Fast Segmentation of Brain Magnetic Resonance Tomograms

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Abstract. We describe a combination of a region growing and a watershed algo-
rithm optimized for the detection of homogeneous structures in magnetic reso-
nance (MR) volume datasets. No prior knowledge is used except a segment
model. The adaptation to different data sets is controlled by parameters which
can be determined interactively due to the high speed of the algorithm. Results
are shown for the segmentation of the basal ganglia and the white matter of the
brain.

1 Introduction

The basic idea of the segmentation method described in this paper is to combine a
region based approach using homogeneity and connectivity to yield segments with an
morphological approach using watersheds on gradients to achieve a good localisation
of the segment borders. The segmentation method is based on a simple but very gen-
eral segment model which is defined in section 2. An extremly efficient implementa-
tion of this algorithms is given in section 3. Except the segment model no other a priori
knowledge is used. The algorithm is adapted to different data sets by parameters,
whose values can be determined automatically or interactively. The results shown in
section 4 are generated with the second method, which is favored because of the short
computing times even for large datasets. An approach for the knowledge based auto-
matic determination of the parameters for a similar algorithm can be found in [1].

As a testbed for our algorithm we have selected the detection of the white matter and
the basal ganglia in brain MR tomograms. A special property of the algorithm needed
to segment these structures is its ability to differentiate very similar neighboring struc-
tures that are seperated only by a very slight inhomogenity.

2 The Algorithm

To segment the structures of the brain mentioned above a segment model is defined:

*A segment is a connected, homogeneous region surrounded by inhomogeneous
regions (edges) or by other segments (with different mean gray values).*

Homogeneity refers to a suitable predicate. If a segment is not enclosed totally by edges it must have neighboring segments with a smooth intensity transition between them. These smooth transitions appear frequently in MR brain images but can hardly be detected by a purely gradient oriented segmentation approach. Nevertheless for both types of neighbors the segment borders should be located at the local extreme values of the gradient between the structures. To achieve these goals the following region growing algorithm is proposed:

The growing starts at the most homogeneous regions, found due to their small gradient magnitude and continues to the less homogeneous regions. Therefore the voxels are sorted by their gradient magnitude and are processed in that order. This avoids expensive neighbor search during the segmentation and makes the algorithm orders of magnitude faster than classical approaches [3]. Interestingly, this procedure is comparable to the implementation of the watershed algorithm based on immersion simulation [2].

During the region growing process the assignment of voxels to segments is controlled by a voxel-segment homogenity predicate. To avoid the creation of one segment for each local minimum, what happens if the watershed transformation is applied, a segment-segment merging step is introduced. It is controlled by a segment-segment homogeneity predicate. This algorithm yields stable results since the segments grow at first as large as possible in the homogenous regions. Additionally, the algorithm needs no seed points and the shape of the segments is purly data driven. However, with increasing gradient magnitude during the segmentation process an increasing fragmentation would occur. To prevent this, two methods are proposed:

a) "Relaxed region growing": the voxel-segment and the segment-segment homogeneity predicate are relaxed with increasing gradient magnitude.

b) "Region growing plus watershed": the region growing with fixed homogenity predicates is stopped at a certain gradient magnitude and the segmentation is completed with a modified watershed transformation.

"Relaxed region growing" has the advantage to form large segments even in less homogeneous areas. But regions may be connected if they are separated only by a slight edge. Hence this method is suitable to segment regions with neighbors of different intensity values for example the white matter of the brain (Fig. 2).

"Region growing plus watershed" stops the region growing process as soon as the gradient magnitude reaches the parameter value h_{stop}. This value should be chosen small enough to avoid the formation of many small segments. The result would be an incomplete segmentation. The idea is to extend the existing segments up to the surfaces of maximum gradient magnitude of the neighboring edges. We achieve this by a modified watershed transformation, which let the segments grow up to the next neighboring edge. Consequently all edges with magnitude $> h_{stop}$ lead to segment borders. Hence the separation of distinct structures can be forced if an edge lies between them.

