

User guide

Dynamic Susceptibility Contrast-enhanced (DSC) MR — LIFEx —

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Chapter 1
Introduction

1.1 Three major approaches

1.1 Three major approaches

There are three major approaches to measure cerebral perfusion using MRI:

1. **DSC.** The first is the use of an exogenous, intravascular, nondiffusible contrast agent, usually a gadolinium-based contrast agent, that enhances either the susceptibility effects of gadolinium-based contrast agents on the echo signal, namely first-pass dynamic susceptibility contrast-enhanced (DSC) MR perfusion;
→ The DSC-MR protocol of LIFEx uses this technique to derive perfusion-related parameters using exogenous gadolinium-based contrast agent dynamic methods.
2. **DCE.** The second is based on relaxivity effects of gadolinium-based contrast agents on the echo signal, namely dynamic contrast-enhanced (DCE) MR perfusion.
→ Not yet available in LIFEx.
3. **ASL.** Arterial spin labeling (ASL) MR perfusion consists in the use of an endogenous contrast agent using magnetically labeled arterial blood water as a diffusible flow tracer in arterial spin labeling MR perfusion.
→ Not yet available in LIFEx.

Chapter 2

DSC-MR Perfusion

2.1 Current knowledge

2.1.1 Background

Dynamic Susceptibility Contrast or DSC is a method for measuring cerebral blood flow, ie blood flow to the brain. The technique requires intravenous contrast delivered through an automated power injector attached to an IV. The scanner creates an image reflecting multiple cerebral perfusion parameters including cerebral blood flow (*CBF*), mean transit time (*MTT*), and negative enhancement integral or cerebral blood volume (*rCBV*). These techniques are most beneficial to patients with vascular stenosis, stroke, and brain tumors.

2.1.2 Benefits

DSC perfusion gives the most thorough evaluation of cerebral blood flow. In addition to flow, the technique gives other parameters such as blood volume and transit time that

2.2 Inputs

allow the neuroradiologist to more accurately depict the true state of brain perfusion. These additional parameters have been thoroughly studied with regard to stroke and tumor evaluation.

Stroke and Transient Ischemic Attack (TIA). The perfusion parameters can show brain tissue at risk of stroke before the stroke occurs. The best example of this is a patient with a transient ischemic attack or TIA . These patients have brief stroke-like symptoms and but may have a normal MRI. DSC perfusion can reveal subtle perfusion changes that could allow possible therapeutic interventions to prevent a future stroke

Tumors. Cerebral blood volume correlates with the tumor grade or how malignant the tumor is. Brain tumors are frequently heterogeneous when looked at under the microscope. Perfusion can help guide the neurosurgeon to obtain the most accurate biopsy sample of the tumor to optimize therapy after surgery. Perfusion can also help distinguish between brain metastases, primary brain tumors, and an infectious process prior to surgery.

2.2 Inputs

In this context, perfusion is one of the most important physiologic and pathophysiologic parameters and can be assessed with MRI. The Dynamic Susceptibility Contrast (DSC-MR) protocol and measurement of conventional parameters from images are based on a number of rules related to the image series, ROI and pixel values, as described below:

Image series. DSC protocol is currently only supported for MR; MR Perfusion sequences are EPI T2* weighted with a short repetition time (TR) (often 2 sec) and a short echo time (TE) (often 40 to 60 ms); if the patient moves during the acquisition, it is possible to perform a temporal and spatial registration before calculating perfusion parameters ; see the "Estimation of the tissue motion section" for more information (section 2.3.1 p.8).

Input parameters. No input parameters are needed to calculate perfusion parametric maps. These are all calculated from perfusion images: index of first image after signal stabilisation, index of image of start time of bolus, index of image of end time of bolus.

Input ROI. No ROI is needed to calculate perfusion parametric maps.

2.3 Estimation of conventional parameters?

2.3.1 Correction for tissue motion

Tissue motion. The analysis of MR perfusion can be hampered by tissue motion.

Align button. By pressing the "run" button in the DSC-MR menu / Time alignment submenu, the Montreal Neurological Institute (NMI) registration is carried out. To do this, a reference volume is required and has to be specified in the "Time of reference (sec)" entry. This time defines the reference volume for registration. All time volumes will be registered on this chosen volume.

2.3 Estimation of conventional parameters?

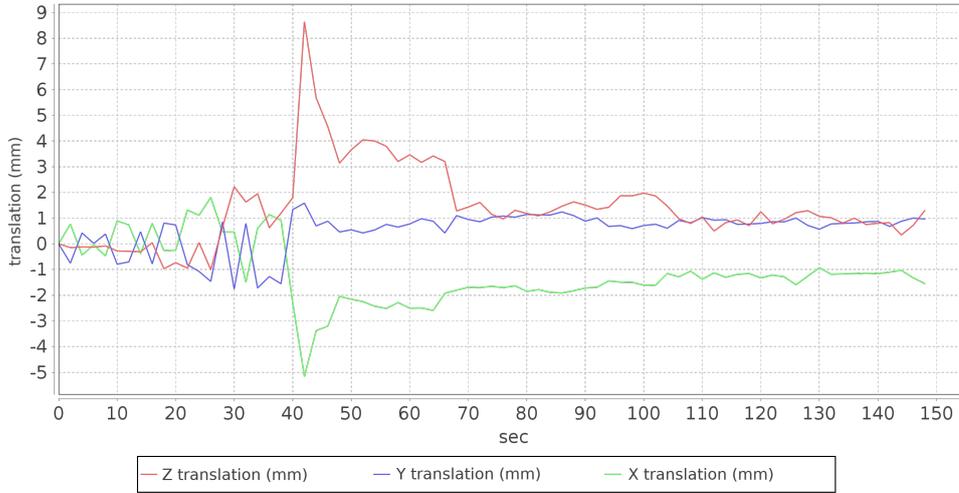


Figure 2.1: translation parameters estimated to realign the MR perfusion volumes

Output results. Beware of the fact that, this step causes a changed of the current series. The new registered series replaces the series previously loaded.

