ASL Modelling and Quantification

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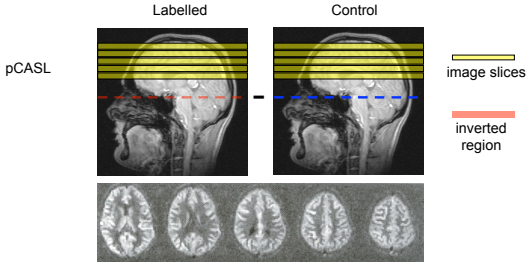
Overview of talk

- Brief review of ASL
- Describe the 2 main ASL quantification models
  - T1 model
  - General kinetic model
- Pros and cons of multi-TI and single-TI
- Quantification methods using single-TI
- Assumptions of the models
- Consensus approach to ASL quantification

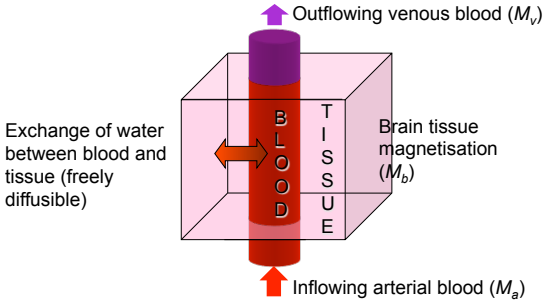
Brief review of ASL



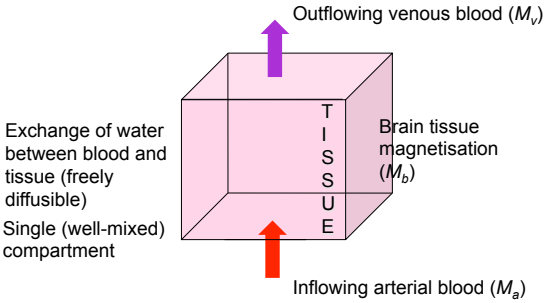
Signal intensity in these images proportional to CBF

Q: How do we convert these images into quantitative maps (ml/100g/min)?

ASL CBF quantification model



ASL CBF quantification model



ASL CBF 'T1 quantification model'

- Modification of Bloch equation (Detre et al MRM 1992)

$$\frac{dM_b}{dt} = \frac{M_b^0 - M_b(t)}{T_1} + f \cdot M_a(t) - f \cdot M_v(t)$$

Relaxation term

Change in magnetisation caused by arterial inflow

Change in magnetisation caused by venous outflow

- Solve to give:

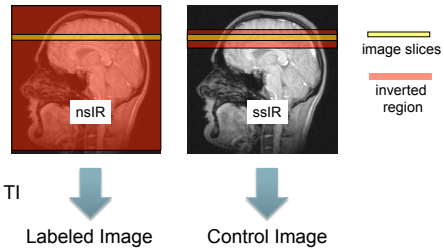
$$f = \frac{\lambda}{T_{1app}}\left(\frac{M_b^{control} - M_b^{labelled}}{2M_b^{control}}\right)$$

where λ is blood:brain partition coefficient

$$\frac{1}{T_{1app}} = \frac{1}{T_{1b}} + \frac{f}{\lambda}$$

PASL CBF T1 quantification model

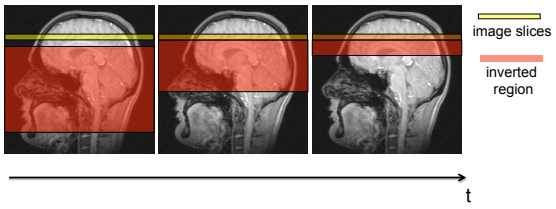
- FAIR technique (Kim and Kwong et al MRM 1995)



- Apparent T1 recovery dependent on state and inflow rate of blood magnetization

ASL CBF 'general kinetic model'

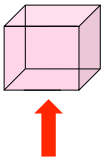
PASL labeling of a proximal slab of arterial blood (EPISTAR)



- Think of this as the inflow of a kinetic tracer (inverted arterial blood water)

ASL CBF general kinetic model

Retention of the tracer in the voxel
Residue function



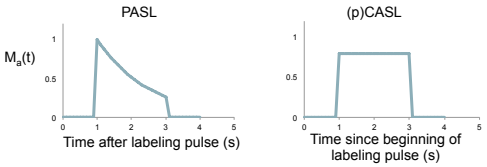
Tissue voxel

Delivery of the tracer to the voxel
Arterial Input Function (M_a)

