Multi-Resolution, Model Based Segmentation of MR Angiograms

Paul Summers, Abhir Bhalerao, David Hawkes

Abstract—Over the past decade, the quality of magnetic resonance angiograms has risen substantially with their clinical utility being progressively demonstrated. This acceptance has created a need for tools with which to summarize and display the information available. We have used a model based segmentation technique to extract vascular morphology and local flow parameters from phase contrast magnetic resonance angiograms. A multiresolution data structure is used as the basis of recursive decision-making to identify regions of blood flow. The resulting data representation allows more efficient data handling in subsequent processing and visualisation, and is directly applicable to the creation of a connected graph model of vascular regions. We describe this flow feature extraction algorithm and demonstrate the utility of the results.

Keywords—MR Angiography, Image segmentation, Flow Visualisation

INTRODUCTION

In addition to the merits of magnetic resonance angiography (MRA) as a non-invasive alternative to techniques relying on ionising radiation and injected contrast agents, it is possible for MRA to provide a full three-dimensional image of vasculature structure and flow. Such MR angiograms are acquired in a volumetric format, routinely yielding data arrays of 25 megabytes and greater. The vascular structures of interest, however, tend to be sparsely distributed within this volume. Thus, interpretation of MR angiograms brings to the fore issues of data handling, segmentation and visualisation.

To be clinically useful, the processing and depiction of the angiographic images must address issues of information content, user interaction, and time. The information contained in an MR angiogram is closely tied to the technique by which it was acquired. Time of flight MRA depicts the inflow of relatively unsaturated blood into a surround of highly saturated static tissue [1]. The straightforward implementation, speed, and consistency of the time of flight technique has led to its widespread use. Phase contrast MRA (PCA) produces a voxel by voxel map of the velocity field which may be depicted as a collection of velocity component images (collectively a velocity image x), or combined to produce an angiographic image closely resembling those of time of flight MRA (loosely termed a speed image x) [2]. A further image exhibiting mixed TI - proton density weighting can also be reconstructed from the acquired data. Thus, an anatomical image, and both quantitative and qualitative angiographic information may be generated during a single scan.

To date, the most important consideration in the use of MR angiograms has been the tendency for the source images to show low contrast between blood and static tissues; particularly for vessels of voxel and sub-voxel dimensions. The clinical potential of MRA has brought considerable attention to bear on overcoming this limitation. The ensuing progress in MRA has considerably raised the conspicuity of vessels in MR angiograms through strategies to reduce static tissue signal [3] [4] or maximise the blood signal [5] [6] [7]. These improvements in contrast coupled with advances in scanner speed (primarily through gradient rise time and strength) have lead to increases in image resolution. Thus, greater volumes of image data of steadily improving quality are being produced.

In such large image volumes, the complexity of the vessel tree limits slice by slice viewing to the scrutiny of particular regions of interest. Other means, such as maximum intensity projection (MIP) of speed data allow large amounts of angiographic data to be viewed efficiently. Velocity data may be easily displayed with colour as is done with ultrasound, or as arrow overlays. The three-dimensional velocity field map obtained in PCA however, is difficult to interpret from such views. Notably, these common approaches involve no decision about what is vascular, leaving it to the viewer to discern the presence and connectivity of vessels. In preparing views which attempt to depict the three-dimensional vascular structure, or specific attributes of flow, some decision is often needed. Surface rendered views [8], or pseudo-projections of the cross-sectional area [9] require a binarised image in which the vessel lumen and surrounding tissue are classified separately in order to identify the vessel surface. Less stringent decisions are required in volume rendering where each voxel is allocated a measure of probable vessel occupancy (typically based on angiographic image intensity) which may be treated as an opacity to reveal information about the contained region rather than just the vessel surfaces [10]. The planar display of velocities has been extended to three-dimensional streamline-like trajectories by Buonocore [11], but extensive computation, including identification of vessel boundaries through segmentation is required to generate images which are haemodynamically feasible. Both image acquisition and preliminary image processing must therefore be considered central to the process of evaluating MR angiograms.

