Measuring cerebral blood flow and other haemodynamic parameters using Arterial Spin Labelling MRI

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"ASL was performed using PASL with Q2TIPS (TI1=800ms; TI2=2000ms) and a multi-shot 3D GRASE readout scheme.

CBF was quantified using the Buxton kinetic model."

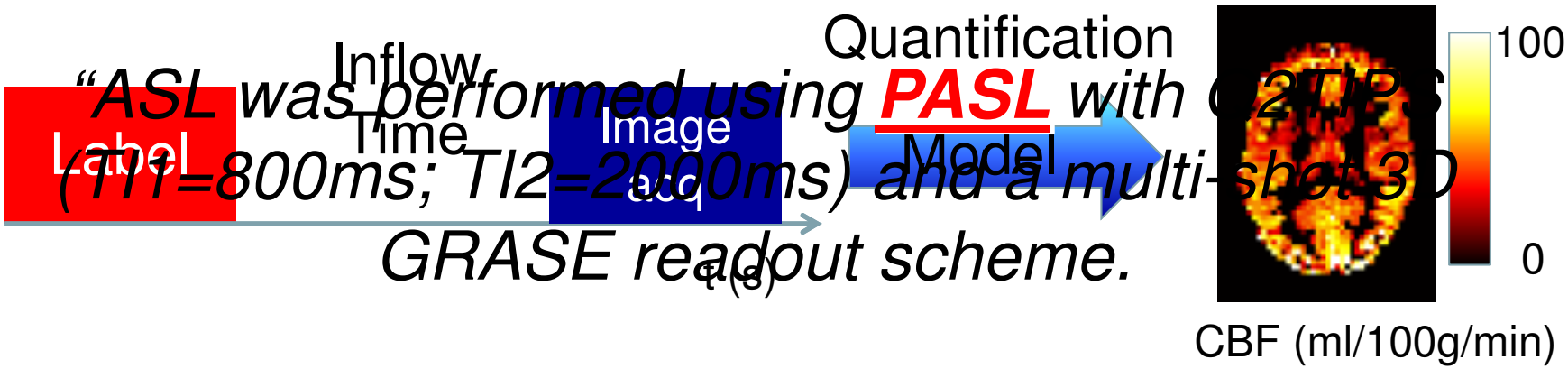
- MRI suffers from Excessive Use of Acronyms
- ASL is particularly guilty of this

Aim: to demystify the jargon and provide an overview of the main concepts underlying ASL

Components of the ASL method

- Magnetic labelling of blood water
  - creation of kinetic tracer
- Delay for the tracer to flow into the tissue
  - Single or multiple inflow times
- Acquiring the image
  - 2D and 3D rapid imaging techniques
- Quantification of CBF
  - Converting from image SI ⇨ ml/100g/min

Components of the ASL sequence



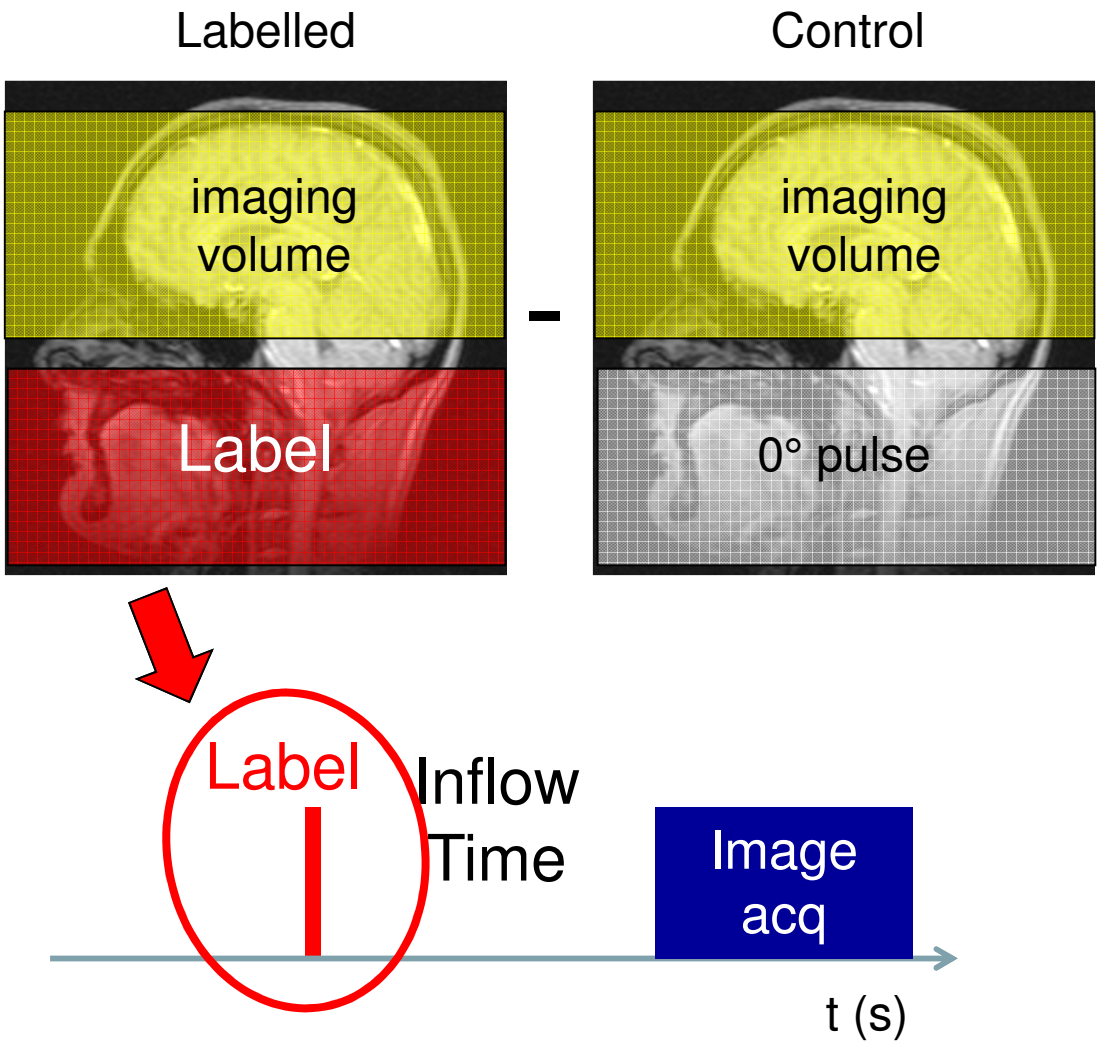
*"ASL was performed using **PASL** with (2TIPS (TI1=800ms; TI2=2000ms) and a multi-shot 3D GRASE readout scheme.*

