Segmentation and Volume Estimation on a Sub-voxel Basis using Quantitative MR: *A Validation Study*

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Introduction: By using quantitative MR on the brain, quantitative maps of relaxation rates, R1 and R2, as well as proton density, PD, can be acquired. Specific brain-tissues typically exhibit a narrow range of R1, R2 and PD values and thus the tissues in the brain can be identified as clusters in the three dimensional R1-R2-PD space. In partial volume voxels (voxels containing two or more tissue types) the R1-R2-PD values are a combination of the values from the contributing tissues. By using a partial volume model the brain-tissue volumes can be calculated on a sub-voxel basis and the dependency on voxel size can effectively be removed. This makes it possible to use larger voxels, increasing SNR and decreasing scan time, while still accurately quantifying brain tissue volumes.

Materials and method: A simulation of partial volume voxels was used in order to determine how voxel positions in R1-R2-PD space relate to tissue fractions. A segmentation method to assess fractional brain-tissue volumes of white matter (WM), grey matter (GM) and CSF for the complete brain on a sub-voxel basis was then created. Finally 7 normal subjects was scanned 8 times each for validation The quantification sequence used was a multi-echo saturation recovery sequence using a repetition time TR = 3.2 s, 6 echoes at multiples of 15 ms and saturation delays of 128, 384, 1408 and 3072 ms *(Warntjes et al., Magn Reson Med 2008:60;320-329)*.

The simulation consisted of (a) A Bloch simulator where the effect of RF-pulses and gradients on several spin-isochromates could be simulated; (b) The quantification sequence and fitting adapted to work with the Bloch simulator and; (c) Partial volume phantoms with known mixtures of tissue types. The simulation was implemented in MATLAB R2008a (MathWorks, 2008).

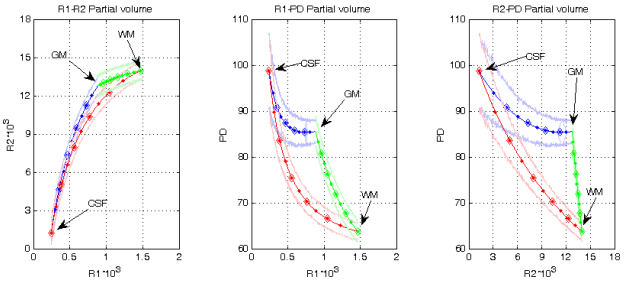

Figure 2*: Simulated partial volume graphs with different volume fractions of WM, GM and CSF in R1-R2-PD space. The green lines show partial volume for GM↔WM, blue lines shows CSF↔GM and red lines show CSF↔WM. Each diamond represents incremental steps of 20% tissue, and similarly each dot represents steps of 10% tissue. The dimmed lines corresponds to 1 standard deviation of noise with SNR=20. Pure tissue positions are marked using labels.*

Finally the quantification method was used to quantify R1, R2 and PD in 7 normal subjects (4 male, 3 female, age 28±5 years). The scanner used was a 1.5T Philips Achieva. Each of the subjects was scanned 8 times. For 6 of the scans the same axial volume was acquired varying the in plane resolution (1.0, 1.2, 1.4, 1.6, 1.8 and 2.0 mm), leaving all other parameters constant, additionally one sagittal and one coronal stack were acquired (2.0 mm in plane resolution). In all scans slice thickness was 5.0 mm. By changing the voxel size or the geometry the partial volume affects the acquired images differently. It is then possible to determine if the segmentation process and volume estimation is sensitive to partial volume effects *in vivo*. Figure 1 show an example of the segmentation of brain-tissues in three different geometries.

Results: Figure 2 show how position in R1-R2-PD space relates to brain tissue fractions. Table 1 shows the resulting brain volumes for WM, GM, CSF, intracranial volume, brain parenchyma and brain filling fraction (=brain parenchyma/intracranial volume) for all 7 subjects comparing the six resolutions. Table 2 shows the same volumes comparing the three different orientations.

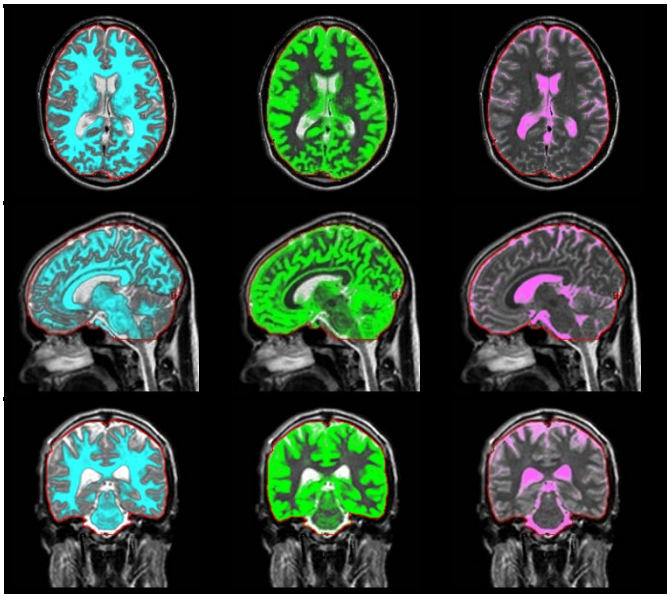

Figure 1: *One slice sample segmentation of brain tissue. From left to right: WM, GM and CSF. From top to bottom: axial plane, sagittal plane and coronal plane. Radiological convention was used for L/R orientation.*

Subject	WM [ml]	GM [ml]	CSF [ml]	Intracranial Volume [ml]	Brain Parenchyma [ml]	Brain Filling Frac. [%]
F38	605±10	742±4	95±1	1442±10	1347±9	93±0
F26	631±16	789±17	100±1	1521±8	1421±7	93±0
F24	468±8	591±10	145±1	1204±4	1060±4	88±0
M29	530±6	740±10	136±1	1405+7	1270±7	90±0
M32	698±15	839±21	101±4	1638±23	1537±20	94±0
M26	671±7	847±8	141±4	1660±9	1518±11	91±0
M23	575±10	833±9	140±3	1550±11	1409±10	91±0

Table 1: *Brain volumes for WM, GM, CSF, intracranial volume, brain parenchyma and brain filling fraction comparing the six resolutions.*

Subject	WM [ml]	GM [ml]	CSF [ml]	Intracranial Volume [ml]	Brain Parenchyma [ml]	Brain Filling Frac. [%]
F38	609±38	753±41	82±12	1444±8	1362±9	94±1
F26	650±52	780±69	88±12	1518±13	1430±9	94±1
F24	426±42	645±54	136±8	1207±8	1071±14	89±1
M29	523±12	761±25	126±8	1410±12	1284±14	91±1
M32	680±33	850±24	87±12	1618±27	1530±16	95±1
M26	633±45	903±49	124±13	1660±11	1536±4	93±1
M23	552±41	873±48	125±12	1550±7	1425±7	92±1

Table 2: *Brain volumes for WM, GM, CSF, intracranial volume, brain parenchyma and brain filling fraction comparing the three different geometries.*

Conclusion: Total brain-tissue volumes can be calculated accurately using the described method, independent of voxel size and geometry. When comparing different geometries (i.e. axial, sagittal and coronal) the brain volumes of the different tissues differ slightly. The intracranial volume, brain parenchyma volume and brain filling fraction are, however, still determined with high accuracy. The presented method can be used to quantify brain tissue volumes on a sub-voxel basis. This is very important for epidemiological studies where large groups are compared as well as for different age related diseases, such as dementia where brain degeneration can be seen as a decrease in brain tissue.