The progressive improvement of MR angiograms should
make segmentation and visualisation easier, but does not
obviate the need for efficient tools with which to achieve
optimal image segmentation, or enhancement of the dis-
play. Simple segmentation techniques (e.g. thresholding)
and projection views are hampered by the overlap between
the upper end of the background tissue’s intensity distri-
bution and the intensities of slow flowing and small vessels.
Du et al [12] have shown that zero-padding the acquired
data prior to Fourier transformation distributes the noise
and effectively sharpens the edges of small vessels giving
them improved delineation in MIP displays. MIP displays
may be further improved by limiting the projection vol-
ume to exclude high intensity background [13]. While this
type of pre-processing is typically done by the viewer an
automated approach is desirable. An example of such an
approach is coarse vessel identification based on knowledge
of the image, such as the assumption that large vessels will
exhibit the highest signal intensity. This is used as a guide
to limit the MIP process to neighbourhoods of voxels sat-
isfying a threshold criteria and has been demonstrated as
a means of reducing background signal in MIP views [14].

An further instance of a prior knowledge is that vessels
tend to resemble line segments over small distances.
This has been used in the application of anisotropic filters
which enhance locally line-like intensity features while suppres-
sing noisy (point-like) intensity variations in an image [15].
Used as a pre-processing step such filters can improve ves-
sel conspicuity in MR angiograms and MIP views [16] [17].
An anisotropic model of a vessel segment has been used in
correlation with the image data to estimate the position
of vessels [18]. A decision based on the agreement of the
model with the data is used to binarise the data volume
onto vessel segments and background. The estimate must
be repeated for different vessel orientations and diameters
making the process time-consuming. We have adopted and
extended the use of the line segment model of the blood ves-
sels into a segmentation technique to extract vascular mor-
phology and local flow velocity from phase contrast MR
angiograms.

Method - Theory

To relate the PCA data to vessel structure, we assume
that the blood flow is sufficient to cause a variation in the
local intensity of the speed image, and that direction of
blood flow is consistent with the vessel axis. While these
assumptions are not always valid, they produce a simple
image model of vessels as as piecewise linear curves in 3D
(Figure 1) in the angiographic image, and directed curves
in the velocity image. Modelling the vessels in this way is a
direct extension to 3D of a 2D curve model for the used by
Calway [19] for finding curves in natural scenes and elab-
orated in [20]. The model belongs to a general class of
multiresolution image models first introduced in Chipping-
dale [21] which have a number of interesting and important
properties and have been successfully applied to a wide va-
riety of image processing tasks including segmentation and
analysis. For simplicity’s sake, our segmentation is wholly
performed in the spatial domain though a Fourier domain
based method such as that of Calway et al may have a num-
ber of advantages when analysing MR data. Although the
model may be applicable to time of flight MR angiograms,
the results presented in this paper are based solely on the
PCA information.

Figure 1 illustrates how a 3D curve can be approximated
by a series of linear parts (features) at different scales or
resolutions. The features of any single curve are bounded
by cubic regions (blocks) of different sizes which form an
inhomogeneous tessellation of the image. Each block is
subjected to the constraint of containing a single local fea-
ture. Large, isolated features are then represented by big-
ger blocks at coarser spatial resolution whereas details i.e.
high curvature or bifurcations, are represented by smaller
blocks. The segmentation process amounts to estimation
of parameters for the features in the 3D curve model i.e.,
block offset $\xi$, feature centroid $\chi$ and feature orientation $\delta$
(Figure 1). The output of our segmentation is a 3D graph of
the vascular system which is a concise and general purpose
representation and can provide information for subsequent
visualisation, quantification or flow modelling.

Multiresolution Analysis

In the adopted curve model, we expect different sized
blocks to tessellate the image. To efficiently generate a
multi-scale block structure, the image is represented at a
number of resolutions by recursive averaging. The scale
at which a feature is best represented is identified directly
from this multi-resolution representation.

Multiresolution image processing methods are usually
characterised by a two stage process: building some multi-
scale or phase-space representation, such as an oct-tree (see
below), followed by a ‘coarse-to-fine’ refinement strategy
whereby parameter estimates are propagated back down to
regain full spatial resolution. A global structure is identi-
ﬁed at a coarse scale and then gradually refined using detail
from finer scales [22]. Such coarse-to-fine analysis leads to
highly efﬁcient estimation procedures; decisions made at
low resolutions that encompass large blocks of the image
can quickly help reject parts of the image where there is
little or no signiﬁcant activity.

In 3D image analysis the simplest spatial multiresolu-
tion structure is the oct-tree. This consists of a stack of
coarser and coarser resolution images created by averaging
non-overlapping groups of 8 voxels (Figure 2). The spatial
resolution is reduced by a factor of two in each direction at
each successive level. For a slice volume size $N \times N \times N$
there will be $M = \log_2 N + 1$ levels with a total storage of
$\approx 10^3 N^3$ (an overhead of 43%).

