Fabber DCE documentation

Release 0.0.1

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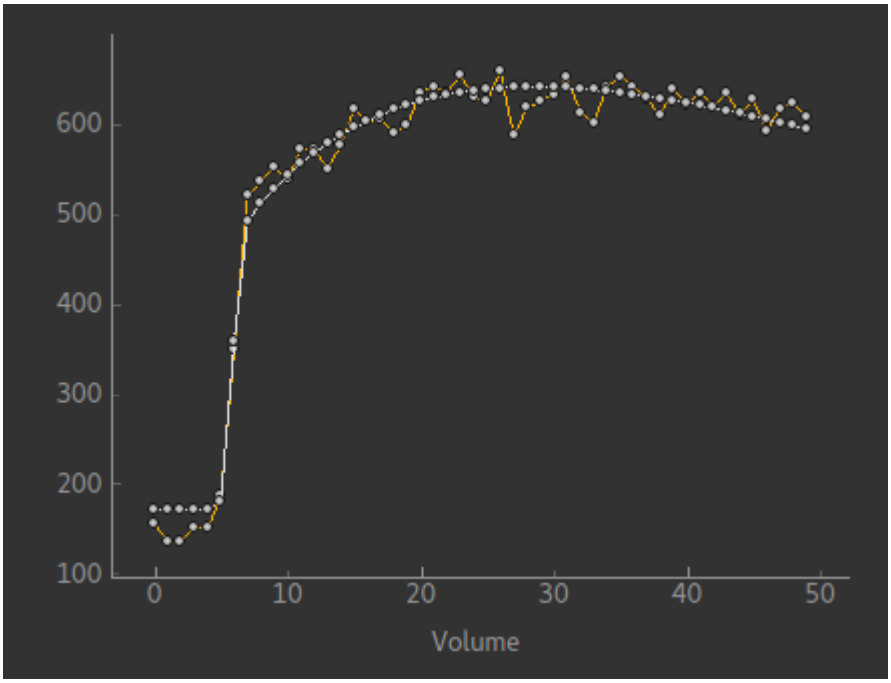
Contents



These models use the Fabber Bayesian model fitting framework[1] to implement a number of models for Dynamic Contrast Enhanced MRI (DCE-MRI).

[1] *Chappell, M.A., Groves, A.R., Woolrich, M.W., "Variational Bayesian inference for a non-linear forward model", IEEE Trans. Sig. Proc., 2009, 57(1), 223–236.*

CHAPTER 1

Getting FABBER_DCE

The DCE models are not currently included as part of FSL. To get the models you will either need to build from source using an existing FSL 6.0.1 or later installation, or download the pre-built Fabber bundle which contains the latest DCE release alongside other models in a standalone package.

CHAPTER 2

Models included

Currently four models are included in the maintained release:

2.1 The standard and extended one-compartment Tofts model[2]

This model is selected using `--model=dce_tofts`. Options are:

--ktrans	Initial and prior Ktrans value
--ve	Initial and prior Ve value
--kep	If using `--infer-kep`, initial and prior Kep value
--vp	If using `--infer-vp`, initial and prior Vp value
--infer-vp	Infer the additional Vp parameter (i.e. use the Extended Tofts model)
--infer-kep	Infer Kep instead of Ve - the two are related by Kep = Ktrans / Ve. Often inferring Kep enables a better fit to be found however the resulting derived values of Ve may be greater than 100%. This may reflect an innaccurate T10 value.
--force-conv	Force numerical solution of the convolution equation even when an analytic solution exists. Currently an analytic solution is only possible when using `--aif=orton`

2.2 The two-compartment exchange model[3]

This model is selected using `--model=dce_2CXM`. Options are:

--fp	Initial and prior flow in min-1 (default 0.5)
--ps	Initial and prior permeability surface area product in min-1 (default 0.05)

[2] http://www.paul-tofts-phd.org.uk/DCE-MRI_siemens.pdf
[3] https://onlinelibrary.wiley.com/doi/full/10.1002/mrm.25991

--vp	Initial and prior plasma volume in decimal between zero and one (default 0.05)
--ve	Initial and prior extracellular space volume in decimal between zero and one (default 0.5)
--conv-method	Method to compute convolution, trapezium, matrix or iterative. Default is iterative

The default prior value for F_p corresponds to a value of 50 ml/100g/min in conventional units. However this prior is relatively uninformative with a default variance of 100 min-1.

The prior for PS is based on the 'permeability limited' regime where $PS \approx K_{trans}$, however the default prior variance of 10 min-1 allows the parameter to increase in leaky vasculature (the 'flow limited' case).

The prior for V_p is based on common values in the range 1-10%. This parameter is constrained to lie between zero and 1. Similarly V_e typical ranges are 10-60%.

See[8] for an overview of these parameters.

