π.pmod Biomedical
Image Quantification

PNEURO Workbook Version 3.4

Scope and Intended Use

This document has been prepared for the *PMOD Brain PET / MR Analysis Course* in Zürich, March 13, 2013. It is an addition to the PNEURO User's Guide and aims at illustrating PNEURO operation with some application cases. The workbook starts with step-by-step descriptions and progresses towards higher-level outlines. Note that bold face is used for indicating strings corresponding to elements in the user interface of PNEURO.

Copyright and Disclaimer

The example data for the course demonstrations and exercises are organized in the **Neuro** database. This database is not included in the standard distribution but is available upon request for PNEURO users. The data are by courtesy of the Nuclear Medicine Department, University Hospital, Zürich, Switzerland. Note that the original data have been processed and optimized for training purposes.

PNEURO Application Cases

Three example data sets are available in the **Neuro** database (DB). In order to reduce the RAM requirements during the PNEURO analyses the MR images have been resampled to 1.2mm isotropic pixel size. This allows running the Maximum Probability Atlas (MPA) analysis with systems having 4GB of RAM, and the T_1-Parcellation analysis with 8GB RAM.

The following sections describe typical analyses with the example data. It is recommended reading them sequentially, as the level of description detail decreases progressively. The **Neuro** DB has been configured in the course software environment. However, if you downloaded the **Neuro** DB on your own and use it in your private environment, please make sure that you configure the DB using the **Config** facility as described in the *Readme* which accompanies the data.

## 1. MRI and Dynamic ^{11}C-Raclopride PET

The data set of "patient" **MRI-Raclo Dynamic** includes a dynamic PET acquisition of ^{11}C-Raclopride during 60 minutes as well as a resampled T_1-weighted MRI. The brain anatomy in the PET image is not ideal for brain VOI generation, as the initial frames are very noisy and late uptake concentrates in the basal ganglia. Therefore the brain structures will be derived from the MR image and applied to the PET series for regional statistics. The MPA and the T_1-Parcellation approaches are described in the following.

Analysis using the Maximum Probability Atlas Method

PET Image Loading, Averaging and Cropping

Please start the **Neuro** tool from the PMOD ToolBox and select the **Maximum Probability Atlas** tab. Activate the **Load PET** button with the database (DB) format configured. In the appearing DB interface make sure the **Neuro** DB is selected. 3 "patients" are listed in the **Patients** area. Select **MRI-Raclo Dynamic**, and in the updated **Series** list the **Dyn 60 min** PET. Load the data with the **Open** button. The images appear in an orthogonal layout with the default PET color table. Note that the original dynamic PET images are fused with an image calculated from averaging a range of dynamic frames.

The averaged PET will be used for the rigid matching with the MR, so the frame averaging should provide an image containing information about the whole brain with sufficient quality. The optimal averaging range strongly depends on the tracer uptake characteristics. For the present Raclopride PET please define the frame range **From** and **To** as **10** and **31**, respectively. Whenever the range definition is changed, the average image is updated immediately. To only see the average PET drag the fusion slider fully to the right.
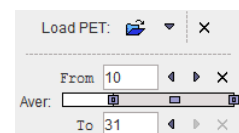
For avoiding excessive RAM needs and speeding calculations up, the image is then cropped to the relevant portion of the data. Activate the **Crop** box and place the appearing yellow crop box such that the brain is completely enclosed. The box position can be changed by simply clicking at the brain center in all plane orientations. If needed, the box edge sizes can be adjusted by the three size selection buttons.
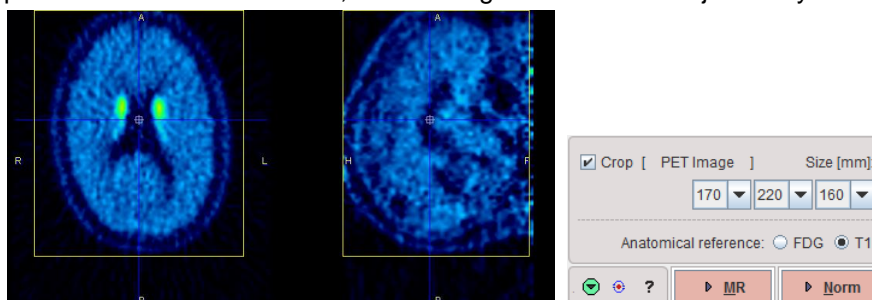
Activate the **PET image** button next to the **Crop** checkbox in order to execute image cropping. This completes the preparation of the PET image.

The next step is to load an anatomical image. Ideally, a T_1-weighed MR image is available which presents the brain anatomy with good resolution in all directions. If this is not the case, an FDG image might be used alternatively. As the MRI is available for this exercise please select the **T1** radio button and activate the **MR** action button in the lower right. Correspondingly, the program switches to the **MR** loading page.