Labelling options for ASL

PASL: Pulsed ASL
CASL: Continuous ASL
pCASL: pseudo-continuous ASL

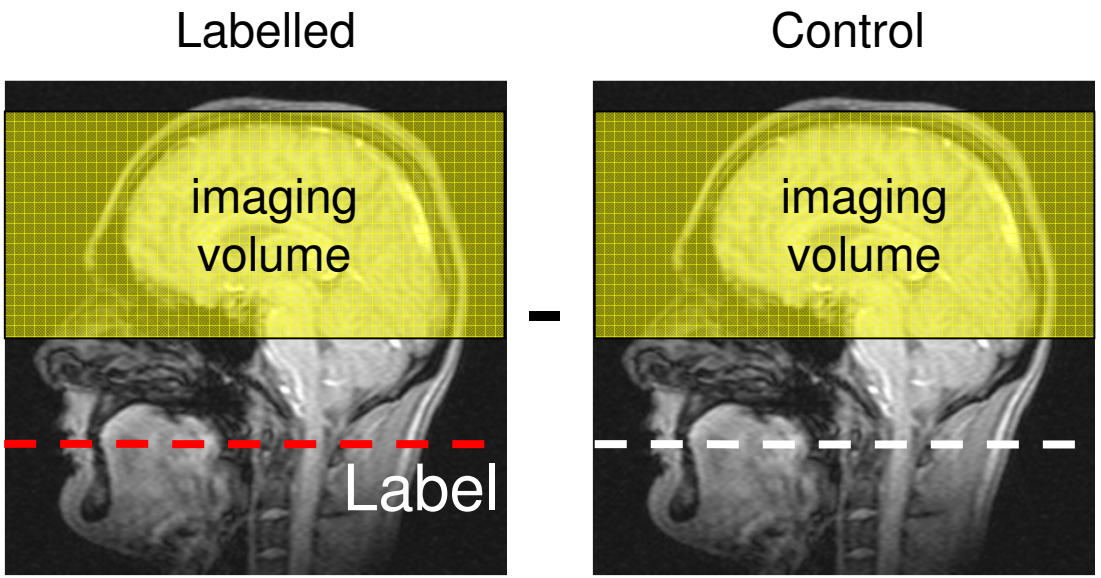
Labelling options for ASL

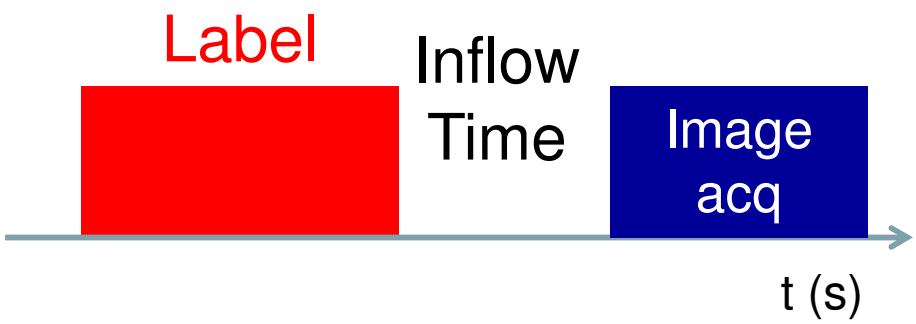
PASL



Labelling options for ASL

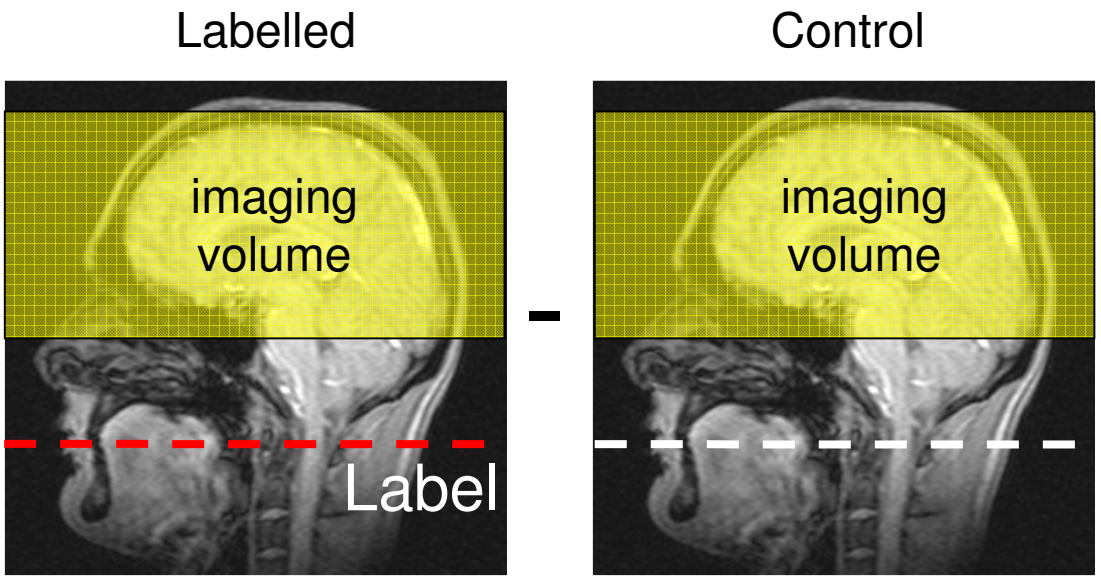
CASL

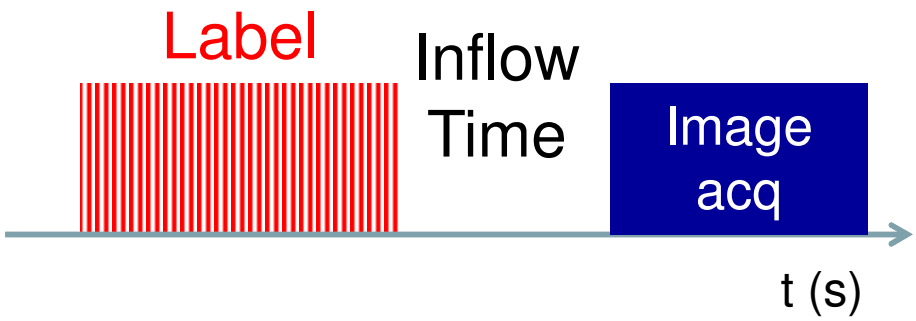




Labelling options for ASL

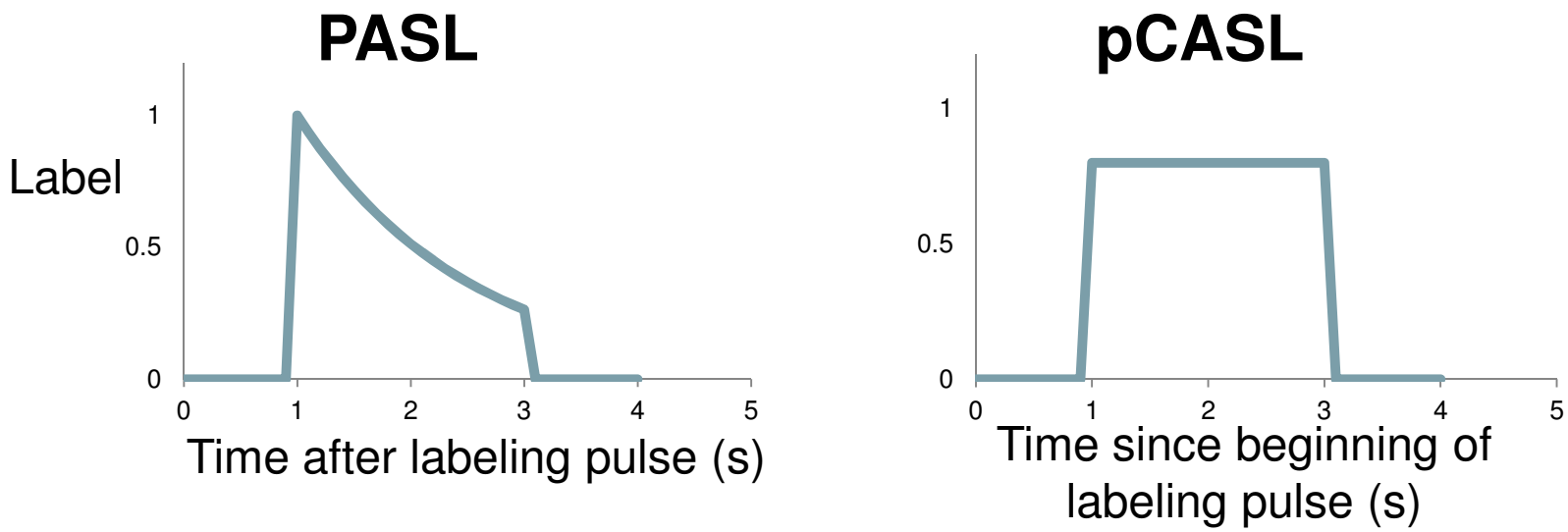
pCASL





pCASL vs PASL

- Arterial input function



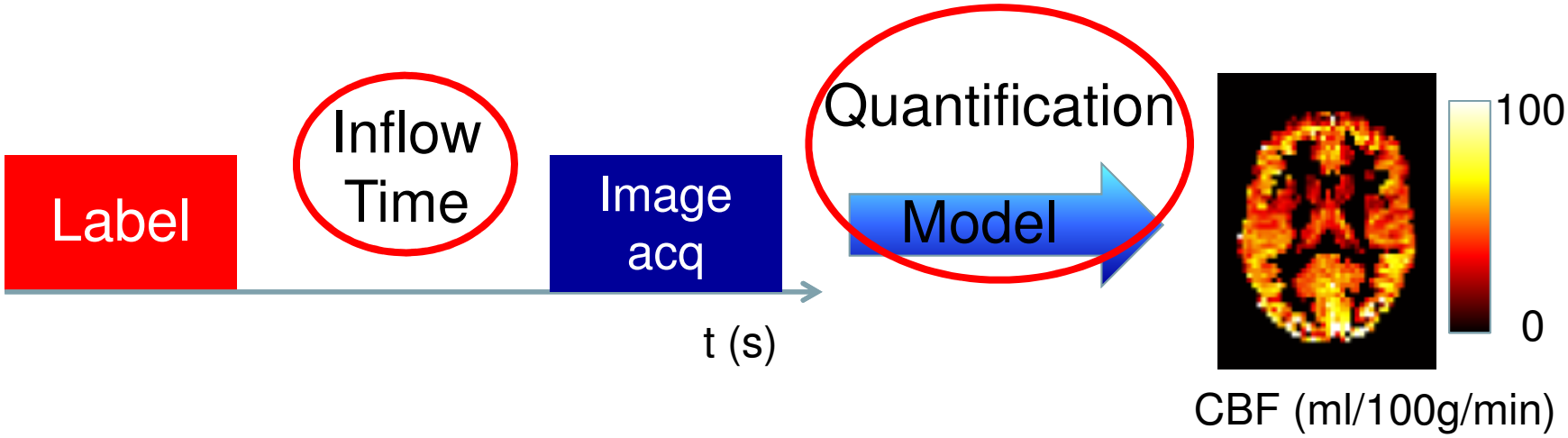
