

User's Guide

# PMOD Brain Database Tool (PBRAINDB)

Version 3.3



PMOD Technologies



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# PMOD Brain Database Tool Introduction

The PMOD Brain Database Tool (short Brain DB tool) is a general tool for establishing the normal pattern of a certain type of brain images, and to compare patient images against it.

The process of constructing the normal pattern - named the *Normal Database* or *Brain Norm* - in principle consists of the following steps:

- ▶ The acquisition of images from a set of normal controls. Preferably the same acquisition and image reconstruction protocols should be used as in the patient studies.
- ▶ The stereotactic normalization of the control images, so that the anatomy of the normalized images is comparable across the controls.
- ▶ The scaling of the pixel values in the normalized images relative to an internal reference. The resulting normalized values allow pooling of the data.
- ▶ The analysis of the values across the control collective in each pixel of the stereotactic anatomy. Hereby the normal values and their deviation across the set of normal data is established in each pixel.

During the analysis, patient images are normalized and scaled in the same way as the control images, and the resulting pixel values compared with the normal values. This process results in a map showing the differences between the patient images and the normal pattern, expressed as a z-score value. The z-score map can be investigated in a multitude of ways including fusion with the patient images and 3D rendering (separate option).

The Brain DB Tool is started using the



button on the PMOD ToolBox. It pops up a new window which contains four different pages, representing the different phases of data processing:

- 1) Loading of the patient data.
- 2) Stereotactic normalization of the patient images to the template of the database.
- 3) Quality control of the normalization result.
- 4) Comparison with the database pattern and display of the difference (z-score) maps.

The elements on the different pages are explained in the Patient Data Analysis *section* (on page 12). The Normal Database is created and extended with new control series in a dedicated **Create Norm / Edit Norm tool** (on page 3).

# Normal Database Creation

The creation of a Normal Database requires the availability of a number of control images. These images must beforehand be saved in a PMOD database, where they are in DICOM format and include information such as the age or sex of the controls, and the anatomical image orientation.

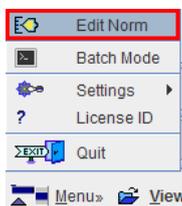
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**Note:** Controls can always be added to an existing database to extend the statistical power of the analysis. To this end, the new control images are normalized and scaled using the same approach as when building the database initially, followed by a new calculation of the pixel distribution of the extended control set.

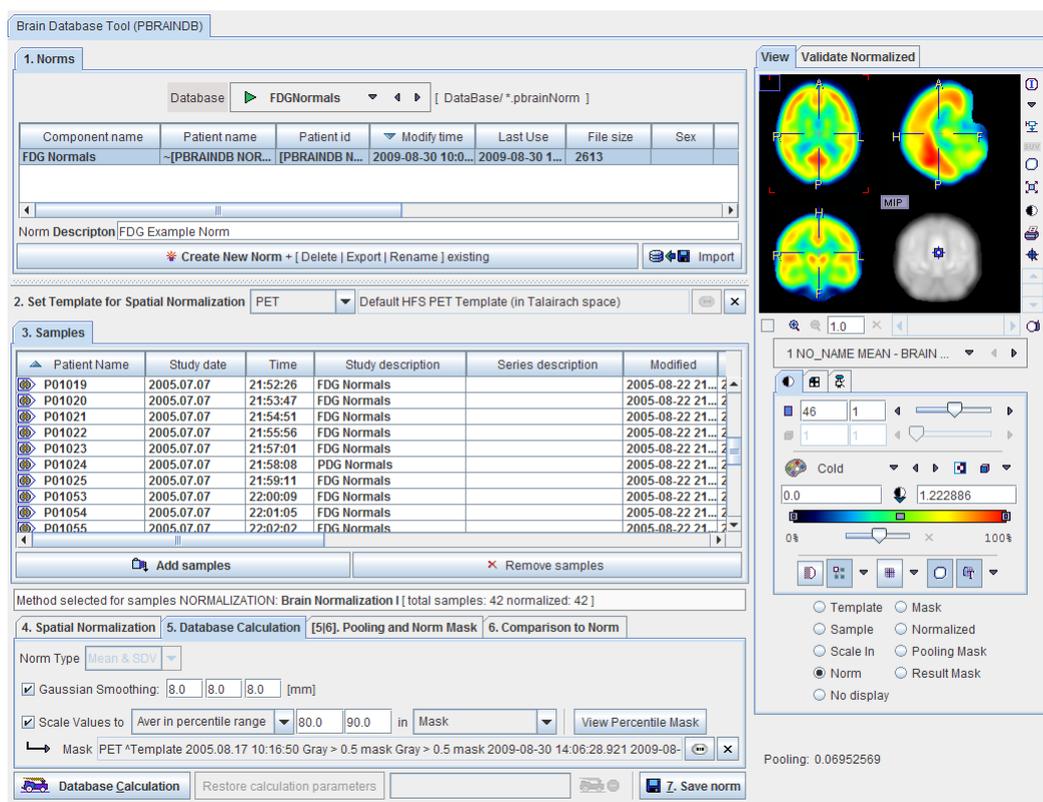
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## Brain Norm Editor

The tool for Brain DB creation and maintenance can be started using the **Edit Norm** entry in the **Menu**.



The dialog window illustrated below appears.



The image viewer to the right allows displaying the different data sets involved in the Normal Database calculation. From top to bottom:

- Template Mask** Show the template of stereotactic normalization, or the normalization mask.
- Sample Normalized** Show the original images of the currently selected control sample, or the images after spatial normalization.
- Scale In Pooling Mask** Show the mask used for finding the reference value for scaling, or the mask used in the pooling operation of the standard deviations.
- Norm** Show the result of the database calculation. The **MEAN**, the **STDV** and the **Pooled STDV** image are available here. Note the selection below the image to switch the images.
  - 1 PET ^Template ...
  - 1 PET ^Template FDG Template MEAN - BRAIN NORM
  - 2 PET ^Template FDG Template STDV - BRAIN NORM
  - 3 PET ^Template FDG Template STDV POOL - BRAIN NORM
- Result Mask** Mask outside which the database comparison is cleared.

The different elements are explained in detail in the following sections.

## Brain Norm Creation

The principle in the Brain DB editor is to work from top to bottom following the numbering of the elements.

### Steps for creating a new Brain DB (or Brain Norm)

#### 1. Create empty Brain Norm

Activate the **Create new norm** button.