The difference between the modified and the morphological watershed transformation is that the assignment of a voxel with several segmented neighbors is still controlled by the voxel-segment homogeneity predicate, i.e. the voxel is assigned to the most suitable segment. Problems with deviated watershed lines [2] does not occur.

3 Implementation

The voxels are segmented from the minimal gradient magnitude up to $h\_max = h_{stop}$ ("Region growing plus watershed") or to $h_max = $ maximum gradient magnitude ("Relaxed region growing") (see Fig. 1).

```
for ( h = 0; h < h_max; h = h + 1) {
    while there are unsegmented voxels v with gradient magnitude h {
        while there are voxels g of v have neighboring segments {
            put voxels g in queue Q;
            for all voxel x in Q {
                if x can be merged with best matching neighboring segment then { (**)
                    voxel-segment merge;
                    if segments have become new neighbors then try seg.-seg. merge; }
                else create new segment; }}
        /* Treat local minima now: */
        for all unsegmented voxels v create new segment; } }
    if "Region growing plus watershed" then perform modified watershed transformation;
```

Fig. 1. Segmentation algorithm

The final modified watershed transformation ("Region growing plus watershed") is equivalent to the region growing algorithm except that the segment-segment merge is omitted and the statement in line (**) is unconditional.

Both the region growing and the subsequent watershed algorithm use the same data structures and exploit the excellent performance $O(n)$ (without sorting, n number of voxels) of this implementation. Furthermore they are independent of the underlying coordinate grid and can be extended to graphs and m dimensional images.
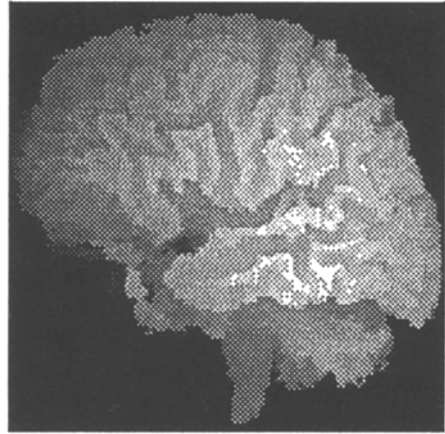
4 Results and Discussion

We have applied the algorithm to segment the white matter and the basal ganglia of the brain. Fig. 2.a) shows the segment border of the single segment containing the white matter superimposed on the initial volume (slice 110 from 256 slices, size 256 x 109 voxel). The 3D visualization in Fig. 2.b) is computed with the V-Buffer algorithm [4] using the volume with the segment labels. For this segmentation the "Relaxed region growing" has been used. In spite of considerable intensity changes in the white matter a single segment is formed.

Next, results of the segmentations of the basal ganglia are presented:

Fig. 3 shows a computed segmentation of the caudatum. The used volume consists of 154 slices with 127 x 154 voxel. Here and in the following all computations were made using the "Region growing plus watershed" algorithm. The segmentation compares well to hand segmentations although the border lines are more jagged. All segmentations are computed without smoothing the data to avoid suppression of small structures (Canny operator: $\sigma = 0.7$).
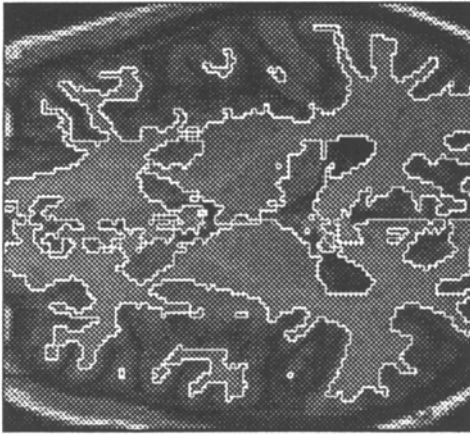
Fig. 2. a) Segmentation of the white matter   Fig. 2. b) Visualization of the white matter