➡ In pCASL, more tracer delivered ∴ higher SNR

- But higher power deposition

➢ **pCASL 'method of choice' but PASL also good**

Components of the ASL sequence

"ASL was performed using ~~PASL~~ with Q2TIPS (TI1=800ms; TI2=2000ms) and a background-suppressed, multi-shot 3D GRASE readout scheme. CBF was quantified using the Buxton kinetic model."

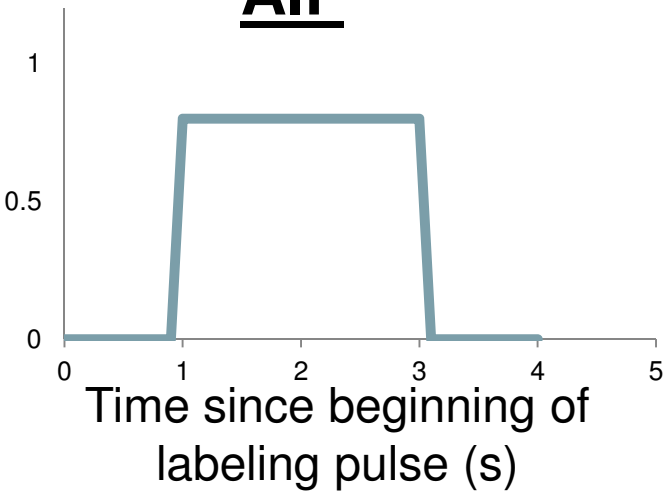


ASL general kinetic model

- General kinetic model (Buxton *et al.* 1998)
  - ⇨ assumes water is a freely diffusible tracer