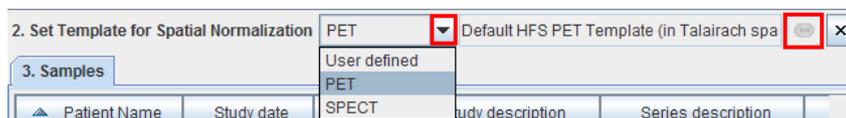
In the appearing dialog select the PMOD database in which the Brain DB definition will be saved, then enter a DB name,



and activate the **Create new Brain Norm** entry button.

#### 2. Specify Normalization Template

Define the template used during the stereotactic localization.



The list selection allows switching between standard MNI templates for **PET** and **SPECT**, or alternatively a **User defined** template. With **User defined** please use the button to select the template in a database (files outside databases are not supported).

The defined template will serve as the reference image (representing the stereotactic anatomy) during the spatial normalization of all control and patient images. For new tracers, the user may first have to generate a suitable template outside the brain database tool.

#### 3. Add Control Samples

The button **Add samples** brings up a database selection dialog. In this dialog bring one or more image sets of normal controls into the **Selected for loading** area and quit with the **Set series** button. The samples are listed in the **Samples** section

3. Samples					
▲ Patient Name	Study date	Time	Study description	Series description	Mod
P01018	2005.07.07	21:51:06	FDG Normals		2005-08
P01019	2005.07.07	21:52:26	FDG Normals		2005-08
P01020	2005.07.07	21:53:47	FDG Normals		2005-08
P01021	2005.07.07	21:54:51	FDG Normals		2005-08
P01022	2005.07.07	21:55:56	FDG Normals		2005-08
P01023	2005.07.07	21:57:01	FDG Normals		2005-08
P01024	2005.07.07	21:58:08	PDG Normals		2005-08
P01025	2005.07.07	21:59:11	FDG Normals		2005-08
P01053	2005.07.07	22:00:09	FDG Normals		2005-08

▲ Add samples      ✖ Remove samples

#### 4. Define the Spatial Normalization and Normalize the Samples

The next step is to define how the stereotactic normalization of the control samples is performed.

A mask is required to cut off signal from outside the brain. It is specified using the **Mask for Spatial Normalization** selection. For the standard **PET** and **SPECT** templates there are default masks available, for **User defined** templates the user has to select an appropriate mask series in a database.

Since the normalization template is typically quite a smooth image, a similar smoothing of the target images is also needed. To this end a **Gaussian smoothing** filter may be defined by its full width at half maximum in all directions ( $x,y,z$ ). An additional selection allows switching between three different function bases.

Then normalize the control images by selecting the new samples in the list and activate the **Normalize Selected** button. The normalization is performed in the background, and finally confirmed by a message. Note that control data which have already been normalized are marked in the **Samples** list with a special symbol.

3. Samples			
▲ Patient Name	Study date	Time	Study description
H012	2003.03.23	11:00:00	
P01017	2005.07.07	21:46:40	FDG Normals
P01018	2005.07.07	21:51:06	FDG Normals
Ⓢ P01019	2005.07.07	21:52:26	FDG Normals

Note that although smoothing is applied for the purpose of the normalization, the resulting normalized images are not smoothed by the specified filter.

#### 5. Define the Database Properties

The database properties are defined on two tabs. The first contains the following:

A **Gaussian smoothing** filter is available for smoothing the normalized control images before the database calculations.

In order to perform a pooled analysis it is required that the control images have comparable pixel values. In most cases the image values must therefore be scaled. This is achieved by scaling the pixel values by the inverse pixel average in stable reference tissue. Several user interface elements in the **Scale Values** to line allow flexible scaling strategies.

The first selection lets define how the reference value is calculated within a spatial extent defined by the second selection.

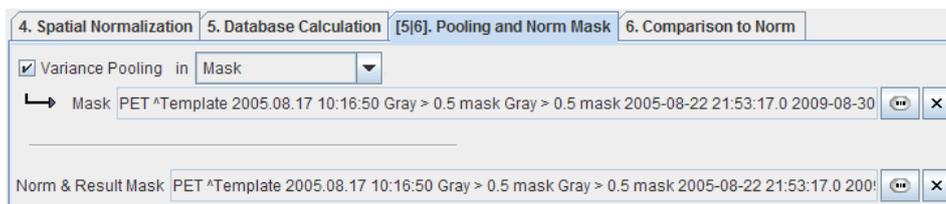
<b>Aver</b>	Average value in the reference pixels.
<b>Max</b>	Maximal value in the reference pixels.
<b>Aver above % of Max</b>	Average of those pixels in the selection which are larger than the entered percentage of the reference maximum.
<b>Aver in percentile range</b>	A pixel value histogram is done in the spatial selection. The average value is calculated in the percentile range value specified.

The second selection allows defining the spatial extent within which the reference value is determined. The restrictions are

<b>VOI</b>	A volume-of-interest which can be selected in the database.
<b>Mask</b>	A mask file which can be selected in the database.
<b>Sample</b>	No restriction, all data pixels are used.

In the example shown above the average is calculated of all pixels in a gray matter mask which are in the 80% to 90% percentile range. This definition may represent an approach to exclude diseased hypometabolic (low pixel values) and activated (highest values) pixels.

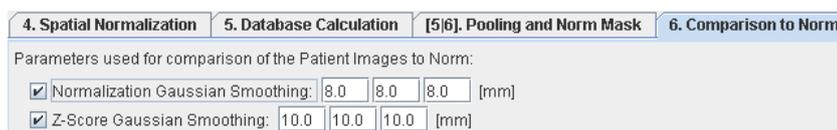
The z-score calculation is based on the standard deviation of the normalized values across the controls data sets. If the number of control samples is low, the statistical power may not be sufficient for calculating reliable standard deviations in each individual pixel. In this case **Variance Pooling** on the **Pooling and Norm Mask** tab should be enabled.



If **Variance Pooling** is enabled, the user can define a spatial extent, in which the pixel standard deviations are averaged to derive a pooled standard deviation which will be used for all pixels. A **VOI**, a **Mask**, or the whole **Normalized sample** can be employed for variance pooling. Finally, a **Result Mask** is needed outside which the calculation results are cleared because they are meaningless.

## 6. Define z-Score Calculation

The patient images which are to be compared against the Normal Database are also first normalized. The smoothing filter during this normalization can differ from the filter applied to the control image normalization and can be specified with the **Normalization Gaussian Smoothing** values. Due to the pooling of many samples and some optional filtering, the database is inherently smoothed. Therefore, some smoothing of the normalized patient images is most likely required to reduce disturbing edge artifacts. This smoothing can be specified with **Z-Score Gaussian Smoothing** values.



