Feasibility of using Non-Contrast Spoiled Gradient Echo Magnetic Resonance Fingerprinting for the Quantification of Cerebral Blood Volume

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Assessment of vasculature is essential for the monitoring of a wide range of neurological diseases. One aspect of that is the quantification of blood volume.

We propose a method for the quantification of blood volume using the magnetic resonance fingerprinting (MRF) framework[1] with a spoiled gradient echo (SPGR) acquisition to efficiently exploit the differences in native longitudinal relaxivity between blood and tissue and use simulations to explore the impact of noise on the method's accuracy and precision.

Methods

- The signal simulation was modelled using an array of isochromats governed by the Bloch equations.
- Different fractional blood volumes (v_b) from 0.5 to 10% in steps of 0.5% (denoted: [0.5,10,0.5]%) were simulated by varying the proportion of array isochromats with blood properties.
- Fingerprints were created that were unique to each combination of tissue compartments by varying input flip angle (α) **(Fig. 1a)** and repetition time (*TR*) **(Fig. 1b)**, while assuming a short and unvarying *TE,* for 1000 repetitions of *TR*.

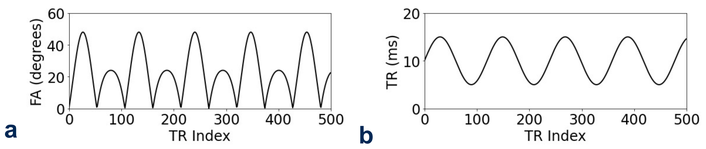

Fig. 1: *Partial representations of the variation in* ***(a)*** *flip angle, and* ***(b)*** *repetition time, used to generate the fingerprints*

- We assume that that the noise in MRF signals can be modelled as zero-mean complex Gaussian noise with a standard deviation σ_G on each isochromat.
- Optimisation of sequences was done using a branch and bound technique, outlined in Cohen et al. [2]

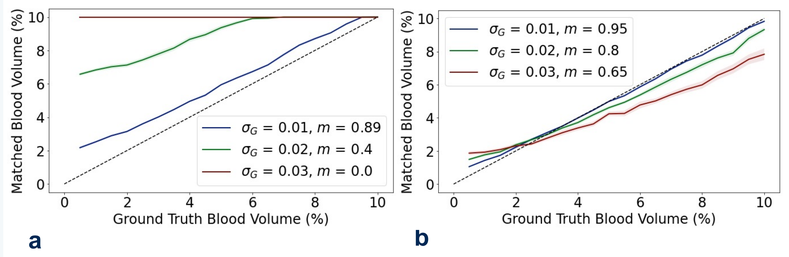

Fig. 2 *Matching of blood volume at three noise levels with* ***(a)*** *non-optimised acquisition parameters* ***(b)*** *optimised acquisition parameters, with 95% confidence intervals shaded*

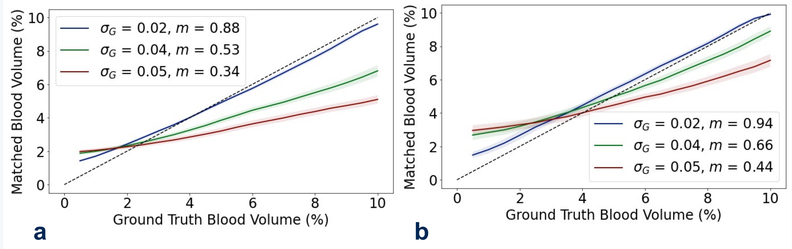

Fig. 3 (a) *Matching of blood volume at three noise levels with single dimension dictionary in v_b, and a four-dimensional sample [v_b,$T_{1,b}$,$T_{1,e}$, and B_1^+] **(b)** Matching when the dictionary is expanded to include the range of $T_{1,b}$,$T_{1,e}$, and B_1^+ values, with 95% confidence intervals shaded*

Experiments

1. Comparison a non-optimised and optimised dictionary with variation in blood volume, v_b: [0.5,10,0.5]%. Initial, 'non-optimised' values for these parameters were chosen to closely match the variation chosen by Ma et al.[1] These parameters were then optimised for v_b.
2. Next, a sample data set with variation along v_b ([0.5,10,0.5] %) $T_{1,b}$(1500,1900,200]ms), $T_{1,e}$ 1000,2000,200]ms), andB_1^+ (0.8,1.2,0.1] x B_1), was then matched to the v_b - only dictionary, to look at robustness of matching when these parameters are not known *a priori.*
3. Finally, the four-dimensional sample, was matched to a dictionary of the same variation to test the feasibility of determining each parameter simultaneously.

Results

- **Fig. 2a** shows the success of matching blood volume at three noise levels for the optimised dictionary. At the middle shown noise level optimisation increases slope (*m*) from 0.40 to 0.80. (Perfect matching would result in a slope of unity).
- When assumptions regarding $T_{1,e}$, $T_{1,b}$, and B_1^+ are inaccurate there is a loss of accuracy seen most prominently at higher noise levels, **Fig. 3a**.
- If the dictionary is extended to explicitly account for unknown variation in $T_{1,e}$, $T_{1,b}$, and B_1^+ the precision and accuracy improves, **Fig. 3b**. Improvement becomes more pronounced at higher noise levels

Discussion

- Optimisation of the acquisition parameters showed a marked improvement in matching success at lower noise levels.
- Understanding gained from these experiments will guide our development of in vivo acquisitions protocols.
- Requiring prior knowledge of $T_{1,e}$, $T_{1,b}$, and B_1^+ would require a set of pre-scans that would increase scanning time. It is therefore encouraging that each of these parameters can be estimated simultaneously with v_b with reasonable accuracy.

SPGR magnetic resonance fingerprinting acquisition for the quantification of blood volume is feasible. However, for the best accuracy, this will require either a pre-scan or simultaneous quantification of T1 of the intravascular compartment, T1 of the extravascular component, and a B_1^+ field map. We are in the process of confirming these findings *in vivo.*

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1. Ma D, et. al. Nature.; 495:187–192 (2013)
2. Cohen O, et al. Magnetic Resonance Imaging. 41:15–21 (2017)