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A multi-site round robin assessment of ASL using a perfusion phantom

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Synopsis

Arterial Spin Labelling shows great promise for perfusion measurements; however, despite numerous volunteer reproducibility studies, comparisons have not been made using a phantom to establish differences due to the acquisition hardware and pulse sequences. We present data from a multi-site study using a perfusion phantom, targeting 3T MRI systems from a single vendor running the same software version.

Introduction

The measurement of Cerebral Blood Flow (CBF) using Arterial Spin Labelling (ASL) has recently seen a renewed interest following the publication of the Position Paper providing a set of very clear guidelines on how to set up an ASL experiment[1]. In particular, it has been shown to be valid as a biomarker of neurological disease onset[2] and response to therapy[3]. Indeed, based on numerous reproducibility studies[4], the coefficient of variation of CBF has been well established, enabling its use as a biomarker in cross-sectional studies[5]. However, while the sources of potential physiological confounds are well established[6], it has so far not been possible to compare all ASL implementations depending uniquely on potential hardware differences.

In this study, we set out to assess the effective reproducibility of CBF estimates by ASL using a recently developed Perfusion phantom[7] at 11 different sites with a range of scanner manufacturers (total 17 systems) working on various software levels. We present here the preliminary data from the first 5 scanners from 3 sites working on Philips 3T MRI scanners with software release R5.3.

Materials and Methods

A perfusion phantom was transported by car to 3T MRI imaging centres in the Netherlands over the course of a week and scanned on 5 Philips 3T MRI systems running software release R5.3 (detailed in Figure 1.a). On each system, ASL measurements were made using the product ASL sequence, comprising of pCASL labelling with a 4-shot 2D-EPI segmented acquisition. Measurement parameters are detailed in Figure 1.b. Data were acquired with 'normalisation' turned on; the first dynamic a long-TR without background suppression or labelling pulses for an M0 image, followed by 3 dynamics of control-label pairs. Measurements were made at two flow rates; 200ml/min and 350ml/min, and computer software monitored and recorded the phantom flow rates during scanning. At each site, care was taken to ensure the phantom was reproducibly placed on the patient couch (see Figure 2), and the FOV was centred at a landmark at the centre of the porous material and rotated into alignment with the phantom.

Analysis was performed in Matlab R2016b (The Mathworks, Natick, MA, USA). Dicom images were converted to NIFTI dicm2nii[8], and CBF maps calculated using the single subtraction equation for pCASL[1]:

$$\mathrm{CBF} = \frac{6000 \cdot \lambda \cdot (\mathrm{SI}_{\mathrm{control}} - \mathrm{SI}_{\mathrm{label}}) \cdot e^{\frac{\mathrm{PLD}}{T_{1b}}}}{2 \cdot \alpha \cdot T_{1b} \cdot \mathrm{SI}_{\mathrm{PD}} \cdot \left(1 - e^{-\frac{\tau}{T_{1b}}}\right)}$$

where α=0.85, λ=0.32, T_{1b}=1800ms, τ=1800ms, PLD=1800ms. The M0 image from dataset was registered to a structural atlas image of the phantom, from which an ROI mask of the entire porous material was generated (see Figure 3). The mean CBF and standard deviation within this ROI were then calculated.

Results

Figure 4.a shows representative CBF maps of the fifth slice from each data set. Figures 4.b and c show the CBF value distributions within each mask for MRI System 5. The mean CBF values and standard deviations within each mask for each system and flow rate are shown in Figure 5.a and b. Across all systems, the mean CBF was 33.7±3.1 ml/100g/min at 200ml/min, and 76.7±9.0 ml/100g/min at 350ml/min.

Discussion

Across the MRI systems, the coefficient of variance of the mean CBF was 9.2% at 200ml/min and 11.7% at 350ml/min. As Figure 4.b and 4.c show, the actual voxel value distributions within the masked regions are complex and simple mean/standard deviation statistics do not capture this, leading to an underestimation in the perfusion signal CBF, and perhaps underestimate the differences between MRI systems. At the higher flow rate the difference between systems in both the mean CBF and standard deviation of CBF is greater. In particular, System 2 shows a mean CBF and standard deviation that is noticeably higher than the other four systems. The corresponding CBF map for System 2 at 350ml/min shows a similar level of noise, but a slightly more hypointense signal. Possible reasons for this might be improved labelling efficiency, or this could be a receive coil effect as this was the only system using an 8 channel head coil. No repeat measurements were made at each site, so there is no metric of intra-session variability which might also explain some of the variations observed between systems.

Conclusion

We have presented a multi-site assessment of 2D-EPI pCASL measurements on Philips 3T MRI systems running the same software version, using a perfusion phantom. In general, measurements made across all systems are in good agreement with each other; however, further analysis and measurements are required to determine a statistically significant difference between systems.

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Figures

a.

MRI SYSTEM NO.	MRI VENDOR	MODEL	SOFTWARE VERSION	RECEIVE COIL
1	Philips	Ingenia	R5.3.1	32ch
2	Philips	Achieva	R5.3.1	8ch
3	Philips	Ingenia	R5.3.1	32ch
4	Philips	Ingenia	R5.3.0	32ch
5	Philips	Achieva dStream	R5.3.1	32ch

b.