4. Spatial Normalization	5. Database Calculation	[5]6. Pooling and Norm Mask	6. Comparison to Norm
Parameters used for comparison of the Patient Images to Norm:			
<input checked="" type="checkbox"/>	Normalization Gaussian Smoothing:	<input type="text" value="8.0"/> <input type="text" value="8.0"/> <input type="text" value="8.0"/>	(mm)
<input checked="" type="checkbox"/>	Z-Score Gaussian Smoothing:	<input type="text" value="10.0"/> <input type="text" value="10.0"/> <input type="text" value="10.0"/>	(mm)

## 7. Database Calculation and Saving

After these definitions have been completed, the Normal Database can be calculated. The button **Database Calculation** initiates the calculation encompassing all samples which have been added and normalized. The following processing steps are performed.

- 1) For each normalized control sample the reference value is calculated, and all pixels are scaled by its inverse. As a result, the values typically range from 0 to somewhat above 1.
- 2) The scaled images are smoothed with the Gaussian filter.
- 3) For each pixel the distribution of the scaled values in all samples is calculated.

As a result, the average value (representing the expected normal value) and the standard deviation (a measure of uncertainty) are known. These results are saved in the database as new series of the normalization template study (MEAN, STDV).

At the end, save the database using the **Save norm** button.

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**Note:** New samples can incrementally be added. In this case, and if one of the definitions has been modified, it is required to recalculate the database.

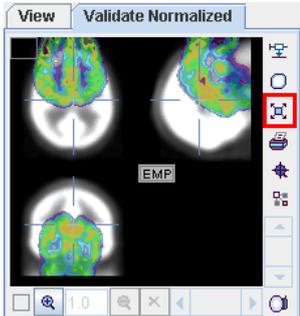
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## Quality Control

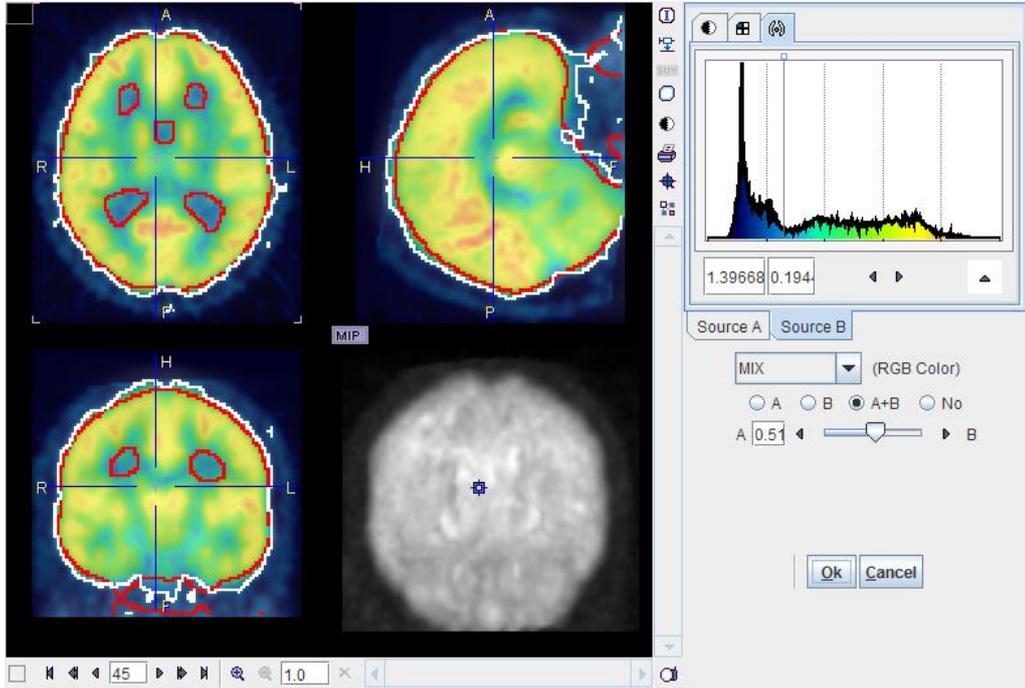
When creating a Normal Database it is important to ensure that only correctly normalized samples without truncated areas are included. Although a certain inaccuracy of the mapping from the patient anatomy to the stereotactic template cannot be avoided, samples showing gross deviations should be dropped from the analysis.

A fusion display supporting the quality control of spatial normalization is integrated in the Brain DB editor tool. When the **Validate Normalized** tab is selected, the image display shows a fusion of the template with the normalized patient images.

The easiest way to quickly check the normalized samples in the database is to switch to the orthogonal view of the **Validate Normalized** tab, select the first sample, and with the **CURSOR DOWN** key browse through the **Samples** list. Each time a new sample is selected the view gets updated. The example below clearly indicates a failed normalization.



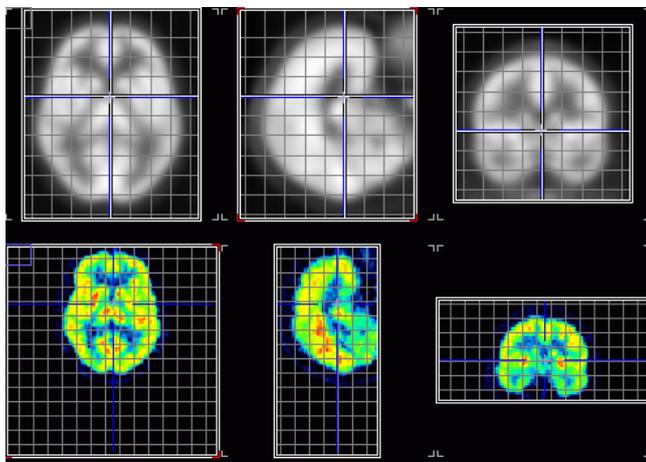
For a detailed analysis the fusion display can be blown up using the large view button indicated above.



In this large view display the images from both sources are always fused. **Source A** represents the template, and **Source B** the normalized patient images. The tabs allow to switch between the two data sets, for example to adjust the color tables or to define the iso-contour level. The relative contribution of the two components to the fusion image is governed by the fusion balance slider.