Central to our approach are the joint concepts of hy-
pothesis testing over scale, and scale consistency [20]. The
assumption is made that a given feature can be positively
detected at more than one scale. Decisions are made based
on scale consistency criteria with the aim of tessellating the
data into the smallest set of disjoint blocks for which the
data is consistent with the model. The appropriate scale
of a feature is determined by estimating features at each
scale independently, and then checking the results for con-
stency between scales until an acceptable level of confidence is achieved. Using the oct-tree representation allows the hypotheses to be fixed and the scale to be efficiently and consistently varied. The nodes of the four-dimensional oct-tree are thus pruned to provide a non-overlapping set of blocks in the final representation of the vasculature.

Segmentation Steps

The first stage of the segmentation process involves the building of two oct-trees; one of what we have called the “speed” data \( (x) \) which is used to test a vessel versus background hypothesis, and one of the velocity vector data \( (x) \) to test whether the flow in a given neighbourhood is sufficiently coherent to suggest the presence of a single vessel segment (Figure 3). The speed data is tested over scales for the likelihood of a vessel being present in each node of the oct-tree. Nodes having sufficiently high probability of containing a vessel, and which share a common face are regarded as adjacent or neighbours allowing a region adjacency graph to be formed. Scale selection is then performed on the flow vector data to identify a set of nodes from which parameters of the piece-wise linear curve model are determined. These blocks are linked together to form a boundary adjacency graph. The segmentation is the output of an interaction process between the ‘region’ and ‘boundary’ adjacency graph structures.

1. Oct-tree generation

A recursive, low-pass filtering operation is used to generate an oct-tree of the PCA velocity vector data. The filter kernel in this case is of size \( 2 \times 2 \times 2 \). For a cubic volume of side \( N = 2^M \) the exponent \( M \) determines the number of levels in the resulting oct-tree \( x_{ijk}(l), 0 \leq i, j, k < 2^l, 0 \leq l \leq M \) where \( l \) is the scale index, and the spatial indices are given by subscripts. The general form of process required to construct an oct-tree is given by the expression:

\[
x_{ijk}(l) = \sum_{m,n,o=0}^{1} A_{mno} x_{(2i+m)(2j+n)(2k+o)}(l+1)
\]

where \( 0 \leq l < M \), and the base of the oct-tree is the image \( x_{ijk}(M) = x_{ijk} \). The multiplier \( A_{mno} = 0.125 \), \( 0 \leq m, n, o \leq 1 \) is a blurring filter kernel. A similar process is performed on the speed image data \( x_{ijk} \).

2. Vessel occupancy

Use of the oct-trees begins by identifying nodes which are likely to contain a vascular feature. Working from fine (the source images) to coarse resolution in the speed image oct-tree, the local variance in the speed values \( v^2_{ijk}(l), 0 \leq l < M \) is calculated at each node using the locally averaged speed at that node \( x_{ijk}(l) \) and within its daughter nodes:

\[
v^2_{ijk}(l) = \sum_{m,n,o=0}^{1} B(l) [x_{(2i+m)(2j+n)(2k+o)}(l+1) - x_{ijk}(l)]^2
\]

where the averaging filter kernel is fixed in our implementation as \( B(l) = 0.125 \). The sample variances \( v^2_{ijk}(l) \) are compared with their level’s mean variance \( \bar{v}^2(l) \) allowing the homogeneity of the node values to be tested. Voxels straddling vessel surfaces should form a population with significantly higher variance than is expected among voxels in nodes entirely interior or exterior to the vessels [23]. This allows the simple classification:

\[
\text{If } v^2_{ijk}(l) > \alpha \bar{v}^2(l), 1 < l < M
\]

Then the node \( \xi = (i, j, k, l) \) is marked as a surface node [4].

The mean intensity of the surface nodes on a given level is used as a threshold to classify the remaining nodes on the level as either interior or exterior to vessels. In general the interior nodes are small, arising mostly from the finest or next coarsest voxel resolution. The set of interior nodes are then connected based on neighbourhood adjacency to form a region adjacency graph. The lowest marked surface node in any subtree acts as a leaf of the region representation.