Output charts. One graph shows the estimated translation parameters (fig. 2.1) while another graph displays the estimated rotation parameters (fig. 2.2).

Is it necessary to register the volumes? Registration should absolutely be performed for movements that can be visually detected (by scrolling through the dynamic series using the time cursor). When no motion can be visually perceived, registration is not recommended.

2.3.2 Estimation of the perfusion

Bolus. The transit of the contrast agent in the cerebrovascular system responds to a monocompartmental model. After bolus injection, the vascular transit of the contrast product induces a variation of the local magnetic field with an artificial phase shift of the spins (R effect, denoted $R2^*$ in $T2^*$ weighting) in a space equivalent to that of the vessel. This magnetic susceptibility induces a shortening of the relaxation time with a significant drop in the signal (Fig. 2.3).

Estimation of the perfusion parameters. In the absence of a recirculation phenomenon of the contrast agent or crossing of the blood brain barrier (BBB), the $rCBV$ is proportional to the area under the curve (Fig. 2.4) of the concentration of the contrast agent as a function of time. This concentration (eq. 2.1) is proportional to the variation of the phase shift of the transverse relaxation $\Delta R2^*$ of $\frac{S(t)}{S_0}$, calculated using:

$$C(t) \propto \Delta R2^*(t) = \frac{-k}{TE} \cdot \ln \frac{S(t)}{S_0} \quad (2.1)$$

with:

2.3 Estimation of conventional parameters?

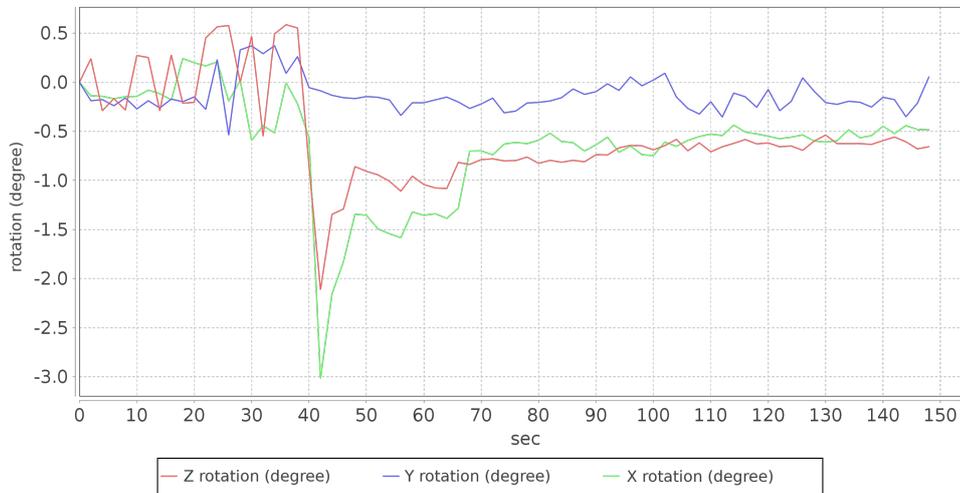


Figure 2.2: rotation parameters estimated to realign the MR perfusion volumes

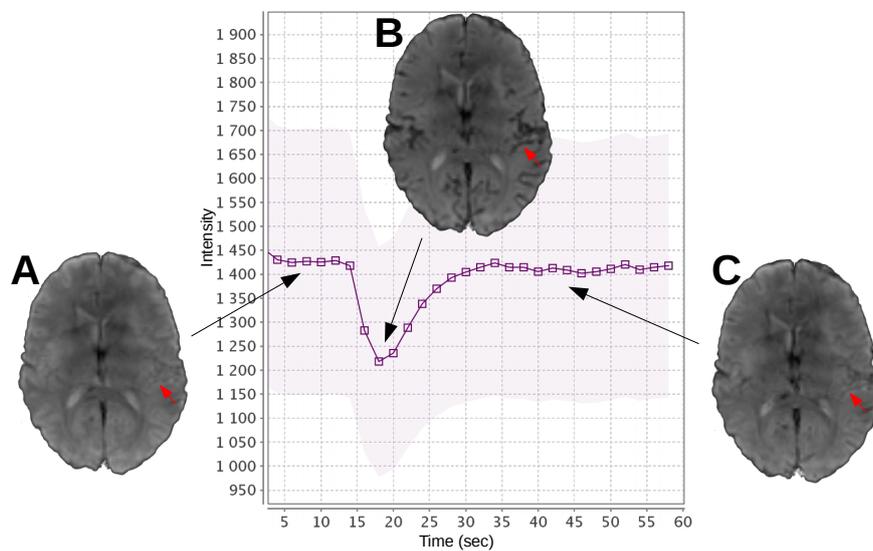
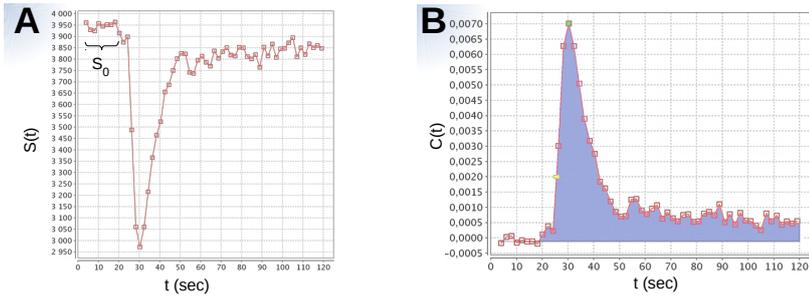