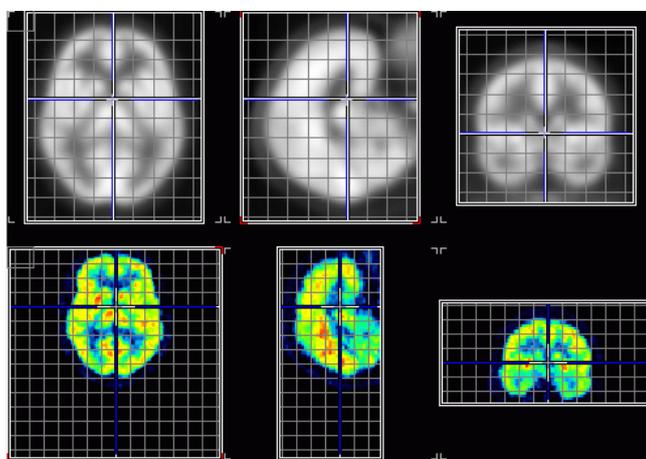
## Solving Normalization Problems

Often failure of normalization is caused by a gross mismatch between the template and the control image. The example below illustrates such a case.



Note that the grid has been enabled, indicating the origin as the intersection of the heavy lines. Obviously, the origin in the template (upper row) is placed in a well defined anatomical position, while it is located at the border in the control image (lower row). There the blue lines indicate the approximate position of the template origin. A simple procedure with the data inspector allows setting the origin to this anatomical location.

The origin of an image defines the center of the coordinate system in mm calculated from the front upper left hand corner. The origin is a concept of Analyze data written by SPM. For formats that support images positions (DICOM, ECAT) the origin values are calculated from the position of first slice. For other formats the origin setting is available for change in the loading dialog. If it is not changed, the default values are used.



Although the control images are shifted towards the end of the field-of view, the normalization worked after saving the images with the modified origin and using them instead of the original data.

## Sharing Databases

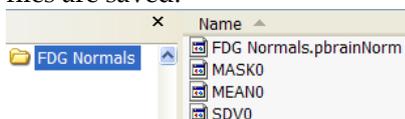
Establishing a brain database requires a substantial effort. Therefore, a brain database represents a valuable asset which should be sharable with others. The PMOD Brain DB tool supports the easy export/import of databases. Note that only the compiled information is exported, not the original control data sets, so it can only be modified by the owner of the controls data.

### Exporting a Brain DB

- 1) To export a Brain DB open the Brain DB Editor.
- 2) Activate the button **1. Create new norm + [Delete | Export | Rename] Existing**.
- 3) A dialog opens for defining the Brain DB to be exported.

Component name	Patient name	Patient id	Modify time	Last Use	File size	Sex	Birth date	High	We
FDG Normals	~[PBRAINDB NOR...	[PBRAINDB N...	2009-08-30 10:0...	2009-08-30 1...	2613			0.0	0.0

- 4) Select the **Data Base** containing your Brain DB, and then the list entry.
- 5) Activate the **Export** button. A new dialog appears for defining the destination directory. In this directory a new subdirectory (**FDG Normals**) is created wherein the definition files are saved.



### Importing a Brain DB

The DB import requires the whole contents of the directory created during the DB export.

- 1) Open the Brain DB Editor and select the database into which you intend to import the DB definition.
- 2) Activate the **Import** button. In the appearing file selection dialog navigate to the directory containing the Brain DB files, select the definition file (**FDG Normals.pbrainNorm**).
- 3) When **Set file(s)** is activated the different files are loaded and stored together with the processing definition in the selected database.

After the import, the brain DB can immediately be used for analyses.

# Patient Data Analysis

For the analysis of patient data with an existing Normal Database the PMOD Brain DB tool is started from the PMOD ToolBox with the **Brain DB** button. The appearing application contains four pages for the different stages of processing.

## Image Loading - Page 1

The first page **1. Load Images** displays a database loading area. Please select the right **Data Base** and then the patient in the **Patients** list. Select the appropriate series in the **Series** and start processing with the **Open** button.

The screenshot displays the '1. Load Images' page of the PMOD Brain Database Tool. The interface includes a search bar at the top, a patient list table, a series list table, and a series image preview window.

Patient name	Patient ID	Modify date	Sex	Date of Birth
PKIN1	Dyn. CFFPX bolus & MRI	2011-10-20 19:55:40.198	M	1981.01.01
PALZ1	Highly abnormal, T-Sum 48219	2011-09-21 11:01:16.798	F	1956.04.29
PFLU4	MRI and SPM Contrasts for 3 S...	2011-09-21 11:37:56.603		
PFLU1	Multimodality PET & MRI	2011-09-21 11:15:24.436	M	
PKIN2	Dyn. DASB without blood & MRI	2011-09-21 11:14:10.338		
P3D1	Mouse CT & SPECT	2010-09-03 18:43:01.149	F	
PETCT-Example	PETCT-Example	2010-09-03 16:32:31.06	M	
Example Brainnorm	Example for Normal Database	2010-09-03 14:12:47.216		1956.10.11
PKIN3	Dyn. FDG scan with whole bloo...	2010-08-27 15:20:40.196	M	
PCARD2	Rb Cardiac PET	2010-08-19 15:06:52.92	M	1956.06.17
PKIN5	Tracer with Metabolites, KM Fil...	2010-08-17 10:05:51.972		

Patient Name	Study date	Time	Study description	Series description	Modified	Last Use	Mod	nz	rv
PALZ1	2011.09.14	13:52:50	Alzheimer's Case	L_MAP [CLUSTERS]	2011-10-05 11...	2011-10-05 11...	PT	68	1
PALZ1	2011.09.14	13:52:50	Alzheimer's Case	L_MAP [VALUES]	2011-10-05 11...	2011-10-05 11...	PT	68	1
PALZ1	2011.09.14	13:52:50	Alzheimer's Case	NORMALIZED	2011-10-05 11...	2011-10-05 11...	PT	68	1
PALZ1	2011.09.14	13:52:50	Alzheimer's Case	NORMALIZED	2011-10-04 16...	2011-10-05 13...	PT	68	1
PALZ1	2011.09.14	13:52:50	Alzheimer's Case	T-Sum 48219	2011-09-21 10...	2011-10-07 11...	PT	47	1