3. Flow feature selection

The velocity vector oct-tree is then traversed from coarse to fine resolution to identify nodes likely to contain a flow feature. The criteria here is based on the degree of coherence between the velocity vector in the daughter nodes of a given node. The coherence measure \( c \) at node \( \chi \) is calculated as

\[
c_{\chi} = \frac{|\sum_{\chi} x|}{\sum_{\chi} |x|} \approx \frac{|x_{PCA}|}{x_{vec}}
\]

Which is simply the ‘averaged length of the net flow vector’ over the ‘average length’ of the flow vectors in the daughter nodes [24] [25]. 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 node. The denominator normalises the measure so the relative vector strengths between nodes are compensated for. Notably, this coherence measure can be rapidly calculated by dividing the oct-tree of the vector signal by the oct-tree speed image (assuming \( x \approx |x| \)).

Taking the mean coherence on a given oct-tree level \( l \) as \( \bar{c} \) and the variance in the coherence values at a given level as \( \bar{c}^2 \) we can define a threshold \( T = \bar{c} - \beta \ast \bar{c}^2 \) as the minimum coherence required within a node in order for it to be included in the representation. A decision is taken at each node \( \chi \) to either terminate the tree at this point or to continue the search to the next highest resolution level. The traversal is terminated when the highest resolution is reached. The tree is truncated if the vectors within the node are sufficiently coherent to suggest a single vessel feature, or if the node contains no vessels as indicated by searching the region adjacency graph:

Hypothesis \( H_0 \): there is a coherent feature in block \( \chi \)

Accept \( H_0 \) if \( c_{\chi} > T \)

and \( \xi \in \chi \) for some \( \xi \)

where \( \xi \) is a corresponding speed octree node.
3. Flow feature parameterisation

The nodes $\chi$ in the velocity oct-tree having sufficiently coherent flow, are now used as the blocks of the vascular tesselation. Information from these blocks, and the associated nodes $\xi$ in the speed oct-tree identified as containing a vessel are used to provide the parameters of curve segment contained in the blocks. The offset of the block is simply the spatial offset of the node $\chi$. Within each block the position of the vessel and orientation are also estimated (Figure 1). The orientation $\theta$ of the vessel segment is taken to be that of the mean of the velocity vectors $x_\chi$ in the node. The feature position is estimated by taking the centroid of the associated vessel nodes $\xi$ in the speed oct-tree which lie inside the block $\chi$.

METHOD - IMPLEMENTATION

Using the formulation described, multiresolution vessel segmentation was implemented in C++ on a standard Unix workstation. Initial testing was performed using a model intracranial vasculature obtained by manual segmentation from bi-plane angiography. Levels of simulated noise were added to the model data to test the behaviour of the segmentation under less ideal conditions.

The segmentation process was also demonstrated on data obtained from volunteers. The first volunteer dataset was an intracranial phase contrast MR angiogram (Venc: 70 cm/s, TE 6.1 ms, TR 140 ms, FOV 220 mm, Slice thickness 1.0 mm) obtained in an un gated manner. A second volunteer data set, this time of the renal arteries was also used. Imaging in this case was performed using a gated-sweep phase contrast technique (Venc: 120 cm/s, TE 5.9 ms, TR 13.3 ms, FOV 350 mm, Slice thickness 2.0 mm). All scans were performed on a 1.5T Philips ACS MR Scanner.

The vessel descriptors obtained from the test and in-vivo data are illustrated using a simple projection of the relevant line segments. The effect of varying the threshold parameters $\alpha$ and $\beta$ in the vessel identification and flow coherence testing were examined on the volunteer data as a guide to the sensitivity of the protocol to realistic data.

RESULTS

Figure 4a depicts a surface rendered view of the noise-free model intracranial vasculature. The vessel axis was used as the velocity orientation for the purpose of segmentation. The tesselation and flow features resulting from segmentation are shown in Figure 4b. Since $\bar{v}_\chi^2(l)$ is tested against a 'local' sample variance $\bar{v}_\xi^2(l)$, the surface threshold is adaptive to SNR characteristics. The robustness of this classifier at $\alpha = 2$ is demonstrated in Figure 5 which shows a graph of classification error for a data set to which Gaussian white noise has been added giving effective SNRs between -6 dB to 12 dB. Visual inspection reveals that our experimental PCA data have SNRs greater than 3 dB.