2.3 The Compartmental Tissue Uptake model[4]

This model is selected using `--model=dce_CTU`. Options are:

--fp	Initial and prior flow in min-1 (default 0.5)
--ps	Initial and prior permeability surface area product in min-1 (default 0.05)
--vp	Initial and prior plasma volume in decimal between zero and one (default 0.05)
--conv-method	Method to compute convolution, trapezium, matrix or iterative. Default is trapezium

Priors are as for the 2CXM model

2.4 The Adiabatic Approximation to the Tissue Homogeniety model[5]

This model is selected using `--model=dce_AATH`. Options are:

--fp	Initial and prior flow in min-1 (default 0.5)
--ps	Initial and prior permeability surface area product in min-1 (default 0.05)
--vp	Initial and prior plasma volume in decimal between zero and one (default 0.05)
--ve	Initial and prior extracellular space volume in decimal between zero and one (default 0.5)

Priors are as for the 2CXM model

[8] http://www.paul-tofts-phd.org.uk/CV/reprints/A20_dce_mri_chapter_2013.pdf
[4] https://onlinelibrary.wiley.com/doi/full/10.1002/mrm.26324
[5] https://journals.sagepub.com/doi/10.1097/00004647-199812000-00011

CHAPTER 3

Generic options common to all models

3.1 Acquisition parameters

--delt	Time resolution between volumes, in minutes
--fa	Flip angle in degrees.
--tr	Repetition time (TR) In seconds.
--r1	Relaxivity of contrast agent, In s^-1 mM^-1.

3.2 Optional parameters

The following model parameters can be specified as options, however they can also be inferred as part of the fitting process. If they are inferred the specified value is used as an initial value and also as the prior value.

--t10	Baseline T1 value in seconds. May be inferred.
--sig0	Fully relaxed baseline signal. May be inferred.
--delay	Injection time (or delay time when using measured AIF) in minutes. May be inferred.
--infer-t10	Infer t10 value
--infer-sig0	Infer baseline signal
--infer-delay	Infer the delay parameter

It is quite common to measure a T10 map independently (e.g. using VFA images or a saturation recovery sequence). In this case you can use `--infer-t10` and add an *image prior* for the T10 value. See the examples below for how to do this.

3.3 AIF specification

The arterial input function (AIF) is a critical piece of information used in performing blood-borne tracer modelling, as in DCE and other types of MRI. The AIF can either be specified as a series of values in a text file or a generic 'population' AIF can be used.

If the AIF is suppplied as a signal-curve `--aif=signal` it will be converted to a concentration-time curve using the supplied haematocrit and T1b values `--aif-hct` and `--aif-t1b`.

If using the Orton AIF[6] the parameters may be varied using the options described below. The defaults are those given in the Orton paper. The Parker AIF[7] uses hardcoded parameter values from the paper.

--aif Source of AIF function: orton=Orton (2008) population AIF, parker=Parker (2006) population AIF, signal=User-supplied vascular signal, conc=User-supplied concentration curve

--aif-file File containing single-column ASCII data defining the AIF. For aif=signal, this is the vascular signal curve. For aif=conc, it should be the blood plasma concentration curve

--aif-hct Haematocrit value to use when converting an AIF signal to concentration. Used when aif=sig

--aif-t1b Blood T1 value to use when converting an AIF signal to concentration. Used when aif=sig

--aif-ab aB parameter for Orton AIF in mM. Used when aif=orton

--aif-ag aG parameter for Orton AIF in min^-1. Used when aif=orton

--aif-mub MuB parameter for Orton AIF in min^-1. Used when aif=orton

--aif-mug MuG parameter for Orton AIF in min^-1. Used when aif=orton

3.4 Other options

--auto-init-delay Automatically initialize posterior value of delay parameter by fitting a step function to the DCE timeseries.

[6] Matthew R Orton et al 2008 Phys. Med. Biol. 53 1225
[7] https://onlinelibrary.wiley.com/doi/full/10.1002/mrm.21066

CHAPTER 4

Examples

Tofts model on DCE data collected every 6s using the Orton population AIF:

```
fabber_dce --data=dce_data --mask=roi_img
           --method=vb --noise=white
           --delt=0.1 --fa=15 --tr=0.0027 --r1=3.7 --delay=0.5
           --aif=orton
           --infer-delay --infer-sig0 --infer-t10
           --convergence=trialmode --max-trials=20
           --output=dce_output --overwrite --save-model-fit
```

As above but using a pre-measured T10 map:

```
fabber_dce --data=dce_data --mask=roi_img
           --method=vb --noise=white
           --delt=0.1 --fa=15 --tr=0.0027 --r1=3.7 --delay=0.5
           --aif=orton
           --infer-delay --infer-sig0 --infer-t10
           --PSP_byname1=t10 --PSP_byname1_type=I --PSP_byname1_image=T10_map
           --convergence=trialmode --max-trials=20
           --output=dce_output_with_t10_map --overwrite --save-model-fit
```

CHAPTER 5

References