$$\Delta M(t) = M_0.CBF \times [AIF(t) * Res(t)]$$

AIF

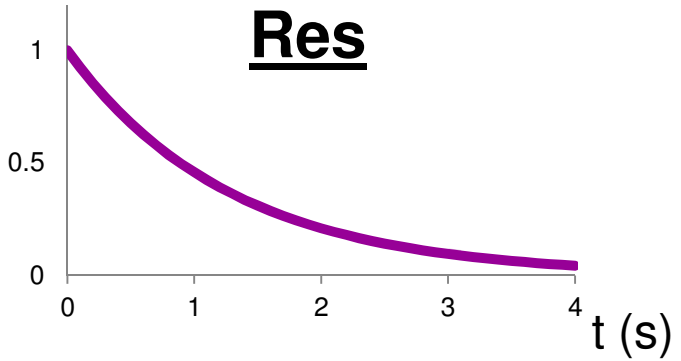


- Residue function (Res) = m(t).r(t)
  - Tracer lost due to venous outflow

    $r(t) = \exp(-CBF/\lambda.t)$
  - Tracer reduces due to T_1 relaxation of label

    $m(t) = \exp(-t/T_1)$

Res



ASL general kinetic model

- Solution of general kinetic model

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

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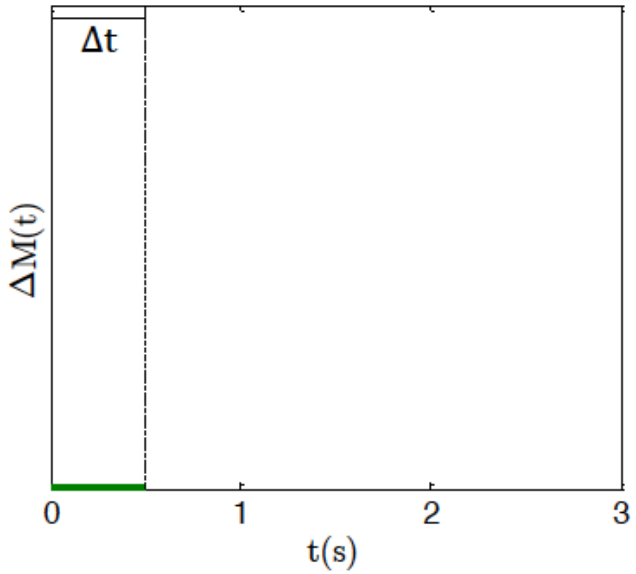

Δt = bolus arrival time (s)

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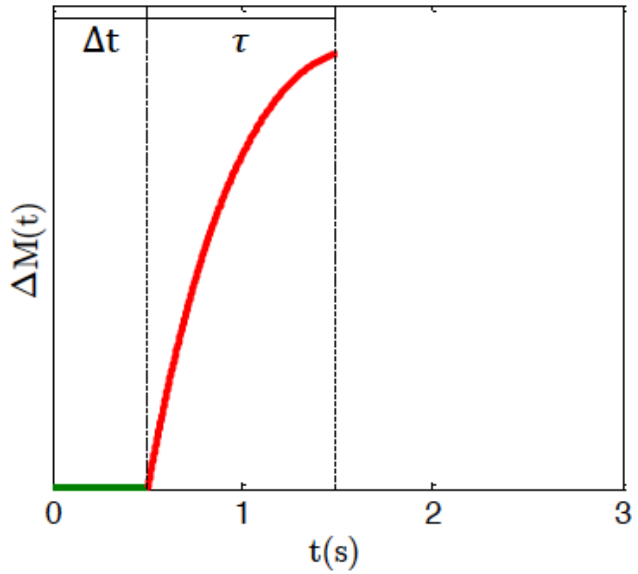

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f = CBF (ml/100g/min)

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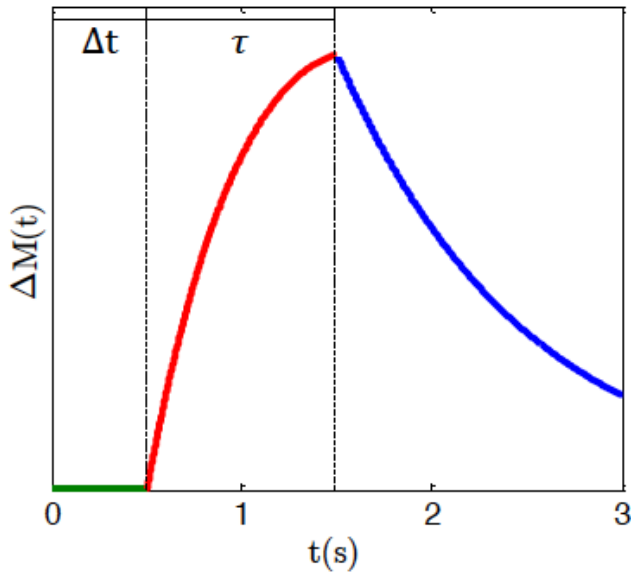

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f = CBF (ml/100g/min)
τ = bolus duration (s)