Figure 2.3: Perfusion signal on T2* ponderation induced by a bolus of gadolinium on cerebral hemispheres (curve). pT2* images corresponding to three different times are displayed. Red arrows indicate the location of a vessel. A — before. B — during. C — after bolus.

2.3 Estimation of conventional parameters?



DSC-MR Perfusion

Figure 2.4: MR perfusion signal and concentration curve. **A** — Intensity of MR perfusion signal. S_0 is the baseline signal. **B** — relative concentration curve.

k : proportionality factor;
 $S(t)$: signal intensity at time t ;
 S_0 : baseline signal before injection;
 TE : echo time of the sequence.

The maximum signal-to-noise ratio for this type of curve is obtained when the minimum signal is around 37% of the signal strength S_0 (Smith MR, Lu H, and Frayne R; 2003; Signal-to-noise ratio effects in quantitative cerebral perfusion using dynamic susceptibility contrast agents. Magn Reson Med, 49 1:122-8).

We characterize the bolus curve, which is also called 1st bolus curve, by 5 key values: BAT, TTP, MTT, AUC and FWHM as defined in Figure 2.5. In order to accurately calculate $rCBV$, the choice of the volume of interest in the pathological area is extremely important.

To define the volume of interest (VOI) corresponding to a pathological zone: you should draw a VOI in the zone where the $rCBV$ appears to be the highest. It is indeed in the zone of maximum angiogenesis that it is preferable to characterize the lesion (Grand S, Lefournier V, Krainik A, Bessou P, Tropes I, Chabardes S, Hoffmann D, and Le Bas JF (2007) MR and CT perfusion imaging of the brain : principles and clinical applications. J Radiol, 88 3 Pt 2:444-71).

To do this, the VOI must be placed outside the large cortical vessels, and outside areas that include deep vessels or part of the choroid plexuses. For this purpose, you can use pT1 axial sections, which are generally obtained at a distance from the injection point.

The VOI you should include several pixels to reduce the impact of the noise. By moving this VOI, can assess the variations of these parameters in different areas of the lesion, and also observe the first pass curve and the quality of the adjustment.

Note, that the location of this VOI is difficult when the tumor is infiltrating due to the lack of anatomical limits of the lesion.

2.3 Estimation of conventional parameters?

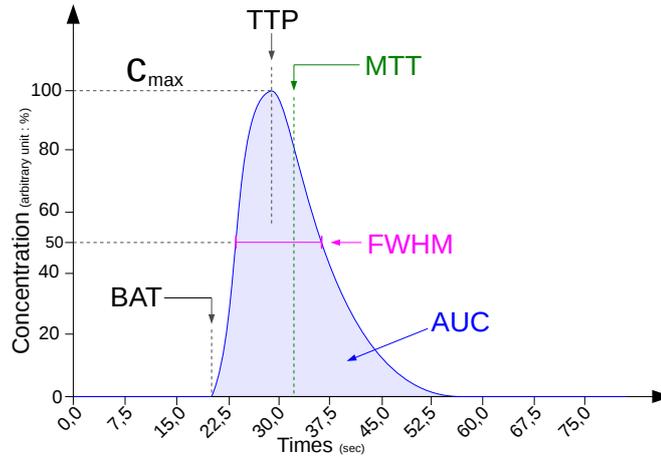


Figure 2.5: MR specifications of bolus curve.

BAT — bolus arriving time.

AUC — area under the curve = $rCBV$.

FWHM — full-width at half maximum.

MTT — mean transit time

TTP — time to peak (C_{max}).

2.3.3 Theorem of the central volume

The central volume theorem is used in compartmental analysis for a non-diffusible paramagnetic tracer, here the gadolinium chelate (Ostergaard L, Weisskoff RM, Chesler DA, Gyldensted C, and Rosen BR (1996b) High resolution measurement of cerebral blood flow using intravascular tracer bolus passages. Part I: Mathematical approach and statistical analysis. Magn Reson Med, 36 5 :715-25).

