Post processing: Kinetics and M0

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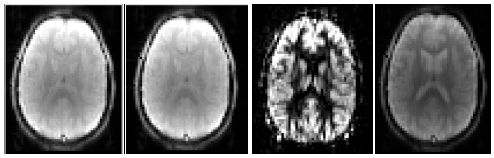
FSL & BASIL

- FSL: The FMRIB Software Library (v5.0)
  - ➡ www.fmrib.ox.ac.uk/fsl
- BASIL: a toolset for resting ASL quantification:
  - ➡ CBF quantification.
  - ➡ Calibration / M0 estimation
  - ➡ Registration.
  - ➡ Partial volume correction.
  - ➡ Command line tools
    `oxford_asl, basil, asl_reg, asl_calib`
  - ➡ Graphical User Interface (beta in v5.0.4/5.0.5)
    `Asl / Asl_gui`

What Have I Got Here!?

- What I have...
- What I want...
- What should I do?



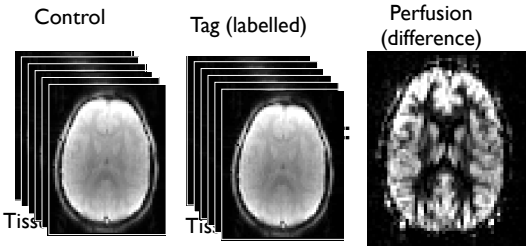
I just want to do something simple/easy!

I must have absolute perfusion (ml/100g/min)

```
Command line instructions here for future reference...
```


Example (simple)

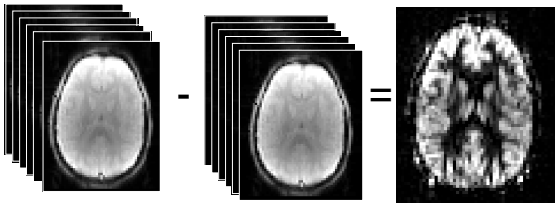
- What I have...
  - ➡ ASL data!
- What I want...
  - ➡ A perfusion image (in this subject).
- What should I do?
  - ➡ Tag-control subtraction
  - ➡ Average




```
asl_file --data={ASLdata.nii.gz} --ntis=1 --iaf=tc --diff --out={diffdata.nii.gz}
asl_file --data={ASLdata.nii.gz} --ntis=1 --iaf=tc --diff --mean={diffdata_mean.nii.gz}
```

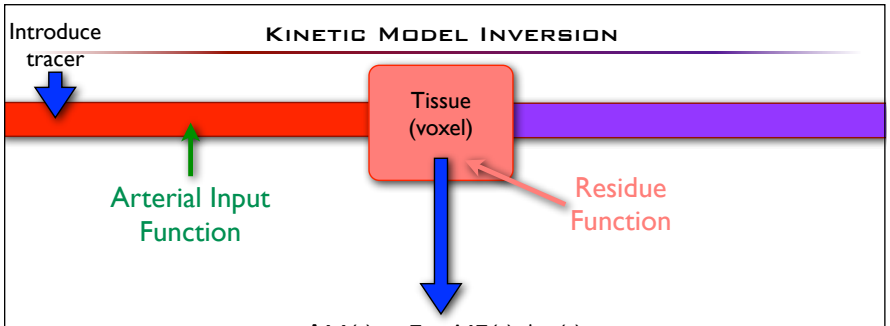
Example

- What I have...
  - ➡ ASL data
  - ➡ (calibration images)
- What I want...
  - ➡ Perfusion in ml/100g/min



