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## 6 Perfusion Imaging

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Perfusion imaging tracks the transient passage of a Gd-based contrast agent bolus by means of a fast dynamic scan:

- Contrast agent will be injected as a bolus.
- Simultaneously, a fast dynamic scan will be started.
- This dynamic scan will be evaluated with post-processing packages.

Perfusion imaging can be performed in two different ways. Both techniques are described in this chapter. Working with the online user documentation, click on a link to go to the corresponding description.

- Basic T1 Perfusion
  - Overview
  - Workflow 'Basic T1 Perfusion'
  - Results - Basic T1 Perfusion
- Neuro T2\* Perfusion
  - Overview
  - Workflow 'Neuro Perfusion'
  - Results - Neuro Perfusion

- User Interface - Perfusion Postprocessing packages

As the user interface of the two perfusion postprocessing packages is more or less identical, it is described within one section.

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## 6.1 Basic T1 Perfusion

This chapter provides an Overview on Basic T1 Perfusion and describes the Workflow 'Basic T1 Perfusion' of the corresponding postprocessing package.

### 6.1.1 Overview

T1 perfusion studies are based on the fact that Gd-based contrast agent shortens the T1 relaxation times of tissues.

#### Acquisition

In order to observe the changes of the T1 relaxation time and in such a way the contrast-uptake, a T1w dynamic fast perfusion scan has to be executed, e.g. 3D T1-FFE or -TFE scan.

#### Applications

Typical applications are contrast-uptake studies in the body, e.g. abdomen and thorax.

#### Contrast agent bolus injection

Contrast agent has to be injected as a bolus.

#### Postprocessing

Evaluation of the scan can be done with the 'Basic T1 Perfusion' package.

The Basic T1 Perfusion package calculates functional and parameter maps for any kind of contrast-uptake dynamic study. New imaging series can be easily generated and stored.

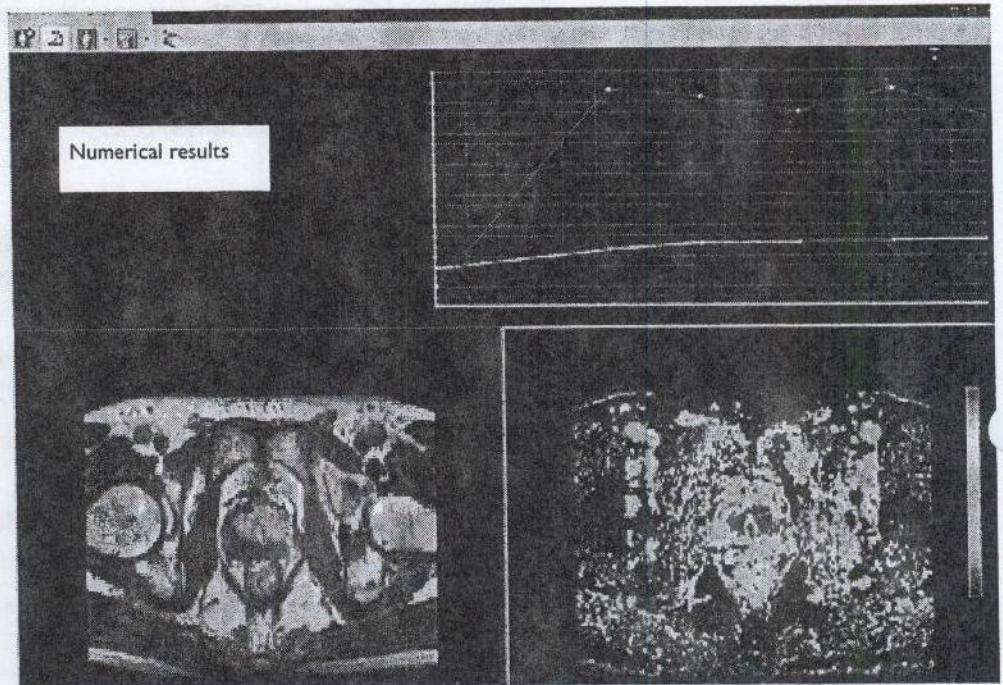
Analyses are stored in the current ExamCard and performed automatically when the ExamCard is executed again. For more information, see chapter on ExamCards, Inline Processing.