- Need to know what these functions are

ASL CBF general kinetic model

- Arterial Input Function (AIF)



$M_a(t) = 0$ when $t <$ bolus arrival time (Δt)
$M_a(t) = 0$ when $t > \Delta t +$ bolus duration (τ)

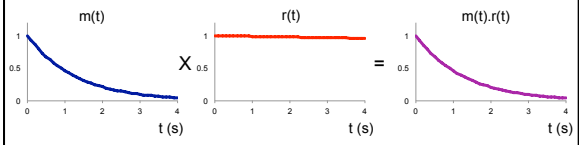
$M_a(t) = 2M_a^0.\alpha.\exp(-t/T_{1b})$ *for PASL*
$M_a(t) = 2M_a^0.\alpha$ *for (p)CASL*

α = inversion efficiency

ASL CBF general kinetic model

- Residue function (Res)
  - Tracer reduces due to T_1 relaxation of label
    $m(t) = \exp(-t/T_1)$
  - Tracer lost due to venous outflow
    $r(t) = \exp(-f/\lambda.t)$

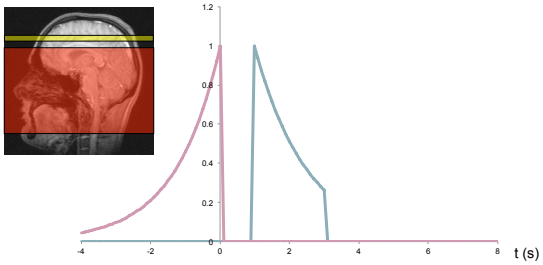
$Res = m(t).r(t)$



ASL CBF general kinetic model

- Equation for general kinetic model

$\Delta M(t) = CBF \times [AIF(t) * Res(t)]$



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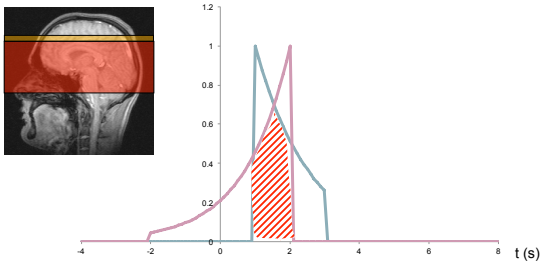

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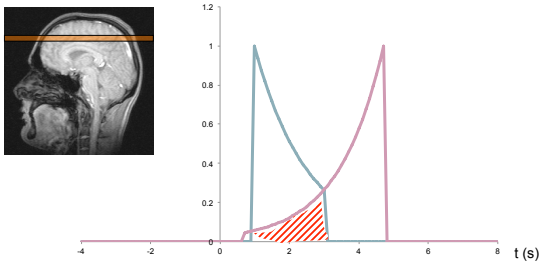
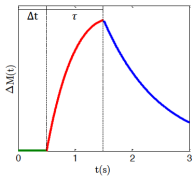


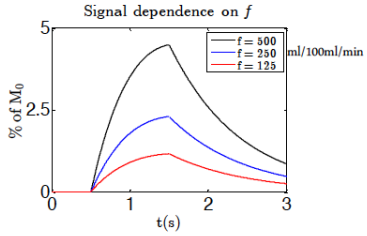
ASL CBF general kinetic model

- Solution for general kinetic model

$$\Delta M(t) = \begin{cases} 0, & 0 < t < \Delta t \\ 2M_{0b} f (t - \Delta t) \alpha e^{-\frac{t}{T_{1b}}} q_p(t), & \Delta t < t < \Delta t + \tau \\ 2M_{0b} f \tau \alpha e^{-\frac{t}{T_{1b}}} q_p(t), & t > \Delta t + \tau \end{cases}$$

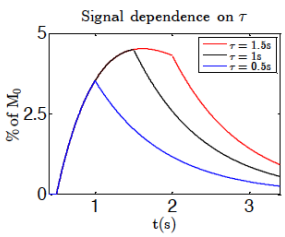


Parameters of the general kinetic model



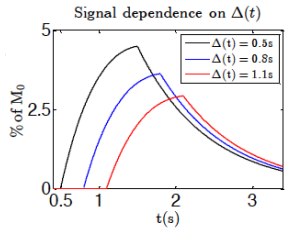
Sensitivity to blood flow

Parameters of the general kinetic model



Sensitivity to bolus width

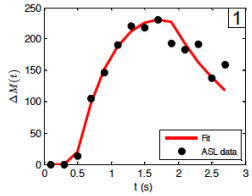
Parameters of the general kinetic model



Sensitivity to bolus arrival time

Quantification of CBF using ASL data

- Acquire ASL images over a range of inflow times
- Fit the data to the general kinetic model

