
Verbena documentation

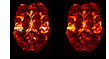
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Martin Craig

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Verbena is a Bayesian Inference tool for quantification of perfusion and other haemodynamic parameters from Dynamic Susceptibility Contrast perfusion MRI of the brain.

VERBENA complements the [OXASL](#) pipeline for the quantification of perfusion using Arterial Spin Labelling MRI and is built on the same core inference algorithm ([FABBER](#)).

VERBENA uses a specific physiological model for capillary transit of contrast within the blood generally termed the ‘vascular model’ that was first described by Ostergaard (see below). In VERBENA the model has been extended to explicitly infer the mean transit time and also to optionally include correction for macro vascular contamination - contrast agent within arterial vessels - more information on the model can be found in the [theory section of the FABBER_DSC documentation](#).

VERBENA takes a model-based approach to the analysis of DSC-MRI data in contrast to alternative ‘non-parametric’ approaches, that often use a Singular Value based Deconvolution to quantify perfusion. An alternative Bayesian Deconvolution approach is also available, but not currently distributed as part of FSL. For more information see the reference below and contact the senior author.

VERBENA is included in [FSL v6.0.1](#).

CHAPTER 1

Running verbena

For the full usage of VERBENA type `verbena` at the command line. A typical usage of VERBENA would be:

```
verbena -i data.nii.gz -a aif.nii.gz -o output_directory -m mask.nii.gz
```

This would process the 4D DSC data in `data.nii.gz` using the AIFs supplied in `aif.nii.gz` and using the modified Vascular Model to estimate (relative) perfusion, commonly referred to as cerebral blood flow ($rCBF$), along with the mean transit time (MTT) and the transit time distribution parameter λ .

Maps of these are placed in the output directory. Analysis is only performed within the mask supplied (`mask.nii.gz`) which will normally have been derived from a brain extraction using BET or other equivalent tool.

1.1 AIFs

VERBENA takes as an input a 4D Nifti file containing the Arterial Input Functions (AIFs) this should have identical dimensions to the data and thus should have a single AIF time course for every single voxel (within the mask).

If the AIF is taken directly from the DSC data it will be in the form of a DSC signal. However if the AIF has been preprocessed using some other tool, or a predefined ‘population AIF’ is being used, it may take the form of a *concentration* time curve. In this case the option `-aifconc` should be given to indicate this. Verbena will perform conversions between signal and concentration curves as required.

Often this will be a single global AIF replicated for every single voxel. However, VERBENA allows for different AIFs to be specified for individual brain regions should a local AIF be available.

We do not currently include a tool for the selection or identification of the AIF. Often the AIF time course will be manually selected from the DSC data by the identification of a major artery, various automated methods have been developed in the literature and it may be possible to find tools that implement them online.

1.2 Acquisition parameters

The `-tr=TR` option is used to specify the time resolution of the data in seconds, i.e. the time spacing between volumes. The `-te=TE` option specifies the assumed TE of tissue, used for conversion of concentration to signal

1.3 Macro vascular contamination

By adding the `-mv` option an additional component will be added to the model (based on the AIF) to account for macro vascular contamination contrast in large arteries, see Theory. When this option is included a further image will be produced in the output directory that maps the Arterial Blood Volume (r_{ABV}) in relative units.

By default the additional macro vascular component is added when the concentration time course of the voxel is calculated, optionally addition of the tissue and macro vascular component can be done as signal time courses using the `-sigadd` option.

1.4 ‘Model-Free’ Analysis

VERBENA takes a model-based approach to perfusion quantification. It is possible to use a more conventional Singular Value Decomposition deconvolution method by choosing the `-modelfree` option.

This ‘model-free’ quantification can also be used to create initial estimates for the main model-based VERBENA analysis using the `-modelfreeinit` option, which may lead to more robust results in some cases.

CHAPTER 2

Referencing

If you use VERBENA in your research, please make sure that you reference Chappell et al¹.

The following articles provide more background on the original vascular model from which the VERBENA model is derived:

An alternative Bayesian ‘non-parametric’ deconvolution approach has been published in:

¹ Chappell, M.A., Mehndiratta, A., Calamante F., “Correcting for large vessel contamination in DSC perfusion MRI by extension to a physiological model of the vasculature”, e-print ahead of publication. doi: 10.1002/mrm.25390