vessels of interest. Much of the post-processing of MRA data is aimed at better visualisation - (e.g. MIP), particularly image enhancement, such as improving contrast and local connectivity [1] [2]. There have also been a number of interesting contributions in the area of the enhancement of MRA data to reduce flow artifacts [3] and to better determine blood flow streamlines [4]. These workers have employed iterative, local optimisation methods to improve flow estimates by essentially smoothing the data constrained by anatomical structure. Relatively little work has been done in using more sophisticated techniques currently being used by researchers in computer vision.

Gering et al. [5] have sought to use the vessel centre lines from the line tracking process to produce a symbolic description of the MRA network which encodes key topological locations, such as branch and end-points and local lumen diameter. Although the segmentation approach described here differs radically from this single resolution approach, they share essentially the same symbolic representation output. A 3D graph of the vascular system is obviously the most concise and general purpose representation (in the sense that it can provide all the necessary data for visualisation, quantification and flow modelling). By using MRA obtained using phase contrast pulse sequences, the direction as well as the speed of the flow can be used to obtain a segmentation and forms an additional parameter to the encoded representation.

This paper considers the automatic extraction of a concise symbolic representation of vasculature. A model based segmentation method to determine the vascular network is described in detail. The algorithm employs a multi-resolution 3D curve extraction method based on an image model where the centre lines of blood vessels are modelled as interconnected, piece-wise linear, 3D curves. Parameters of the model are determined, and hence the segmentation is achieved, by first expanding the image data into an oct-tree representation. Curves segments are identified across a number of voxel resolutions, which represent the current best fit of the data to the model. Probable curves are then inferred through these ‘trace’ points by means of an adjacency graph, which form the basis of the symbolic description. The method’s computational complexity is shown to be low (equivalent to less than a 3 × 3 × 3 filter kernel) and its robustness and accuracy is demonstrated on examples of real MRA data.

This model-based approach makes direct use of the vector magnitude and direction information to form velocity averages over a succession of scales. The resulting oct-tree representation in turn is well suited to further extensions and manipulations for display and processing of the data. Moreover, the data volume is reduced in accordance with the sparsity of the vascular network making subsequent manipulations more efficient than is possible when handling the full data volume.
2 A Multiresolution Model for Curves in 3D

2.1 Uncertainty and Multiresolution Analysis

In multiresolution methods an image is analysed over several resolutions or scales. This is equivalent to trading off high position resolution, present at the image plane, for greater class resolution at lower scales (the uncertainty principle in image analysis [6]). Multiresolution methods are characterised by a two stage process of building some multiscale representation (quadtree, pyramidal [7], oct-tree, Wavelet representations [8], Multiresolution Fourier Transform [9]), which is an expansion of the data into the scale-space, followed by a `coarse-to-fine' refinement strategy, propagating parameter estimates back down to the full spatial resolution, whilst maintaining any gains in estimates of class domain parameters. Implicit in this scheme is the notion of scale consistency, which is based on the assumption that there is more than one scale where there is just one object within the neighbourhood of a given point.

In 3D image analysis, the simplest, spatial multiresolution structure is the oct-tree in which spatial resolution is reduced by a factor of 2, in each dimension, at each successive scale. Each voxel at a coarser resolution is an average of 8 voxels on the current level (figure 1). For a 3D volume of size $N \times N \times N$ there will be $M = \log_2 N + 1$ levels. The total storage required for an oct-tree is given by $\sum_{i=1}^{M} 2^3 \approx \frac{16}{7} N^3$. Within the oct-tree structure, each node $i_{ijk}(l)$ can be denoted by the scale-space position vector $\xi(l) = (i,j,k,l)^T$ and represents a cubic voxel region $\Lambda_{\xi}$ of the image volume (at level $M$)

$$\Lambda_{\xi} = \bigcup_{0 \leq m,n,o < 2^{M-1}} (2^{M-l}i + m, 2^{M-l}j + n, 2^{M-l}k + o, M)$$ (1)

Furthermore, $\xi(l), l < M$ has 8 ‘children’ $\xi_{ik}(l + 1), 0 \leq k < 8$, such that $\xi_{ik}(l + 1) \in \Lambda_{\xi}$.