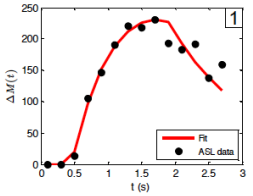


Fitted parameters: **CBF, Δt, τ**

Other parameters needed:
T_{1b} (blood T_1)
M_a^0 (equilibrium blood signal)
Tissue T_1
α (inversion efficiency)
λ (blood:brain partition coeff)

Quantification of CBF using ASL data

- Acquire ASL images over a range of inflow times
- Fit the data to the general kinetic model



Fitted parameters: **CBF, Δt, τ**

Other parameters needed:
T_{1b} Single value - assumed
M_a^0 } Measured – separate scans
Tissue T_1 }
α Single value - assumed
λ Single value - assumed

Pros of multi-TI acquisition

- Allows fitting of ASL data to kinetic model
- Allows measurement of other haemodynamic parameters (e.g. bolus arrival time Δt) as well as CBF

Journal of Cerebral Blood Flow & Metabolism (2014) **34,** 34–42; doi:10.1038/jcbfm.2013.161; published online 18 September 2013

ORIGINAL ARTICLE

Cerebral arterial bolus arrival time is prolonged in multiple sclerosis and associated with disability

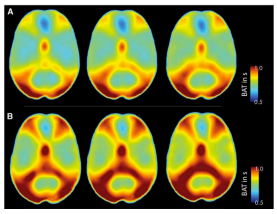
David Paling[1], Esben Thade Petersen[2], Daniel J Tozer[1], Daniel R Altmann[1,3], Claudia AM Wheeler-Kingshott[1], Raju Kapoor[1], David H Miller[1] and Xavier Golay[4]

Pros of multi-TI acquisition

- Allows fitting of ASL data to kinetic model
- Allows measurement of other haemodynamic parameters (e.g. bolus arrival time Δt) as well as CBF

Controls

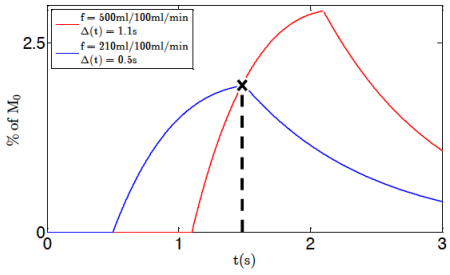
MS patients



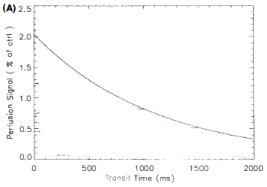
Cons of multi-TI acquisition

- Requires the acquisition of a series of images for single measurement
  - Low temporal resolution
  - Not suitable for dynamic acquisitions e.g. fMRI
- Can have poor measurement efficiency if sampling TIs where SNR is low e.g. TI < Δt
- So, can we quantify using a single TI?

Problem for single TI quantification



Problem for single TI quantification



Alsop and Detre JCBFM 1996

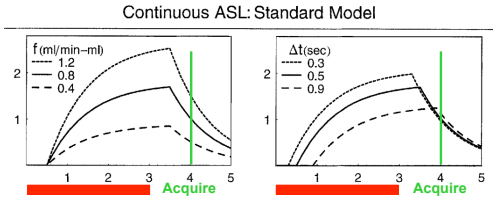
Δt and CBF both have strong influence on ΔM

High CBF, long Δt

Low CBF, short Δt

Solution for single TI CASL quantification

- Use a **post-labeling delay** (Alsop and Detre JCBFM 1996)

