

# Method for accurate tumor volume estimation in the brain using healthy tissue subtraction

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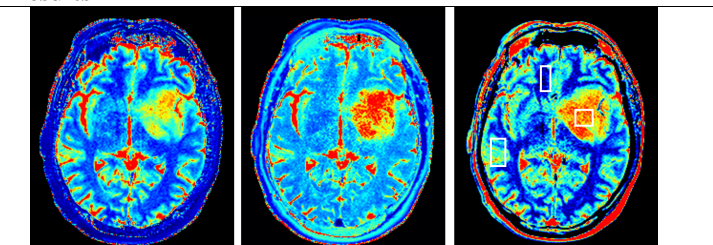
## Introduction

Quantitative Magnetic Resonance Imaging (qMRI) of multiple ( $n$ ) MR parameters can be used to create an  $n$ -dimensional parameter space for Functional Relaxometric Classification ('FRC-space'). Since each tissue has a unique combination of MR parameters it will form a cluster in the FRC-space, characterized by its position and its statistical distribution. If an image-voxel contains two tissue types, it has coordinates between the cluster positions of the separate tissues. Hence an estimation of tissue probability can be retrieved geometrically from FRC-space, assuming a certain model for the contribution of each tissue corresponding to the weighted parameter average. For an individual patient, removal of the recognized healthy part from the complete brain image volume may leave a certain volume with predominantly abnormal tissue. In most cases one might assume that this 'remaining part' is pathological in nature. This approach may provide an accurate estimate of the size of a brain tumor and may assist in the recognition of tumor type. The validity of both the approach and the hypothesis was explored in this contribution.

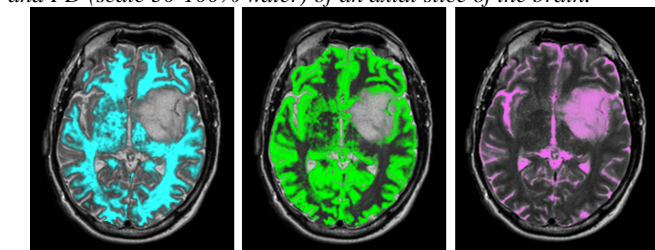
## Materials and Methods

A recently published rapid quantification method (Warntjes *et al.*, Magn Reson Med 2008;60:320-329) was added to the standard examination of a group of patients, diagnosed with different types of brain tumors. Using this method the T1 relaxation and T2 relaxation and the proton density (PD) was simultaneously measured for 24 slices with a resolution of 1 mm and a slice thickness of 5 mm on a 1.5 T Achieva scanner (Philips Healthcare, the Netherlands). The scan time was 5:34 minutes. Reference cluster positions and distributions of white matter (WM), grey matter (GM) and cerebrospinal fluid (CSF) were established by application of the same scan on a group of 21 healthy volunteers (16 male, 5 female, average age  $29 \pm 7$  years). The healthy tissue probability was calculated assuming a linear relation of cluster distance in R1-R2-PD parameter space (where the relaxation rate  $R1 = 1/T1$  and  $R2 = 1/T2$ ). Subtraction of healthy tissue from the complete brain results in the remaining tissue image. Pathology volume was defined as the sum of voxels where the deviation from normal was larger than 10%.

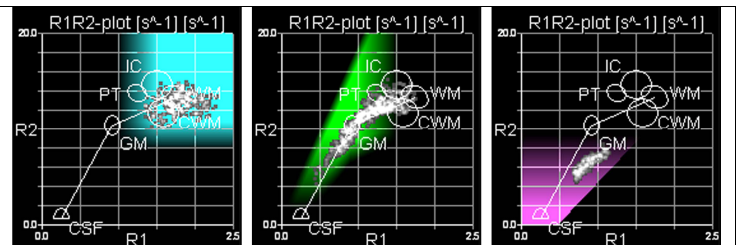
## Results



**Fig. 1.** T1 relaxation (scale 0-2000 ms), T2 relaxation (scale 0-200 ms) and PD (scale 50-100% water) of an axial slice of the brain.



**Fig. 3.** Coloured classification overlays corresponding to the WM, GM and CSF classes, based on the probability regimes in the plots of Fig. 2.



**Fig. 2.** The reference cluster regions of healthy CSF, GM, subcortical WM, central WM (CWM), putamen (PT) and internal capsule (IC) in a relaxation rate plot of R1 versus R2 (a projection of the R1-R2-PD space). The colors (blue, green, purple) show the probability regimes of WM, GM and CSF. The clusters from the ROIs of Fig. 1c (PD map) are also plotted as individual data points. The tumor data points are positioned significantly off-line from the partial volume connectivity between CSF and GM. Hence it seems to contain partly CSF, but no WM or GM.

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**Fig. 4.** Slice 13 - 8 of 24 of the same patient where the yellow overlay indicates remaining tissue that does not correspond to normal, healthy values. The red line indicates the edge of the brain. The estimated tumor volume was 5.2, 6.7, 9.1, 11.2, 12.3 and 10.6 mL respectively, giving a total of 55.1 mL in the displayed slices. In reality the tumor stretched over slice 14 - 4 resulting in a total estimated size of 70.1 mL. Slice 10 was used for Figs. 1-3.

## Conclusion

Subtraction of healthy tissue from the complete brain seems to be a promising method to find tissue that deviates from normal. In case of a tumor this approach can be used to obtain an estimate of the total tumor volume.