MR Image Loading and Cropping

Data loading is started using the **Load MR** button. In the DB window select the same patient **MRI-Raclo Dynamic**, and in the **Series** list the **Brain MR**. Load the images with the **Open** button and then define a crop box in the same way as for PET. Activate **MR image** to effectively crop the data. Note that during loading the MR images are always brought to standard radiological orientation, even if the data was acquired in sagittal orientation.

In the next step, probability maps of grey matter (GM), white matter (WM) and cerebrospinal fluid (CSF) will be calculated. This process is tailored by some parameters above the red action button: **Denoising strength** can be set to different levels. It may improve the image quality and consequently the outcome of segmentation. As it is quite time-consuming and the MR image quality is sufficient, please select **None** to skip this pre-processing step. The **Bias regularization** and **Cleanup threshold** parameters are related to the actual segmentation. Please set both of them to the default value of **Light**. **Sampling** is an important parameter as it determines how much of the data is actually used for segmentation. The smaller the sampling size becomes, the more information is used and the longer the segmentation will take. With the present data, **6mm Sampling** works properly. In other cases, *if the segmentation outcome is unsatisfactory, please try smaller sampling settings*, starting with the default setting of **3 pix**els.
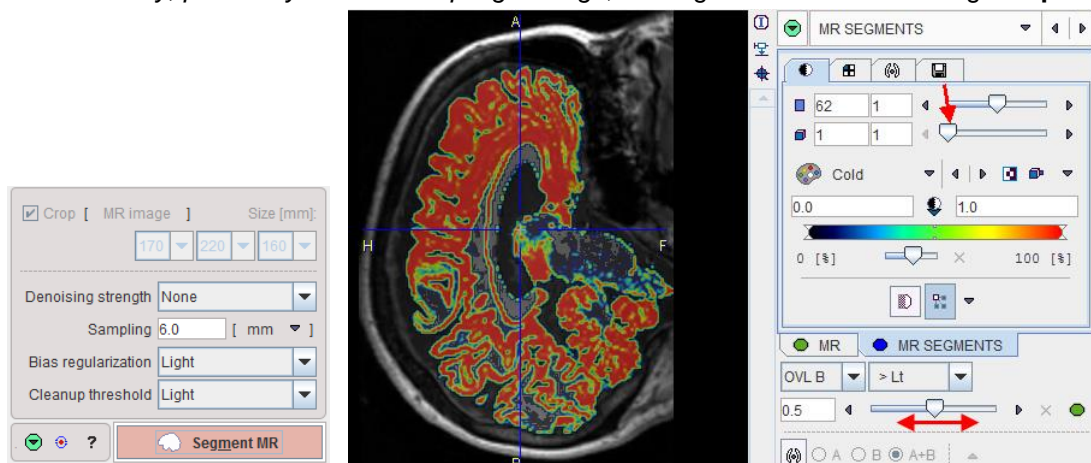

Finally, activate **Segment MR** to start the segmentation process. Calculation time may be around 2 minutes on a decent notebook system. The segmentation result is shown on the next page as illustrated above. Note that the GW, WM and CSF probability maps are compiled as a "dynamic" series on the **MR SEGMENTS** tab, so that they can be inspected with the indicated frames slider.

MRI-PET Matching

The next step establishes the mapping between the MR and the PET spaces. To this end the average PET image is rigidly matched to the MR image using the Normalized Mutual Information criterion. The only available parameter for this procedure is **Matching sampling.** Activating the *default* button as

indicated below set it to **3 pix**els. If the data were already matched, this step could be skipped by checking the box **PET already matched to MR**.
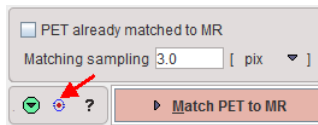

Activate **Match PET to MR** to start rigid matching. The result is shown as a fusion image on the **MATCHED PET** page. Please check the alignment quality of the two images using the fusion slider.
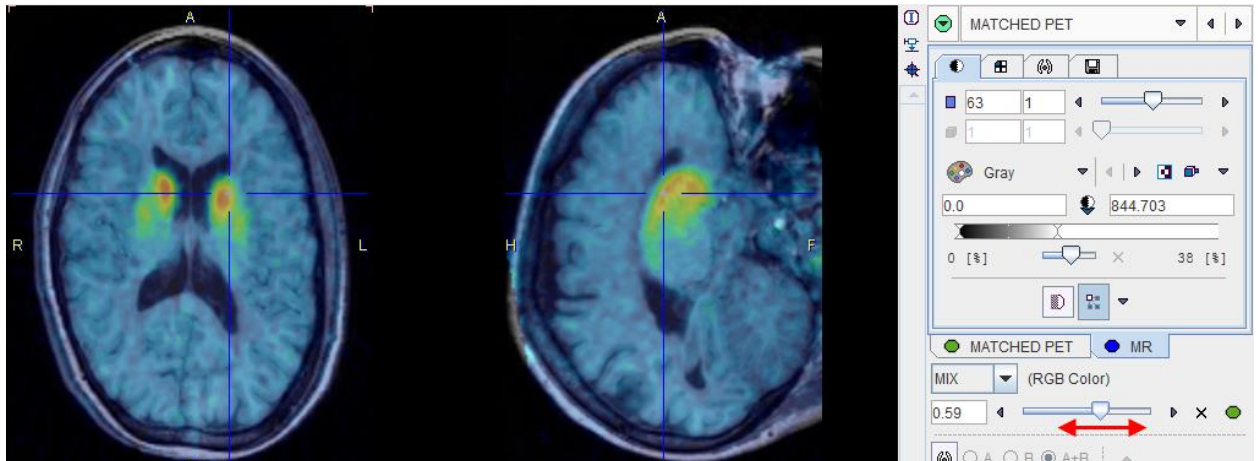
In this exercise the matching outcome is satisfactory. In case of a failure there are three options to try:

1. Interactive correction: activate the **Adjust Matching** button and drag/tilt the PET images in all directions.
2. Return to the **MR SEGMENTS** page using the list selection illustrated below,
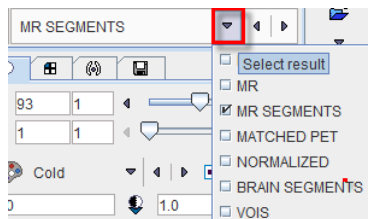
    reduce the **Matching sampling** parameter, and start matching again.
3. Match the PET externally to MR, save it, load the matched PET into PNEURO, and skip matching.

MR-based Normalization

The next step establishes the stereotactic transformation between the patient brain anatomy and the standard anatomy in the MNI space (Montreal Neurological Institute). Actually, this transformation was already determined during the segmentation process. It is now applied to the MR image by activating the **Normalize** button. The result is shown on the **NORMALIZED** page as a fusion of the T_1 MNI **TEMPLATE** together with the **NORMALIZED** MR. Shift the fusion slider left/right in order to validate the outcome. Additionally, iso-contours can be introduced into the images for highlighting boundaries in the brain as illustrated below. To arrive at this representation proceed as follows: Enable the iso-contours, select the **NORMALIZED** image tab, activate the iso-contour tab, change the contour color to blue and finally adjust the iso-contour level. Next, adjust the iso-contour level of the **TEMPLATE** image similarly.
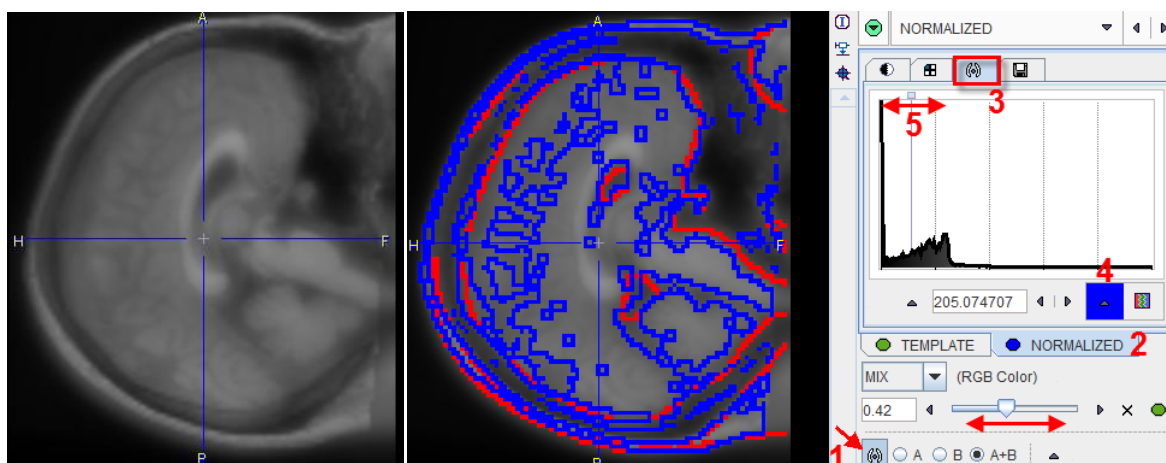
Atlas Transformation

At this time, the rigid transformation between MR and PET is known as well as the stereotactic transformation between the patient brain and the template. Therefore, all images as well as the atlas regions can be transformed to any involved space: the MNI atlas space, the patient MR space which probably has the highest resolution, and the patient PET space. In the next step, these transformations are applied to the data so that the user can inspect the VOI results on top of the PET and the MR images in any space.