## 6.1.2

# Workflow 'Basic T1 Perfusion'

In the Advanced Viewing Environment

- 1 Right click on any perfusion data set in the pictorial index.  
A context menu appears.
- 2 Click on 'Basic T1 Perfusion'.  
The Basic T1 Perfusion package opens.



**Figure 6.1** Example of 'Basic T1 Perfusion' screen with numerical results, graphical display (curve), an original image and a resulting map.

Entering the package, immediately the results will be presented for the image in the middle of the volume. Moving the cursor over either the original image or the map, the curve and the numerical results originating from the current pixel will be shown.

## Navigate through images

### *Through slices/dynamics*

To select the slice/dynamic of interest:

- 3 Drag the left mouse to the left or to the right within the image viewport to scroll through dynamics.
- 4 Drag the left mouse up- or downwards within the image viewport to scroll through slices.

### **Through maps**

To select the map of interest:

- 5 Drag the left mouse to the left or to the right within the map viewport to scroll through maps.

Moving the mouse up- or downwards with the mouse button being pressed doesn't have any effect in this case.

### **Adjust Threshold**



Setting a threshold mask will exclude background pixels from the functional map calculations. Only pixels with intensity above the mask value are used for the calculations.

Entering the package, the threshold function is automatically enabled. This means that the threshold mask will be overlaid to the original image.

- Click on the Threshold ON/OFF icon to enable or disable the display of the overlaid threshold mask.

- 6 Right click and move the mouse up- and downwards with the right mouse button being pressed to adjust the threshold.

All pixels with values below the mask value will be displayed blue.

### **Apply spatial smoothing**



It is possible to smooth the original images and in such a way also the resulting map.

- 7 Click on the 'Spatial Smoothing' icon.
- 8 Select either of the possible settings by clicking:
  - None (no smoothing).
  - Weak.
  - Medium.
  - Strong.

## Select the colors for the maps

It is possible to display either colored or greyscale maps.



- 9 Click on the 'Color LUT' (look-up table) icon.
- 10 Select either of the possible settings by clicking:
  - Blue to Red
  - Greyscale.

Values:	Minimum				Maximum
<b>Display</b>					
Blue to Red	Blue	Green	Yellow	Orange	Red
Greyscale	Black		Grey		White

## Generate results per pixel

This package provides graphical and numerical results.

- The graph correlates to a specific pixel and shows the intensity value (intensity) over the time for this pixel.
- The numerical results are displayed in a table.  
More information on the results can be found in the 'More about ...' paragraph.

In order to generate results, it is necessary to select a pixel. This can easily be done by positioning the pointer at a specific position on either the original image or the map.

Prerequisite is that the pointer is in the 'Follow Mouse' mode.

- 11 Right click on the curve view port.
- 12 Click to enable 'Follow Mouse'.
- 13 Move the pointer over the image.  
Results will be displayed and automatically be updated with every move of the pointer.

## Generate results per ROI

If necessary, results per ROI can be generated.

- 14 Set the Interaction mode to 'Draw ROI' via the right mouse menu on one of the image viewports.

- 15 Drag the left mouse over the image to draw a ROI. Releasing the left mouse button, the ROI will be closed.

Numerical and graphical results can now be shown as ROI average.

To do so:

- 16 Select 'ROI average' from the right mouse menu on the graph.

In order to delete an existing ROI, right click on the ROI and select 'Delete'.

### **Generate new imaging series**



- 17 Click on the 'Generate series' icon.  
A new imaging series will be generated within the current examination.
- 18 Define a name for the new series in the entry field.

