Computer Assisted Detection in FLAIR and Diffusion Tensor neuroimages: automatic segmentation and volume assessment of cerebral gliomas

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Gliomas account for more than 70On the contrary, MR Diffusion Tensor Imaging (MR-DTI) is sensitive to subtle disruption of white matter tracts and can detect abnormalities around gliomas that appear normal on conventional imaging. DTI is a technique sensitive to the anisotropic diffusion of water along WM tracts, and can identify WM abnormalities in various kinds of disorders. Preliminary studies suggested that DTI might identify tumoral and peritumoral WM abnormalities in gliomas that can be referred to areas of disruption of cerebral tissue or regions of infiltration surrounding the gross tumor core, as confirmed by image-guided biopsies in small cohorts of patients. In particular the tumor core is characterized by reduced anisotropy and increased isotropy, while, around this area, tumor infiltration shows increased isotropy, but normal anisotropy. Early diagnosis and comprehensive evaluation of tumor extent and relationship with surrounding anatomical structures are crucial in determining prognosis and treatment planning. Automated methods for segmenting and evaluating cerebral gliomas may be useful for preoperative assessment of tumor extension, for radiation therapy planning, and to assess response during chemotherapy follow-up. They can decrease inter/intra-observer diagnosis subjectivity, while enhancing sensitivity. The aim of this study is to characterize pathological and healthy tissue in several MR datasets of patients with cerebral gliomas by 3D statistical Texture Analysis, developing an automatic segmentation technique (CAD, Computer Assisted Detection), also providing volumetric assessment. In particular, we tested our system (hereafter called GlioCAD) on DTI scans and on FLAIR (Fluid Attenuated Inversion Recovery) images, commonly used in clinical diagnosis.

DT-MR images were acquired at 3T at Scientific Institute and University Vita-Salute San Raffaele (Milan, Italy). MR datasets were collected from 48 patients harbouring cerebral gliomas (divided into two sets, made of 19 patients for training and testing the CAD system, 29 patients for verifying segmentation quality), and from 10 healthy subjects. DTI consisted of a single-shot EPI sequence (TR/TE 8986/80 ms) with parallel imaging (SENSE factor, R = 2.5). Thirty-two diffusion-gradient directions (b=1000 s/mm2) and one image set without diffusion weighting were obtained. The sequence was repeated twice and the data was averaged off-line to increase signal-to-noise ratio; DTI datasets were aligned off-line to the echo-planar volume without diffusion weighting on a PC workstation using the AIR (Automatic Image Registration) software to correct artifacts due to rigid body movement during scan acquisition. T2-weighted Turbo-Spin-Echo (TSE) and T1-weighted Fast-Field-Echo (FFE) conventional imaging was performed for anatomic guidance and morphological characterization of the lesions. Isotropic and anisotropic maps (MD, FA, p, and q) were calculated. In order to build a supervised procedure, manually-defined pathological regions of interests (ROIs) were drawn in consensus on each map by two experienced neuroradiologists using MRIcro software (http://www.mccauslandcenter.sc.edu/CRNL/tools). Scalp masks were generated using a combination of thresholding and mathematical morphology in order to automatically exclude the background voxels and the bone of the skull. These masks were applied on each map. 3D Texture analysis was applied to the segmented ROIs. A total of 126 features from Grey-Level Histogram (GLH), Gray-Level Cooccurrence Matrices (GLCM), and Grey-Level Run-Length Matrices (GLRLM), were calculated using a sliding-window approach: the (dilated) bounding boxes of

the ROIs were regularly partitioned into small overlapping sub-volumes of interest, called svois, in which the features were estimated. In this way, spatial distributions of features were assessed in each map (within the bounding boxes, where the tissue is essentially pathologic). In order to identify discriminating features, the same feature calculations were also performed in the contralateral (usually healthy) ROIs (partitioned into csvois). Each svoi and each csvoi were labeled as healthy or pathologic according to the class of its central voxel. In the supervised classification step, the image-feature dataset was split into a train and a test subset obtained by Leave One Patient Out (LOPO) cross-validation, a special case of k-fold cross-validation where k equals the number of patients. The feature-space dimensionality was reduced by Linear Discriminant Analysis (LDA), which allowed tissue classification by simple thresholding. Classification quality for each diffusion map was assessed by ROC (Receiver Operating Characteristic) curve calculation on the test set. A set of images that had not been used for training were automatically segmented by local tissue classification (again with a sliding-window approach, this time performed on the whole brain), and finally a system for false-positive rejection (based on 1st-order features) was developed and applied. The automatic segmentations were compared with the manual ones by the Jaccard similarity coefficient (JC), so giving a measure of the CAD-system quality. The JC measures similarity between sample sets (the CAD and manual ROIs, in our case), and is defined as the size of the intersection divided by the size of the union of the sample sets. All the software was written in the MATLAB environment (http://www.mathworks.it/products/matlab/), using the Image Processing toolbox and the MATLAB tools for NIFTI and Analyze image processing. With the purpose of allowing remote fruition of the CAD tool, a GUI (Graphical User Interface) was designed as a plugin for well-known visualization tools, such as Dycompiler and Osirix. The purpose of the interface is to offer a simple way of loading and displaying images, uploading them to a remote server, remotely running the CAD system with the chosen options, receiving the output of the segmentation process and visualizing the automatically-created ROI on the initial image, together with volumetric measures of the identified tumor regions.

For each map, classification sensitivity, specificity, and ROC curves were calculated: preliminary results were obtained for the MD map (AUC = 0.95, 11Twenty-nine images for each modality were automatically segmented: manual and automatic segmentations were compared, and the JCs were satisfying, with an inferior result for q maps (0.710.10 for MD and p maps, 0.610.12 for FA maps, 0.390.18 for q maps and 0.700.09 for FLAIR). Some false positive findings were spread throughout the brain tissue, lowering the JC values: the automatic system for false positive rejection proved to be quite effective in enhancing the JC. Figure 1 shows an example of automatic segmentations.

We described a method for automatic detection of cerebral gliomas in conventional and DT-MRI scans, by means of a classifier trained on 3D statistical texture features. According to our tests, the computed segmentations are in acceptable accord with the tumor contours as drawn by our radiologists. The results show that this approach could allow objective tumor identification and quantitative measurements, with good accuracy. Our system, GlioCAD, is proposed as a new tool, based on statistical textural analysis, for the automatic segmentation and volume assessment of brain gliomas, and for the quantitative analysis of the histograms in the regions of interest.
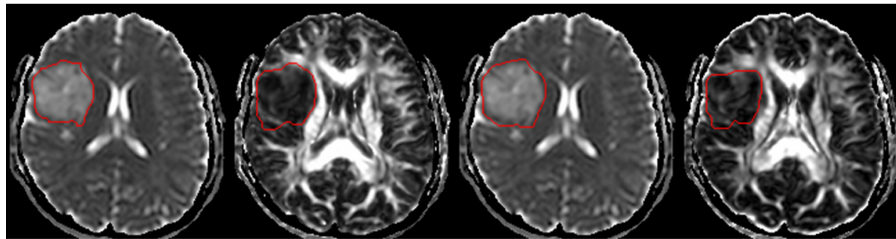

Figure 1. Oligodendroglioma WHO II, F 29 y. Left to right: MD (J = 0.83), FA (J = 0.73), p (J = 0.82), and q (J = 0.61) maps. The red line is the CAD segmentation