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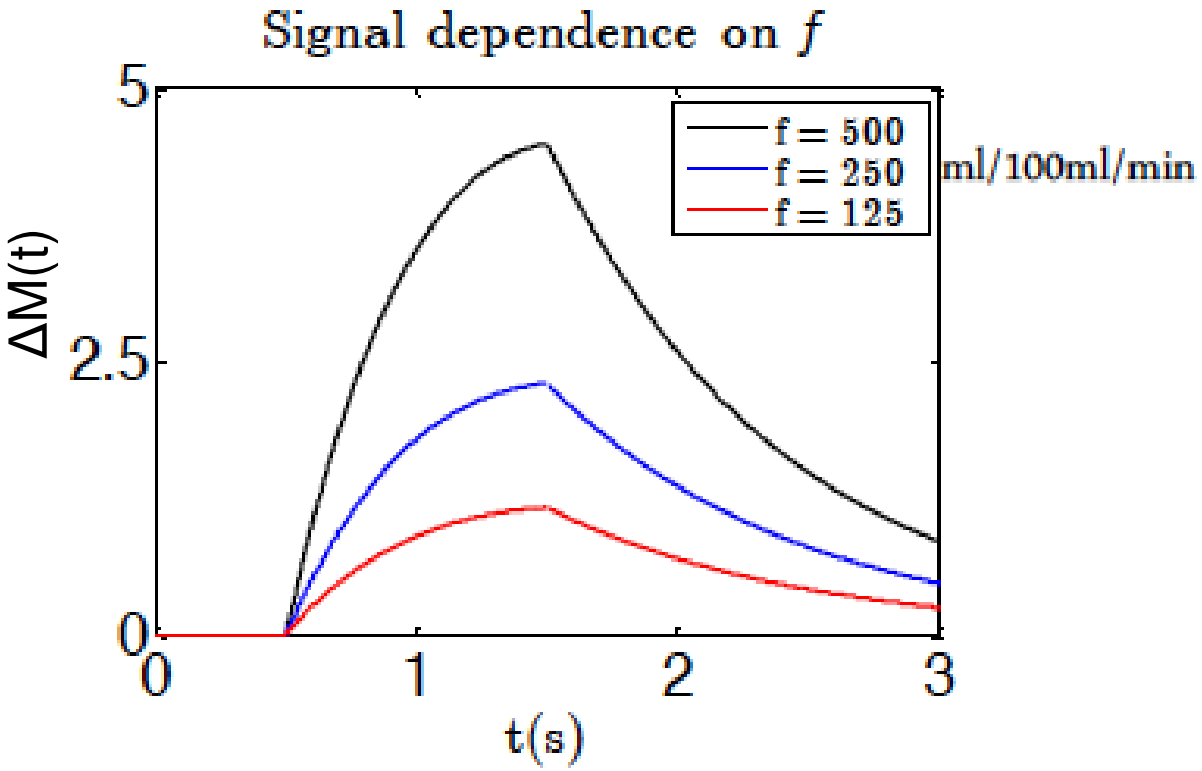
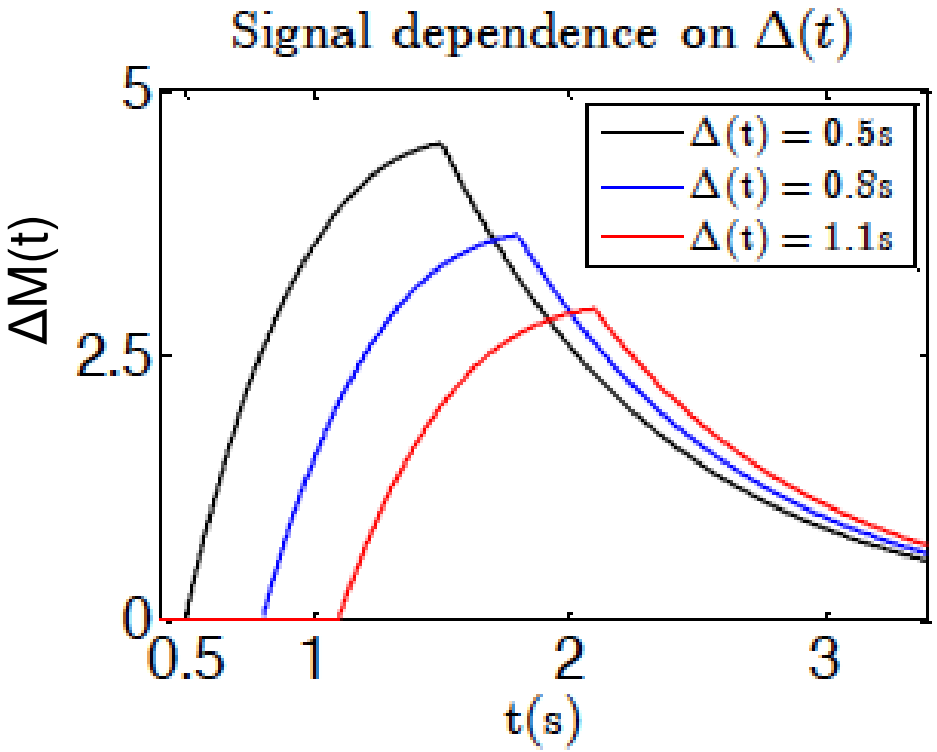


Sensitivity to CBF

Parameters of the general kinetic model



Sensitivity to bolus arrival time Δt

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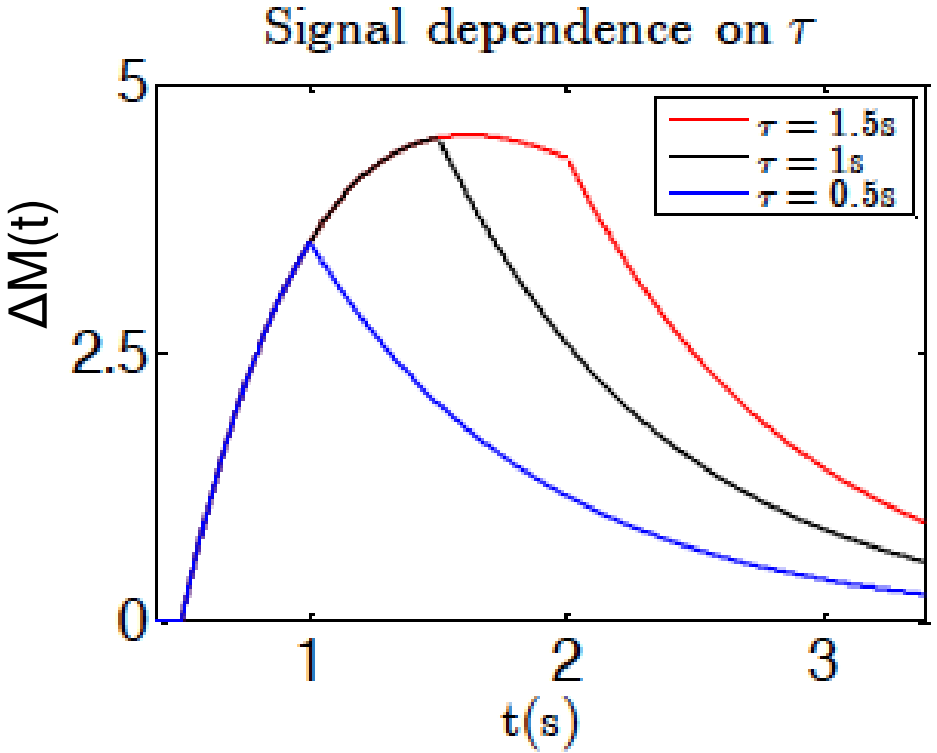

Sensitivity to bolus duration τ

Quantification of CBF using ASL data

- Acquire ASL images over a range of inflow times (TI)
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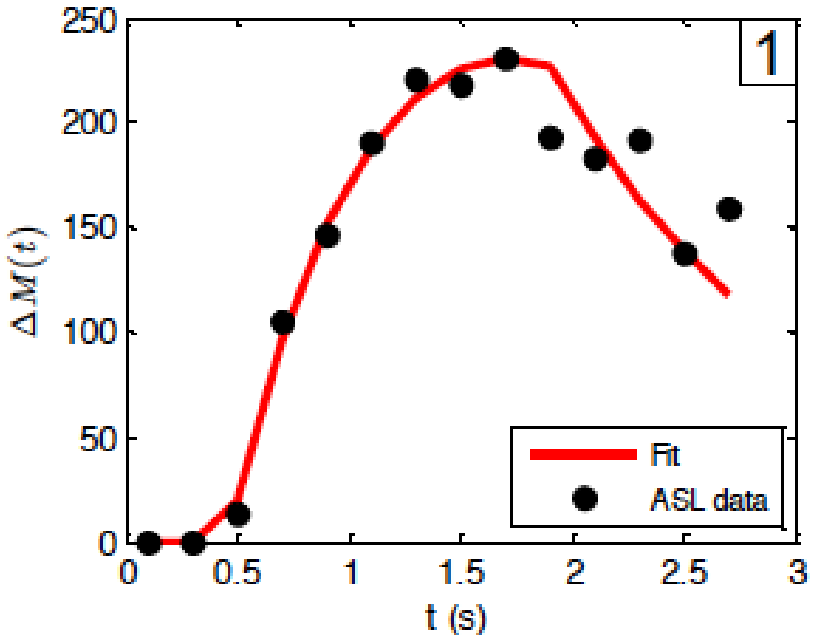