2.2 Linear Multiresolution Image Models

The model used here for the segmentation of MRA data is an extension to 3D of the simple 2D curve segmentation model used by Culway [10] and is based on a general class of linear multiresolution image models [11]. The generalised linear multiresolution image model may be defined by a recursive operation:

$$s_{ijk}(l) = \sum_{mno} A_{ijk,mno}(l) s_{mno}(l - 1) + \sum_{pqr} B_{ijk,pqr}(l) u_{pqr}(l)$$ (2)
where \( s_{ijk}(l) \) is the ‘image’ at level \( l \) of the model given by taking a linear combination of the level above (lower spatial resolution) plus an innovations image \( w_{pq}(l) \). The linear operators \( A \) and \( B \) ‘construct’ the image by controlling the features from the coarser, ‘parent’ resolution and the innovations used to form the ‘child’ level. The resulting image \( s_{ijk}(M) \) is given by level \( M \) of the model. Figure 2(a) show a typical realisation of the 2D model for a curve network. Local image features are represented at different scales, creating an inhomogeneous tessellation of the image into square regions (blocks) of different sizes. The larger features are represented by larger blocks at coarser spatial resolutions whereas detail, e.g. high curvature, is represented by smaller blocks. Each of these regions is subjected to the constraint of containing a single local feature.

The curve model is particularly simple to generate as these linear operators act as selection functions taking an appropriate octant of the previous level or of the innovation level. Each block is a locally defined real function which has an associated orientation and position vector, which models a single line feature in each block (prototype)[10]. The prototype can be extended to model both region and boundary features, including corner and branch points [12].

There are three main stages in deriving the image signal from the model: a trace process, a curve process and a segment process [9]. The network of generated curves then represent the centre lines of a given vascular system.

1. The Trace process

A set of trace points, \( \zeta(l) \) is defined for the 3D curves

\[
\zeta(l) = \zeta_i(l) + \bar{v}_i(l)
\]

where \( \bar{v}_i(l) \) is the offset of the trace point in the block. Associated with each trace point are the parameters \( a_i(l) \), an amplitude and \( \bar{v}_i(l) \) which is an estimate of the tangent of the curve through the block (figure 2(b)). The set of parameters defining the trace points are selected from the parameter field \( \phi_i(l) \) within each spatial oct-tree block \( \zeta_i \) and is modelled as an evolution through scale, as in equation (2), using the conditional probabilities

\[
P(\phi_{i,k}(l+1) | \phi_{i,k}(l)), 0 \leq k < 8
\]

subject to the initial conditions \( P(\phi_{i,k}(0)) \) at the coarsest scale. The amplitude parameter \( a_i(l) \) serves both as an estimate of strength of a curve element in the block and, if set to 0 or -1, as a scale selection parameter. This allows the successive approximation through scale to be terminated before the full spatial resolution is regained.
2. The Curve process

The trace points are linked together based on their orientation and position estimates. A set of connections or links $\lambda_{ij}(l, m)$ is defined between pairs of neighbouring oct-tree blocks $\xi_i(l), \xi_j(m)$

$$\lambda_{ij}(l, m) = 1, \text{ if } \chi_i(l) \text{ is linked to } \chi_j(m)$$  \hspace{1cm} (5)

A simple model for this is defined through the conditional probabilities

$$P(\lambda_{ij}(l, m) \mid \phi_i(l), \phi_j(m)) = f_1(\theta_i(l) - \theta^*_{ij}(l, m)) f_2(\theta_j(m) - \theta^*_{ij}(l, m)) f_2(\| \theta_{ij}(l, m) \|)$$  \hspace{1cm} (6)

where $\theta_{ij}(l, m) = \chi_i(l) - \chi_j(m)$ is the displacement vector between the two trace points. The link states thus specify a curve as an ordered set of points $\Gamma_i = \{ \phi_{i_1}(l_1), \phi_{i_2}(l_2), \ldots, \phi_{i_n}(l_n) \}$ for which

$$\lambda_{k,k+1}(l_k, l_{k+1}) = 1, 1 \leq k < n$$  \hspace{1cm} (7)

Note that this does not cater for branching of curves which is dealt with by starting a new curve whenever a probable branch is encountered (i.e. when an encountered block has only one link to a neighbour).

3. The Segment Process

In [9] and [10], the image signal produced from the parameters selected by the curves in the model were used to generate the coefficients of the appropriate Multiresolution Fourier Transform (MFT) blocks. This was done by modelling the image features (edges) by a Markov process in the Fourier domain and applying an inverse MFT.

