



Diffusion Imaging Perfusion Imaging

Application Brochure

MAGNETOM Avanto
MAGNETOM Espree
MAGNETOM Symphony a Tim System
MAGNETOM Trio a Tim System
MAGNETOM Verio

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Application Brochure

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MAGNETOM Verio

This brochure informs you about diffusion and perfusion imaging with *syngo* MR. It addresses medical personnel working in the area of MR tomography.

To optimize the user-friendliness of this brochure, the contents are divided into several areas:

The first part of the brochure focuses on the basics and fundamental knowledge of the subject matter. The second part is directed toward practical applications and describes their use on the basis of sample examinations. The third part provides evaluation possibilities based on the Neuro 3D (diffusion) and Perf MR (perfusion) task cards.

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Overview of diffusion and perfusion imaging

Modern MR diffusion and perfusion imaging techniques have greatly simplified routine examinations. Together, they serve as an effective instrument for functional diagnosis and therapy planning/control, especially for stroke cases.

Application range of diffusion imaging

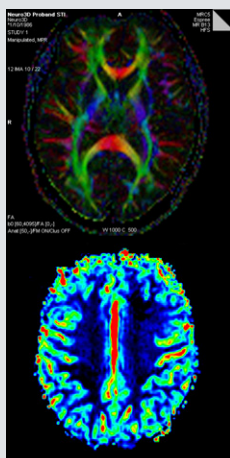
- Differential diagnosis in the early phase of a stroke and evaluation of the progression of a disease
- Visualization of the course of diffusion paths

Application range of perfusion imaging

- Evaluation of the ischemic penumbra to support decisions regarding therapy for a stroke, and validation of treatment strategies
- Preoperative classification and grading of brain tumors

Ischemic penumbra

Zone around the center of the infarction with reduced cerebral blood flow. It comprises functionally damaged but structurally intact cells that are potentially treatable.



*Diffusion map
(FA map)*

*Perfusion map
(relCBF map)*

Diffusion contrast and its application

Functional MR imaging may be used to diagnose and confirm a stroke in a very early phase (just a few hours after the attack).

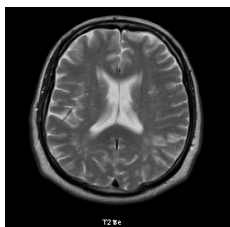
Diffusion

Diffusion is produced by the thermal movement of molecules (Brown's Motion). The diffusion of water in tissue forms the basis of diffusion imaging in MR.

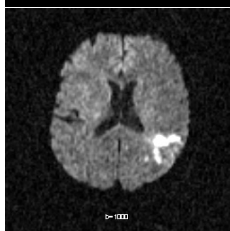
Diffusion contrast

The diffusion contrast in the image represents the strength of the microscopic motion of water molecules. To create diffusion contrast, diffusion-weighted sequences switch special diffusion gradients.

Areas with high diffusion, that is, areas with water molecules of strong mobility show a weaker signal in the diffusion image than the surrounding tissue (are shown in a darker color).



*Anatomic
T2 image
is free of pathology*



*Diffusion images
display areas of
reduced diffusion
(pathogens)*

Areas with reduced diffusion show a stronger signal (brighter) in the diffusion image.

Effect of diffusion weighting on contrast

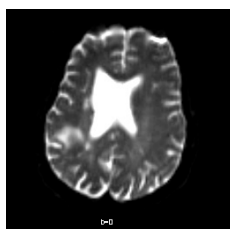
Diffusion imaging displays the microscopic movement of water molecules in the image.

We would now like to examine how we can effect diffusion contrast.

**Diffusion
weighting
factor
(b-value)**

Diffusion weighting b identifies the measurement's sensitivity to diffusion. The b -value determines the strength and duration of the diffusion gradients.

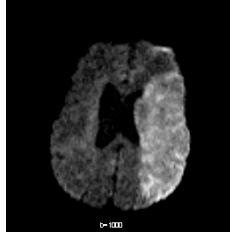
In the range of clinically-relevant b -values (i.e., up to approx. 1,000), the following applies: The greater the b -value, the stronger the diffusion weighting and the higher the contrast in pathogenic regions.



$b=0$
no diffusion
weighting,
low-resolution
T2 comparison
image



$b=500$



$b=1000$

From the diffusion image to the diffusion map

In addition to diffusion contrast, diffusion images also have an overlaying T2 contrast. In regions with long T2, this can simulate reduced diffusion (“T2 Shine-Through”). These portions of the signal can be eliminated by calculating a pure diffusion coefficient.

Diffusion coefficient

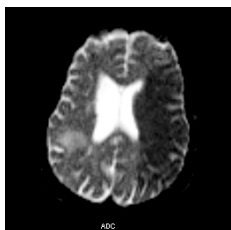
The diffusion coefficient is a measure of the strength (velocity) of diffusion in tissue.

The stronger the diffusion, the greater the diffusion coefficient.

ADC map

Diffusion imaging determines the averaged diffusion coefficient calculated for each voxel. This is called the “Apparent Diffusion Coefficient” (ADC). The ADC map is the pixel-by-pixel display of all diffusion coefficients. It displays the pure diffusion contrast and shows the *strength* of diffusion.

Calculating the ADC requires at least two measurements with different b-values.



ADC map

The diffusion image displays reduced diffusion as hyperintense (brighter pixels); in contrast the ADC map displays it as hypointense (darker pixels).

Eliminating the dependency on orientation (I)

In tissue the diffusion of water is not free, but limited by e.g., tissue boundaries.

Anisotropy

Anisotropy indicates spatially disparate diffusion.

Example:

In the case of commissures, diffusion is severely limited *perpendicular* to the fibers due to the surrounding myelin layer. In contrast, there are few or no limitations *along* the fibers.

Anisotropy may have a strong effect on measurement results. To measure the *diffusion strength* independent of anisotropy, diffusion images of different orientation are measured and averaged.

Trace-weighted image

Geometric averaging of three measurements in different directions results in the trace-weighted image (TraceW map).

Like the ADC map, the TraceW map shows the *strength* of the diffusion and not its orientation.

Orientation and number of measurements

Depending on the alignment and number of averaged orientations, the following are distinguished:

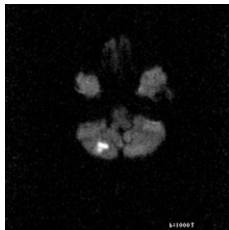
- Orthogonal

Measurements are performed in the orthogonal orientation. It is not possible to display the original images.

- 3-Scan Trace

The measurement directions are *not* oriented orthogonal to one another. The gradient directions are optimized which leads to slight image distortions. For this reason, original images cannot be displayed.

- MDDW (> p.14)



*TraceW map:
averaged diffusion strength,
independent of orientation*

Eliminating the dependency on orientation (II)

Individual ADC map

Individual ADC Maps are generated for *one* orthogonal orientation.

You can select them only for the diffusion mode Slice, Read and Phases.

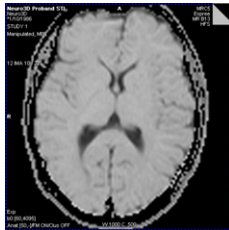
Averaged ADC map

Averaging ADC maps from three different orientations results in the averaged ADC map. It shows the *diffusion strength* independent of orientation.