Fitted parameters: **CBF, Δt, τ**

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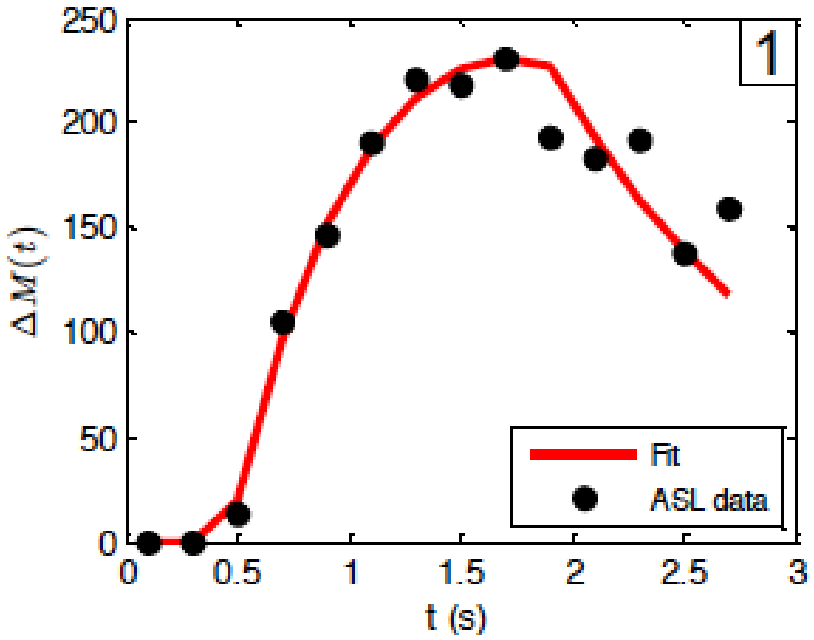

Fitted parameters: **CBF, Δt, τ**

Other parameters needed:

T_{1b} blood T_1
α inversion efficiency
λ blood:brain partition coeff
M_0
Tissue T_1

Quantification of CBF using ASL data

- Acquire ASL images over a range of inflow times (TI)
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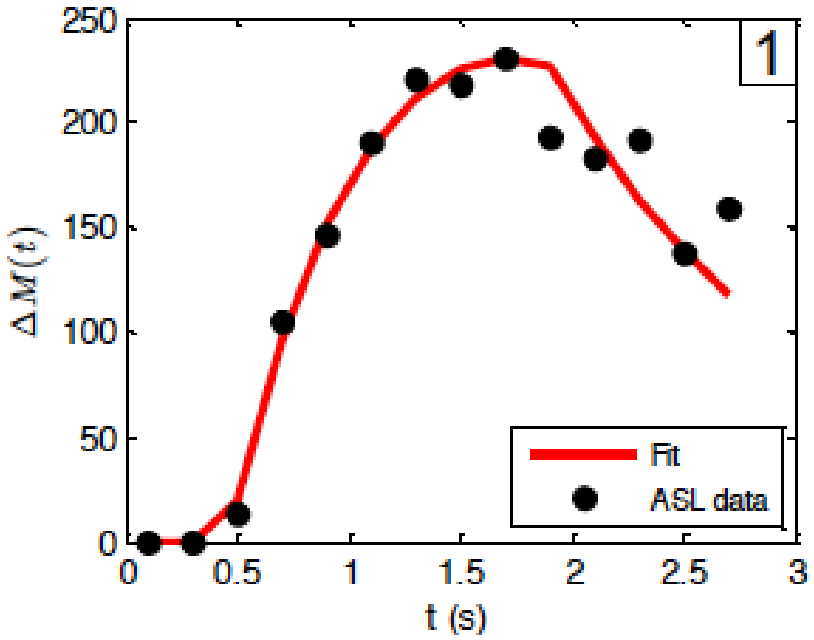

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T_{1b}
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Tissue T_1

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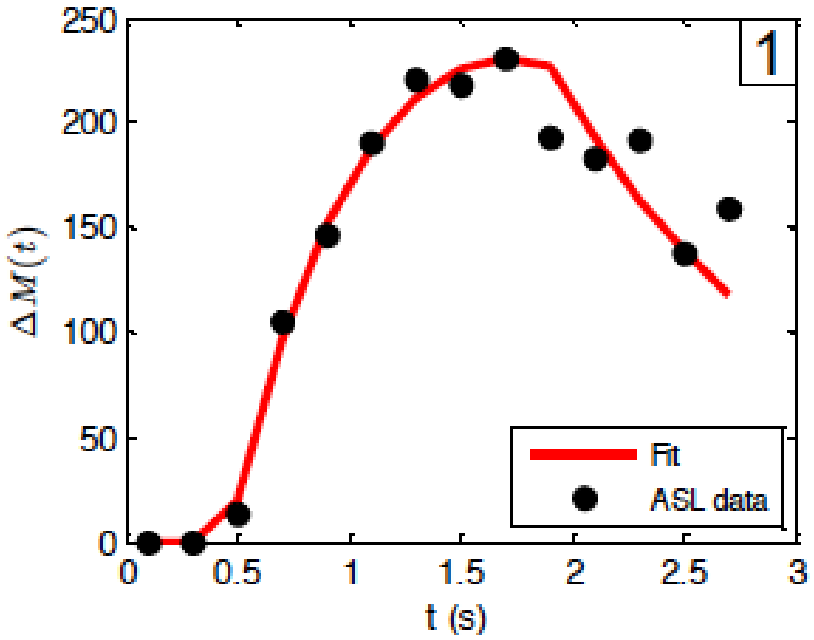

Fitted parameters: **CBF, Δt, τ**

Other parameters needed:

T_{1b}, α, λ } Single values – assumed

M_0, Tissue T_1 } Measured in separate scans

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

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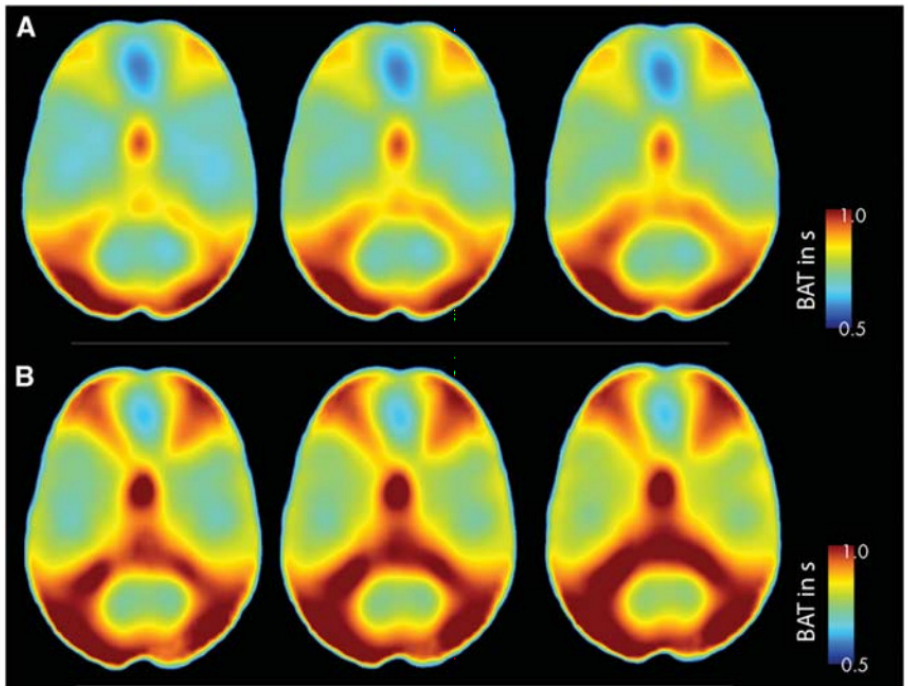
Δt (controls)

Δt (MS patients)



Paling et al 2014

Cons of multi-TI acquisition

- Requires the acquisition of a series of images
  - Long scan time
  - Not suitable for dynamic acquisitions e.g. fMRI
- Poor measurement efficiency if sampling TIs where SNR is low e.g. $TI < \Delta t$

Cons of multi-TI acquisition

- Requires the acquisition of a series of images
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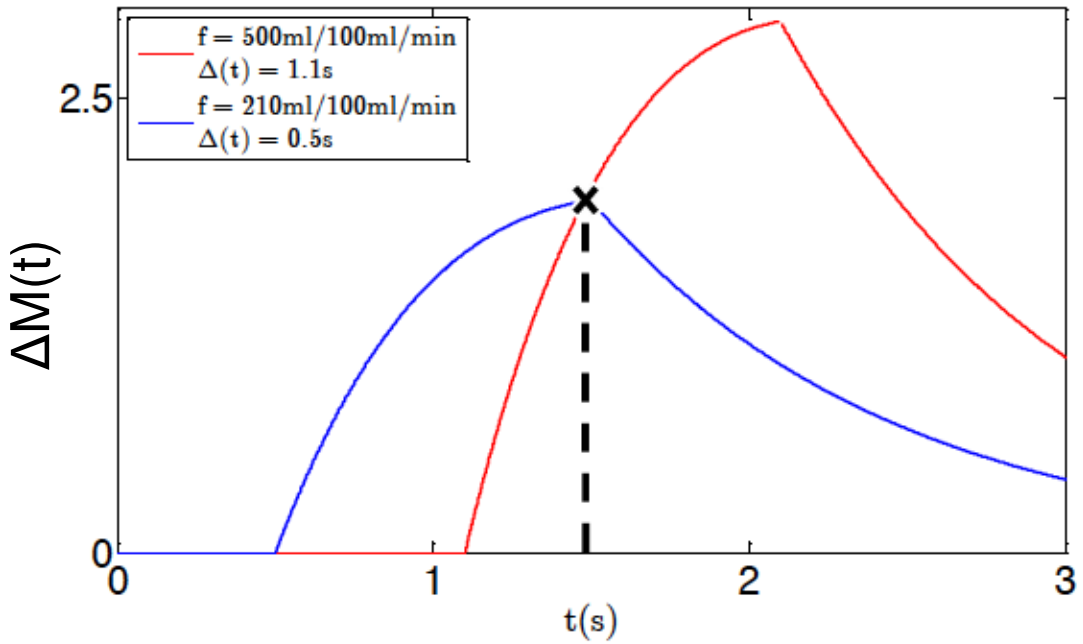
- Poor measurement efficiency if sampling TIs where SNR is low e.g. TI < Δt
- So, can we quantify using a single TI?