In this work, the segmentation is performed wholly in the spatial domain, using a block based Hough transform, so the signal to be produced is modelled in the appropriate Hough accumulator space. The dimensionality of the Hough space is reduced by knowing the tangent of the curve segment in the block $\theta^*_i(l)$ and reduces to a 3D accumulator array for the position estimator $\theta^*_i(l)$ only. The image signal is then simply the 3D lines in the selected image blocks $\Lambda_m$, which have the parametric equations

$$x_{ijk} = 2^M - l(\chi_m(l) + \theta^*_m(l)), \forall m$$  \hspace{1cm} (8)

where $\theta$ is normalised and the indices $ijk$ are constrained to lie within the block $\Lambda_m$.

3 Segmentation: Estimating parameters of model

Within the framework of the 3D model, the segmentation process amounts to estimation of its parameters with decisions based on scale consistency criteria, whose aim is to tessellate the phase-space (oct-tree) into the smallest set of disjoint regions for which the data are consistent with the model. The best-fit tessellation is then transformed into a Boundary Adjacency Graph which is a symbolic representation of the feature blocks and their neighbourhood relationships. From this 3D curves, representing the vessel centre lines, are inferred by a relaxation process. Because of the great data reduction achieved by this stage, it is possible to use exhaustive graph-theoretic methods without the fear of exponential computation burden.

1. Oct-tree generation

The first step is to generate an oct-tree of the PCA data which is a volume of flow vectors $x_{ijk}, 0 \leq i, j, k < N = 2^M$. Using a lowpass filter kernel $A_{mnos}$, the general form of the processing required to construct the oct-tree is the recursive operation:

$$x_{ijk}(l) = \sum_{n=-K}^{K} \sum_{m=-K}^{K} \sum_{o=-K}^{K} A_{mno} x_{i(2l+m)(2j-m)(2k-o)}(l+1)$$  \hspace{1cm} (9)
where there are $M + 1$ levels, $0 \leq l \leq M$, and the base of the oct-tree is the image $x_{ijk}(M) = x_{ijk}$ and the kernel is of size $(2K + 1) \times (2K + 1) \times (2K + 1)$. Note that the scale index $l$ appears as the argument of the function $x(l)$, whereas the spatial indices are given as the subscripts $x_{ijk}$. The simplest form for the generating kernel is used where the coefficients $A_{mn0} = 0.125, 0 \leq m, n \leq 1$.

2. Tessellation: Single feature hypothesis and orientation consistency

For each block $\xi$, an orientation consistency measure [13] is calculated which estimates the coherence of the flow vectors within the block. This measure is given by

$$c_{\xi} = \frac{|\sum_{ijk \in \Lambda_{\xi}} x_{ijk}|}{\sum_{ijk \in \Lambda_{\xi}} |x_{ijk}|}$$

which is simply the ‘length of the average flow vector’ over the ‘average length’. This measure has the characteristic of being small if the vectors are randomly oriented, i.e. they sum to zero, and large if there is a strongly oriented feature in the given block. Furthermore, this estimator can be rapidly calculated by creating an oct-tree of the magnitude image $|x_{ijk}(M)|$ and dividing into the oct-tree of the signal.

Starting at the coarsest spatial resolution, the oct-tree is traversed in a pre-order traversal (root, followed by sub-trees), and terminated if the highest spatial resolution is reached. A decision is taken at each node to either terminate the tree at this point or to continue the search to the next, higher resolution. The hypothesis testing is done as follows:

Hypothesis $H_0$: there is no feature or a single feature in block

Accept $H_0$ if $c_{\xi} < T_n$ or $c_{\xi} > T_c$ (11)

where the significance level $T_n$ is set low to exclude noisy blocks where there is no significant signal activity, and $T_c$ is set high to include only very consistent blocks. The lower threshold creates the ‘dead’ branches in the resulting tree and the higher threshold the blocks from which the features are extracted. In practice, it was found that setting $T_n = 0.5\hat{c}$ (half the mean consistency across the entire oct-tree) and $T_c = \hat{c}$, gave satisfactory results across a variety of real and and synthetic data sets. However, parameter estimation of the signal and noise variances would be more effective in controlling these confidence levels [12].

A important property of this approach is the ability to repeat the hypothesis testing with lowered significance levels if there is sufficient evidence of a feature in a given locality. This can be used to good effect to close gaps in detected curve segments by re-examining the raw data (see below).

Next, a Hough Transform [14](HT) is used in each trace point block to determine the $\tilde{m}$ since the orientation or slope $\tilde{\theta}$ is already known (figure 2(b)). Given the 3D line in some arbitrary block $\xi$

$$x_{ijk} = 2^{M-l}(\tilde{\chi}(l) + \tilde{\theta}m(l))$$

the HT $H_{ijk}$ reduces to

$$H_{ijk} = \sum_{l=0}^{L} x_{ijk} = 2^{M-l}(\tilde{p}, \tilde{q}, \tilde{r})^T(l) + \tilde{\theta}m(l)$$

and the peak in this array estimates the position $\tilde{m}$.