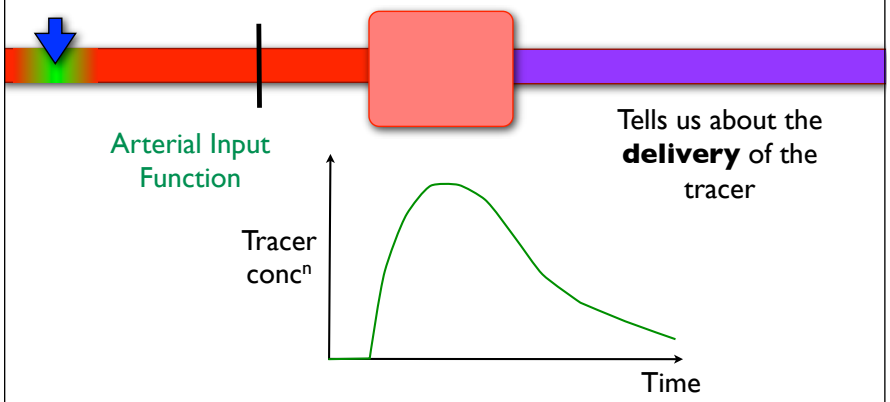
- What should I do?
  - ➡ Tag-control subtraction. ✓
  - ➡ Kinetic model inversion. ←
  - ➡ M0 calculation.

Kinetic Model Inversion



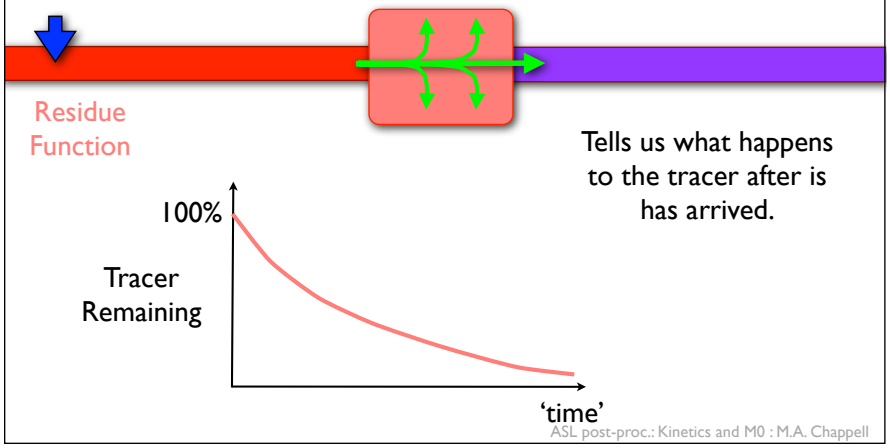
$$\Delta M(t) = F \cdot AIF(t) * r(t)$$

Kinetic Model Inversion



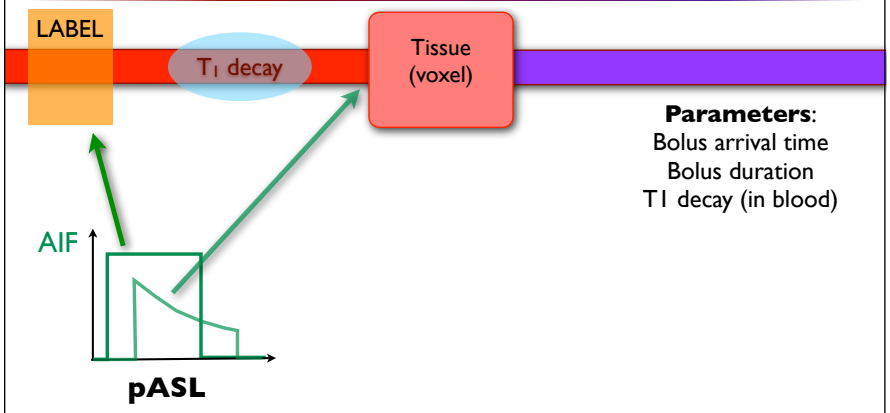
Tells us about the **delivery** of the tracer

Kinetic Model Inversion



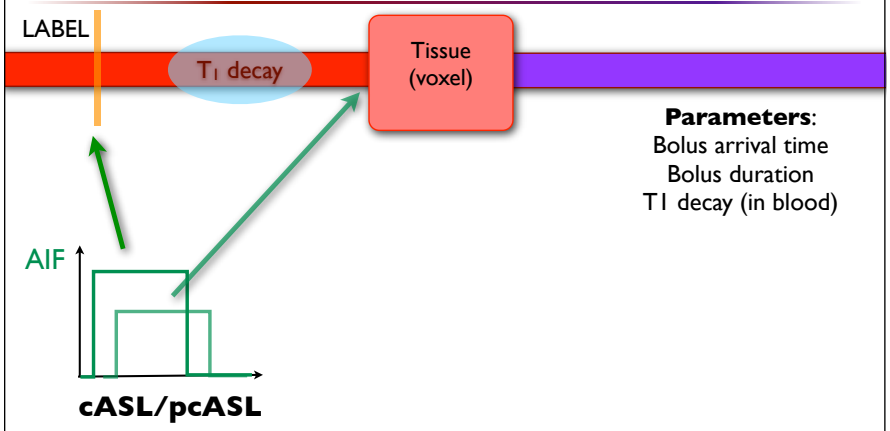
Tells us what happens to the tracer after is has arrived.