Determining the averaged ADC map is important primarily for follow-up studies, because a slight change in patient position causes a displaced orientation of tissue structure compared to the diffusion axes.

Exponential map

While the exponential map (Exp map) shows the diffusion strength as well, it is computed differently. (> p.68). When the Exponential map is compared to the ADC map, the contrast will be displayed inversely.



Exponential map

Display of the dependency on orientation

Maps independent of orientation, such as the ADC map and TraceW map, show the *diffusion strength* by eliminating the diffusion orientation.

If you want to display the *diffusion orientation* of the anisotropic diffusion, other diffusions maps are required.

Tensor

An anisotropic magnitude is mathematically expressed as a tensor. A tensor is a vectored magnitude.

DTI

To measure and display the tensor and subsequently the *direction* of anisotropic diffusion, Diffusion Tensor Imaging (DTI) is used.

MDDW

For DTI, measurements in at least six directions of diffusion are performed. For this purpose, the technique of multi-directional diffusion weighting (MDDW) is used. One diffusion-weighted image each is generated per slice position, b-value, and direction of diffusion (for $b > 0$).

The results are original images (if selected), diffusion maps, and the “tensor data set”. The tensor data set includes a wealth of information regarding the diffusion characteristics of the voxels measured.

To minimize the data volume to be saved, original images are saved as mosaic images, Inline-computed maps are saved normally, and tensor data are saved as DICOM NonImages. Diffusion maps, images, and paths can be reconstructed from tensor data. This is only possible with the Neuro 3D task card. (> p.52).

Display of isotropic and anisotropic diffusion

Anisotropy stands for spatially unequal diffusion characteristics. Isotropic diffusion, however, distributes equally in all directions. Both diffusion characteristics can be displayed as graphics.

Displaying isotropy

Isotropic diffusion is shown as a sphere. The distribution of diffusion is the same in all directions.

Displaying anisotropy

Anisotropic diffusion is shown as an ellipsoid, since diffusion is *not* the same in all directions. The form of the ellipsoid depends on the anisotropic degree:

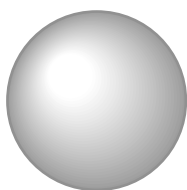
- The more direction-dependent the diffusion, the more elongated the ellipsoid.
- The weaker the anisotropy, the rounder the ellipsoid.

The form of the ellipsoid is determined through the *Eigen values*.

Eigen value

The size of the three eigen values determines the length of the axes of the ellipsoid:

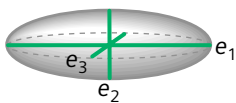
- e_1 : Eigen value 1, longest axis of the ellipsoid
- e_2 : Eigen value 2, medium axis of the ellipsoid
- e_3 : Eigen value 3, shortest axis of the ellipsoid



*Isotropic
diffusion*



*Anisotropic
diffusion*



*Display of
eigen values
(green)*

Diffusion maps with anisotropic diffusion display

To display anisotropic diffusion in diffusion maps, color courses and ellipsoids are used. Much more rarely, grey images are used as well.

While the direction of diffusion is shown voxel-by-voxel in the tensor graphic, all other maps show diffusion across all voxels.

FA map

The FA map (Fractional Anisotropy) displays the anisotropic *degree*.

Color FA maps include information to track diffusion, where and in what direction diffusion is taking place.

The relationship between the course of color and the direction of diffusion is illustrated using an orientation sphere.

Tensor graphic

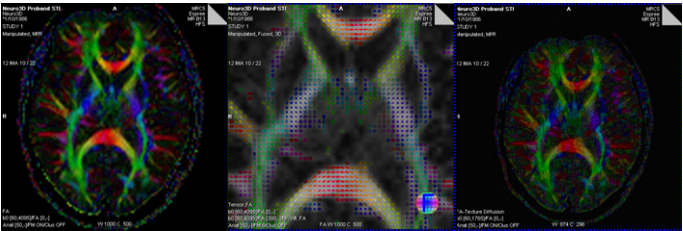
The tensor graphic shows the direction of diffusion voxel-by-voxel. The *degree* and *direction* of diffusion are shown via an ellipsoid. The color of the ellipsoid indicates the direction of diffusion, its size as well as its color intensity the strength of the preferred direction.

Texture diffusion

The texture diffusion image is the prestige to diffusion tractography (> p.58). It shows the course of anisotropic diffusion across the entire slice, resulting in an overview of the diffusion tracks.

Eigen value maps

The eigen value maps (E1, E2, E3) represent the *direction* of the anisotropy. They show the diffusion along the directions of the eigen values.
Example: The E1 map shows the diffusion along the eigen value 1 (as a magnitude).



FA map

Tensor graphic

Texture diffusion

Dynamic perfusion imaging

Perfusion imaging visualizes the diagnostically relevant parameters of tissue perfusion in the image.
syngo MR creates dynamic studies of a contrast medium bolus with direct quantitative evaluation in Inline technology.

Perfusion Perfusion refers to the flow of nutrients to the capillary bed of the tissue to supply the cells.

First Pass First Pass refers to the initial passage of the contrast medium bolus through the perfused brain tissue.

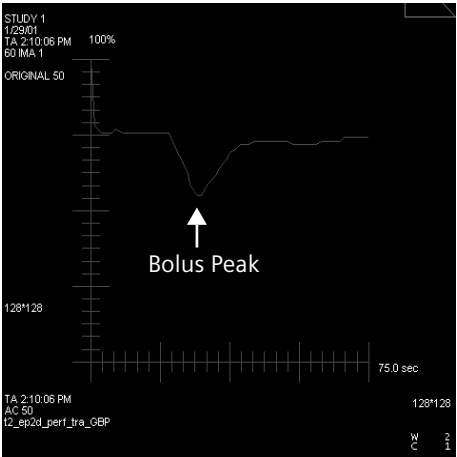
Significant reduction of signal indicates high perfusion, because the bolus perfuses quickly and almost completely.

Global Bolus Plot (GBP) The global bolus plot displays the signal curve created by the bolus along a time axis. It is used to evaluate the quality of the bolus passage.

Arterial input function (AIF)

The AIF is determined from the time plot of the CM concentration in an artery. It used to compute perfusion parameters. The AIF is measured together with the CM concentration in tissue.

The Global Bolus Plot (GBP) displays the time response of the bolus compared to the baseline

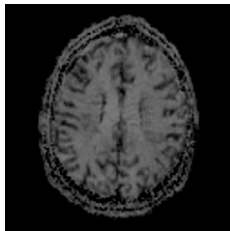


Perfusion cards display pathogenic perfusion

The existing technique for perfusion contrast is based on tissue-specific $T2^*$ differences after administration of contrast medium (dynamic susceptibility). It displays disturbances in perfusion.

PBP map

The “Percentage of Baseline at Peak” (PBP) determines the amount of the bolus peak relative to the baseline. Its pixel-by-pixel display results in a PBP map.

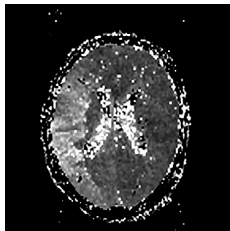


PBP map

Areas where the signal is reduced less by the First Pass of the bolus produce brighter pixels in the PBP map.