3. Curve Inference and Tracing

The oct-tree nodes selected from the tessellation process are linked together to form an Adjacency Graph [15]. Nodes are considered neighbours if they either share a face, an edge or a vertex, or
a combination of these attributes. In a homogeneous 3D grid, a node would have altogether 26 possible neighbours: 6 face, 12 edge and 8 vertex.

Let $\mathcal{N}_x$ denote the neighbourhood of node $x_i$, then it has cardinality $\text{card}(\mathcal{N}_x)$ links given by

$$\mathcal{L}_{x_i} = \bigcup_{x_j(m) \in \mathcal{N}_x} \lambda_{ij}(l,m)$$

Each link $\lambda_{ij}(l,m)$ is given a link strength based on the orientation of the link, given by the angle of the displacement vector $\gamma_{ij}(l,m) = x_i(l) - x_j(m)$, and the orientation (slope) of the feature estimates of the blocks it connects. The link probability is given by

$$P(\lambda_{ij}(l,m) | \phi_i(l), \phi_j(m)) = f_1(\theta_i(l) - \theta_j(l, m)) \times f_1(\theta_j(m) - \theta_j(l, m))$$

and $f_1(\theta) = 0.5(1 - \cos \theta)$ which is at a maximum at $\theta = \pm \pi$.

Before curves are traced, all possible combinations of pairs of links are examined within each node link set $\mathcal{L}_x$ and ordered into decreasing likelihood that they form a curve segment. For a node with $n = \text{card}(\mathcal{N}_x)$ links, there are a possible $n(n-1)/2$ link pair combinations:

$$\gamma_i = \bigcup_{j=i} \bigcup_{x=0} \bigcup_{k=j+1} \lambda_{x=i} = \{\lambda_{ij}, \lambda_{ik}\}$$

The link pair combinations are indexed $0 \leq x < n(n-1)/2$ and the oct-tree level parameters have been dropped for clarity. Each link pair $\lambda_{x} \in \gamma_i$ is given a probability defined to be

$$P(\lambda_x) = P(\gamma_{x0})P(\gamma_{x1})f_3(\gamma_{x0}, \gamma_{x1})$$

where the subscripts $x0$ and $x1$ refer to the first and second links of the link pair set. The function $f_3(\theta) = 0.5(1 - \cos \theta)$, which has maxima at $\theta = \pm \pi$, expresses the requirement to give the highest probability to the 3-block curve segment with the minimum curvature.

Next, starting from the largest spatial blocks where the feature estimate is likely to be most reliable, curves are traced in both directions. The neighbours $\mathcal{N}_i$ of each block $i$ are examined and the curve is continued by selecting a link $\lambda_{ij}$ if the link is a member of the maximum probability pair in both blocks it connects i.e.

$$\lambda_{ij} \in \lambda_{\text{max}} P(x) \in \gamma_i \text{ and } \lambda_{ij} \in \lambda_{\text{max}} P(y) \in \gamma_j$$

By relaxing this condition to allow for linking through link pairs which have lower probabilities, curves with greater curvature segments will be included. If a curve cannot be traced further within the continuation criteria, it is terminated and a new curve begun. Traced curves are not allowed to visit a given block more than once in an attempt to find as many independent paths through the trace points as possible. Thus far, no attempt has been made to join these extracted curve segments with each other using a higher-order process.

It has been already been demonstrated in [10] [9] etc. that within such a scheme, it is possible to fill gaps where there is no feature estimate and span more than a 1st order neighbourhood within the adjacency graph, by re-examining the original data in light of the greater confidence gained from results of the initial segmentation. Also, the sparseness of the symbolic structure obtained by this stage permits iterative schemes to be used, which would otherwise be computationally prohibitive [12].

4 Results

Figures 3(a)-(d) illustrate stages of the multiresolution curve extraction algorithm run on part of a MRA of the head. The original data set was $256 \times 256 \times 64$ and the figures illustrate one $64^3$ part of this data set.