### **6.1.3**

## **Results - Basic T1 Perfusion**

The package calculates the following types of results:

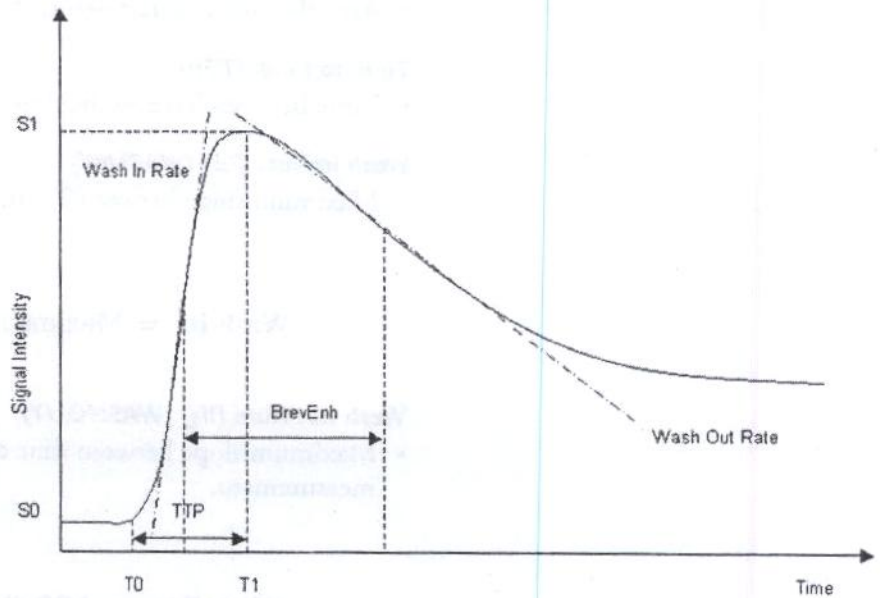
### **Graphical results**

The graphical results present a Time-Intensity Diagram (intensity versus time).

### **Numerical results and maps**

The results will be provided numerically and as maps. Figure 6.2 gives an overview where

- S0 is the initial intensity,
- S1 is the peak intensity,
- T0 is the Time of Arrival (time of initial intensity),
- T1 is the time of peak intensity.



**Figure 6.2** T1 Perfusion - Results.

**Relative Enhancement [%] (RELENH)**

- The signal enhancement of a pixel of certain dynamic relative to that same pixel in the reference dynamic. The reference dynamic is normally the first, pre-contrast dynamic. The reference dynamic can be set to another dynamic via the right mouse menu function 'Set as Subtraction Reference'.

$$\text{Relative Enhancement} = \left[ \frac{I(D)}{I(Dref)} - 1 \right] \times 100$$

- where I(D) stands for pixel intensity of current dynamic and I(Dref) stands for pixel intensity of reference dynamic.

**Maximum Enhancement (MAXENH)**

- Difference between peak intensity S1 and S0.

**Maximum Relative Enhancement [%] (MAXRELENH)**

- Maximum of all relative enhancements over all dynamics.

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***T0 - Time of Arrival [s] (T0)***

- Arrival of the contrast agent, i.e. begin of the enhancement curve.

***Time to Peak (TTP)***

- Time between T0 and the time of peak intensity (T1).

***Wash in Rate [I/s] (WASHIN)***

- Maximum slope between T0 and time of peak intensity T1.

$$\text{Wash In} = \text{Maximum} \left[ \frac{I(D) - I(D-1)}{T} \right]$$

***Wash out Rate [I/s] (WASHOUT)***

- Maximum slope between time of peak intensity T1 and the end of the measurement.

$$\text{Wash Out} = \text{ABS} \left( \text{Maximum} \left[ \frac{I(D) - I(D-1)}{T} \right] \right)$$

***Brevity of Enhancement [s] (BREVENH)***

- Time between point of maximum wash in rate and maximum wash out rate.

***Area under the curve (AREACURV)***

Sum of all intensities under the curve.

Scrolling through the maps, the type of the map is indicated in the map's scan type field. The used values can be found in the descriptions below in brackets.