TTP map

“Time to Peak” (TTP) is the duration from the arterial injection of contrast medium to the bolus peak. Its pixel-by-pixel display is the TTP map.



TTP map

Areas with delayed First Pass produce brighter pixels in the TTP map.

Blood volume and flow indicate disturbances in perfusion

The blood volume taken up in the capillary bed of the tissue and the corresponding blood flow are the primary characteristics of perfusion. The corresponding parameters (relCBV, relCBF, and relMTT) are calculated using the **Perf MR** task card.

relCBV

The relative cerebral blood volume (relCBV) is the volume taken up by the capillary bed within a voxel, based on the mass of the tissue supplied.

relCBF

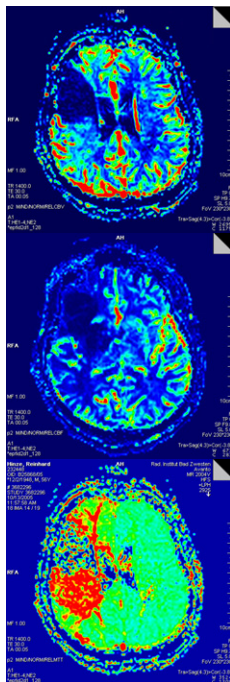
The relative cerebral blood flow (relCBF) is the corresponding amount of flow.

Areas with reduced relCBV and relCBF produce darker pixels in the map.

relMTT

The relative “Mean Transit Time” (relMTT) is the mean duration of the bolus passage through a voxel. Its pixel-by-pixel display results in a relMTT map.

The relMTT is proportional to the ratio of relCBV to relCBF.



relCBV map displays reduced blood volume in the area of the lesion

relCBF map shows reduced blood flow in the area of the lesion

relMTT map shows increased mean transit time in the right half of the brain

Overview—Arterial Spin Labeling (ASL)

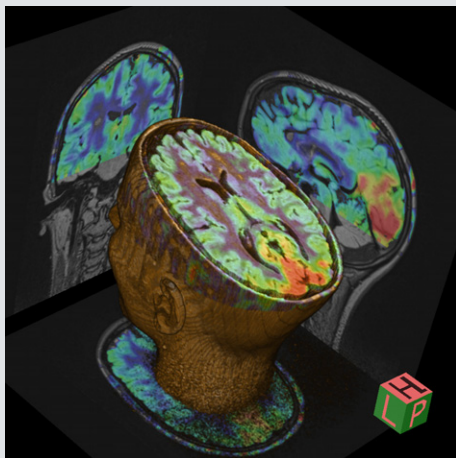
Arterial Spin Labeling (ASL) is an MR technique for non-invasive perfusion determination without administering contrast medium. It uses the water in arterial blood as endogenous contrast medium. By evaluating the relative cerebral blood flow (relCBF), this technique enables insight into perfusion and the functional physiology of the brain.

Applications	<p>Its high spatial resolution makes ASL suitable for:</p> <ul style="list-style-type: none">• Evaluating tumors• Pediatric imaging• Stroke• Degenerative diseases (Dementia, Morbus Alzheimer)• Epilepsy• Functional examinations of the brain based on functional changes of relCBF
---------------------	--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

Implementation

syngo ASL uses the parallel imaging of Tim (Total imaging matrix) and the 12-channel head matrix coil. *syngo* ASL is compatible with GRAPPA.

The integration of the 3-D PACE motion correction makes this advanced application even more robust and increases diagnostic safety.



Principle of Arterial Spin Labeling

Until now, brain perfusion studies in MRT were mostly taken with contrast medium administration. In principle, ASL functions similarly, however it is *completely non-invasive*: It is not required to inject contrast medium.

Labeling

ASL is a technique for labeling the blood bolus: using an inversion pulse, the arterial blood water is magnetically labeled below the region to be examined.

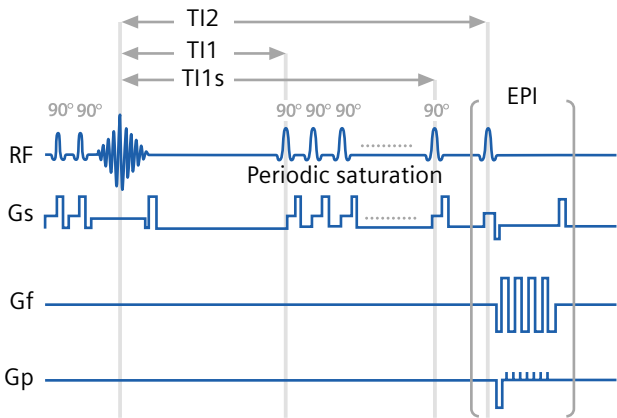
- Tag image** After a certain transit time, the labeled blood has flown into the region of interest where it distributed itself. There the labeled blood spins reduce the tissue magnetization present. If an image is acquired (the tag image), the MR signal is slightly reduced.
- Control image** Subsequently, a control image without blood labeling is measured. The tag images and control images are measured alternately until the planned series is acquired.

Sequence and timing

**PICORE
labeling
scheme**

The application package uses the technique of Pulsed Arterial Spin Labeling (PASL) for perfusion weighting.

The arterial spins are labeled in a thick inversion slab (10 cm) which lies below the image slices ("PICORE" scheme). First, two pulses are used to presaturate the slice group (TR 25 ms) to minimize off-resonance effects. Subsequently, the inversion pulse is applied, and the labeled blood flows into the image slices.



**Inversion
time 1**

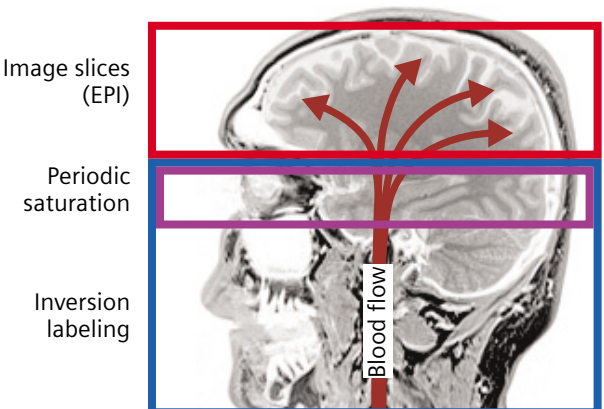
After inversion time T_{I1} , the periodic saturation pulses are radiated into a thin slice at the upper end of the inversion slab (Q2TIPS method) to truncate the bolus and give it a defined length (saturation slab 20 mm, TR 20 ms)

**Saturation
stop time**

Stop time T_{I1s} determines the end of the saturation pulses.