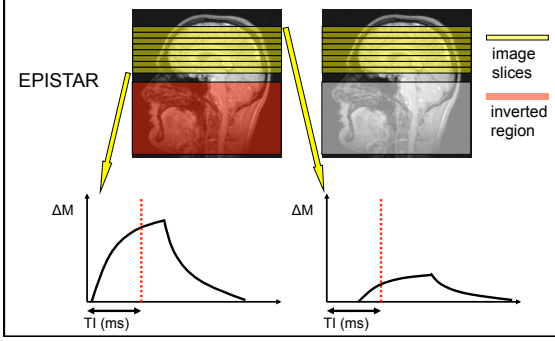


Tagging pulse = 3s; T_1 = 1s

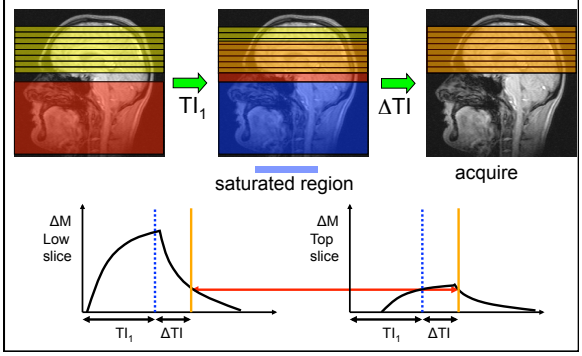
Solution for single TI CASL quantification

- Use a **post-labeling delay** (Alsop and Detre JCBFM 1996)
  - Minimizes the dependence on Δt
  - Also reduces the contribution of intravascular signal
  - BUT lose SNR due to extra T_1 decay

Dependence of PASL on transit time

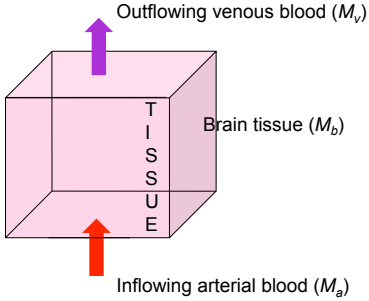


Dealing with PASL transit time: QUIPSS II



Assumptions of the standard models

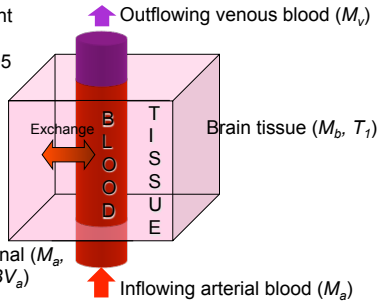
- Instantaneous exchange / single compartment



Assumptions of the standard models

- ~~Instantaneous exchange / single compartment~~

Multi-compartment models e.g. see Parkes JMRI 2005 for review



Assumptions of the standard models

- No dispersion of the bolus
  - Include dispersion as another parameter[1,2]
  - Tag as close as possible to the tissue
- Stationarity of CBF during measurement
  - Another reason to keep scan duration to a minimum

[1]Hrabe and Lewis JMR 2004; [2]Gallichan and Jezzard MRM 2008

Standardization of ASL

- Due to the variety of ASL pulse sequences and quantification models, need for standardization
  - ISMRM Perfusion Study Group
  - EU COST Action: ASL Initiative in Dementia (AID)
- Consensus
  - Published in 'White Paper' in MRM[1]
  - pCASL with post-labeling delay

$$CBF = \frac{6000 \cdot \lambda \cdot (SI_{control} - SI_{label}) \cdot e^{PLD/T_{1,blood}}}{2 \cdot \alpha \cdot T_{1,blood} \cdot SI_{PD} \cdot (1-e^{-\tau/T_{1,blood}})}$$

Constants Measured

Fixed in acquisition
PLD = 1.8 / 2 s
τ = 1.8 s

[1]DOI: 10.1002/mrm.25197

Summary

- ASL provides a non-invasive method for the absolute quantification of CBF (ml/100g/min)
- Two main quantification models
  - T1 model
  - General kinetic model
- ASL can be acquired as multi- or single-TI
  - Multi-TI more robust but time-consuming
  - Single-TI better suited to dynamic imaging but relies on assumptions for CBF estimatation

Useful References

- Detre *et al* MRM 23:37-45 (1992)
- Alsop and Detre JCBFM 16:1236-49 (1996)
- Buxton *et al* MRM 40:383-396 (1998)
- Wong *et al* MRM 39:702-709 (1998)
- Golay *et al* Top Magn Reson Imaging 15:10–27 (2004)
- JMRI 22(6) perfusion review edition (2005)
- COST AID http://www.aslindementia.org/
- ASL White Paper DOI: 10.1002/mrm.25197