Kinetic Model Inversion



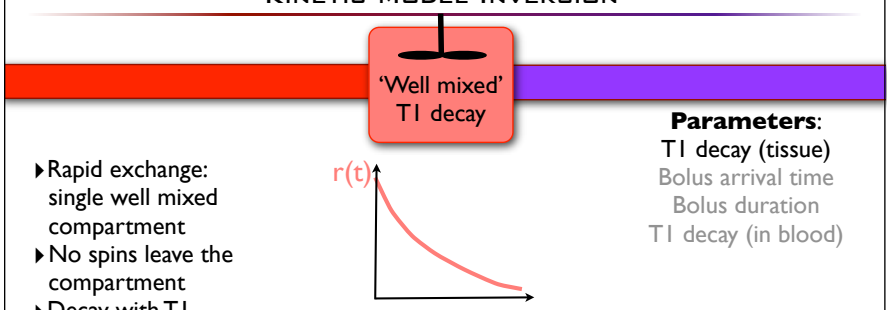
Parameters:
Bolus arrival time
Bolus duration
T1 decay (in blood)

Kinetic Model Inversion



Parameters:
Bolus arrival time
Bolus duration
T1 decay (in blood)

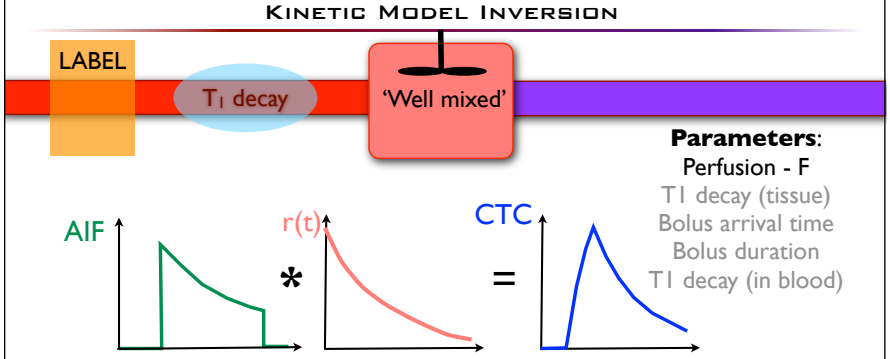
Kinetic Model Inversion



- Rapid exchange: single well mixed compartment
- No spins leave the compartment
- Decay with T1

Parameters:
T1 decay (tissue)
Bolus arrival time
Bolus duration
T1 decay (in blood)

Kinetic Model Inversion

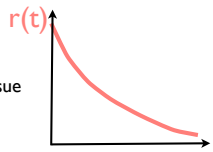


Parameters:
Perfusion - F
T1 decay (tissue)
Bolus arrival time
Bolus duration
T1 decay (in blood)