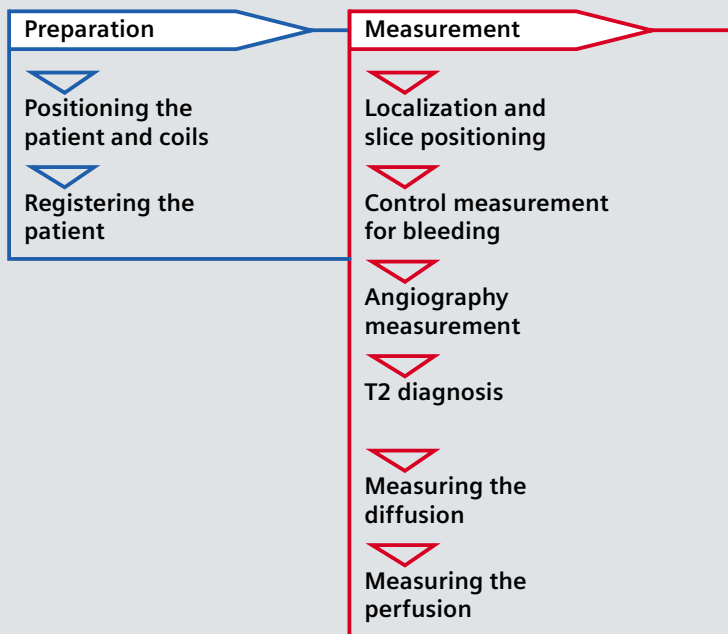
**Inversion
time 2**

During the entire inversion time T_{I2} , the bolus flows into the image slices where it creates a slight decrease in signal. After time T_{I2} , the image is acquired (single or multi-slice EPI)



Diffusion and perfusion imaging procedure

You want to obtain both structural and functional information regarding the pathophysiology of a brain disease. Perform an MR examination by combining anatomical MR imaging with MR angiography as well as diffusion and perfusion imaging.



PROTOCOL

Localizer

T1 TSE

T2 TSE

ep2d_diff

ep2d_perf

Post-processing

▼
Evaluating diffusion
measurements > p.52

▼
Evaluating perfusion
measurements > p.66

TIP

Use an angio/head
protocol (MRA-ToF)
as the protocol for the
angiography measure-
ment.

Measuring the diffusion: Selecting the diffusion mode

**T2 diagnosis
completed/
slice position
transferred**

You want to evaluate diffusion in the brain. In this case, measure transverse slices of the entire head. You set the diffusion-specific parameter on the **Diff** parameter card.

b-value	s/mm ²
b-value[1]	0
b-value[2]	500
b-value[3]	1000

Diffusion mode: 3 Scan Trace

Diff. weightings: 3

Diff. weighted images: ☒

Trace weighted images: ☒

Average ADC maps: ☒

Individual ADC maps: ☒

FA maps: ☒

Tensor: ☒

Noise level: 40

Diff. directions: 6

Example: 3-Scan Trace diffusion mode

Diffusion mode. The diffusion mode describes the measurement procedure. In the following, we are focusing on diffusion modes "3-Scan Trace" and "MDDW".

3-Scan Trace diffusion mode

The measurements are performed in three random directions. 3 scans are required per image. Since diffusion-weighted images are slightly distorted, they are not output.

Original images *cannot* be saved. Trace-weighted images and averaged ADC maps are stored by default.

Diffusion mode MDDW

Measurements are performed in at least 6 directions, a maximum of 256 directions is possible. For $b\text{-value} = 0$, a diffusion-weighted image is generated for each slice position. When the $b\text{-value}$ is > 0 , an image is generated for the $b\text{-value}$ and each diffusion orientation. These images can be saved as original images in the mosaic format. TraceW maps and averaged ADC maps are stored by default. In addition, original images, FA maps and the tensor can be saved.

PROTOCOL

Localizer

T1 TSE

T2 TSE

ep2d_diff

ep2d_perf

Measuring the diffusion: Setting the parameters

Select the requested diffusion mode (3-Scan Trace or MDDW).

Establish the b-value (e.g., 0, 500, 1000) for each diffusion weighting.

You can measure a maximum of 16 different b-values. The maximum value that can be set is 10.000. Higher b-values extend TE.

In the 3-Scan Trace mode:

Select Trace weighted images and Average ADC maps.

The number of **Diffusion directions = 3** is set automatically.

Trace-weighted images and averaged ADC maps are calculated using the Inline technique.

In the MDDW mode:

Determine the number of Diffusion directions.

Select FA maps (Fractional Anisotropy) and the Tensor.

The **Tensor** parameter determines whether the diffusion tensor data are stored to the database. It is therefore possible to evaluate diffusion in the Neuro 3D task card.

Trace-weighted images and Average ADC maps are automatically selected as result images.

Noise level. Use Noise level to establish the intensity at which pixels are included for the calculation of the ADC value.

Start the measurement.
(Apply)

PROTOCOL

Localizer

T1 TSE

T2 TSE

ep2d_diff

ep2d_perf

TIP

It is also possible to retroactively (offline) compute tensor data from diffusion images.

In the **Patient Browser**: select a series with diffusion images.



Start computation of the tensor data.

Measuring the diffusion: Result images

In the 3-Scan Trace mode:

- Trace-weighted images:
per slice position and
b-value > 0
- Average ADC maps:
per slice position

In the MDDW mode:

- Original images in the mosaic format
($> p.35$)
- Trace-weighted images
(computed Inline)
- Average ADC maps
(computed Inline)
- FA maps
(computed Inline)
- Tensor

Measurement

Measuring the
diffusion

PROTOCOL

Localizer

T1 TSE

T2 TSE

ep2d_diff

ep2d_perf

TIP

3-Scan Trace:

ADC maps can be
calculated subsequently

(**Evaluation >**

Dynamic Analysis >

ADC).

Measuring the perfusion

Diffusion measurement has been completed

As a supplement to the diffusion imaging, you want to determine the perfusion parameters in the region under examination. You perform a perfusion measurement with contrast medium administration and 50 measurement repetitions. Use the Inline technology to compute the GBP, PBP and TTP maps .

Transfer the slice position from the T2 TSE protocol.

On the Perfusion parameter card:

Set the number of measurement repetitions (in this case: 50 measurements).

Establish the number of initial measurements that will not be used for the evaluation.

(Starting ignore measurements)

Select GBP, PBP and TTP.

Measurement



Measuring the perfusion

**Start the measurement.
(Apply)**

While the measurement is running, administer the contrast medium intravenously as a bolus.

PROTOCOL

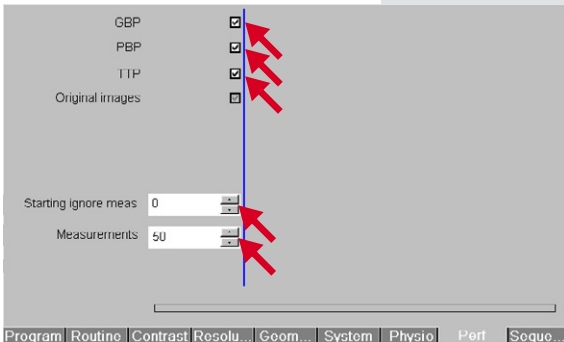
Localizer

T1 TSE

T2 TSE

ep2d_diff

ep2d_perf



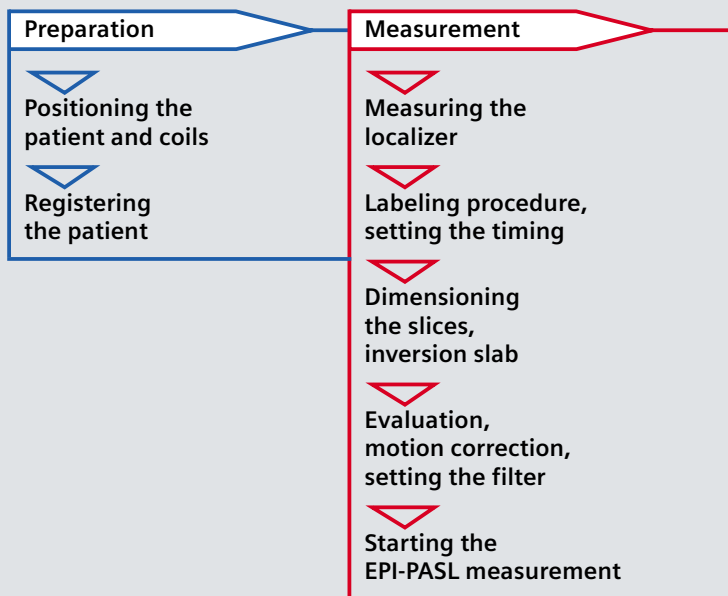
Original images are generated per slice position (1 image/measurement) as well as a GBP, a PBP and a TTP map are computed.