Before proceeding, the user needs to decide on the atlas definition he or she would like to use. There are two atlas choices available in the **Select Atlas** panel: the maximum probability atlas **Hammers N30R83** which is the default choice, and the single-subject atlas **AAL-Merged**.
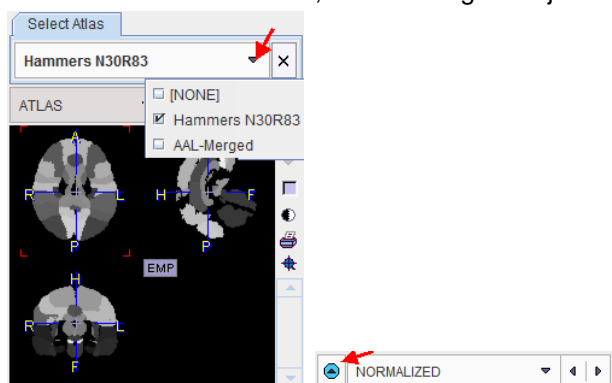

If the **Select Atlas** panel is not visible at the left window side, it can be shown using the atlas show/hide arrow button in the upper right as indicated above.

Please select the **Hammers N30R83** atlas and start the transformation of all data sets with the **Segment Brain** button on the **NORMALIZED** page.

Volume of Interest Outlining

A fusion of the transformed **MR** image and the atlas segments is shown on the **BRAIN SEGMENTS** page. Please verify that there is a good match of the segments with the anatomy. This is again most conveniently achieved by shifting the fusion slider left/right.
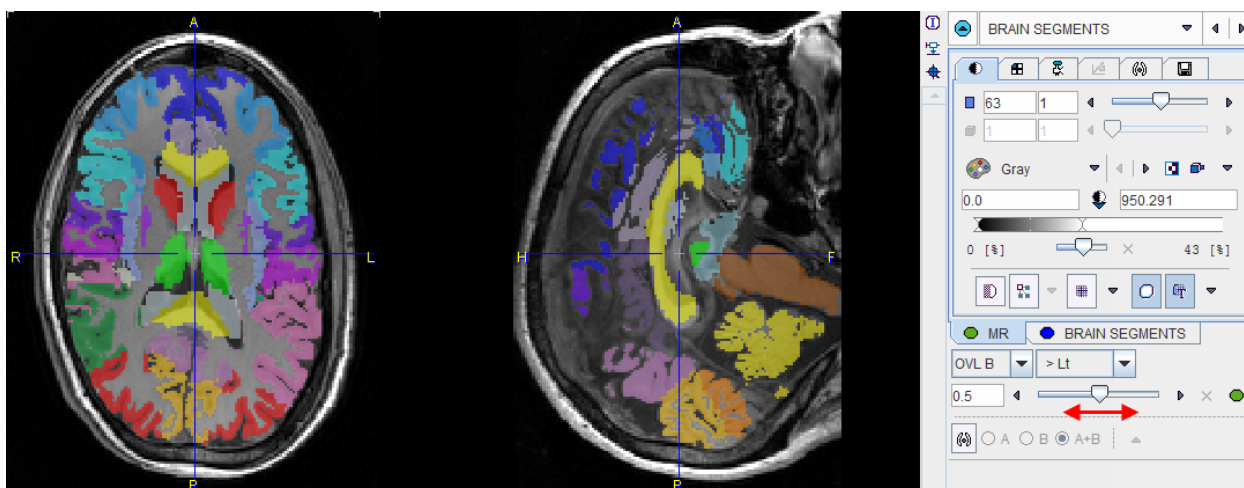
The images are always shown in the **Result space** selected in the configuration area. Please explore the differences in representation when selecting the **Atlas** space, the **Input/MR** and the **Input/PET** space. The image is updated whenever the result space is changed. Because of the superior resolution of the MR images, **Input/MR** brings out most detail.
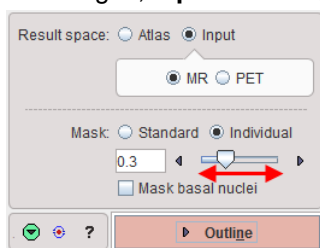

Next, explore the impact of restricting the brain regions to pixels with grey matter probability above a specified threshold. Set the **Mask** radio button to **Individual** for using the GM segment of this particular patient and move the threshold slider left/right. The trimmed regions are updated in the display as soon as it is released. The smaller the threshold values are, the larger the regions become. Switch the **Standard Mask** radio button on to base trimming on a population average GM map. Because of the lower probabilities the regions grow considerably.

The basal nuclei definitions are usually excluded from this masking operation. So see how GM trimming affects them enable the **Mask basal nuclei** box. It is evident, that significant parts of the basal nuclei structures become discarded. Therefore, please define the parameters as illustrated above and activate **Outline** to convert the segment image into an outline definition.