IMAGING PARAMETER	VALUE
LABEL DURATION	1800ms
POST LABELLING DELAY	1800ms
LABEL PLANE LOCATION	60mm from centre of FOV, parallel alignment.
NO. DYNAMICS	3
NO. SHOTS	4
SENSE FACTOR	2.3
FOV	256x192x59mm
PE DIRECTION	AP
ACQUISITION MATRIX (PER SLICE)	128x96
NO SLICES	12
SLICE THICKNESS/GAP	4mm/1mm
TR	5000ms
TE	Min TE selected, given per MRI system 1-5: 11.271, 10.166, 11.283, 11.269, 10.16 ms
BACKGROUND SUPPRESSION	4 pulse product default

Figure 1

Summary of MRI Systems (a). ASL Sequence Parameters (b).

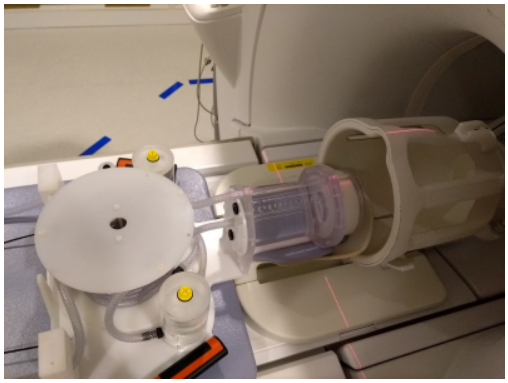

Figure 2

The perfusion phantom consists of an MRI compatible pump that delivers a liquid at a controlled flow rate to a perfusion chamber. The liquid is distributed in a ‘vascular’ network to a porous material cylinder that simulates the capillary bed of diameter 116mm and height 28.5mm. To minimise any variance in measurements due to placement of the phantom, on each MRI system the laser marker was set to the same reference point on the phantom, the phantom was aligned with the laser in the head-foot direction, and the phantom was levelled using foam pads.

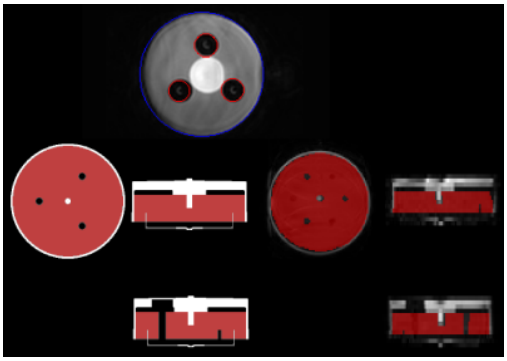

Figure 3

The creation of the image masks is automatic, using the registration of an 'atlas' image of the phantom to the data to be analysed. First, a Hough transform provides candidates for known circular features to be detected which are then exhaustively matched w.r.t. their size and relative location to one another (top). If consecutive slices detect features in a similar location, this location is used as an initialisation to a multi-resolution, multi-transformation (including B-spline) registration to the phantom 'atlas' image (bottom-left), which provides the porous material mask (in red, bottom-right).

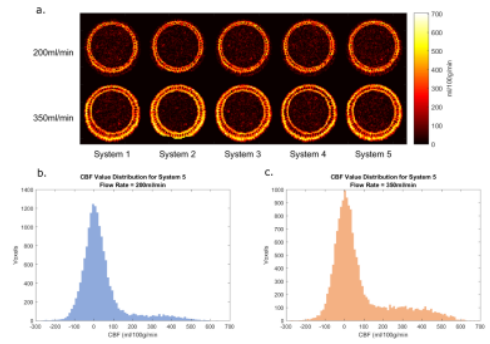

Figure 4

Calculated CBF maps of slice 5 at each flow rate in each data set from all systems (a). Images have been masked with the porous material mask to remove background signal.

Histograms of the CBF value distributions within the mask at a flow rate of 200ml/min (b) and 350ml/min (c) for MRI System 5. The distributions have two components: a Gaussian distribution centred around zero, corresponding to noise in voxels where there is no perfusion signal; and a broader, positive non-zero centred Gaussian distribution of values from voxels that do have a perfusion signal.

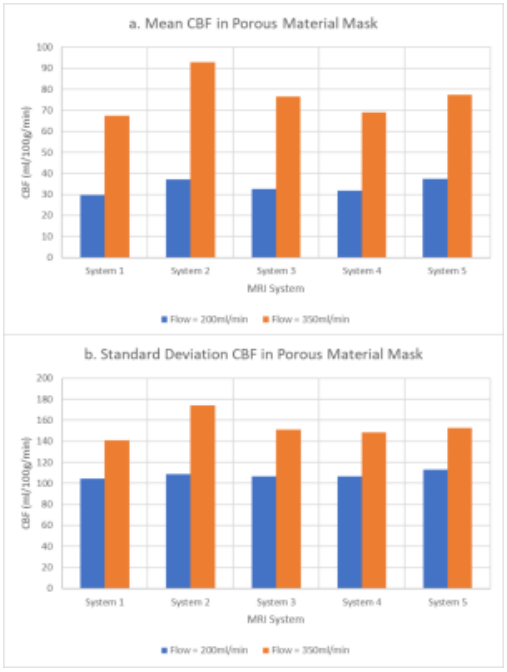

Figure 5

Mean CBF (a) and standard deviation of the CBF values (b) within the porous material masks. Trends in variation between the MRI systems visually correspond at flow rates, with variation at the higher flow rate more pronounced. In all cases, the mean CBF at 350ml/min is more than double that measured at the 200ml/min, despite the flow rate ratio being 1.75. This is because at 200ml/min not all of the labelled bolus has reached the porous

material at PLD=1800ms.