$$\Delta M(t) = F \cdot AIF(t) * r(t)$$

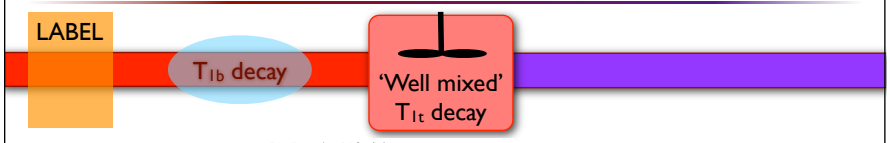
Kinetic Model Inversion

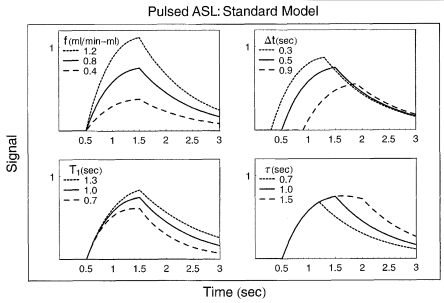
- The 'simple' model
  - ➡ Only one T1 value (blood)
  - ➡ Spins never leave tissue
- The 'standard' model:
  - ➡ Separate T_1 for blood and tissue ($T_{1t} < T_{1b}$).
  - ➡ Spins leave voxel at rate determined by perfusion and partition coefficient.



Buxton *et al.*, MRM 40(3), 1998.

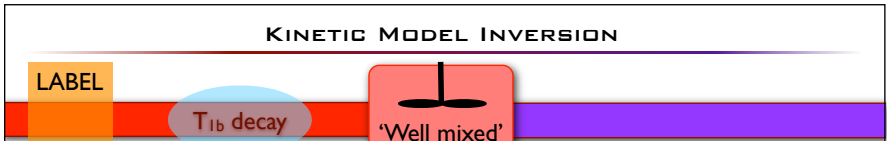
Kinetic Model Inversion

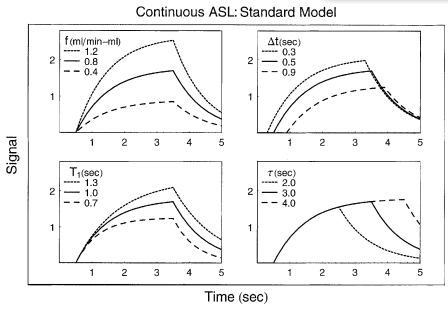




Buxton *et al.*, MRM 40(3), 1998.

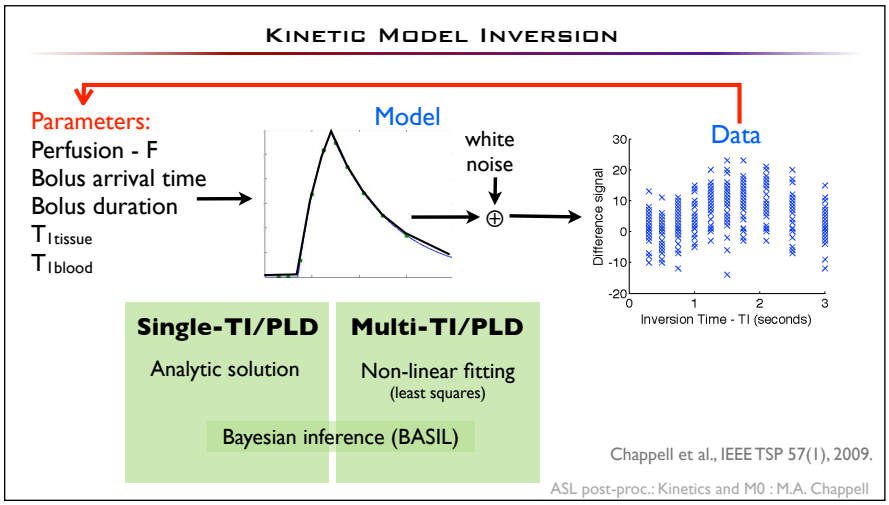
Kinetic Model Inversion





Buxton *et al.*, MRM 40(3), 1998.

Kinetic Model Inversion



Chappell et al., IEEE TSP 57(1), 2009.

Example

- What I have...
  - ➡ ASL data
  - ➡ (calibration images)
- What I want...
  - ➡ Perfusion in ml/100g/min
- What should I do?
  - ➡ Tag-control subtraction. ✓
  - ➡ Kinetic model inversion. ←
  - ➡ M0 calculation.