TIP

For more precise perfusion evaluation: additionally calculate relCBV, relCBF, and relMTT maps (in the **Perf MR** application card).

Examination procedure with ASL— overview

For perfusion measurements with ASL, you use the motion correction under BOLD. You are able to evaluate the image results as usual or you can use the extended functions of BOLD and Neuro 3D.





Post-processing

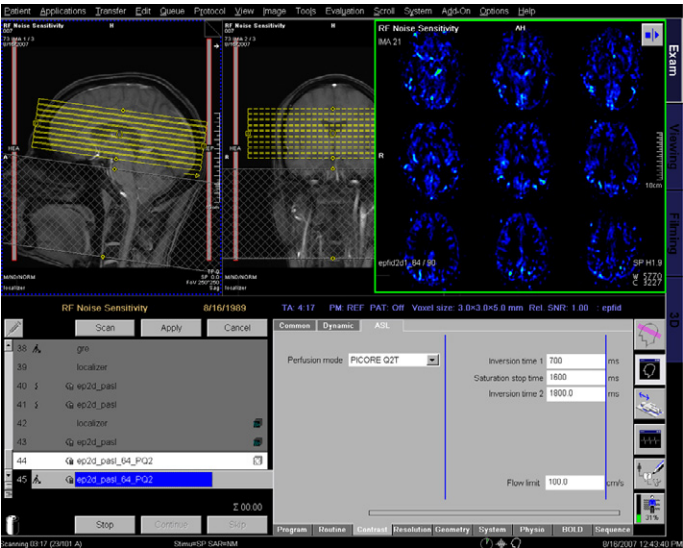
▼
Evaluating the
perfusion images

▼
Generating t-maps
(optional)

▼
Processing
(BOLD, Neuro 3D)

Measuring ASL perfusion

Establish the measurement parameters in the **Exam** task card. During the measurement, the Inline Display shows the perfusion-weighted images that have been generated.



Measurement sequence

The first image volume is measured prior to the preparation scans (M0 volume).

Even numbered/uneven numbered volumes include tag images or control images. These are subtracted from one another, e.g., 3–2, 5–4, and the result is shown in the Inline Display.

Setting parameters

In the **Contrast/ASL** parameter card you select the labeling/timing parameters.

Perfusion mode. PICORE Q2T (fixed)

Inversion time 1 (TI1). Determines the bolus length; start time of the periodic saturation pulses.

Keep the value *below* the actual duration of the bolus. Typical value: 700 ms

Saturation stop time (TI1s).

End of periodic saturation pulses. If equal TI1, saturation is switched off. Typical values: 1200–1600 ms.

The screenshot shows the 'ASL' tab of a software interface. It contains several input fields and a timeline. The 'Perfusion mode' is set to 'PICORE Q2T'. The 'Inversion time 1' is 700 ms, 'Saturation stop time' is 1600 ms, and 'Inversion time 2' is 1800.0 ms. The 'Flow limit' is 100.0 cm/s. At the bottom, there is a timeline for 'Inversion time 1' ranging from 25 to 1600 ms, with a green bar indicating the duration from 25 to 700 ms. The bottom navigation bar includes tabs for Program, Routine, Contrast, Resolution, Geometry, System, BOLD, and Sequence.

Parameter	Value	Unit
Perfusion mode	PICORE Q2T	
Inversion time 1	700	ms
Saturation stop time	1600	ms
Inversion time 2	1800.0	ms
Flow limit	100.0	cm/s

Timeline for Inversion time 1: 25 to 1600 ms. Green bar from 25 to 700 ms.

Labeling procedure,
setting the timing

Inversion time 2 (TI2). Overall time between inversion pulse and excitation of the first slice. The ASL signal increases with lower TI2. However, excessive image intensities are created in the arterial voxels as well.

Flow limit [cm/s]. Strength of the bipolar gradient between excitation and readout. Is used to limit the flow to attenuate the signal from large arteries. TE is increased. At the maximum value 100 cm/s (standard setting), the gradient is switched off.

PROTOCOL

Localizer
ep2d_pasl

TIP

TI2 should be long enough to transport the bolus into the image slices, that is, it should be equal or larger than the arterial transit time. Typical values: 1400–1800 ms.

TIP

With shorter TI2 values (1200–1500 ms), lower **flow limits** of 1–10 cm/s are required.

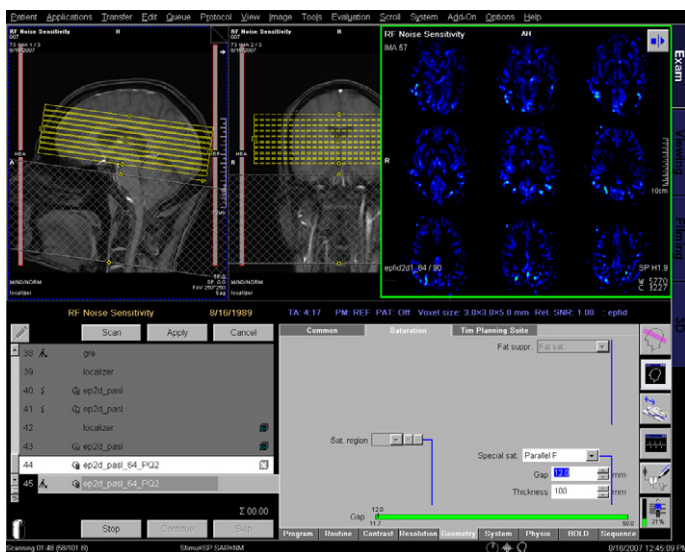
Planning slabs and determining evaluations

You plan the slabs in the **Geometry** parameter card. Evaluation and motion correction is established in the **BOLD** parameter card.

Dimensioning the labeling slab

The graphical slice display on the localizer images shows the inversion slab of the PASL sequence (the saturation slabs are not shown).

Here you are able to select **gap** and **thickness**. As an alternative, you can use the **Special sat.** under the **Geometry**/**Saturation** parameter card.



Inversion slab,
setting the evaluation

Setting the evaluation

- **GLM Statistics**: Typically not used (OFF), If yes, you also have to define a paradigm.
- **Motion correction**: 3-D PACE prospective motion correction.
- **Interpolation**: Select the type of interpolation (3D-K-space).
- **Spatial filter**: Smooths the images with a spatial low-pass filter. Typical filter setting for ASL is 2.0.