Consider a non-diffusible tracer bolus at time $t = 0$. This bolus can be thought of as input to a VOI of tissue. The tracer particles follow different paths through the VOI and their transit times thus have a characteristic flux distribution as a function of the vascular structure (input \rightarrow tissue \rightarrow output). The probability density function of these transit times is denoted $h(t)$, the transfer function. When an arterial input $C_{AIF}(t)$ is given to the VOI, the concentration of the tracer in the Veinous Output Function (VOF), $C_{VOF}(t)$, of the region is given by equation 2.2:

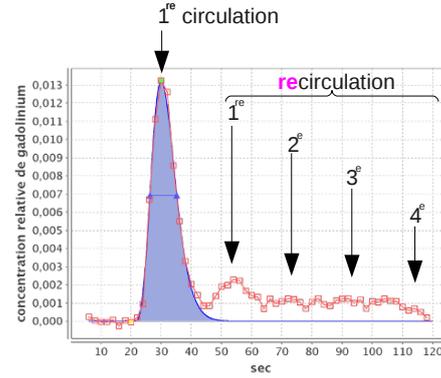
$$C_{VOF} = C_{AIF}(t) \otimes h(t) = \int_0^t C_{AIF}(\tau) h(t - \tau) d\tau \quad (2.2)$$

MTT : the *MTT* for tracer particles is defined as (eq. 2.7):

$$MTT = \frac{\int_{-\infty}^{+\infty} \tau h(\tau) d\tau}{\int_{-\infty}^{+\infty} h(\tau) d\tau} \quad (2.3)$$

The calculation of *MTT* based on a notion of volume, like the $rCBV$, is also affected by the phenomenon of recirculation of the contrast agent that we address in the following paragraph.

Figure 2.6: MR Contrast product recirculation. The actual signal (red curve) has several peaks due to recirculation of the product. The gamma function (blue curve) estimated on the 1st peak does not include that recirculation component.



DSC-MR Perfusion

2.3.4 Recirculation phenomenon

In practice, recirculation influences the measurement before the whole contrast agent has exited the cerebro-vascular system. To overcome this recirculation, the concentration curve is fitted by a polynomial function (incomplete gamma). The contrast medium used is considered locally non-diffusible during the measurement period and remains confined within the cerebral intra-vascular space. The acquisition is therefore performed during the first pass to avoid dilution of the contrast agent and, especially, to avoid the extra-vascular diffusion due to a possible haematoencephalic barrier rupture. This approach therefore requires a sequence with a high sensitivity to magnetic susceptibility, such as the echoplanar gradient echo.

Recirculation phenomena are always present in varying degrees (fig. 2.3.3). They are suppressed by a mathematical function such as "incomplete gamma-variate (eq. 2.4)" (Press WH, Teukolsky SA, Vetterling WT, and Flannery BP (1992) Numerical recipes in C, volume Num Rec In C of Second edition. Cambridge university press. p.216):

$$\Gamma(t) = K_{scale} (t - t_0)^\alpha \cdot e^{\beta(t-t_0)} \quad (2.4)$$

with K_{scale} is an enlargement factor, t_0 the time at BAT, α et β the parameters of the incomplete gamma variate. This function is fitted to the concentration curve of the infusion bolus using the iterative gradient descent minimization method (Levenberg and Marquardt).

2.4 DSC-MR protocol — explanation —

2.4.1 Estimation of the volume of the cerebral parenchyma

The indices of the voxels composing the volume of the parenchyma are denoted by the variable pix_{brain} . The method used to identify these voxels is based on a thresholding technique on EPI-pT2* images in which the absence of structures such as bone or skin simplifies the process.

The mean intensity of the cerebral parenchyma EPI-pT2* images is calculated as the starting point for thresholding. A sampling of 1/4 of number of pixels (magenta grid in figure 2.7) and the parenchyma height threshold is calculated to find parenchyma intensity (green grid in figure 2.7).

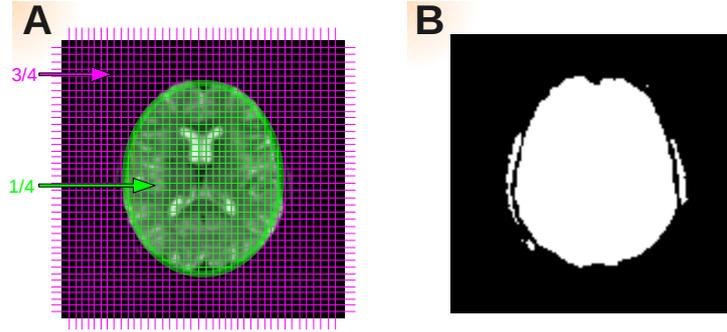


Figure 2.7: MRI Threshold grid of cerebral parenchyma. **A** — Threshold grid, cerebral parenchyma (1/4 green of surface), and black background of image (3/4 magenta of surface). **B** — Resulting thresholded image with threshold value.

This restricted sampling is sufficiently representative of the complete volume and makes it possible to estimate a threshold (fig. 2.7). This threshold that we voluntarily underestimate then allows to have no loss in the volume of the cerebral parenchyma while removing 3/4 of the volume of the image for the calculations (eq. 2.5):

$$pix_{brain}(i) \begin{cases} i, & \text{if } s(i) > \rho, \\ \emptyset, & \text{else} \end{cases} \quad \forall i : 1 \mapsto n \quad (2.5)$$

with pix_{brain} the indices of the pixels containing the cerebral parenchyma, and $s(i)$ signal of pixel i . The vector pix_{brain} has a size of n_{brain} pixels.

The following steps are performed on this part of the image: pix_{brain} .

The second step is the calculation of the average perfusion signal of the entire cerebral parenchyma.

2.4.2 Mean signal of the cerebral parenchyma

The average signal of the whole parenchyma is estimated as follows (eq. 2.6):

$$s_{moy}(t) = \frac{1}{n_{brain}} \sum_i s(pix_{brain}(i), t) \quad \forall t : 1 \mapsto nt \quad (2.6)$$

with $s(x, t)$ the signal of pixel x at t time.

