Purpose: To develop a whole-brain acquisition protocol based on dynamic contrast enhanced (DCE) MR imaging that is able to provide absolute brain tissue perfusion estimates and to assess, evaluate and minimize the uncertainty in the estimates of contrast agent concentration.

Methods: Preliminary in vivo data was collected using a 3D spoiled-gradient recalled echo (SPGR) sequence with TR/TE/flip angle (FA) = $2.5 \text{ ms}/1.15 \text{ ms}/15^\circ$. The spatial resolution was $1.7 \times 1.7 \times 4.0 \text{ mm3}$. A variable rate k-space sampling scheme and view sharing resulted in a temporal resolution of 2.4 s. The perfusion estimates were calculated using indicator-dilution theory. Based on preliminary data, simulations estimating the uncertainty and sensitivity to misestimated parameters in the concentration measures were performed. Tissue parameters and contrast agent relaxivities were obtained from literature. The SNR before contrast injection was extracted from the preliminary data.

Results: Absolute perfusion maps were successfully generated for the whole brain in all three subjects. As predicted, the low signal enhancement in cerebral tissue, especially in white matter, resulted in noisy perfusion maps. The range of the cerebral blood flow (CBF) and cerebral blood volume (CBV) maps corresponded to the range of the values reported in literature. The mean transit times (MTT) however were overestimated. The simulations showed that a FA of 9° minimizes the concentration coefficient of variation in white matter. However, the sensitivity to misestimated parameters was reduced with increasing FA: a FA > 20° was beneficial. For realistic SNR levels, averaging 5 acquisitions of the signal before contrast agent arrival were sufficient. More baseline measurements did not significantly decrease the signal variance.

Conclusion: It is possible to acquire qualitatively acceptable whole-brain bolus tracking data using a DCE sequence. In addition, the FA influences the uncertainty and sensitivity in concentration estimates when using a SPGR sequence.

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