A GRAPH METHOD FOR THE CONSERVATIVE DETECTION OF POLYPS IN THE COLON

C. TOMASI; S.B. GOKTURK
Department of Computer Science, Stanford University, Stanford, CA
Department of Electrical Engineering, Stanford University, Stanford, CA

I. PURPOSE

A method employing sphere fitting and graph-based clustering is presented to determine possible locations of polyps in a CT colon image dataset. The method is conservative in that it misses essentially no polyp greater than a specified minimum size, at the cost of several false positives. The output from the algorithm is sufficiently small that more sophisticated classification methods can be subsequently run on the polyp candidates it produces.

II. METHODS

Recent methods in virtual colonoscopy have modeled polyps as essentially spherical structures. However, bounding surfaces of polyps are often more complex surfaces composed of many small, approximately spherical patches of different radii of curvature, but with nearby centers of curvature. In our method, we find these structures by a combination of sphere fitting, and a graph algorithm that determines clusters of centers of curvature. First, and in contrast with previous methods, we do not compute the precise location of the interior surface of the colon. Instead, we model the colon wall as a thick region of high gradient valued voxels that have densities intermediate between tissue and air, and fit spheres to patches in this region. Sphere fitting is a linear problem that can be solved fast, as opposed to computing surface curvature. Fitting local isodensity contours, rather than the fully reconstructed inner colon surface, saves additional computation. Second, an adjacency graph is built to connect nearby sphere centers that are closer than one voxel to each other. This proximity threshold is principled, because a convex surface sampled on a one-voxel grid must produce centers of curvature that are less than a voxel apart. A depth-first traversal algorithm finally determines the connected components of this graph in time proportional to the number of its edges. Sufficiently large connected components are declared to be polyp candidates. This graph method is superior to binning techniques because it can find clusters that spread without gaps over a wide volume, without committing to a particular bin size.

III. RESULTS

The algorithm has been parameterized for detecting polyps greater than 10 mm in size. The detection rate was 100% with a high number of false positives (as high as 50 per dataset of 300 slices of 512x512 voxels) in 5 datasets containing a total of 10 significant polyps. Most of the false positives occur on the thick folds of the colon wall.

IV. CONCLUSION

Modeling polyps as more complex than spheres may be essential for eliminating false negatives in virtual colonoscopy. Our method based on a graph-theoretical clustering of centers of curvature provides the appropriate foundation for finding these complex shapes automatically. Computational complexity is reduced by (i) modeling the colon wall as a thick region, (ii) fitting spheres rather than ellipsoids, and (iii) employing geometric hashing techniques when searching for clusters of centers of curvature. The algorithm yields essentially no false negatives above 1cm, but produces relatively numerous false positives. These need to be eliminated by a second stage, currently under investigation, that employs a more complex, knowledge-based automatic 3-D shape classifier.