Volume of Interest Exploration

The resulting VOI outlines are shown on the **VOIS** page together with the tools for manipulating them. Initially, a fusion of the MR and the PET images is shown in the selected result space using an orthogonal layout. As the images may be small, use the layout tab to change the representation to a single axial slice. Next, bring the fusion balance fully to the right to show the MR image only.
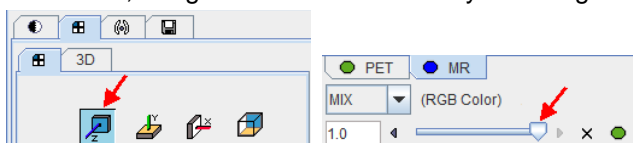
In this representation the region contours can be conveniently explored by scrolling through the slices. It is evident how the cortical VOIs follow the grey matter boundaries. The basal nuclei, however, show some aberration from the anatomy. Initially, all the VOIs are shown in the image overlay. The tree in the **VOI Group** panel organizes the VOIs hierarchically into left/right branches followed by lobe/central structure branches. Individual VOIs or whole branches can be hidden or shown by checking the corresponding box as indicated in the illustration below. *Note that the S checkbox has to be active for this selective visualization to work*. Otherwise, all VOIs will be shown irrespective of the settings in the tree.
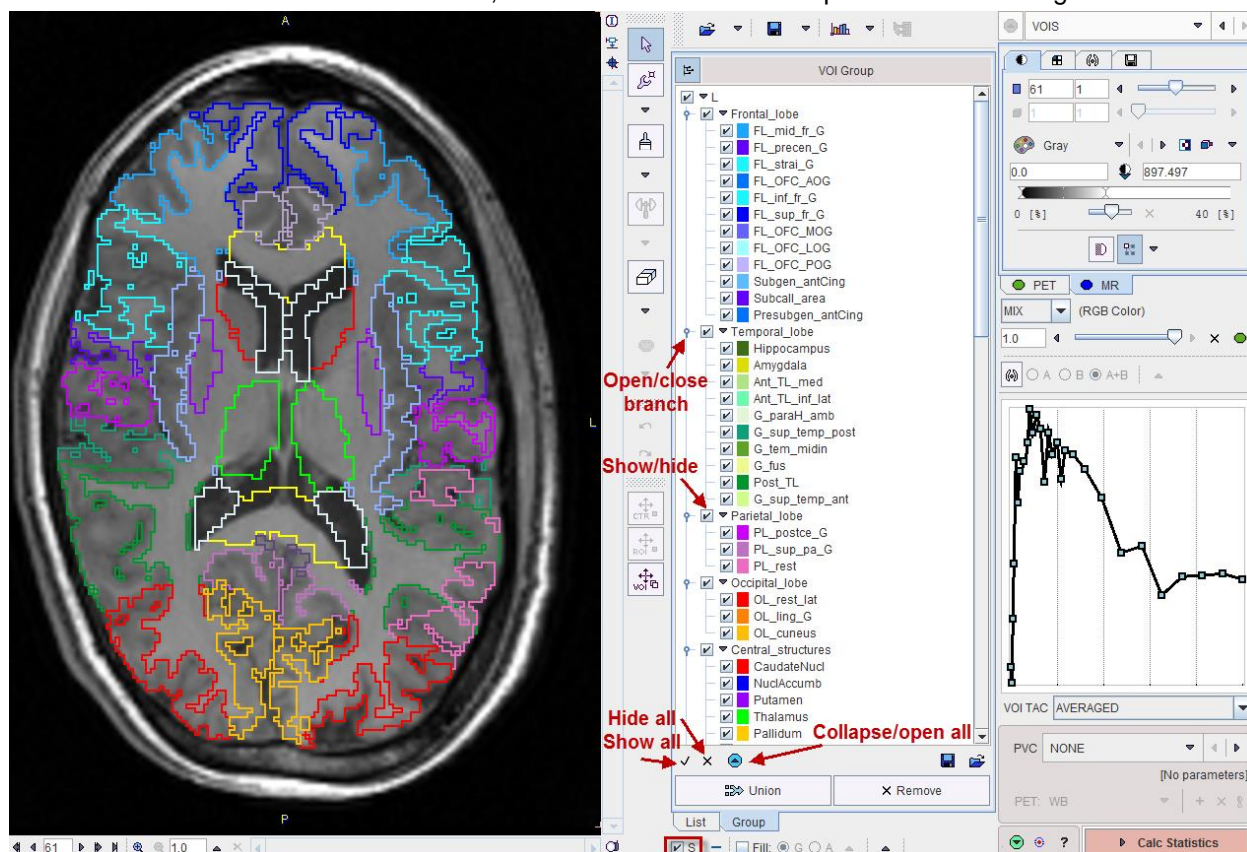
Modifications can be applied to the VOIs in many ways as described in the *PMOD Base Users Guide*. For instance, while the **Group** tab is active, all VOIs selected in the tree can be shifted. As illustrated below, activate the **x** button for disabling all VOIs, then click into the **Central_structures** check box of the **L** branch. Only the 5 central structures are shown in the overlay. Next activate the **VOI** operation button.
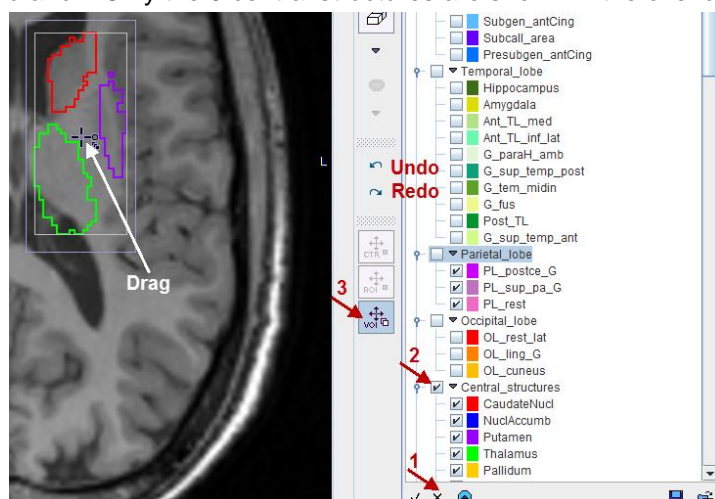
A box appears around the contours with a handle in the middle. Try out how the group of VOIs can be moved by dragging the handle, and scaled by dragging the edges of the bounding box. Finally use the *Undo* button multiple times to bring the VOIs back to the original position.