The third step estimates the time to peak bolus and mean transit time, key points of perfusion and starting points for gamma function adjustment.

2.4.3 Quick pre-calculation of Time To Peak (TTP) and Mean Transit Time (MTT)

From the average signal s_{avg} , the average transit time is calculated as the area under the time curve formed by the product of the signal by the time divided by the area under

the time curve of the signal (see eq 2.7 page 15).

$$MTT = \frac{\int_0^{nt} (t \times s_{avg}(t)) dt}{\int_0^{nt} s_{avg}(t) dt}. \quad (2.7)$$

The TTP value (eq. 2.8) corresponds to the time at which the time signal is minimal:

$$TTP = \left\{ t, \text{ if } s_{avg}(t) = \underset{t}{\text{arg min}}\{s_{avg}(t)\} \right\} \quad (2.8)$$

The adjustment of the gamma function requires knowledge of the transit times of the bolus. These are defined by the presence of a pre-bolus and post-bolus signal plateaus.

2.4.4 Plateau of pre-bolus

The pre-bolus plateau is the baseline of signal intensity before injection. This plateau is characterized by three main parameters: the plateau start time, the average plateau intensity, and the plateau end time.

To determine these values, we use the following algorithm.

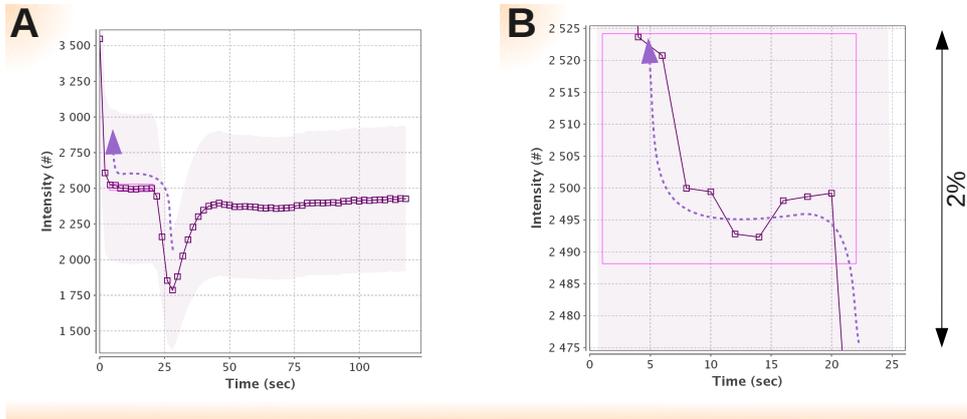


Figure 2.8: MRI temporal curves of the cerebral parenchyma (pre-bolus). The search for the pre-bolus start and end points takes place from the TTP towards the beginning of the acquisition (purple dotted arrow). **A** — Representation of the temporal signal over 120 sec. **B** — 2% of the average signal of the plateau (expansion of the view A).

The identification of the pre-injection plateau starts at the TTP time.

By going back in time ($t - i$) (purple dotted arrows in figure 2.8), the gradient of the signal is compared (eq. 2.9) to an arbitrary value of 2% of the signal ($t - i$). As soon as the amplitude of the gradient becomes less than 2%, we set the pre-bolus plateau end time ($lastPre$).

The algorithm is identical to determine the start of the plateau (*firstPre*) but with an amplitude search greater than 2% (eq. 2.10). We avoid all problems of local minima by averaging the $\sim 100,000$ voxel signal that makes up the brain parenchyma (*pix_{brain}*) and using this curve for the determination of the general plateau.

$$lastPre \left\{ t, \text{ as soon as } \left[|s_{avg}(t) - s_{avg}(t-1)| < 2\% \times s_{moy}(t) \right] \quad \forall t : TTP \mapsto 0. \quad (2.9)$$

$$firstPre \left\{ t, \text{ as soon as } \left[|s_{avg}(t) - s_{avg}(t-1)| > 2\% \times s_{moy}(t) \right] \quad \forall t : lastPre \mapsto 0. \quad (2.10)$$

Additional controls are necessary to ensure the accuracy of the subsequent estimation of the gamma function, including the presence of a sufficient number of points in the pre-bolus plateau. Two points (at least 2 seconds) are needed to have a minimum plateau after which the injection is supposed to be too early for a good stability of the signal and the examination becomes invalid.

2.4.5 Incomplete Gamma Variate

The *Bolus Arrival Time* (BAT) point t_0 (see fig. 2.5, p. 12) is the starting point of the function. The gamma function, frequently used in MR-perfusion, is an incomplete gamma function since it is defined on the $]t_0; +\infty[$ interval:

$$y(t) = \Gamma(t) = t^\alpha e^{\beta t} \quad (2.11)$$

The gamma function is fitted to the data based on the Levenberg-Marquardt method. The evolution of the algorithm is controlled by the merit function $\chi^2(a)$ (not shown) with a the parameters of the model to find.