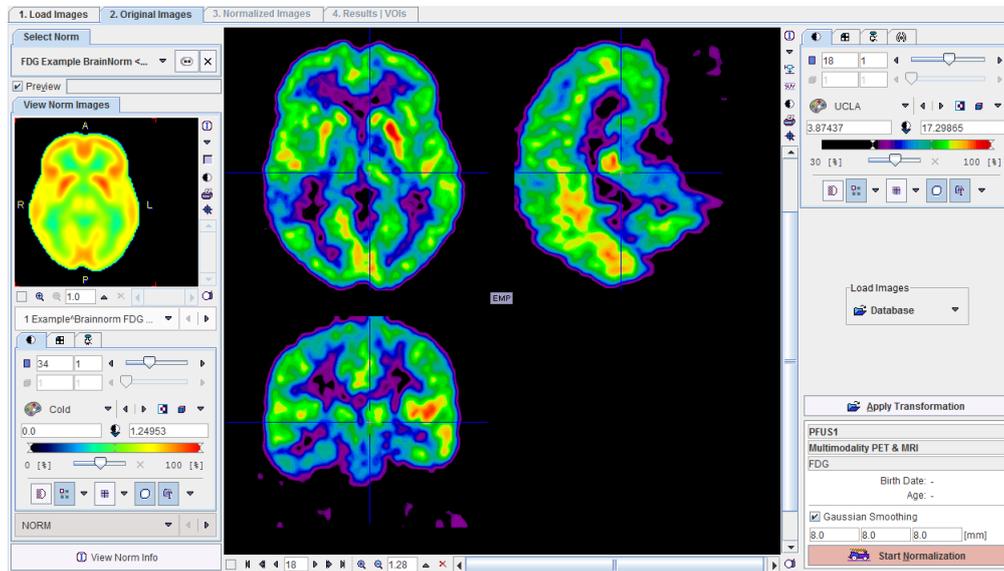
The series image preview window shows a brain scan with a color scale from 0.0 to 13.53109. The image is labeled 'LOADED' and includes controls for zooming, panning, and other viewing options.

As soon as loading completes, the display switches to the second page **2. Original Images**.

## Stereotactic Normalization - Page 2

After loading, the second page **2. Original Images** gets active. The loaded images are shown in the large image area and can be viewed with the standard controls.

The Norm section is to the left. **Select Norm** allows opening a database browser to look for a brain norm definition. Initially, the norm is shown which was used in the last analysis. If different norms are available we recommend different PMOD user accounts, one for each norm. The radio buttons allow to switch between the different image sets of the norm such as the normalization **Template**, the normalization **Mask**, the **Norm** images (MEAN, STDV, STDV POOL), and the **Result Mask**. The **View Norm Info** button pops up a dialog summarizing the different database parameters.



The **Load Images** button allows loading images from other sources than a database, and even in other image formats.

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**Note:** Images loaded in formats other than DICOM must be checked for correct display orientations. Please load an image of this particular type wherein all three orientations can be unambiguously identified. Then, in the orthogonal planes view, the patient coordinates must match the radiological convention as indicated in the images above.

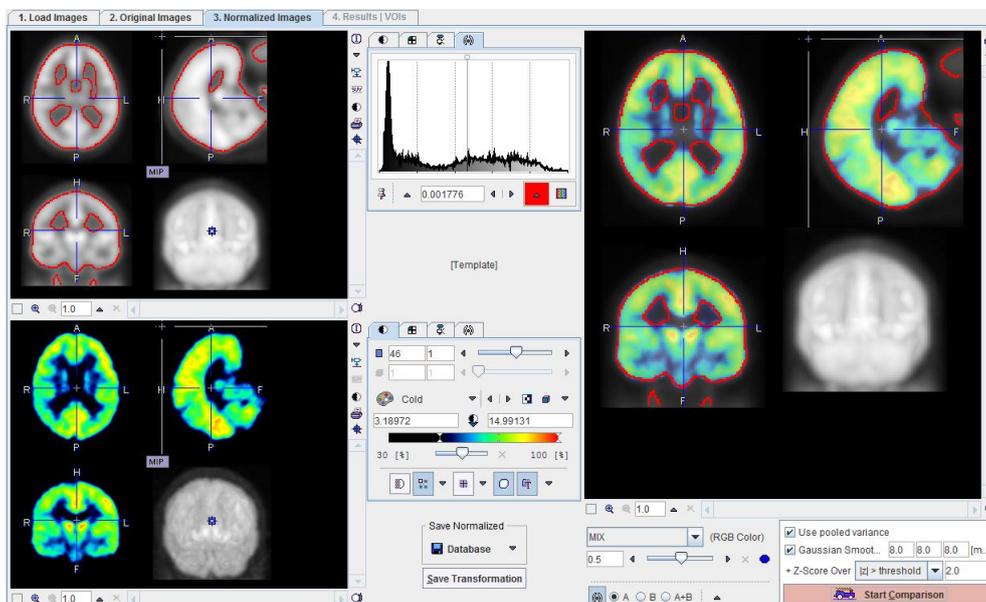
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In the normalization section at the lower right the smoothing parameters are initialized by the definition in the brain norm. Their values can be overwritten if needed, for instance if a normalization procedure fails. The **Start Normalization** button starts the stereotactic normalization calculations. As soon as the calculation completes, the display switches to the third page **3. Normalized Images**.

The **Apply Transformation** button allows retrieving a saved normalization transform, which is subsequently applied to the patient images.

## Quality Control - Page 3

The **3. Normalized Images** page shows the normalization template (upper left) together with the normalized patient images (lower left). The fusion of both images is shown in the large image are to the right.



The purpose of this page is to verify that the spatial normalization was successful, meaning that the agreement of the anatomy in both images is sufficient. The standard image fusion capabilities of PMOD can be used to assess the match. For instance, iso-contours can be overlaid as in the example above. Alternatively, the normalized images can be switched to a color display, and the **Balance** between the two contributions in the fusion image shifted back and forth.

The block in the lower right serves for configuring and starting the z-score calculation. The initially appearing configuration is the one defined in the Brain Norm definition, but it can be modified current image quality. If the size of the control group is small, the **Use pooled variance** box should be checked to use a single averaged standard deviation value for all pixels. Otherwise, the individual pixel-wise standard deviation determined is used. A **Gaussian Smoothing** filter should normally be applied to the normalized images before comparing them with the normal database, because the pooling process inherently smooths the average image. It will be a matter of some optimizations to find out the reasonable filter parameters which brings both data sets to about the same resolution.

