Experiments on the Use of Fast Marching for Feature Identification

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We propose a *fully automatic* method for feature identification. Our main application is the identification of abdominal organs in computerized tomography (CT) scans. We use 3D medical data although this method is not data specific. The main steps of the method are (1) segmenting the scan data, followed by (2) applying the Fast Marching Method in order to extract feature shapes.

We segment the scan volumes using algorithms devised within the Spatial Reasoning Group here at Oxford [1, 2], which output an *image partition forest (IPF)*, a hierarchy of adjacency graphs that partition the volume (and hence each individual slice image). Significantly, the segmentation is successful at dividing the image into regions of semantic importance. However the resulting regions do not shape feature boundaries accurately: they only approximate abdominal features roughly. Thus we rely on the IPF to initialise the Fast Marching Method, but we need a post-processing step in order to detect the true boundaries.

The *Fast Marching Method* is an efficient iterative algorithm, introduced by Sethian [3, 4], for numerical approximation of the development of propagating fronts, closed hypersurfaces moving in the direction of the surface normal. Representing the front implicitly through the arrival time function $T : \mathbb{R}^n \to \mathbb{R}$ (the front reaches the point $\boldsymbol{x}$ at time $T(\boldsymbol{x})$), it solves the *eikonal* equation $|\nabla T(\boldsymbol{x})| = \frac{1}{F(\boldsymbol{x})}$ with a discretised model on a lattice, appropriate upwind schemes and optimal ordering of points in space.

Given a particular abdominal feature (such as an organ), we filter the IPF for regions based on that feature's anatomical knowledge. For instance, regions corresponding to the right kidney should be in a high layer of the IPF, have a mean greyscale value in a certain interval (known from radiology studies [5], inferred from the typical radiodensity Hounsfield Unit (HU); the right kidney should be 'west' of the spine in an axial slice, and anatomically close to the spine; also, the right kidney should span a reasonable number of voxels (depending on the number of slices in the image), etc.

Having identified a suitable region corresponding to our chosen feature, we choose points within that region which are within a fixed greyscale range (again, inferred from the feature's typical HU). We use these as *seed points* to initialise the Fast Marching algorithm.
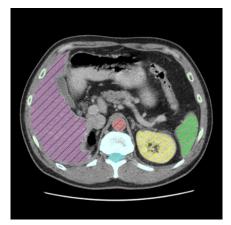
This process is repeated for each feature of interest (mainly organs, bones or blood vessels) within the abdomen.

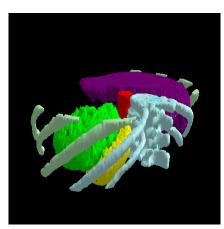The advancement of the Fast Marching front is governed by *speed functions* of the form

$$F(\boldsymbol{x}) = \frac{1}{\left(1 + \left(\frac{|\nabla I(\boldsymbol{x})|}{C}\right)^n\right)^m}, \quad C > 0, \ n, m \in \mathbb{N} \quad \text{or}$$

$$F(\boldsymbol{x}) = e^{-C|\nabla I(\boldsymbol{x})|}, \ C > 0$$

These were compared and tuned on CT data pre-processed with windowing or smoothing.

The development of the front in Fast Marching slows down at points with high gradient magnitude values (in particular, in the neighbourhood of organ boundaries). We captured such slow development of the front and used this as a *stopping criterion* for the Fast Marching. We finalised the identified regions with several iterations of morphological closing in

(a) Final results shown on a single axial CT slice.

(b) A 3D reconstruction of the identified features using the *marching cubes* algorithm which constructs a polygonal mesh around features which belong together.

Fig. 1. The results of 3D abdominal feature identification with Fast Marching Method. Aorta , kidneys , liver , ribs , spine , spinal cord and spleen are visible in their respective colour.

order to remove spurious holes and to smooth out the boundaries. The results of our procedure on a typical CT volume are illustrated in Figure 1.

We carried out extensive empirical experiments to identify the impact of various parameter choices on the performance of the Fast Marching Method. In particular, we determined appropriate parameter values to apply Fast Marching to 3D medical data, and we used these in our implementation, thus automating a process which was previously deemed to be carried out 'manually'.

Extensive analysis of the method's parameters allowed us to achieve significant identification results while employing a comparably simple algorithm. Results are currently validated only by a human judge. Future quantitative analysis is needed to give a more precise assessment to the performance of the method and compare it with other approaches. Also, experiments on a wider class of image volumes are needed since new medical scanners produce images with higher resolution and better precision.

References

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