2.4.6 Levenberg-Marquardt method

The initial parameters *MTT* and *TTP* are calculated as we have seen previously for each studied pixel index *pix_{brain}*. The signal is converted into concentration using equation 2.1, p. 9. The 3 parameters **a** (eq. 2.12) are initialized according to the *MTT* and *TTP* of the studied pixel and extracted from the equation of the gamma function (eq. 2.4, p. 13).

$$\begin{aligned} \mathbf{a}[2] &= \beta &&= 1 / (TTP - MTT) \\ \mathbf{a}[1] &= \alpha &&= TTP \times (-\beta) \\ \mathbf{a}[0] &= K_{scale} &&= (S(TTP) - S_0) \exp(\alpha \times (1 - \ln(TTP))) \end{aligned} \quad (2.12)$$

The set of pixels *pix_{brain}* is thus processed. The functions used are those of the book *Numerical Recipes in C, Second Edition* transcribed in Java, and implemented in our application: *mrqmin* and *mrqcof*.

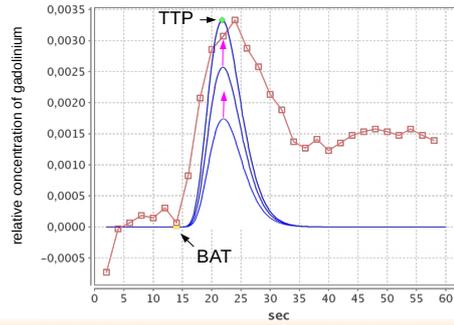


Figure 2.9: Iterative intermediate results of the minimization of χ^2 by the Levenberg-Marquardt method. The BAT point determining the bolus start (**yellow square**) and the TTP point determining the maximum peak (**green diamond**) are identified before the start of the algorithm. The first curve of the lowest gamma function (**blue curve**) corresponds to the non-optimized response of the algorithm, followed by two iterations (**magenta arrows**).

The Levenberg-Marquardt estimation is not yet sufficiently correct without a search for the $[lastPre; firstPost]$ interval of the bolus transit. The algorithm is strongly dependent on this interval which is difficult to estimate properly using 1 pixel (lower SNR ratio than on the mean of the cerebral parenchyma). Typically in the example of figure 2.9 the detected interval of $[14; 30]$ seconds is not sufficient. We have developed an additional method to reduce these curve deviations by optimizing the bolus search interval.

2.4.7 Optimization of the time interval of the bolus

The mean TTP ($meanTTP$) over the whole brain is calculated and an interval defined as $[meanTTP - 5s; meanTTP + 5sec]$ is defined. For each voxel, if the TTP extracted from the voxel signal is out of this interval then $meanTTP$ is used for that voxel, instead of the TTP derived from the voxel signal.

The mean TTP ($meanTTP$) over the whole brain is calculated. This average gives a temporal confidence interval with a search of ± 10 sec. If the TTP of the signal is out of this interval then the $meanTTP$ is considered as more appropriate to start the search of the transit of bolus.

The technique used is to automatically introduce time offsets on the search interval. These offsets are partitioned into physiologically possible values. Values between $[meanTTP - 12 sec]$ and $[meanTTP + 35 sec]$ are tested with a gap of one second.

All combinations are tested and the values of the \mathbf{a} and χ^2 parameters are recorded.

The interval with the smallest χ^2 is kept (see fig. 2.10, p. 18). In this example, the interval of $[10; 42]$ seconds retrieves the parameters of the gamma function closest to the actual signal. Let $S_0 = 1702.2$, $\alpha = 5.67758$, $\beta = -0.40554$, $K_{Scale} = -3.09287E - 7$.

We can now extract analytically the desired parameters and in particular the cerebral blood volume as follows.