Note also the **Union** button which combines all VOIs selected in the tree into a single new VOI. To try this out clear all selections with **x**, enable the left and right **Cerebellum**, activate **Union** and enter **Merged_Cerebellum** as the new VOI name in the confirmation dialog window. As a result, a new VOI branch appears at the end of the VOI tree while the original VOIs disappear at the same time. This is necessary to ensure proper operation of the optional partial-volume correction (PVC). Please return to the original VOI set by activating the *Undo* button.

The editing of single VOIs is done in a different way. First, the **List** tab has to be activated. On this list, the VOI arrangement is linear. Double-click at VOI 57 **CaudateNucl_l** to select it. It is not clearly seen among all the VOIs. Therefore enable the **S** checkbox which became disabled when switching the panels. Now, only the left caudate VOI is shown. Scroll to slice 63 and note that the VOI seems to be somewhat too large. To trim its size interactively select the *Eraser* tool and drag along the VOI boundaries to wipe away pixels. Alternatively, try out the *Hammer* tool and the tool for the erosion/dilation. Note the small arrows which allow configuring the tool sizes.

Finally reset all changes with the *Undo* button. As an alternative for establishing the standard VOI definition, return to the **BRAIN SEGMENTS** page with the selection in the upper right and activate the **Outline** button once again.

Results Saving
After completion of the VOI adjustments save the VOIs with the corresponding button above the VOI list

and name it **Max. Probability MR space**. Any time later, this VOI set can be retrieved and applied to any data in the MR space.

PNEURO offers a convenient facility for saving all generated data at once with the *Save all* button in the lateral taskbar. As can be seen in the illustration below, the images are available in all spaces, as well as the spatial transformations between all the spaces. Note that the transformations can not only be applied to the images, but also for transferring the VOIs between the different spaces.

Another way of saving work is using the **Save Protocol** button in the status line. Activate the button and save the protocol as **MaxProbability-MR-PET**. This saves the processing settings together with the final VOIs.
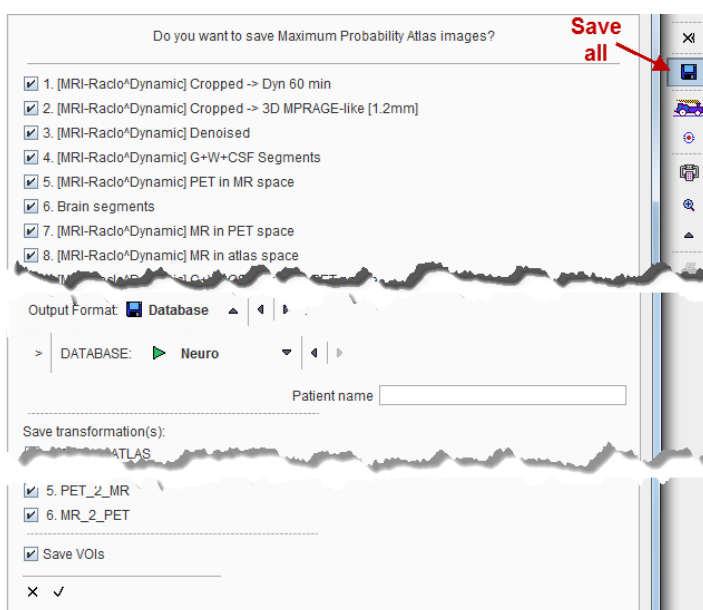
### Statistics Calculation and TAC Transfer to Kinetic Modeling Tool

Finally, start calculation of the regional PET statistics with the **Calc. Statistics** button. PNEURO switches to the dedicated **Statistics** page and shows 83 tissue time-activity curves(TAC) representing the regional PET average in the dynamic frames of the Raclopride PET series.