When the **Start Comparison** button is activated, the z-score is calculated for each pixel in the result mask, and the z-score map generated. The **Z-Score Over** selection serves for creating an additional truncated z-score map. It can be configured to

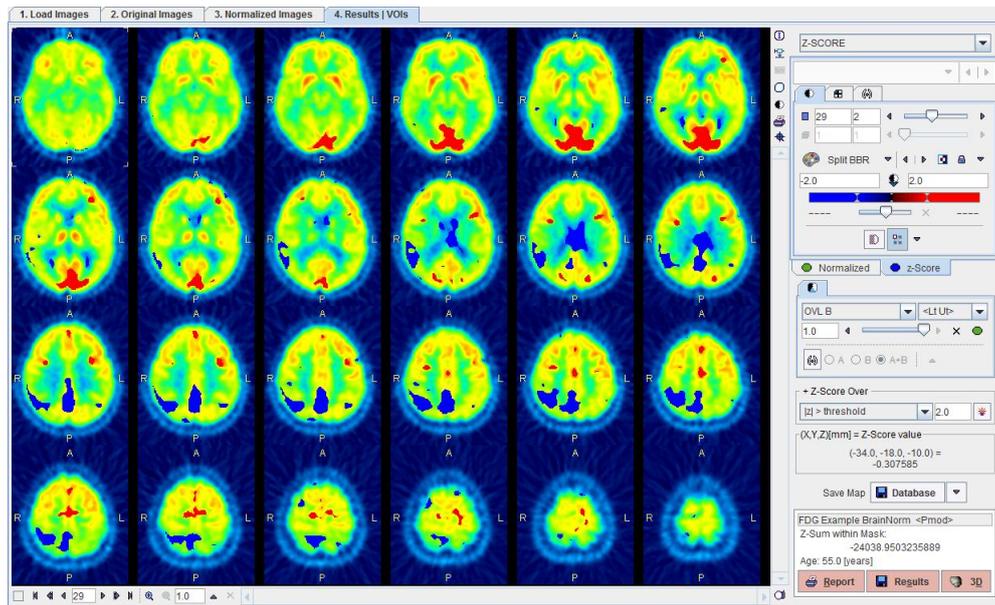
- $z < \text{threshold}$**       Keep only z-score values smaller than the entered threshold. All others are set to zero.
- $z > \text{threshold}$**       Keep only z-score values larger than the entered threshold. All others are set to zero.

$|z| > \text{threshold}$  Keep only z-scores with absolute values larger than the entered threshold. All others are set to zero.

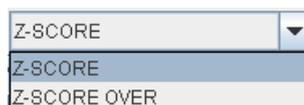
As soon as the calculation completes, the display switches to the page **4. Results | VOIs**.

## Results Analysis - Page 4

The **4. Results | VOIs** page has many helpful analysis functions built into. The normalized patient images and the z-score maps are essentially presented in an image fusion layout. To make optimal use of the available features, please make sure to read the image fusion guide.



Two types of images are available and fused: the **Normalized** patient images, and a **Z-Score** map. The properties of the images can be modified by activating the corresponding tab in the image control area and changing the settings such as the color table and the contrast. When the **Z-Score** images are active, an additional selection in the top right becomes available



**Z-SCORE** will show the z-score values in all pixels, while the values in **Z-SCORE OVER** are truncated according to the threshold configuration. The **Z-SCORE OVER** map can quickly be recalculated for a different threshold configuration using the button



in the **Z-Score Over** section.

### Fusion Capabilities

The fusion settings are located below the image controls. There are two selections for choosing between the different fusion renderings, a **Contours** section for enabling the iso-

contour overlays, and the balance slider to blend the contributions of the two images in the fusion.

The fusion methods available are:

- MIX**      Alpha Blending: weighted adding of the RGB values of both images.
- OVL A**     Shows the z-score images (B) as background image and a part of the normalized patient images (A) as the overlay.
- OVL B**     *Probably most useful in this context:* Shows the normalized patient images (A) as the background image, and a part of the selected z-score map (B) as the overlay. The z-score part to be shown is defined in the threshold selection to the right (see below).
- WIN A**     Shows the z-score images (B) as the background. When clicking into an image a rectangle appears which overlays the patient image (A).
- WIN B**     Shows the normalized patient images (A) as the background. When clicking into the images a rectangle appears which overlays the z-score (B).

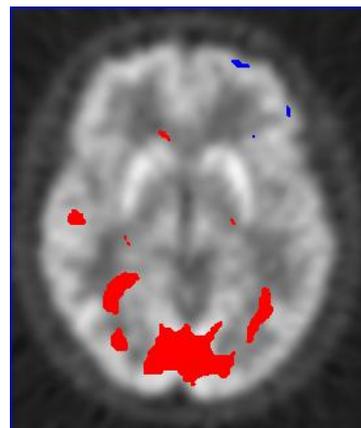
When **OVL A** or **OVL B** is selected, different threshold settings are available in the selection to the right:

- > Lt**      Only the pixels (in A for **OVL A** , in B for **OVL B**) with values above the lower threshold are displayed.
- < Ut**      Only the pixels (in A for **OVL A** , in B for **OVL B**) with values below the upper threshold are displayed.
- >Lt Ut<**    Only the pixels (in A for **OVL A** , in B for **OVL B**) with values between the lower and upper threshold are displayed.
- <Lt Ut>**    Only the pixels (in A for **OVL A** , in B for **OVL B**) with values smaller than the lower threshold or greater than the upper threshold are displayed. Note that only the first and last colors of the selected color table are applied in this setting. A suitable selection in this configuration is the **Split** table.

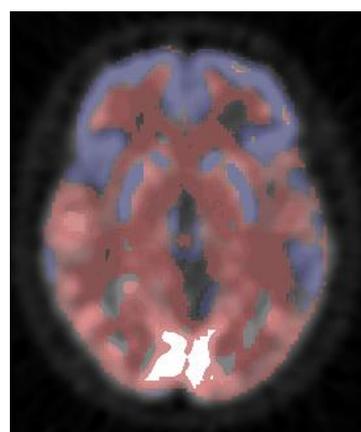
For the illustration of some of the capabilities please see the examples below. The full **Z-SCORE** map is used, and the color table is always configured as



Example z-score overlays:



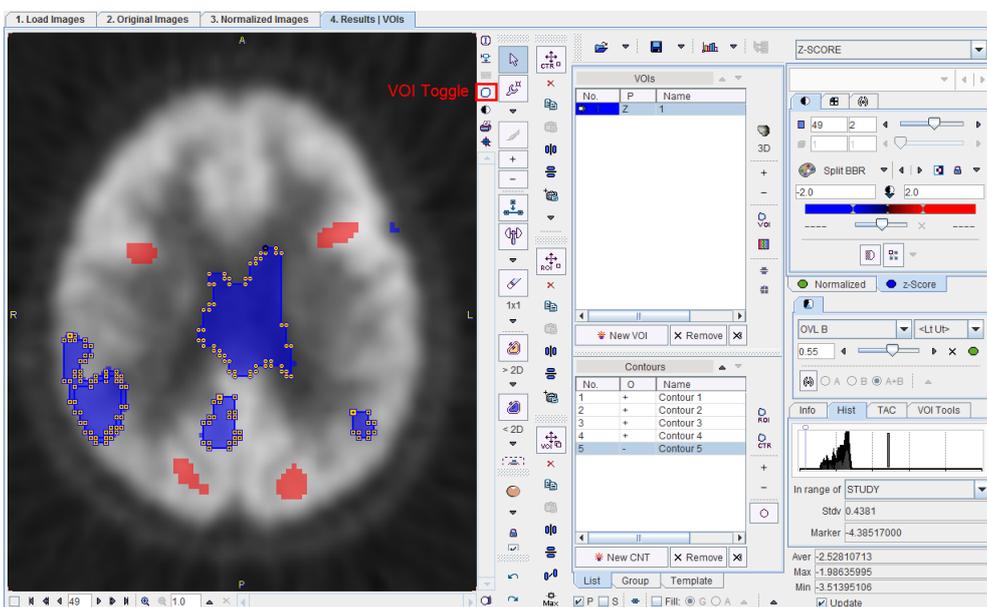
Only z-score values  $< -2$  and  $> 2$  are shown, without transparency. Because only the minimal and the maximal colors are use, the result has a binary character. Red are all pixels with an activation of more than two standard deviations, and blue all the pixels with the uptake reduced by at least two standard deviations. This is probably the most useful configuration for exploring the deviations from the standard pattern.



Only z-score values between  $-2$  and  $2$  are shown. Some blending is used to give an impression of transparency.

### VOI Statistics

The image display on the fourth page can be switched between the *Fusion only Mode* shown above and the *VOI Mode* shown below. The button highlighted by the red rectangle allows rapidly switching between the two layouts.



**Note:** The VOI functionality operates on the images selected by the tab **Normalized** or **z-Score** in the image control area.

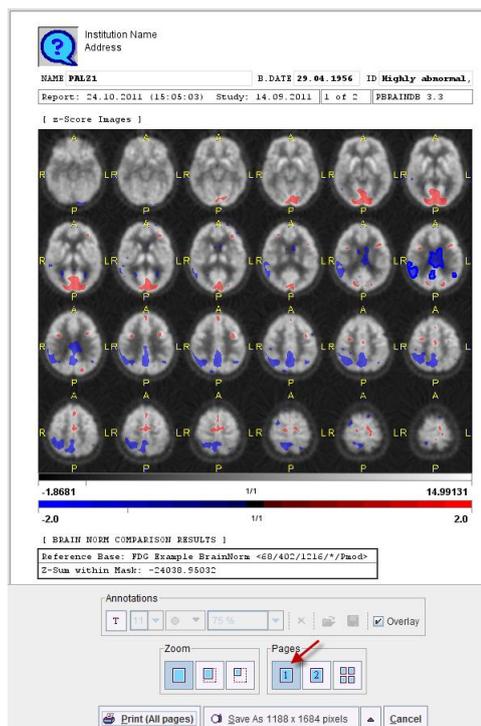
In the example above, the VOI operations run on the **z-Score** map. The blue posterior area were enclosed in a rectangle and the three contours generated with the Auto-Isocontour tool. The **Histogram** tab shows the z-score distribution in the VOI, and an average z-score value of -2.6026. Other VOIs could be added with any of the available tools, and their detailed statistics calculated with the **Statistics** button. Please refer to the documentation of the VOI tool for an in-depth description of all the capabilities.

## Saving Results

The **Save Map** button in the results area allows saving the z-score maps for use in another context. Please select the map you want to export (**Z-SCORE OVER** or **Z-SCORE**), configure the button to the image format of your choice, and then select it for saving.

The program calculates the total z-score in the result mask. This information is displayed together with the name of the Brain Norm and the age of the patient. It can be saved to the database or a text file using the **Results** button in the form of a diskette.

When the **Report** button is activated, a dialog pops up showing the images in the current configuration together with header information and the z-sum. The page can be annotated, printed, and saved as a JPEG or TIFF file, or as a DICOM secondary capture object. The second page of the report contains a summary of the database configuration, and allows entering comments.

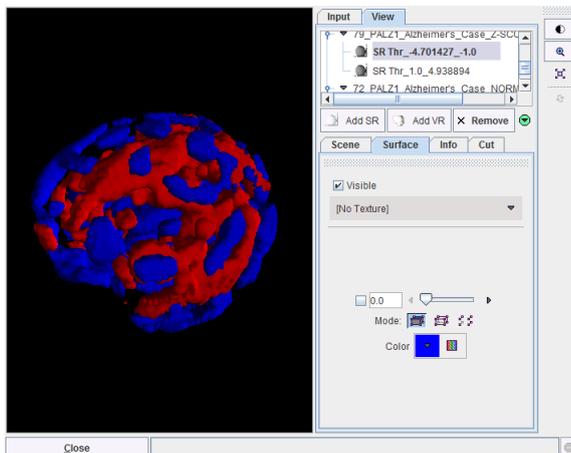


### 3D Rendering (Option)

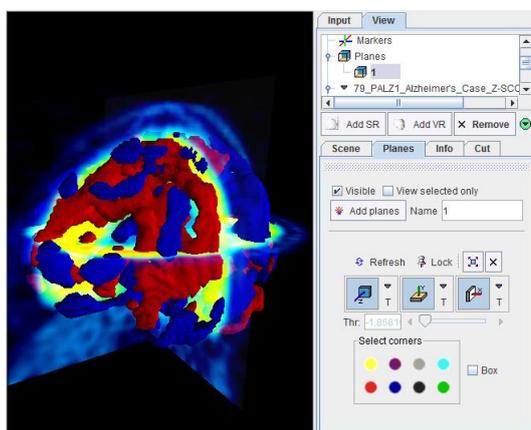
If the 3D option has been purchased and installed the button



appears and can be used to rapidly transfer the normalized patient images and the **Z-SCORE OVER** map to the 3D tool. Rendering is immediately initiated and a result shown such as the example below.



