

Content-Based Image Retrieval Using Feature Density Estimates

William Speier, MS¹, Corey Arnold, PhD¹, William Hsu, PhD¹, Alex Bui, PhD¹
¹UCLA Medical Imaging Informatics, Los Angeles, CA

Abstract

Tumor detection and delineation is a necessary first step for a content-based retrieval system for brain cancer images. The proposed system uses Speeded Up Robust Features (SURF) and kernel density estimation to match feature distributions in a query image to a library of annotated images. The system successfully detects regions of tumor enhancement in a sample of patients with glioblastoma multiforme.

Introduction

The potential impact of content-based image retrieval (CBIR) in radiology has been widely discussed [1-2] with areas of application including decision support, teaching, and research. In brain tumor imaging, CBIR has potential impact in identifying patients with similar lesion locations and morphologies, providing a mechanism by which a patient of interest may be compared to cases in a hospital picture archive and communication system. In this work we describe a tumor detection algorithm based on SURF and present initial results on a dataset of patients afflicted with glioblastoma multiforme (GBM).

Methodology

A library of features is first created by running the SURF detection algorithm on each slice of the images in the training set. The dimensionality of the descriptors is reduced by running k-means in the 36-dimensional descriptor space. Based on manual annotations, each feature is then classified as *tumor* or *not tumor*. Each class is then represented by the distribution of the associated features over the clusters. Then, to locate tumor regions in a query image, features are generated and assigned to one of the k-means clusters. Kernel density estimation [4] is then applied to determine the distribution of each cluster over the volume. The cluster distribution for each voxel is then compared with the known distribution from the training data. Finally, voxels are labeled according to maximum similarity.

Results and Discussion

Preliminary results indicate the algorithm accurately detects enhancements, but has low precision due to false positive candidate volumes (Fig. 1b) and over-conservative detection of enhancement edges (Fig. 1d). False positive candidates are a result of an insufficient model for normal brain tissue. Tumor edge detection can be improved by making the selection threshold more aggressive or by post-processing the segmentation with edge detection.

Conclusion

On a preliminary test set the algorithm accurately detected tumors. This supports its use as a first step to finding candidate volumes that may then be further refined by post-processing methods. Future work consists of improving the model of the non-segmented portion of the brain, which will reduce the number of false positive areas selected.

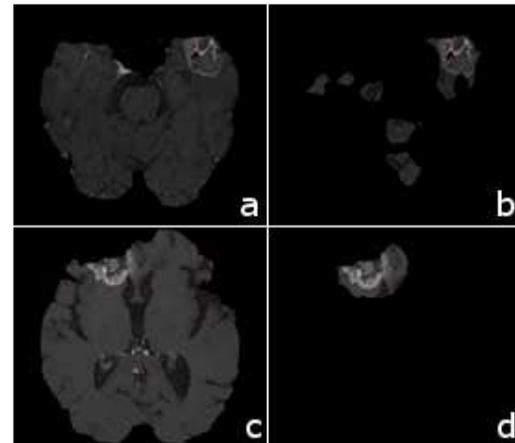


Figure 1: Results of tumor detection (b,d) with the corresponding original images (a,c). SURF features detected in the image are represented by red points.

References

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