Often, PET scans are static rather than dynamic. To see how the result would look like for an acquisition 50-60 minutes after tracer injection average the last two 5 minutes frames as follows. With the **TACs** radio button enabled set the lower range value to **30** (50-55min) and the upper to **31** (55-60min).
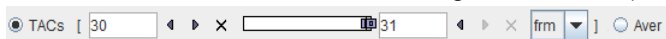
Then switch the **Aver** radio button on. Immediately, the TAC curves are replaced by a table which shows the average uptake per region as well as the region volume. To transfer these results activate **Copy to Clipboard**, start a program like Excel and select the *Paste* operation. The full table is pasted and can be further processed.

Return to the TAC display by switching again the **TACs** radio button on. These TACs can be quantified by the *Simplified Reference Tissue* model using cerebellum uptake as the reference. In order to obtain an averaged cerebellum signal from left and right proceed as follows: Use **Deselect All** to switch off all curves. Look for the **Cerebellum_r** and **Cerebellum_l** entries towards the end of the list and check both of them. Activate the *Merge* menu as illustrated below, choose the **Selected** entry, and enter **Cerebellum** as the TAC name.
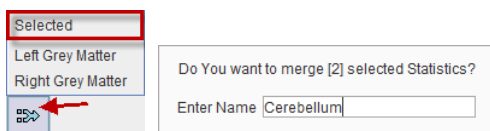
A volume-weighted average of the two curves is calculated and assigned to the TAC **Cerebellum** which appears at the end of the list. Note that opposed to the VOI merging the original curves are still available. Finally, activate the **Kinetic Modeling** button to transfer all curves to the PKIN tool.

Analysis using the T1-Parcellation Method

When exploring the outcome of the MPA analysis in the exercise above it turned out that the basal nuclei definition - which is most relevant for Raclopride - was not ideal. The following exercise applies the T_1-based parcellation approach which is specialized for those structures. Many of the processing steps are the same as for the MPA method and will not anymore be described in detail.
Please close and restart PMOD first to free RAM. This is important because the parcellation is challenging for most non-workstation systems.

PET Image Loading, Averaging and Cropping

Start the **Neuro** tool and select the **Brain Parcellation** tab. Using the **Load PET** button, load the **C11-Raclopride PET** series of the **MRI-Raclo Dynamic** patient, average the frame range **10** to **31**, and **Crop**. Move on to MR loading with the **MR** action button.

MR Image Loading, Averaging and Cropping

Using the **Load MR** button load the **3D MPRAGE-like [1.2mm]** series and **Crop**. Before proceeding switch the **Denoising strength** to **None** because the data quality is good and denoising takes significant calculation time. Continue with the **Denoising** action button.
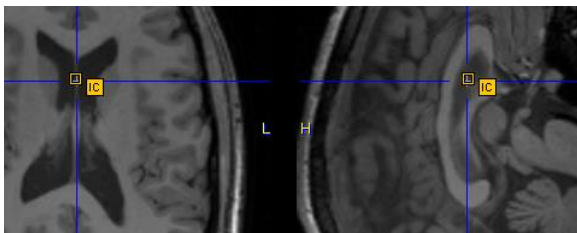
Landmark Definition

An important difference of the T_1-parcellation method to the MPA method is that the user has to manually define 4 anatomical landmarks in the MR image on the **DENOISED** page. Start marker definition mode by activating the indicated button in the **Set markers** area.

From now on, whenever you click into the image, a marker will be placed in the prescribed sequence IC, AC, PC, IH. Please select the **?** button to display a window indicating where these landmarks have to be set.

IC (inter-caudate) is the first landmark to place. Triangulate the slices by clicking into the image while *holding down the Shift and Ctrl keys* to avoid placement of the IH mark. Once the position is found simply click, and a labeled marker appears.

Automatically, PNEURO switches to **AC** (Anterior Commissure) definition mode. Now triangulate the AC, the **PC** (Posterior Commissure) and a inter-hemispheric (**IC**) point. During the process of localizing the anatomical position, the landmark setting can also be temporarily deactivated by selecting the ⤢ button, and re-enabling marker definition mode later on with ⤡.