2.4 DSC-MR protocol — explanation —

DSC-MR Perfusion

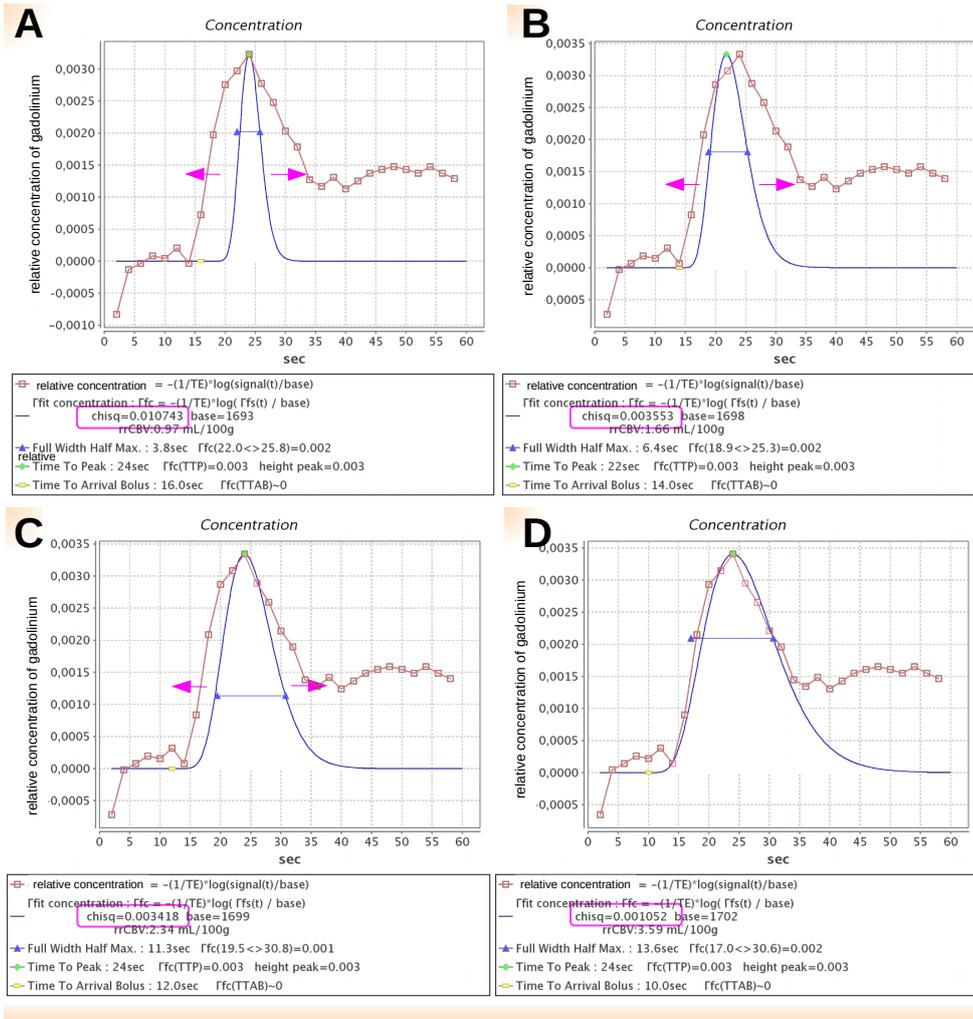


Figure 2.10: MR Optimization of the time interval of bolus. The search interval, A→B, is iteratively increased (**magenta arrows**). **A** — search interval of [13-34] seconds. **B** — search interval of [14-30] seconds. **C** — search interval of [12-38] seconds. **D** — search interval of [10-42] seconds with the minimum χ^2 .

2.4.8 Analytical parameters of the gamma function

Density of brain tissue. Brain tissue has a tissue density of ρ (brain parenchyma attenuation, or density of brain tissue, (Rempp KA, Brix G, Wenz F, Becker CR, Geckel F, and Lorenz WJ (1994) Quantification of regional cerebral blood flow and volume with dynamic susceptibility contrast-enhanced MR imaging. Radiology, 193 3 :637-41.) (Axel L (1980) Cerebral blood flow determination by rapid-sequence computed tomography : theoretical analysis. Radiology, 137 3 :679-86.):

$$\rho = 1.04 \text{ g/cm}^3 \quad (2.13)$$

Hematocrit. When calculating blood volume from exogenous tracers, we must exclude the volume occupied by the cells (red blood cells, leucocytes). We call hematocrit the relative percentage of the volume of cells circulating in the blood relative to the total volume of blood. The average hematocrit rate used in humans is $H_{large \text{ vx}} = 45\%$ for large vessels and $H_{small \text{ vx}} = 25\%$ in small vessels (capillaries). The remaining hematocrit fraction (eq. 2.14) corresponds to the blood volume in which this type of tracer is distributed (Rempp KA, Brix G, Wenz F, Becker CR, Geckel F, and Lorenz WJ (1994) Quantification of regional cerebral blood flow and volume with dynamic susceptibility contrast-enhanced MR imaging. Radiology, 193 3 :637-41.).

$$k_{hematocrits} = \frac{1 - H_{large \text{ vx}}}{1 - H_{small \text{ vx}}} = 73.33\% \quad (2.14)$$

Incomplete Gamma Variate. The incomplete gamma variate function estimates (eq. 2.15) the concentration $Conc(t)$, the signal $S(t)$, the time corresponding to the bolus peak TTP , and the average transit time MTT of the bolus. In addition, the cerebral blood volume $rCBV$ per 100g that corresponds to the area under the curve, which takes into account the hematocrit $k_{hematocrits}$ (see eq. 2.14, p. 19) and the brain density ρ (see eq. 2.13, p. 19) can be estimated.

$$\begin{aligned} Conc(t) &= -K_{scale} \cdot \exp(\alpha \ln(t) + \beta t) \\ S(t) &= S_0 \cdot \exp\{-Conc(t)\} \\ TTP &= -\alpha / \beta \\ MTT &= -(\alpha + 1) / \beta \\ rCBV &= |S_0 \cdot \exp\{\ln\Gamma(\alpha + 1) - (\alpha + 1) \ln(-\beta)\}| \times \frac{k_{hematocrit}}{\rho} \times 100 \\ rCBF &= rCBV / MTT \end{aligned} \quad (2.15)$$

All previous calculations are performed for each voxel.

The estimate of $rCBV$ can also be made from the set of pixels contained in an ROI as explained in the next section 2.5, p.20.

2.5 GUI of DSC-MR protocol

DSC-MR Perfusion

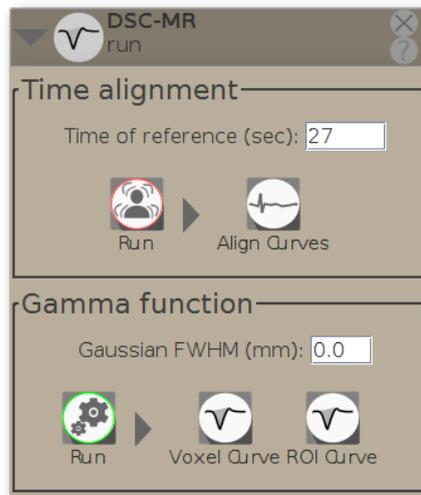


Figure 2.11: GUI of DSC-MR protocol

2.5 Graphic User Interface

- the DSC-MR (fig. 2.11) includes five buttons:
 - the "Run" Alignment button to start the temporal image registration (section 2.3.1, p.8);
 - the "Align Curve" button to display all curves registration;
 - the "Run" Gamma button to start the calculations;
 - the "Voxels Curve" button to display the voxelwise analytic results.
 - the "ROI Curve" button to display the ROI-based analytic results.

