On-line Appendix

The bookend technique requires the combination of 3 consecutive image series to produce quantitative perfusion measurement with patient-specific calibration via an arterial input function–independent steady-state measurement of qCBV. Two segmented, multiphase inversion recovery look-locker-EPI scans are required, 1 before and 1 after a DSC gradient-echo EPI perfusion-weighted scan, to obtain estimates of T1 in a single section containing normal WM, before and after contrast agent injection. The bookend technique calculates qCBV based on changes in the estimated T1 values in WM in relation to these changes in the blood pool.[1,2] This approach relies on careful modeling of the effects of intravascular-to-extravascular water exchange,[1] which is a well-known confounding effect in determining qCBV from pre- and postgadolinium T1 changes.[3] To quantify blood volume in WM, first the steady-state blood volume in WM, $CBVss_{WM}$, is calculated from the T1 changes in WM and the blood pool, under the fast-water-exchange approximation, by the following equation[1]:

$$1) \qquad CBVss_{WM} = \frac{(1/T_1^{Post} - 1/T_1^{Pre})_{WM}}{(1/T_1^{Post} - 1/T_1^{Pre})_{Blood}} * 100\%$$

where T_1^{Pre} and T_1^{Post} are T1 values before and after contrast agent injection. Then, qCBV (in mL/100 g) in WM is calculated as follows:

$$2) \qquad \mathrm{qCBV_{WM}} = WCF(\Delta R_1) * \frac{1}{\rho} * \frac{1 - Hct_{LV}}{1 - Hct_{SV}} * CBVss_{WM}$$

where $\mathrm{qCBV_{WM}}$ is the quantitative CBV value in WM, $WCF(\Delta R_1)$ is the water correction factor determined from the change in inverse T1 values of the blood pool following contrast injection, ΔR_1 is the change in inverse T1 relaxivity (ie, $1/T_1^{Post} - 1/T_1^{Pre}$), ρ is the average attenuation of a brain voxel (1.04 g/mL), and Hct_{LV} and Hct_{SV} are the hematocrit levels in large and small vessels, respectively.

$$3) \qquad WCF(\Delta R_1) = 2.2334 \cdot 10^{-14}\Delta R_1^2 + 0.2539\Delta R_1 + 0.0792$$

For DSC analysis, rCBF is determined by deconvolving the individual tissue concentration versus time curves by the arterial input function using singular value decomposition, and rCBV is computed from the ratio of the area under the curve of a tissue concentration versus time curve to the area under the curve of the arterial input function, according to Sakaie et al.[2] MTT is calculated as the ratio of rCBV to rCBF, based on the central volume theorem. Final perfusion quantification in a brain voxel is calculated using the following equations:

$$4) \qquad \mathrm{qCBV} = \mathrm{rCBV} * \frac{\mathrm{qCBV_{WM}}}{\mathrm{rCBV_{WM}}}$$

$$5) \qquad \mathrm{qCBF} = \mathrm{rCBF} * \frac{\mathrm{qCBV_{WM}}}{\mathrm{rCBV_{WM}}}$$

where $\mathrm{rCBV_{WM}}$ is the rCBV value in WM.

References

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