In the example the truncated z-score maps were calculated with  $|z| > 2$ . Therefore, the red objects enclose all areas with a z-score above 2, while the blue objects enclose the areas with z-score below -2. The scene can interactively be rotated and zoomed. Additionally, more information can be added, for example the brain shape, and/or planes of the normalized images.



## Application Notes

The results of database comparisons will crucially depend on the parameters used for database creation.

- ▶▶ When calculating the reference value for scaling the pixel values, diseased tissue should always be avoided. Therefore it might be helpful to have databases available with

differing reference calculation, for example one using a gray matter mask, and another using a cerebellum mask.

- ▶▶ Resolution mismatches between the database template and the processed patient image and inaccuracies in spatial normalization will result in edge artifacts in the z-score maps. This effect can be reduced by sufficient image smoothing. Again, it might be helpful to have databases available with different smoothing, to be applied depending on the size of the effect one is looking for.

Currently it is not possible to maintain several database definitions with the same set of control samples. However, an easy work-around is the following:

- 1) Calculate a database with specific settings and an appropriate description, then save.
- 2) Export the database. In the export dialog, before actually exporting, change the component name.
- 3) Import the database again. It is now a standalone definition without a relation to the control samples .

To create a modified database change the parameters and recalculate (overwriting the prior definition), and repeat the steps 1. - 3. This procedure can be repeated as many times as required to prepare a collection of databases covering the different situations expected in patient studies.

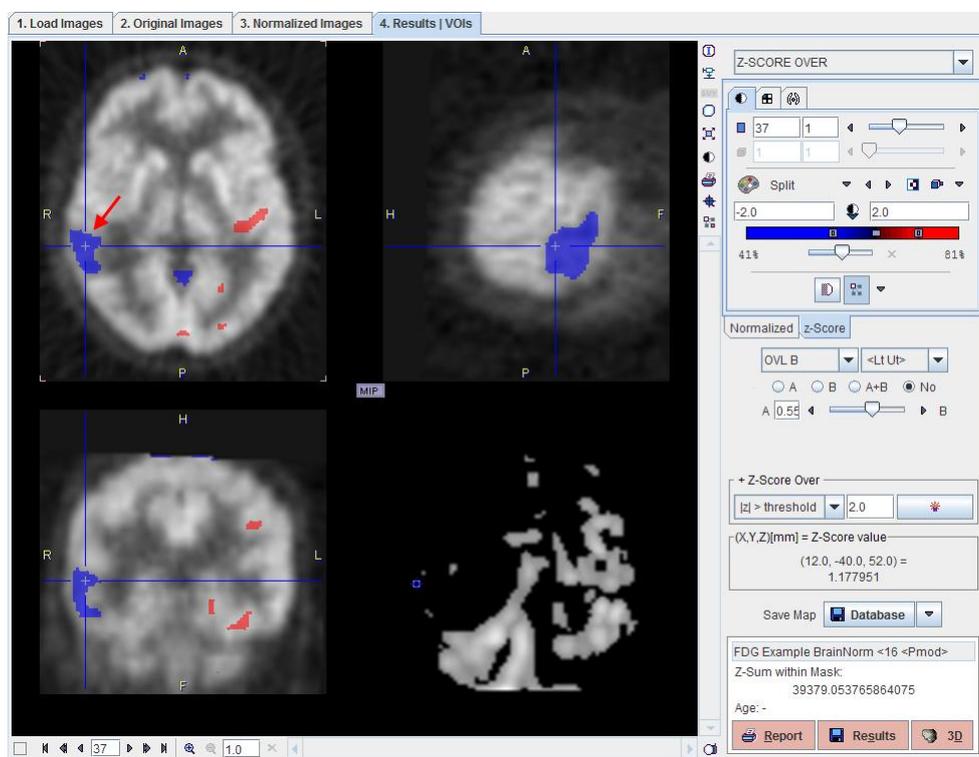
---

**Note:** Functionality for an age correction is not included in the current version of the Brain DB tool.

---

## Example Database

Included in the distributed Pmod database is an example **FDG Example BrainNorm** database. FDG images for testing the Brain DB functionality are available under the PALZ1 and PFUS1 example patients. Shown below is the PFUS1 FDG example. The extended blue area clearly marks the location of the tumor, while red areas indicate activations. Peripheral differences can be attributed to inaccuracies in stereotactic normalization.




---

**DISCLAIMER:** The example database is only intended for testing the functionality of the Brain Database tool, and is in no way a validated FDG Normal Database.

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# Glossary of Terms

## N

### Normal Database

In certain situations it is possible to compare patients images against a reference image to localize alterations from the normal uptake pattern. There are two requirements for such methods:

- 1) Anatomical normalization: To compare the patient images with the reference the patient anatomy must be adjusted to the standard anatomy. There are two domains where this task has proven to be successful. With heart studies the anatomy is usually reduced to a simple geometric model such as an ellipsoid. With brain studies, an elastic transformation is derived which warps the patient images into the stereotactic coordinate system. If functional brain images do not show sufficient anatomical details, the transformation may indirectly be obtained using a set of anatomical brain image of the same patient, such as magnetic resonance images.
- 2) Standard uptake pattern: Studies must be performed with a large enough set of normal controls, the data anatomically normalized, and the results statistically analyzed. It is important to bear in mind that patient preparation, the acquisition protocol, and reconstruction usually have an impact on the resulting images and therefore study guidelines must be established and followed. As tissue function tends to change with age, the control group should ideally be age-matched to the target patient group. The statistical analysis has to demonstrate a consistent uptake pattern with a sufficiently small standard deviation.

In PMOD a Normal database is also called a Brain Norm.

## O

### Origin

The origin of an image defines the center of the coordinate system in mm calculated from the front upper left hand corner. The origin is a concept of Analyze data written by SPM. For formats that support images positions (DICOM, ECAT) the origin values are calculated from the position of first slice. For other formats the origin setting is available for change in the loading dialog. If it is not changed, the default values are used.

## Z

### z-score

The z-score defines the deviation of a sample with respect to the mean of a distribution. It is defined by the formula

$$z = (x-m)/\sigma$$

where  $x$  is the sample value,  $m$  the sample mean, and  $\sigma$  the standard deviation of the distribution. Therefore  $z$  describes the deviation from the mean in number of standard deviations and is positive, when the sample is above the mean, and negative when below.