

Towards User-Independent ADC Quantification in Gliomas

Dirk Simon¹, Jan Klein², Jan Rexilius², Bram Stieltjes¹

¹Radiology, German Cancer Research Center, Heidelberg, Germany,

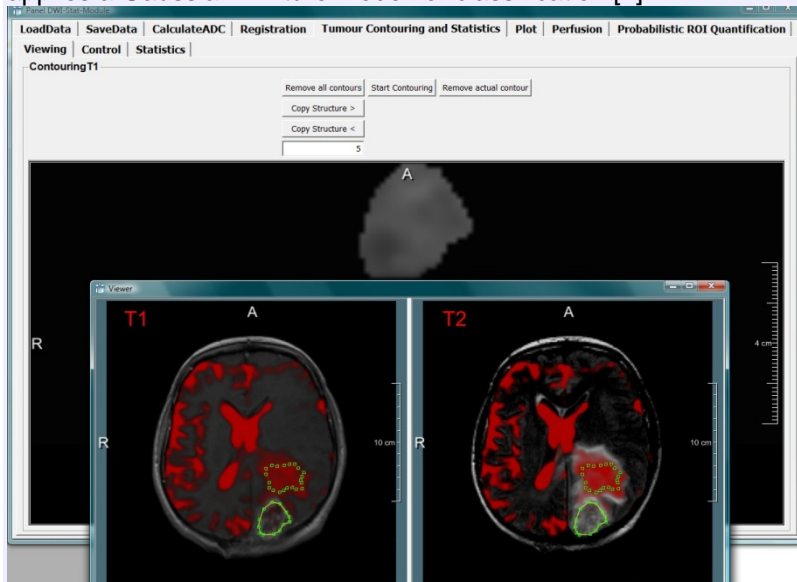
²MeVis Research, Bremen, Germany.

Purpose/Introduction:

Diffusion Weighted Imaging (DWI) derived apparent diffusion coefficient (ADC) values are known to correlate inversely to tumour cellularity in brain tumours [1]. Thus, high- and low malignant areas can be determined before treatment and treatment response can be monitored. However, fast and robust quantification of the ADC using routine ROI-analysis in heterogeneous tumours is impeded by several factors including poor data resolution and little contrast between high and low malignant areas. The main purpose of our project was to develop a software platform that enables the automated delineation and ADC quantification of different tumour sections in a fast, objective, user independent manner.

Subjects and Methods:

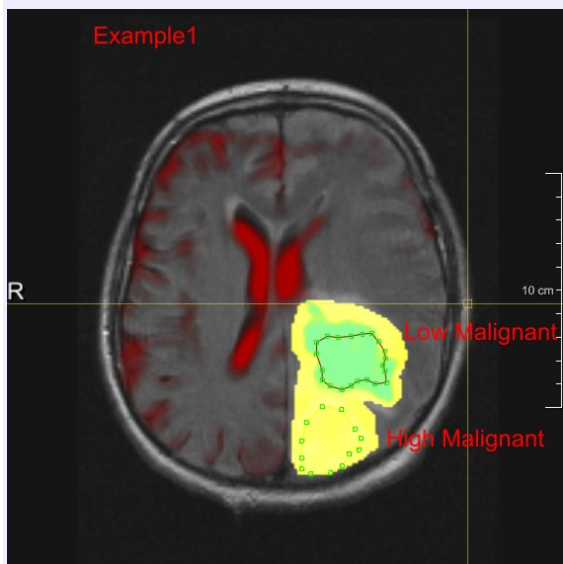
We included 5 patients with high grade gliomas. We used a 1.5 T scanner, routine imaging and DTI was performed. DTI parameters: SSEPI, TR/TE 4700/78, FOV 240 mm 2.5 mm³, 6 gradient directions, two b-values (0, 1000), 10 averages. The platform was developed using MeVisLab. We evaluated the ADC distribution in different tissue types. For ADC distribution analysis, a physician drew conservative ROIs indicating low malignant (T2) and high malignant areas (T1) (example1, example2: red low-yellow high malignant). In a second step, we used an Expectation Maximization (EM) algorithm that applies a Gaussian mixture model for classification [2].



For initialisation, a seed ROI was set in both areas of the Gross Tumor Volume (GTV).

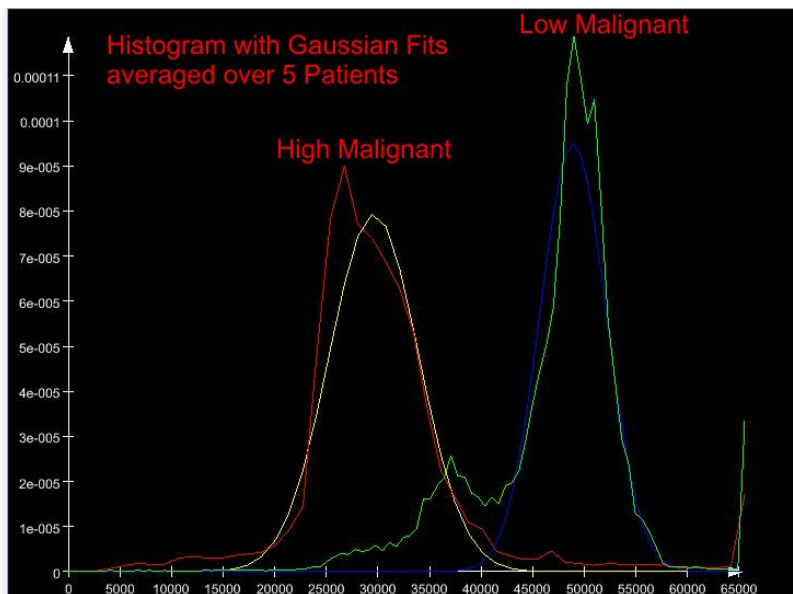


Subsequently, the two areas were automatically clustered. The clustering result was compared to the manually drawn ROIs.



Results:

The manual ROI-placement yielded Gaussian distributions in different areas. Moreover, peaks are distinguishable by their means and theoretically, a clustering algorithm with Gaussian distributions could be applied (histogram). The results from the automated clustering compare well to the hand-drawn ROIs proving the validity of the clustering. Furthermore, the objectiveness of the clustering results could be proven by variation of seed points.



Discussion/Conclusion:

The applied method is appropriate to objectively determine tumour heterogeneity in gliomas. Also, our data indicate that an automatic initialisation should be possible. However, there are challenges considering the boundaries of normal tissue near low malignant tissue. Due to comparable ADC values and partial volume effects, normal tissue may be marked as high malignant tumour (example1), whereas CSF and necrosis (spot in high malignant area) may be marked as low malignant tumour. These issues could be resolved by algorithms using pre knowledge such as Markov Random Fields [3].

[1] Chenevert, TL, J. Natl. Cancer. Inst, Vol 92, No 24. (2000), pp. 2029-2036

[2] Dempster, A. P., Journal of the Royal Statistical Society, Vol. 39, No. 1 (1977), pp. 1-38

[3] Pérez, P, Irisa/Inria, Vol. 11 (4), pp. 413-437