TIP

Optimizing the ASL signal:
Select a minimal **gap** to the slab.

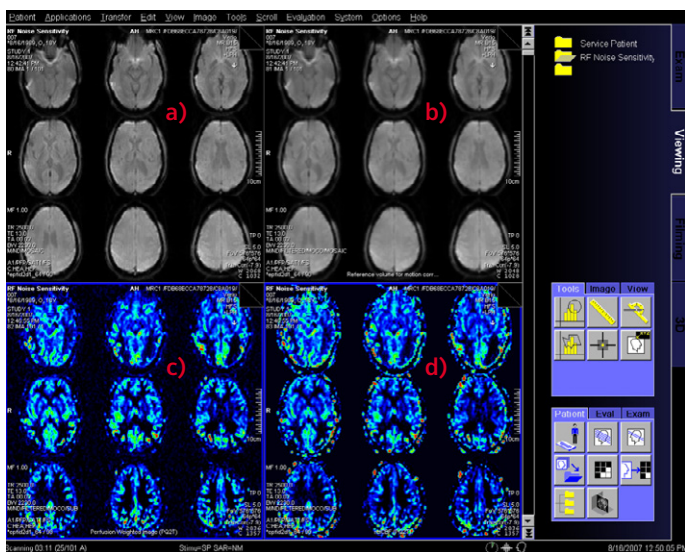
GLM Statistics <input type="checkbox"/>		Motion correction <input checked="" type="checkbox"/>	
Dynamic t-maps <input type="checkbox"/>		Interpolation 3D-K-space ▾	
Starting ignore meas 1 ▾		Spatial filter <input checked="" type="checkbox"/>	
Ignore after transition 0 ▾		Filter setting 2.0 ▾	
Model transition states <input type="checkbox"/>		Measurements 101 ▾	
Temp. highpass filter <input checked="" type="checkbox"/>		Delay in TR 0 ▾ ms	
Threshold 4.00 ▾		Multiple series Off ▾	
Paradigm size 4 ▾			
Meas[1]	Baseline ▲		
Meas[2]	Active ▼		

Program Routine Contrast Resolution Geometry System Physio BOLD Sequence

Evaluating ASL data

For further processing, the image results obtained are displayed in the **Viewing** task card.

- a) Original EPI image series
- b) Motion-corrected EPI image series
- c) Perfusion-weighted images (PWI)
- d) relCBF images



GLM Statistics

The **GLM statistics** under BOLD enable further post-processing on the original or motion-corrected EPI series.

A perfusion-weighted map can be computed as a t-map, similar to the BOLD evaluation.

You are able to use the following parameter settings:

- **Starting ignore meas.:** 1
- **Model transition states:** OFF
- **Paradigm size:** 4
- **Paradigm:** Baseline, Active, Baseline, Active

The resulting t-map corresponds to the perfusion-weighted map. Further processing is possible with the **BOLD** and **Neuro 3D** task cards.

TIP

ASL evaluation with **GLM statistics** can be performed retroactively (Off-line) with the **BOLD** card.

Task card Neuro 3D

The optional Neuro 3D task card allows you to evaluate diffusion measurements as well as generate and store diffusion images or maps. In addition, you can superpose diffusion images with functional images from BOLD measurements of the same study.

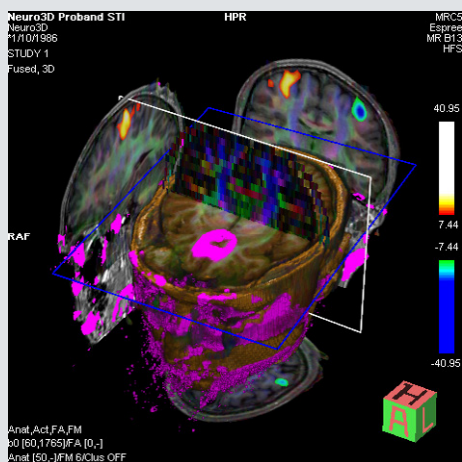
Neuro 3D provides different work modes depending on the data volume and the evaluation target planned.

Diffusion mode

In the diffusion mode, different diffusion maps can be computed from the diffusion data (= tensor) and displayed synchronously (> p.54).

Fusion mode

In the Fusion mode, diffusion data can be displayed in connection with anatomical data (2D/3D) and superposed with functional data (> p.56).



*Fusion mode:
 3D view with diffusion data*

Neuro 3D: Diffusion mode

Neuro 3D displays diffusion maps that are computed from tensor data.

Standard view In the standard view, Neuro 3D shows the following displays:

- FA
- ADC
- TraceW
- b0

Color coded display With colored diffusion maps, the voxel color is derived from the display of the preferred diffusion direction of the voxels on a colored sphere:

- Red: right – left
- Blue: head - foot
- Green: anterior – posterior

Tensor graphic In addition to other display types, Neuro 3D also offers the possibility of displaying tensor graphics. The direction of diffusion is shown voxel-by-voxel. In addition to pure tensor graphics, two combined display types can be selected as well:

- Tensor graphic – FA map
- Tensor graphic – Anatomy

Synchronous scrolling

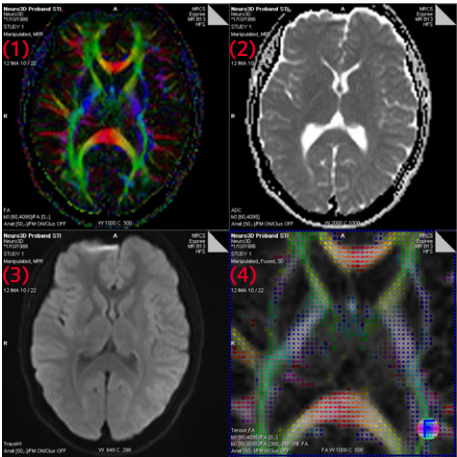
The displays in the image segments are linked. When scrolling in an image segment, the slices in other image segments are automatically scrolled as well.

Variable thresholds

The display of undesirable diffusion values can be suppressed by adjusting the threshold values.

Diffusion mode:

- (1) FA map
- (2) ADC map
- (3) TraceW map
- (4) Tensor graphic



Neuro 3D: Fusion mode

The fusion mode provides the following displays.

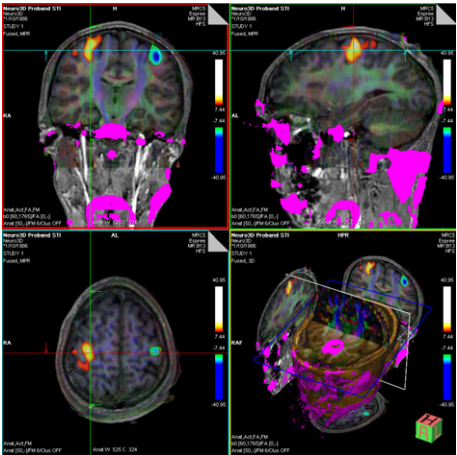
Displays in general

- Overlays in MPR display (2D):
direct overlay on the cut
- MPR series: Series of parallel MPR thick slice images that can be reconstructed in three orthogonal directions.
- 3D view: Overlay of the diffusion data directly on the surface and as floating MPR planes.