In the in-vivo examples, phase contrast MR angiograms were obtained using velocity sensitivities chosen to minimise the likelihood of phase aliasing in vessels of interest. This slightly diminishes the quality of the MIP views (see Figure 6a and Figure 7a) but ensures the coherence testing is not complicated by the presence of a branch cut in the phase angle calculations. The estimates of speed and direction of flow, and the size of regions exhibiting coherent flow are represented by the colour, orientation, and length of arrows. In contrast to the single feature per vessel segment of the simulated data, the in-vivo segmentation changes dependent on both the $\alpha$ and $\beta$ decision thresholds can be seen in projection views of the extracted flow features. With $\alpha = 2.0$ decreasing $\beta$ from 2.0 to 0.0 and $-0.5$ as in Figures 6b, c and d respectively. This corresponds to testing for successively greater feature coherence and results in vessels being sub-divided into more numerous, small features. More pronounced are the differences in the segmentations resulting from changing the value of $\alpha$. Figures 7a, c and d show the flow features resulting from segmentation with thresholds of $\alpha = 2.0$, 1.0, and 0.0 ($\beta = 2.0$). As the $\alpha$ threshold is lowered, vessels which showed low contrast in the MIP are included in the segmentation. The incidence of false positive identification of vessel regions may be an issue where there are ghosts or other variations in intensity occur.

The parameter $\alpha$ determines which blocks are recognized as lying interior to vessels based on the mean and variance of the intensity distributions in the oct-tree. Over a span of five standard deviations about the mean of the intensity distribution the dependence of the number of interior blocks observed on the value of $\alpha$ for $64 \times 64 \times 64$ voxel regions of the circle of Willis and renal artery studies are shown in Figure 8. The sigmoidal shape appears to be stereotypical of the approach to the decision. The ratio of internal to external regions identified ranged from 125 in the intracranial angiogram to 1:10 for the renal angiogram reflecting the differences in vessel size to image resolution between the studies. For values of $\alpha < -0.5$ interior and exterior blocks were all identified at the voxel level. With increasing values of $\alpha$, external regions were identified as high as the fourth level of the oct-tree. The interior regions however were limited to the lowest two (highest resolution) levels of the oct-tree.

The number of interior regions identified by the intensity testing serves as an upper bound on the number of regions which may be identified under the coherence testing. Subject to this maximum, the dependence of the the number of identified blocks on $\beta$ also shows a sigmoidal pattern of behaviour (Figure 9). The differences in shapes of the curves between the alpha and the beta testing likely illustrate differences in the statistics of the speed and the spatial variation of the velocity. Raising the value of $\beta$ relaxes the degree of coherence required for acceptance of a flow feature under the model. Thus, the progression is away from individual voxels being maintained as the scale of representation through progressive uniformation of the features. In the extreme (typically $\beta \geq 5$), any blocks are accepted at the largest scales for which local interior regions were found in the testing of the speed oct-tree. This amounts to no testing performed on the velocity vector data and should be equivalent to running on time of flight data. Processor
times depended on the values of $\alpha$ and $\beta$ selected. With $\alpha = 2.0$ and $\beta = 1.0$ the running time for segmentation of a 64x64x64 sub-block from the image volumes was approximately thirty seconds.

**Discussion**

The multi-resolution image segmentation technique presented here quickly produces a concise representation of the flow field mapped by PCA. The simplistic assumptions underlying the vascular model has two notable failings. Firstly, the in vivo flow is often not uni-directional at a given vessel cross-section. For low values of beta (demanding high coherence) the image model results in the identification of sub-regions as individual flow features. Moreover, turbulence and high velocity gradients may cause intravoxel dephasing in the acquired angiograms, and may compromise the validity of the velocity estimates at the voxel level. Where signal intensity is lost, the speed image may be affected preventing identification of vessel segments, or weaken confidence in the feature estimates. Secondly, the ghost artefacts which accompany the MR imaging of pulsatile flows possess intensity and phase indistinguishable from those of flow features. As seen in the area below the aorta in Figure 6 flow features may be extracted for these ghosts as well as the relevant vasculature. A third, aesthetic limitation of the current implementation is a degree of non-uniqueness in the final representation. Depending on the choice of origin in the data, slightly different segmentations may result. We do not consider this a major problem as the feature content appears consistent in the data studied to date.

