Quantification of Multiple Boli Arterial Spin Labelling in Mice and Rats

Samantha Paterson[1], Camille Graff[2], Antoine Vallatos[3], William Holmes[1]
[1]GEMRIC, Institute of Neuroscience & Psychology, University of Glasgow, Glasgow
[2]Grenoble INP, Grenoble, France
[3]Centre of Clinical Brain Sciences, University of Edinburgh, Edinburgh

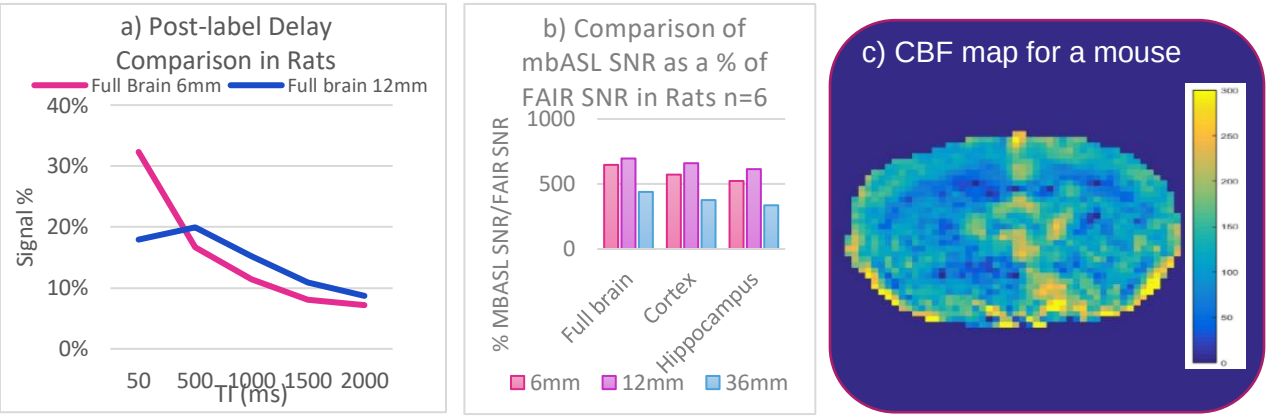
Introduction

There is a need for high SNR quantitative ASL. We introduce a quantitative model for the high SNR ASL sequence (mbASL) in rats and mice, which uses a train of adiabatic pulses to label multiple boli of arterial water[1]. mbASL can be described as a hybrid of PASL and CASL: either as a multiple PASL with limited labelling thickness or a large thickness CASL. We proposed a model describing the mbASL signal based on Buxton's PASL model[2] and have shown its validity by producing quantitative high-SNR CBF maps in rats and mice that agree with the literature values.

Methods

Variable thickness mbASL experiments were performed using C57 mice (n=5) & Wistar rats (n=6). Distance between labelling and imaging slice was kept constant. Exploration of the labelled bolus arrival at different post-label delay times used 1-shot mbASL with an inversion time (CI) of 500ms and a time after inversion TI= 50:500:4050ms (NA=10). CBF maps were produced using a T1 map and a 4-shot mbASL (NA=10, CI = 5000ms, TI = 50ms). mbASL was compared with FAIR, NA= 10, TI = 1750ms.

Results & Discussion



The number of pulses for optimal signal decreased as the thickness of the labelling slice increased. The arrival of the labelled bolus changes distribution as the slice thickness increases shifting from a CASL-like shape to a PASL-like one, as shown in (*Fig a)*. This reflected the theoretical predictions from the model that the ΔM distribution would change at different post label delays with increasing thickness. The model was used to acquire high SNR mbASL CBF maps (*Fig c)* in rats and mice that agree with the literature. The sequence has shown a large increase in overall signal and SNR compared to the standard FAIR sequence (*Fig b)*.

Conclusion

We have been able to fully quantify the mbASL sequence and produce quantitative CBF maps for mice and rats which agree with literature values[3,4]. The sequence has shown high signal and SNR over the standard FAIR sequence in both mice and rats.

[1]Vallatos, A et al. (2017), [2]Buxton, R. B. et. al. (1998), [3]Muir, E. R. et al. (2008), [4]Sicard, K. M et al. (2005).