What you need to know about your data:

Labeling	pASL (pulsed)	or	pcASL (continuous)
	Inversion time(s)		Post-labeling delay(s)
	Bolus duration (TI_1) (if QUIPSS/Q2TIPS)		Labeling duration

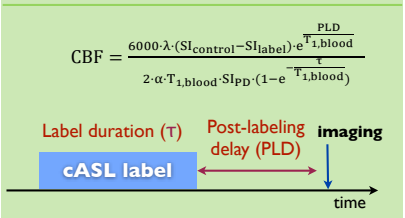
Model	T1 (tissue and blood?) Bolus arrival time

Kinetic Model Inversion

Analytical solutions - Simple model (ASL 'white paper'):

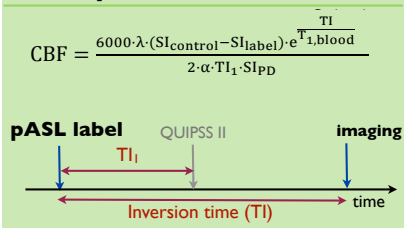
pcASL

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



pASL QUIPSS II

$$CBF = \frac{6000\cdot\lambda\cdot(SI_{control}-SI_{label})\cdot e^{\frac{TI}{T_{1,blood}}}}{2\cdot\alpha\cdot TI_1\cdot SI_{PD}}$$



Fixed value:
T_{1blood} = 1650 ms (3T)

Analytical solutions - Standard model ('Buxton'):

pASL QUIPSS II

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

with

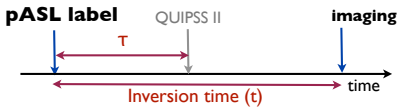
$$q_p(t) = \frac{e^{kt}(e^{-k\Delta t}-e^{-kt})}{k(t-\Delta t)} \qquad \Delta t<t<\tau+\Delta t$$

$$= \frac{e^{kt}(e^{-k\Delta t}-e^{-k(\tau+\Delta t)})}{k\tau} \qquad \tau+\Delta t<t$$

$$k = \frac{1}{T_{1b}} - \frac{1}{T_1'}$$

$$\frac{1}{T_1'} = \frac{1}{T_1} + \frac{f}{\lambda}$$

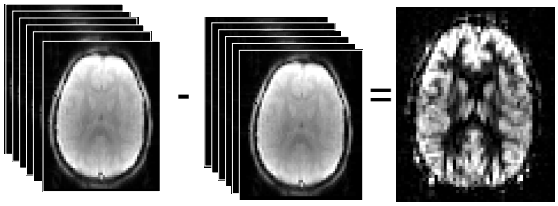
Buxton *et al.*, MRM 40(3), 1998.



A less neat analytic solution for perfusion (*f*)
Simplify by assuming q_p=1

Example 1

- What I have...
  - ➡ ASL data
  - ➡ (calibration images)
- What I want...
  - ➡ Perfusion in ml/100g/min
- What should I do?
  - ➡ Tag-control subtraction. ✓
  - ➡ Kinetic model inversion. ←
  - ➡ M0 calculation.



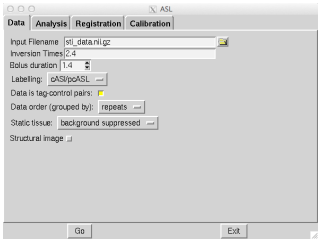
pcASL with
labeling duration: 1.4 s
post-label delay: 1.0 s

Assume
T1 (blood): 1.6 s
T1 (tissue): 1.3 s
BAT : 1.3 s

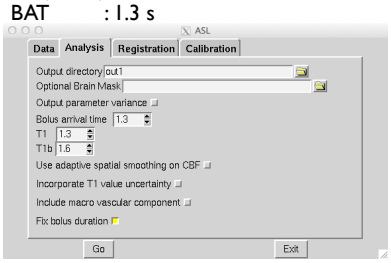
```
oxford_asl -i {ASL_diff_data.nii.gz} -o {result_dir}
  --casl --tis 2.4 --bolus 1.4 --bat 1.3 --artoff --fixbolus
```

Example 1

pcASL with
- tagging duration: 1.4 s
- post-label delay: 1.0 s



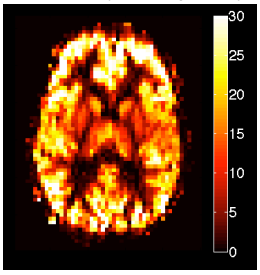
Assume
- T1 (blood): 1.6 s
- T1 (tissue): 1.3 s
- BAT : 1.3 s




```
> asl_file --data=sti_data.nii.gz --ntis=1 --iaf=tc --diff --out=sti_diffdata.nii.gz
> oxford_asl -i sti_diffdata.nii.gz -o out1
   --casl --tis 2.4 --bolus 1.4 --bat 1.3 --artoff --fixbolus
```