In the above results, the confidence testing variables $\alpha$ and $\beta$ were shown to have complementary effects. The optimal parameters would produce a minimum of both false positive and true negative vessel identifications, and produce a accurate representation of the vascular anatomy. While values of these variables may be fixed or estimated from the data such an approach limits the user’s ability to appreciate their effect of the result. In a clinical implementation these would be under the control of the user in a manner similar to controls for windowing conventional MIP views. While the processing time for a sub-region is not prohibitive, and compares favourably with other segmentation tools, treating a full angiographic data set cannot be handled interactively on most current machine architectures.

A number of variations on the processing implemented for feature recognition and position estimation could be considered. The centroid of the associated region nodes inside $\chi$ were used herein to define the feature offsets. This approach has the advantage of speed. An alternative would be to use a Rough Transform where $\theta'$ is given [26]. Currently we are examining the use of a similar image model with time-of-flight (TOF) MRA data, where the feature block parameters are modelled with 3D local Fourier spectra. This has a number of attractions, including the potential to directly model and detect bifurcations, and is closer to the ideas first presented in [19]. The velocity information would be incorporated by estimating average flow in the blocks identified from the TOF tessellation which is more akin to the strategy used by Gerg et al [27] [28]. The processing, modelling and hypothesis testing are however more complicated than our current spatial domain approach.

Although our method differs radically from Gerg’s single resolution approach, they share essentially the same output symbolic representation. Whereas we segment the PCA data directly so that the direction of flow is inherently encoded in the output, their vascular network is determined from TOF sequences and then parameterised by velocity data from a PCA sequence of the same patient. They have sought to use the vessel centre lines from a line tracking process to produce a symbolic representation network of blood vessels that encodes key topological locations such as branch and end points and local vessel diameter. After a binarisation of the image data, they produce a map of mid-line points along the vessel path by a process of erode and open operations that retain the vessel topology. Such a point list can be stored as a summary of the vascular tree with tremendously reduced storage requirements over the image data.

Having obtained a series of feature estimates that form sections of piecewise curves, the logical next step is to attempt to join these together. In [26] we presented results of a graph theoretic relaxation technique which produced indifferent results. One of the reasons for its poor performance is that the velocity estimates produce multiple flow streams within larger vessels. Thus far we have not investigated the use of physical models such as a conservation of mass constraint to help estimate connectivity.

We have demonstrated a novel approach to the segmentation of MR angiograms that overcomes some of the time limitations of single resolution methods. Multiresolution modelling is both simple and effective resulting in fast and automated processing schemes which are adaptive to the data, especially in respect of SNR. With processing times of a few tens of seconds it is realistic to examine the results of several different thresholds in forming an impression of the results. The graph representation and bounding boxes of flow features also allow the raw data to be efficiently re-examined to estimate other attributes such as calibre and pressure gradients [29], or in the generation of limited MIPs. More importantly perhaps, the list based output representation are compact, requiring less than 10% of the original data whilst retaining the salient features. Thus, once segmented, the features can be re-displayed from arbitrary viewpoints on the fly making it possible to interactively examine a vascular network. The vector representation of the flow features is an intuitive way of visualising the vascular network and may be used anywhere flow direction is important, arterio-venous malformations being but one example. With continued improvements in spatial and temporal resolution creating ever greater data volumes, the efficiency of the flow feature representation will be attractive in studying vascular dynamics in the hepatic vessels, cardiac chambers, and the circle of Willis.
REFERENCES


Fig. 1. Piece-wise linear curve representation and model parameters: block offset $\chi_i$, intra-block offset $\eta_i$ and orientation $\theta_i$ of the feature in block $\xi_i$. 
Fig. 2. Oct-tree structure showing parent (left) and child nodes (right).
Fig. 3. Algorithm flow chart.
Fig. 4. a. Maximum intensity projection, and b. extracted features for a noise-less model of the cerebral circulation.
Fig. 5. Vessel-occupancy classification errors ($\alpha = 2$).
Fig. 6. a. Maximum intensity projection view, and b. flow features extracted of the renal arteries in a volunteer $\alpha = 1.5, \beta = 2.0$. In c. and d. the effect of changing the coherence threshold is seen ($\beta = 0.0$ and $-0.5$ respectively).
Fig. 7. a. Maximum intensity projection view, and b. flow features extracted of the cerebral arteries in a volunteer $\alpha = 20, \beta = 20$. In c. and d. the effect of reducing the intensity threshold $\alpha$ to 1.0 and 0.0 respectively is seen.
Fig. 8. \( \alpha \) Dependence of Feature Recognition \((\beta = 2)\).
Fig. 9. $\beta$ Dependence of Feature Identification.