<table>
<thead>
<tr>
<th>Procedure</th>
<th>Storage (voxels)</th>
<th>Multiplications per voxel</th>
</tr>
</thead>
<tbody>
<tr>
<td>Original Image Volume</td>
<td>$N^3$</td>
<td>0</td>
</tr>
<tr>
<td>Oct-Tree</td>
<td>$\frac{N^2}{10}N^3$</td>
<td>$\frac{N^2}{10} \times 8$</td>
</tr>
<tr>
<td>Node Selection</td>
<td>$\frac{N^2}{10}N^3$</td>
<td>$\frac{N^2}{10}$</td>
</tr>
<tr>
<td>Tessellation</td>
<td>Nodes $\frac{N^2}{10}N^3 \times 10$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Links $\frac{N^2}{10}N^3 \times 3$</td>
<td>0</td>
</tr>
<tr>
<td>Block Hough Transform</td>
<td>$\frac{N^2}{10}N^3$</td>
<td>$\leq 1$</td>
</tr>
<tr>
<td>Curve Tracing</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>$4N^3$</td>
<td>14</td>
</tr>
</tbody>
</table>

Table 1: Computational requirements of curve extraction

Figure 3(a) is a surface view of the region at a manually set threshold of about 3%. The result of the initial segmentation where the data set is tessellated into voxel blocks is shown in figure 3(b). The block structure shown by the red wire-frame cubes has been overlaid on to the original. The larger voxel blocks originate from coarser resolutions of the oct-tree expansion of the original data, whereas the smaller blocks have been chosen from the finer spatial resolutions. Notice that the single feature criterion tested by the hypothesis of equation (11) results in relatively large features being represented at the coarser resolutions and the finer detail and high curvature at the higher spatial resolutions. The background area of the image are areas of no significant activity (or noise blocks) and will be dead-branches in the octree. Each of the feature voxel blocks will equate to a trace point in the remainder of the algorithm.

Figure 3(c) shows estimates of the slope of the features within each selected block, with each feature having a position offset within the block from the HT stage. The final part of the algorithm is to infer curves from these trace points. The result of this is shown in figure 3(d) where each contiguous segment has different colours. Overall, there is good structural correspondence between the vessels seen in the voxel surface rendering and the extracted curves. In particular, local connectivity is established by the curve extraction in instances where there is fragmentation of the surface rendered view.

Figures 4(a)-(d) illustrate the curve extraction results for two parts of a head-neck data with figure (d) showing internal and external carotids.

**Computational Requirements**

Table 1 shows estimates for storage and computation required (expressed in multiplications per voxel) for the main steps in the curve extraction algorithm. An estimate of 4% has been used for the typical number of extracted trace points with an average connectivity of 8 [15]. Note that although the block based HT is expensive to calculate, requiring a computation order of $O(n^4)$ for block sizes of $n$, the figure in multiplications per voxel works out to be negligible. The bottom row shows that approximately 14 multiplications per voxel are necessary to complete the computation, which is less than that required to run a filter kernel of size 3 (equivalent to 27 multiplications per voxel) over the original data set.

5 Conclusions

This paper has considered a multi-resolution, model based segmentation method for MRA. It is a spatial domain based technique and an extension to 3D of a 2D curve segmentation method reported elsewhere (e.g., [9]). It was demonstrated to produce a concise symbolic description of the MRA data (in the form of vessel centre lines) and is efficient in its computational complexity, and based on a
generalised and flexible image model which has great potential as a basis for both qualitative and quantitative assessment of MRA data.

The work and results presented thus far are preliminary and currently there are several areas where consolidation and enhancement is necessary. There is a need to assess the levels of noise in the data in situ (as in [16]), to better control the confidence levels used for the hypothesis testing. Curve tracing is currently done probabilistically based purely on the local curvature. By considering the physical measurements of the data being imaged, speed of blood and the vessel diameters, local connectivity could be established using a conservation of mass constraint. Also, there is need to explicitly defined bifurcations as part of the signal model.

With regards to visualisation, some experimentation has already been carried out to represent flow direction by pseudo-colour and using the multi-resolution vectors for generating a limited MIP and predicting probable flow, similar to the bolus injection experiments described in [17]. There is also potential to use the symbol structure to analyse variability between patients by building point based distribution models (PDMs [18]) and for flow modelling, if the MRA flow estimates can be relied upon.

Acknowledgements

The authors would like to thank the radiographers and radiologists at the MR units at both St. Thomas’ and Guy’s Hospitals. They would also like to acknowledge the help and enthusiasm from the members of the Image Processing Group of Radiological/Neurological Sciences, UMDs at Guy’s Hospital. Particular thanks to Dr. David Hawkes for his ideas and continuing support.

This work is supported by the Special Trustees of St. Thomas’s Hospital Trust.

References


Figure 3: Results on one part of head data set
Figure 4: Results on head-neck data set