The segmentation in slice 55 (Fig. 3.b) shows that the caudatum splits into two segments. The reason are different gray values in the area of the tail of the caudatum. As can be seen in Fig. 4 the gray values of the caudatum and the putamen are very similar where they are close together. So an increased homogenity threshold parameter would
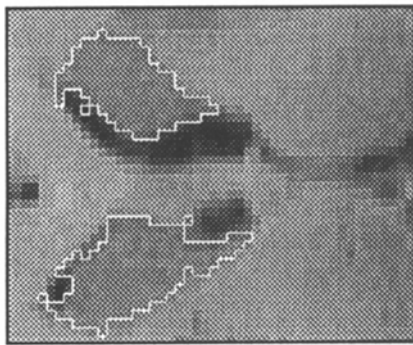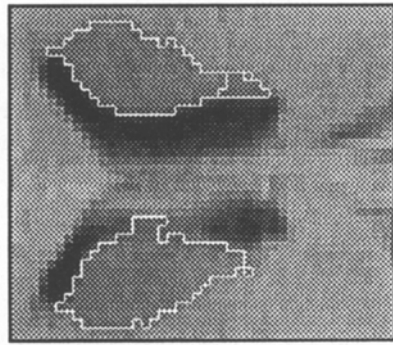
Fig. 3. Segmentation of the caudate nuclei. a) Slice 59, b) Slice 55

yield an incorrect segment merge. For the same reason the putamen and the thalamus (Fig. 4) also split into two main segments. This splitting is a principle property of this segmentation approach when segmenting structures of a high inhomogeneity relative to their vicinity. The complexity of the named brain structures can not be modelled perfectly with our simple segment model. Rather, the complex objects decompose into their homogeneous substructures. Because of its high speed the algorithm seems to be well suited to serve as a tool for higher level systems to achieve a first decomposition of an image into a small number of homogeneous regions highly correlated with the anatomical strucure.

The computing time including the sort on a SUN Sparc 10/40 for the first data volume (14 MBytes) is 142 seconds, for the second data volume (6 MBytes) 69 seconds. For

repeated segmentations of the same volume the algorithm may be speeded up by storing the array of sorted voxels once it is computed.
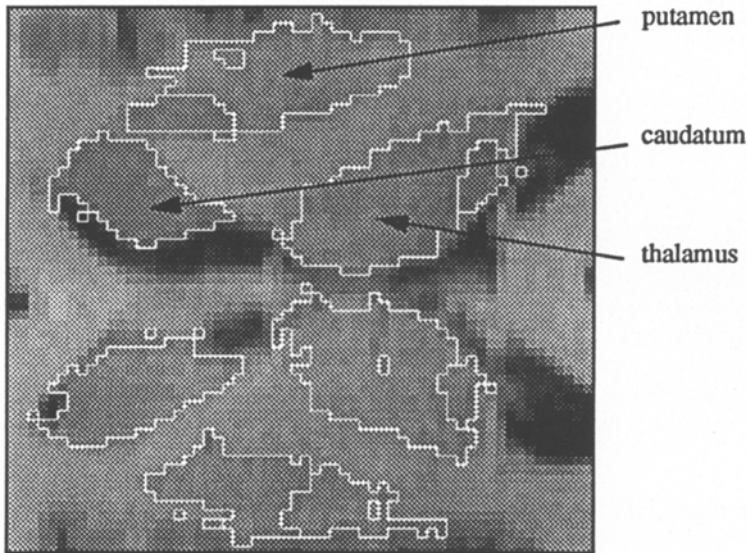
Fig. 4. Segmentation of thalamus and putamen

5 Conclusions

We have presented a 3D segmentation algorithm optimized to segment homogeneous structures in MR data volumes at a very high speed. The algorithm is based on a segment model exploiting homogenity as well as inhomogenity. The implementation is a very efficient immersion simulation [2]. Results are shown for the segmentation of the basal ganglia and the white matter of the brain. Two different variants of the algorithm are given. One is optimized for the segmentation of inhomogenous regions well seperated from similar structures, the other for the segmentation of adjacent structures with very alike properties. It shows that complex objects decompose into their homogenoeus substructures that may be reassambled later by an expert (system). This seems to be a good result since the number of substructures is small and depends only on the complexity of the object.

References

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