Displaying functional data

Additional activation maps can be loaded in the fusion mode which were measured during a BOLD experiment of the same study. Diffusion data and active areas are overlaid and displayed together in 2D as well as in 3D.

Fusion mode



Neuro 3D: Diffusion tractography (I)

Diffusion tractography computes and graphically displays anisotropic diffusion as diffusion tracts.

Prerequisites

- Tensor data
- Highest resolution 3D data set
- Fusion mode, 3D view

Quicktrack

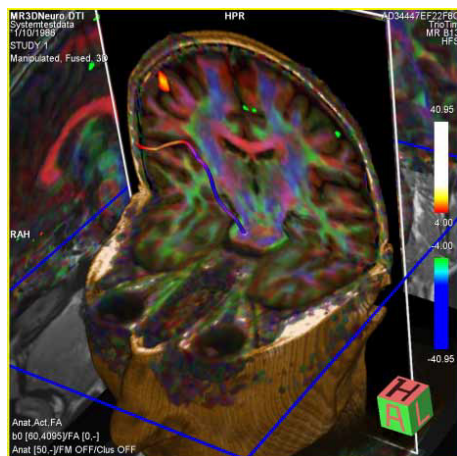
For fast overview, tract computation per voxel.

Press and hold the Shift key.

Move the mouse pointer across the view.

The results are shown automatically in step with the movements of the mouse.

*3D view with
Quicktrack*



Seed points

To compute the tract in selected areas, either set a seed point as the start area or two seed points as the start and target area. Seed points can consist of one or several voxel(s).

Creating seed points:

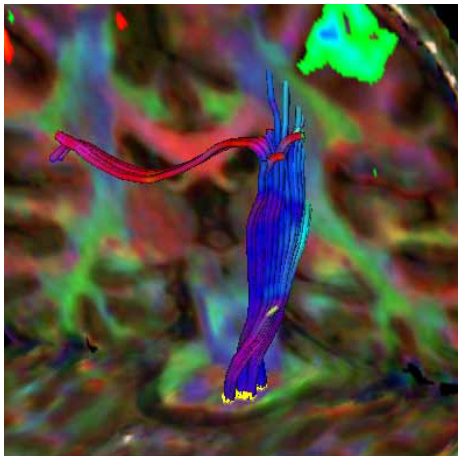
Press and hold the Ctrl key.

- Click the requested voxel or
- Pull the mouse across the requested area

Starting calculations:

Select **Start Tractography** in the context menu for the seed point.

*Tractography
with one seed
point*

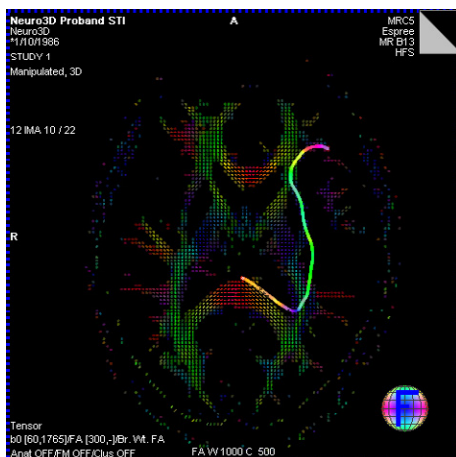


Neuro 3D: Diffusion tractography (II)

Floating MPRs Using floating MPRs, you can compute diffusion tracts across different areas. In this case, set two seed points in two different MPR views.

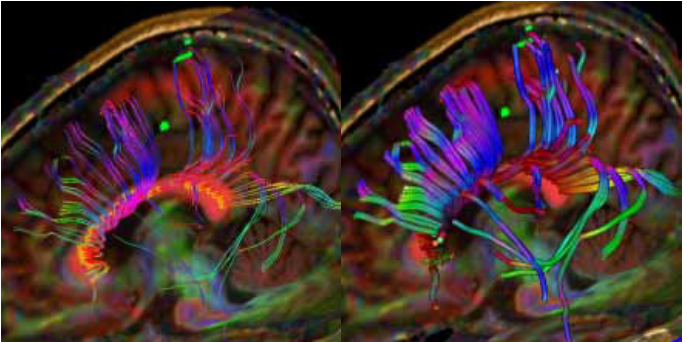
Tensor graphic You are also able to display diffusion tracks via the pixel lens (no computation) in the tensor graphics (diffusion mode). Select **Tools > Pixel Lens**. Move the mouse pointer to the requested pixel.

*Diffusion track
on tensor
graphic*



Setting tractography

You can set the type of display for the tract computation. Select the **Tools > Diffusion Tracts Properties** dialog window.



*Example: Changing the type of display.
Lines (left) and tubes (right)*

Saving seed points/tracts

Tractography data can be stored as:

- NonImage series
- XML file
- 3D series (e.g., for further processing with the navigation software)

Neuro 3D: Evaluation

Neuro 3D provides graphic tools and a diffusion table for evaluation tasks

Graphic tools ROIs and VOIs as well as individual pixels can be evaluated.

Diffusion table The following values are shown per image stack for the selected regions or voxels of interest:

- Mean
Mean pixel value
- Min
Minimal pixel value
- Max
Maximal pixel value
- SDev
Standard deviation
- Size
Size in voxel

ID	ADC		FA		TraceW		Anet	
	Mean	SDev	Mean	SDev	Mean	SDev	Mean	SDev
	Size / Min / Max		Size / Min / Max		Size / Min / Max		Size / Min / Max	
1	853.7	218.4	269.2	149.3	167.4	84.3	257.1	102.5
	1234 / 61 / 1868		1234 / 27 / 1000		1396 / 5 / 459		29542 / 9 / 788	
2	834.1	148.0	268.8	139.7	185.6	57.3	311.3	81.5
	349 / 262 / 1671		349 / 53 / 691		349 / 101 / 408		7742 / 48 / 427	
3	1255.6	531.9	268.5	174.5	154.7	69.6	294.4	84.2
	270 / 54 / 2569		270 / 3 / 1000		270 / 59 / 419		896 / 60 / 413	
4	961.0	0.0	602.0	0.0	211.0	0.0	350.0	0.0
	1 / 961 / 961		1 / 602 / 602		1 / 211 / 211		1 / 350 / 350	

Diffusion table

Neuro 3D: Storage and documentation

Neuro 3D provides the possibility of saving individual images or image series. This allows you to display diffusion images outside of Neuro 3D.

syngo MR includes functions that store the results from Neuro 3D in the database as well as document them on film. This includes:

- Storing individual images grouped according to image type in the database
- Saving images to the database with selectable storage options
- Storing diffusion data as image series
- Exporting images as bit maps into the file system
- Filming images

The images may also be printed in color by using the appropriate printer.

The ability to export result images as bit map files allows them to be used in other applications, such as text or presentation programs.