Problem for single TI quantification



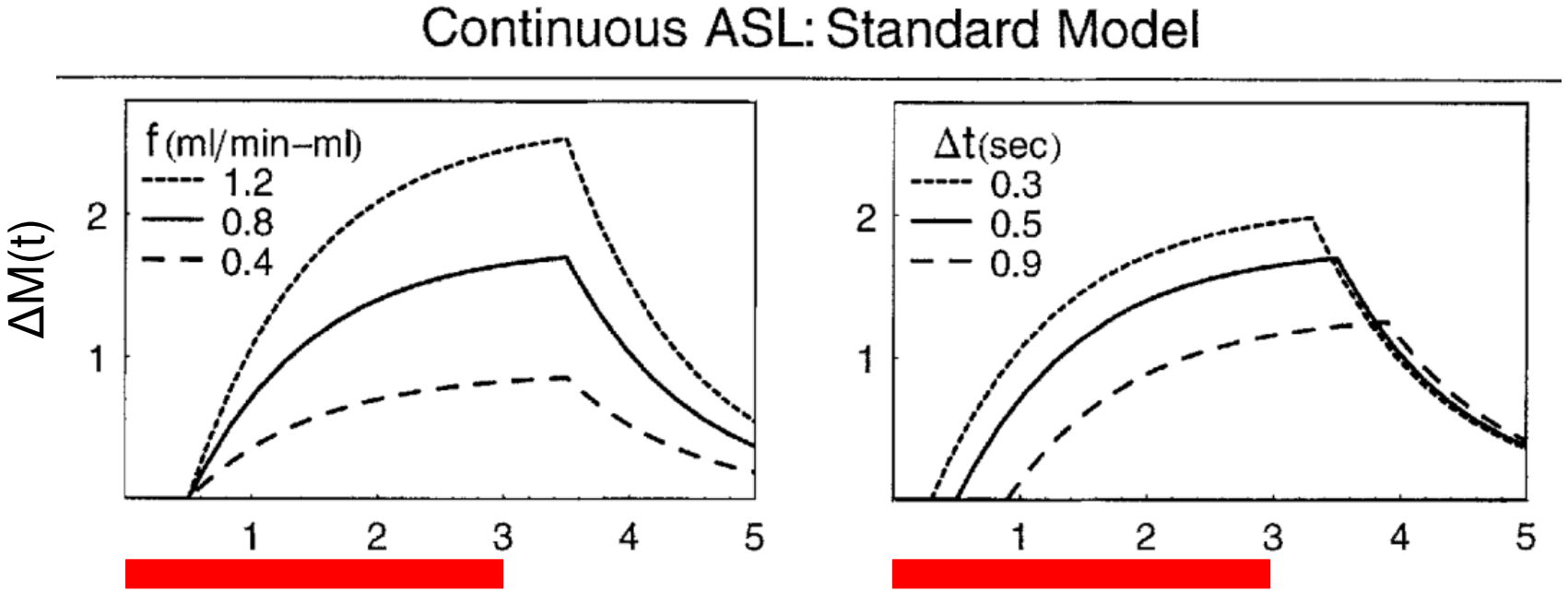
High CBF, long Δt

Low CBF, short Δt

Δt and CBF both have strong influence on ΔM

Solution for pCASL quantification

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



Tagging pulse = 3s

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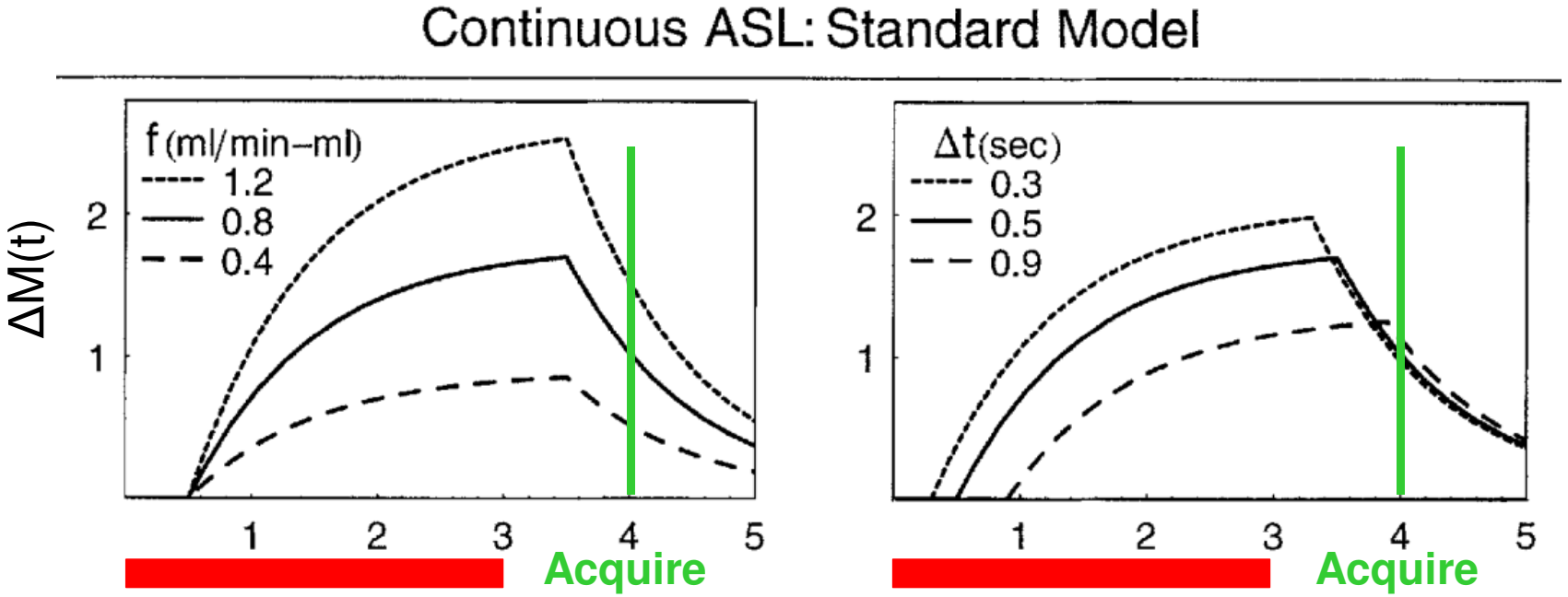
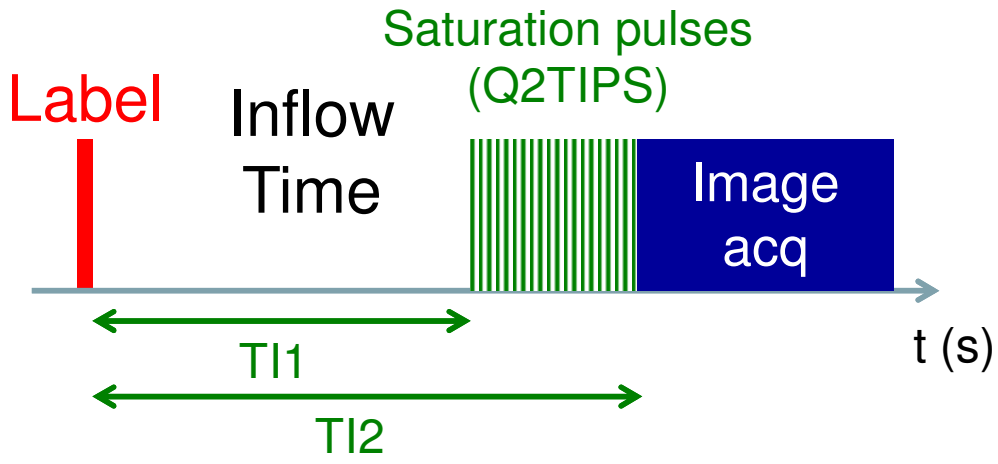


Tagging pulse = 3s

Solution for PASL quantification

- Same principle – but need to use saturation pulses to destroy label



Conditions:

$TI1 < \tau$

$TI2 - TI1 > \Delta t$

$$\mathbf{CBF} = \frac{\lambda \cdot \Delta M \cdot \exp(-TI2/T_{1b})}{2 \cdot \alpha \cdot TI1 \cdot M_0}$$

ASL 'white paper': Alsop et al MRM 2015

Summary

CBF values robust to variations in arterial bolus arrival times

How the labelling was done

"ASL was performed using PASL with Q2TIPS (TI1=800ms; TI2=2000ms) and a multi-shot 3D GRASE readout scheme.

CBF was quantified using the Buxton kinetic model."

Acq parameters in accordance with ASL 'white paper' (Alsop)

Rapid imaging readout

Single compartment freely diffusible tracer model