Example 1

Perfusion (arbitrary units)

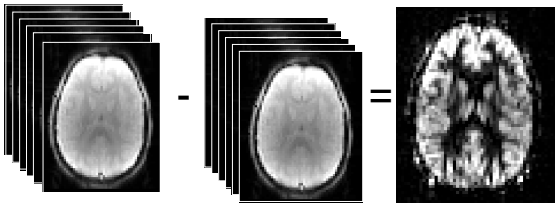


`out1/native_space/perfusion.nii.gz`

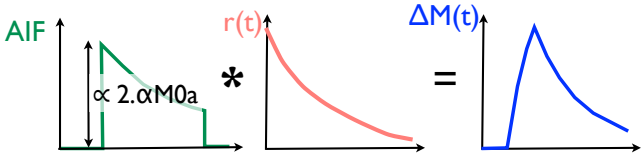
```
> asl_file --data=sti_data.nii.gz --ntis=1 --iaf=tc --diff --out=sti_diffdata.nii.gz
> oxford_asl -i sti_diffdata.nii.gz -o out1
   --casl --tis 2.4 --bolus 1.4 --bat 1.3 --artoff --fixbolus
```


Example

- What I have...
  - ➡ ASL data
  - ➡ (calibration images)
- What I want...
  - ➡ Perfusion in ml/100g/min
- What should I do?
  - ➡ Tag-control subtraction. ✓
  - ➡ Kinetic model inversion. ✓
  - ➡ M0 calculation. ←



M0 Calculation



$$\Delta M(t) = 2 \cdot \alpha \cdot M0a \cdot CBF \cdot AIF(t) * r(t)$$

M0 Calculation

- Cannot measure M0a directly.
- indirect via brain 'tissue' magnetization.
  - ➡ Calculate M0t.
    (M0 of 'tissue')
  - ➡ M0t to M0a.

Steady state magnetization (proton density)

$$S = M_0\left(1 - e^{-TR/T_1}\right)$$

With pre-saturation:

$$S = M_0\left(1 - Ae^{-t/T_{1t}}\right)$$

With background suppression:
No static tissue - need separate calibration images
i.e. a control image with BGS off.

Account for relative proton densities:

$$M_{0a} = \frac{M_{0t}}{\lambda}$$

```
oxford_asl ... -c {calibration_image.nii.gz} -s {structural_image.nii.gz}
asl_calib --mode longtr ...
asl_calib --mode satrecov ...
```


M0 Calculation

- Cannot measure M0a directly.
- indirect via brain 'tissue' magnetization.
  - ➡ Calculate M0t.
    (M0 of 'tissue')
  - ➡ M0t to M0a.
- Practicalities
  - ➡ Reference 'tissue'?
  - ➡ Voxelwise?

Voxelwise	Reference 'tissue'
Calculate M0t	
	Reference tissue mask (CSF or WM)
M0t → M0a	
voxelwise M0a value	Single global M_{0a} value (coil sensitivity correction)

Perfusion (ml/100g/min) = (Perfusion / M_{0a}) * 6000

```
oxford_asl ... -c {calibration_image.nii.gz} -s {structural_image.nii.gz}
asl_calib --mode longtr ...
asl_calib --mode satrecov ...
fslmaths {perfusion.nii.gz} -div [M0a] -mul 6000 {perfusion_calib.nii.gz}
```


M0 Calculation

Analytical solutions - Simple model (ASL 'white paper'):

pcASL

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

$\alpha = 0.85$

pASL QUIPSS II

$$CBF = \frac{6000 \cdot \lambda \cdot (SI_{control} - SI_{label}) \cdot e^{\frac{TI}{T_{1,blood}}}}{2 \cdot \alpha \cdot TI_1 \cdot SI_{PD}}$$