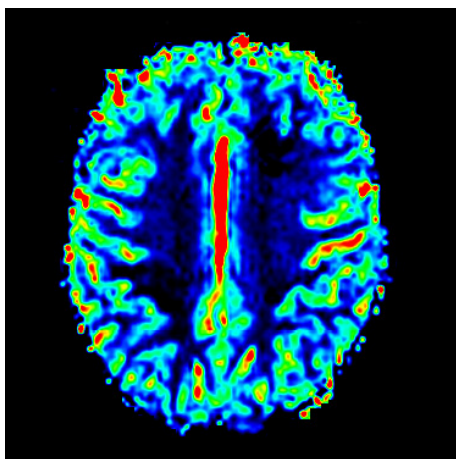
For detailed information on how to handle and run Neuro 3D, see the *Neuro 3D Operator Manual*.

Task card Perf MR

The Perf MR task card lets you evaluate perfusion measurements offline. The computation of different perfusion maps enables detailed evaluations of the perfusion measured.

Perfusion map	<p>You are able to compute the following parameters in the task card:</p> <ul style="list-style-type: none">• relCBV• relCBF• TTP• relMTT
AIF	<p>When computing relCBF and relMTT, the arterial input function (AIF) is included and needs to be defined prior to the computation.</p>
Color display	<p>A color palette is used to display the parameters in color. The color palette can be set differently for the various maps. The images can be saved together with the color palette.</p>

We recommend that only specialists with sufficient experience in MR perfusion diagnostics interpret the parameter maps (relCBV, relCBF, relMTT) obtained.



Diffusion map relCBF

Detailed information regarding the application and the workflow of Perf MR is included in the *syngo MR Operator Manual*.

Diffusion cards (I)

In what follows you will find the formulas for the previously discussed (> p. 18) as well as additional diffusion cards.

ADC map

$$\langle D \rangle = \frac{e_1 + e_2 + e_3}{3}$$

Exp map

$$\text{EXP Map} = \exp(-b\langle D \rangle)$$

TraceW map

$$\text{TW Map} = S_0 \exp(-b\langle D \rangle)$$

FA map

The FA map shows the ratio of the anisotropic diffusion to the medium overall diffusion.

$$\text{FA} = \sqrt{\frac{1}{2}} \left(\frac{\sqrt{(e_1 - e_2)^2 + (e_2 - e_3)^2 + (e_3 - e_1)^2}}{\sqrt{e_1^2 + e_2^2 + e_3^2}} \right)$$

RA map

Like the FA map, the RA map (Relative Anisotropy) displays the anisotropic *degree*. It shows the relationship between anisotropic diffusion and isotropic diffusion.

$$RA = \frac{\sqrt{(e_1 - e_2)^2 + (e_2 - e_3)^2 + (e_3 - e_1)^2}}{e_1 + e_2 + e_3}$$

VR map

The VR map (Volume Ratio) displays the anisotropic *degree* as well. It shows the relationship of the ellipsoid volume to the volume of a sphere having the ratio of a medium diffusion.

$$VR = \frac{e_1 e_2 e_3}{\langle e \rangle^3}$$

Diffusion cards (II)

Linear, planar and spherical map

Linear, planar and spherical maps show the *spatial distribution* of the diffusion.

- Linear map

Shows diffusion taking place in (mostly) one direction only (the ellipsoid is a prolate spheroid)

$$c_l = \frac{e_1 - e_2}{e_1 + e_2 + e_3}$$

- Planar map

Shows diffusion taking place in (mostly) two directions (disk-shaped ellipsoid)

$$c_p = \frac{2(e_2 - e_3)}{e_1 + e_2 + e_3}$$

- Spherical map

Shows diffusion that is (almost) isotropic (sphere-shaped ellipsoid)

$$c_s = \frac{3e_3}{e_1 + e_2 + e_3}$$

Mode

The Mode map displays the form of the diffusion tensor. It connects information about the average diffusion coefficient (ADC), the degree of anisotropy (FA), and the orientation of anisotropy.

$$\text{Mode} = \frac{\sqrt{2\mu_2}}{\sqrt{\mu_1^3}}$$

$$\mu_1 = \frac{(e_1 - \langle D \rangle)^2 + (e_2 - \langle D \rangle)^2 + (e_3 - \langle D \rangle)^2}{3}$$

$$\mu_2 = \frac{(e_1 - \langle D \rangle)^3 + (e_2 - \langle D \rangle)^3 + (e_3 - \langle D \rangle)^3}{3}$$

Diffusion cards (III)

GA map

The GA map (Geodesic Anisotropy) shows the differences in anisotropy by measuring anisotropy similar to "Fractional Anisotropy". In this case, the "geodesic" distance between tensor and the closest isotropic diffusion tensor is measured. (In mathematics, the term "geodesic" is used for theoretically the shortest connection between two points on a curved surface.)

$$GA = \sqrt{(\log(e_1) - \langle \log(e) \rangle)^2 + (\log(e_2) - \langle \log(e) \rangle)^2 + (\log(e_3) - \langle \log(e) \rangle)^2}$$

$$\langle \log(e) \rangle = \frac{\log(e_1) + \log(e_2) + \log(e_3)}{3}$$

Diffusion gradient directions

The following tables provide you with the diffusion gradient directions used for the 6, 12, and 20 diffusion directions that are used during a MDDW measurement.

MDDW 6 directions	Direction vectors in the magnet coordinate system
1	(1.0, 0.0, 1.0)
2	(-1.0, 0.0, 1.0)
3	(0.0, 1.0, 1.0)
4	(0.0, 1.0, -1.0)
5	(1.0, 1.0, 0.0)
6	(-1.0, 1.0, 0.0)

MDDW 12 directions	Direction vectors in the magnet coordinate system
1	(1.000000, 0.414250, -0.414250)
2	(1.000000, -0.414250, -0.414250)
3	(1.000000, -0.414250, 0.414250)
4	(1.000000, 0.414250, 0.414250)
5	(0.414250, 0.414250, 1.000000)
6	(0.414250, 1.000000, 0.414250)
7	(0.414250, 1.000000, -0.414250)
8	(0.414250, 0.414250, -1.000000)
9	(0.414250, -0.414250, -1.000000)
10	(0.414250, -1.000000, -0.414250)
11	(0.414250, -1.000000, 0.414250)
12	(0.414250, -0.414250, 1.000000)

MDDW 20 directions	Direction vectors in the magnet coordinate system
1	(1.000000, 0.000000, 0.000000)
2	(0.000000, 1.000000, 0.000000)
3	(-0.031984, 0.799591, 0.599693)
4	(0.856706, 0.493831, -0.148949)
5	(0.834429, 0.309159, 0.456234)
6	(0.834429, -0.309159, 0.456234)
7	(0.856706, -0.493831, -0.148949)
8	(0.822228, 0.000000, -0.569158)
9	(0.550834, 0.425872, -0.717784)
10	(0.468173, 0.834308, -0.291108)
11	(0.515933, 0.808894, 0.281963)
12	(0.391890, 0.515855, 0.761785)
13	(0.478151, 0.000000, 0.878278)
14	(0.391890, -0.515855, 0.761785)
15	(0.515933, -0.808894, 0.281963)
16	(0.468173, -0.834308, -0.291108)
17	(0.550834, -0.425872, -0.717784)
18	(0.111012, -0.264029, -0.958105)
19	(0.111012, 0.264029, -0.958105)
20	(0.031984, 0.799591, -0.599693)

Direction vectors for additional sets of directions can be obtained through the Application Hotline.

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