2.6 Results

DSC-MR Output map. After calculation, the user interface includes three new parametric map layers (fig. 2.12):

1. the $rCBV$ map;
2. the $rCBF$ map;
3. the MTT map.

The relative cerebral blood volume ($rCBV$), relative cerebral blood flow ($rCBF$) and time to peak (TPP) layers are calculated from each voxel of the perfusion MR series.

DSC-MR Output from ROI. You can extract $rCBV$, MTT , $rCBF$ from ROI (fig.2.13) even if the parametric maps are not calculated. The ROI perfusion calculations are completely independent of the map perfusion calculations.

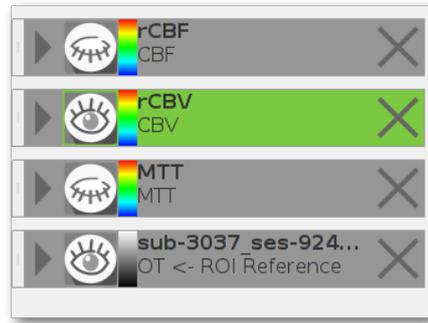


Figure 2.12: 3 new layers of result after DSC-MR perfusion calculation

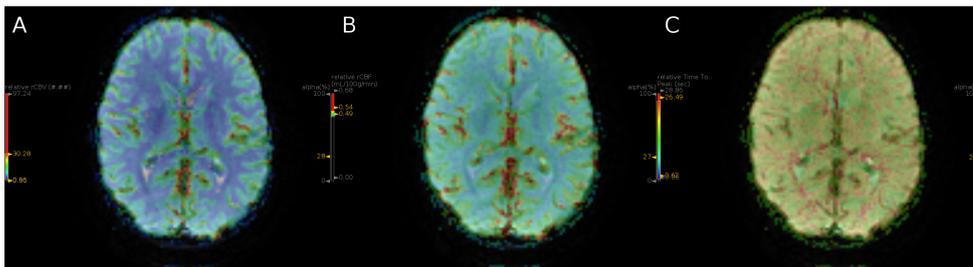


Figure 2.13: rCVB (A), rCBF (B) and MTT (C) result after DSC-MR perfusion calculation.

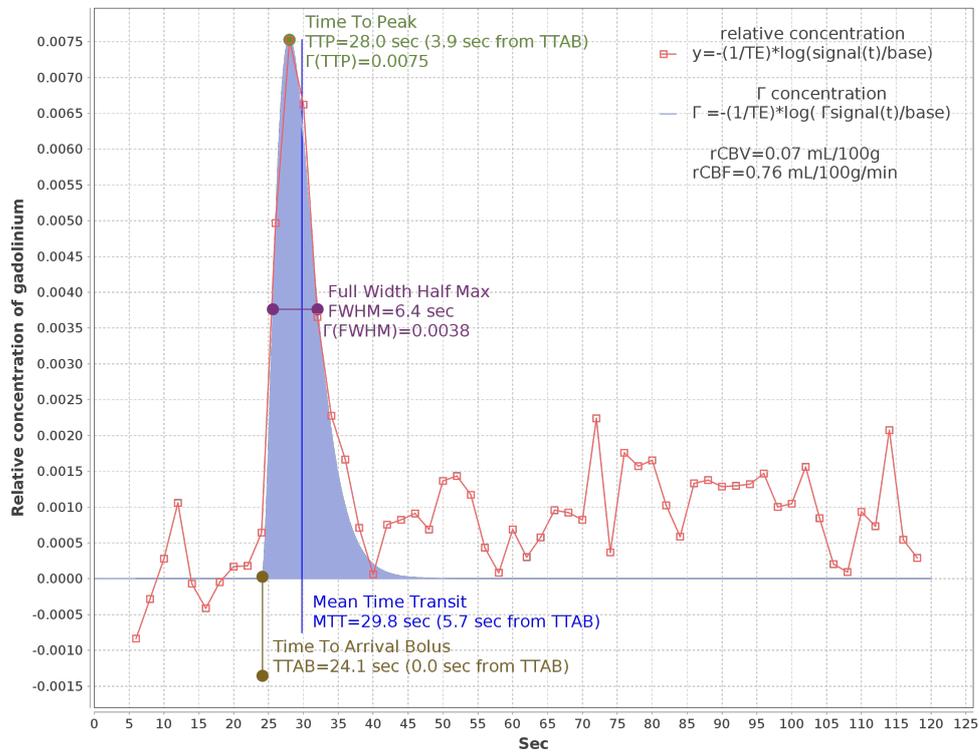


Figure 2.14: Perfusion concentration of the voxel shown by the pointer. Parameters are shown at the top right of the Figure.

2.6 Results

DSC-MR Perfusion

ROI Curves. By selecting the "curve" button, perfusion is calculated from the ROI (visible ROI) and from the series of MR perfusion. The perfusion signal processing is then averaged over the set of voxels of the ROI. The results are displayed as a curve with a new curve for each ROI.