$\alpha = 0.98$

Perfusion (ml/100g/min) = (Perfusion / M_{0a}) * 6000

A 'voxelwise' approach:
$M_{0a} = M_{0t} / \lambda = SI_{PD} / \lambda$ with $\lambda = 0.9$ ml/g

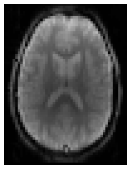
SI_{PD} is a proton density weighted image with 'long' TR
For TR < 5s correct using: $S = M_0\left(1 - e^{-TR/T_1}\right)$

Example 2

- What I have...
  - ➡ ASL data
  - ➡ (calibration images)
- What I want...
  - ➡ Perfusion in ml/100g/min
- What should I do?
  - ➡ Tag-control subtraction. ✓
  - ➡ Kinetic model inversion. ✓
  - ➡ M0 calculation. ←

Background suppression on

Calibration image



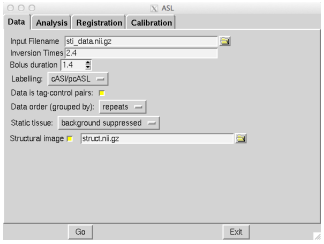
Steady state
TR = 6 s

Calibration reference

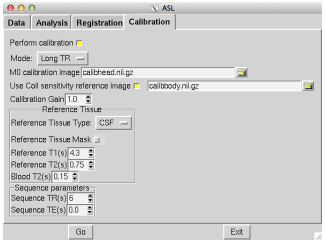
```
oxford_asl -i {ASL_diff_data.nii.gz} -o {result_dir}
  --casl --tis 2.4 --bolus 1.4 --bat 1.3 --artoff --fixbolus
  -c {calibration_image.nii.gz} --tr 6 --cref {calibration_reference.nii.gz}
  -s {structural_image} --regfrom {calibration_image}
```

Example 2

pcASL with
tagging duration: 1.4 s
post-label delay: 1.0 s



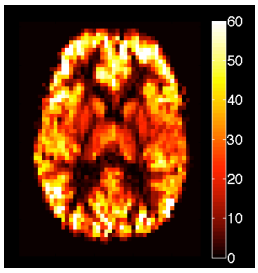
Calibration image with TR = 6 s
Calibration reference (body coil)




```
> oxford_asl -i sti_diffdata.nii.gz -o out2
    --casl --tis 2.4 --bolus 1.4 --bat 1.3 --artoff --fixbolus
    -c calibhead.nii.gz --tr 6 --cref calibbody.nii.gz
    -s struct.nii.gz --regfrom calibhead.nii.gz
```

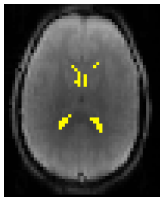

Example 2

Perfusion (ml/100g/min)



out2/native_space/perfusion_calib.nii.gz

Calibration: CSF mask



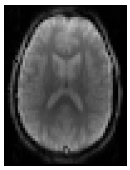
out2/calibration/refmask.nii.gz
(overlaid on raw data)

```
> oxford_asl -i diffdata.nii.gz -o out2
    --casl --tis 2.4 --bolus 1.4 --bat 1.3 --artoff --fixbolus
    -c calibhead.nii.gz --tr 6 --cref calibbody.nii.gz
    --s struct.nii.gz --regfrom calibhead.nii.gz
```


Example

- What I have...
  - ➡ ASL data
  - ➡ (calibration images)
- What I want...
  - ➡ Perfusion in ml/100g/min
- What should I do?
  - ➡ Tag-control subtraction. ✓
  - ➡ Kinetic model inversion. ✓
  - ➡ M0 calculation. ←

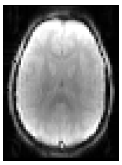
Calibration image



Calibration reference

Steady state
TR = 6 s

Control image



Saturation recovery
t = 2.4 s

```
asl_calib -c {calibration_image / control_image} -s {Structural_image}
  -t {asl2struct.mat} --tissref csf -o {out_dir}
    --mode longtr --tr 6   /   --mode satrecov --tis 2.4
```


FSL: The FMRIB Software Library (v5.0)

➡ BASIL: www.fmrib.ox.ac.uk/fsl/basil
User guide & tutorials

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