Finally, the set of landmarks is available for inspection with the elements in the **Go to** section as illustrated below. Click on the arrows or select a landmark from the list to let the program triangulate this position. Finally, save the set of landmarks using the 🖫 button. If you are not sure about the placement of

the landmarks, please load the definition saved in the **Neuro** DB under the name of **Markers**. The markers loading button is located right to the saving button.
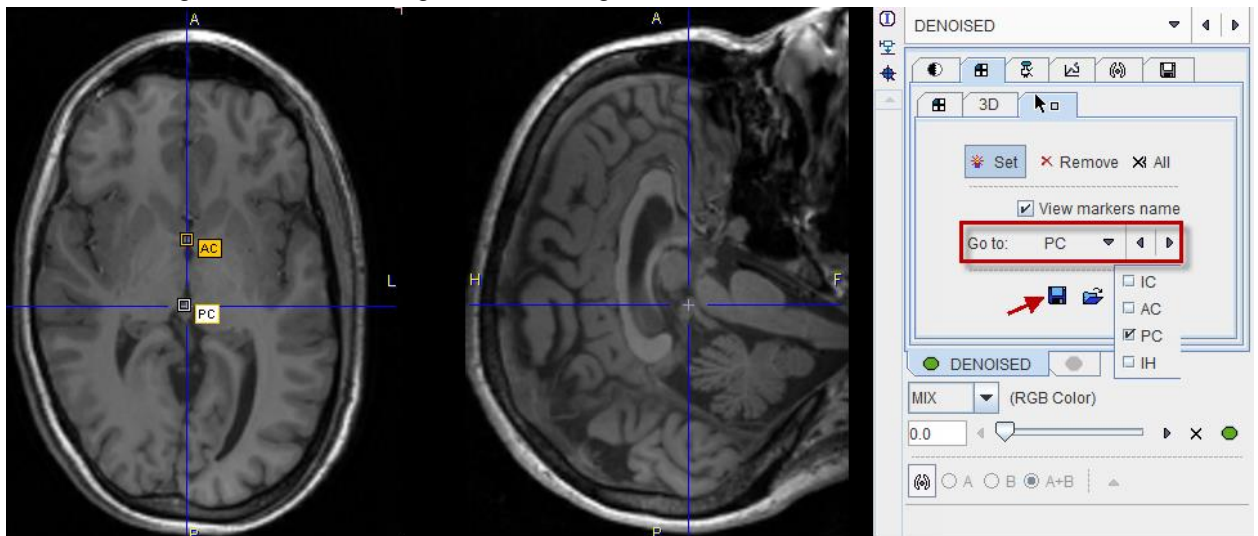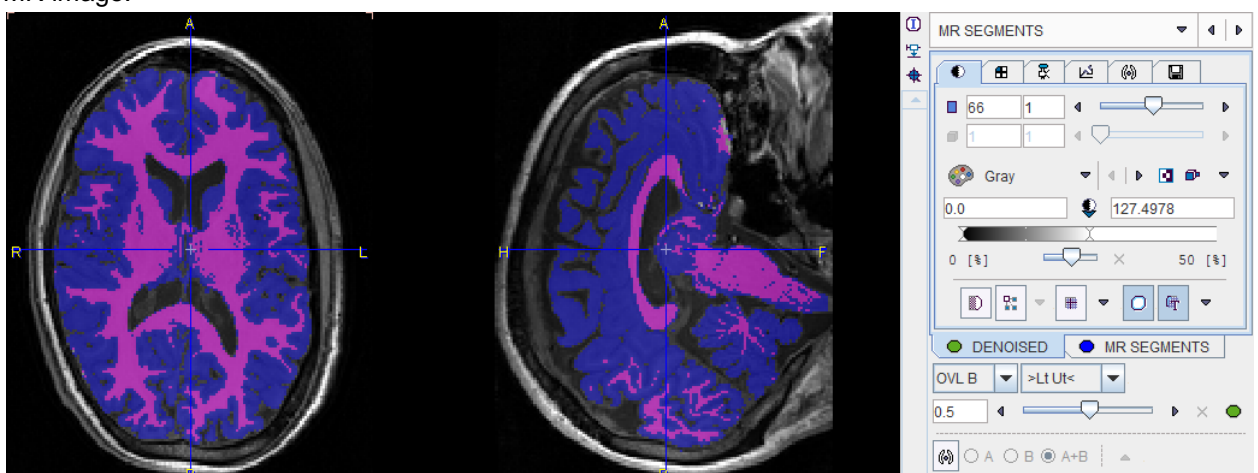

MR Image Segmentation

Still on the **DENOISED** page, set the parameters for the GM/WM/CSF segmentation to the same values as for the MPA method.
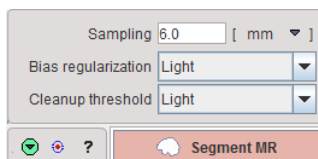

Then activate **Segment MR** to proceed.

Parcellation

The segmentation result is shown on the **MR SEGMENTS** page as a fusion of the GM/WM map with the MR image.

Note that there is a well-defined boundary between the GM (blue) and the WM (pink). It is possible to shift this boundary line towards GM or WM with the tools in the **Seg. Touch-up** panel, but for this exercise the segmentation is accepted.

In the next step, the program will select the most similar hemispheres from the knowledge base (KB) in order to construct an atlas of the basal nuclei. This selection is based on a number of indexes which were calculated during the segmentation. They can be inspected by activating the button illustrated below.
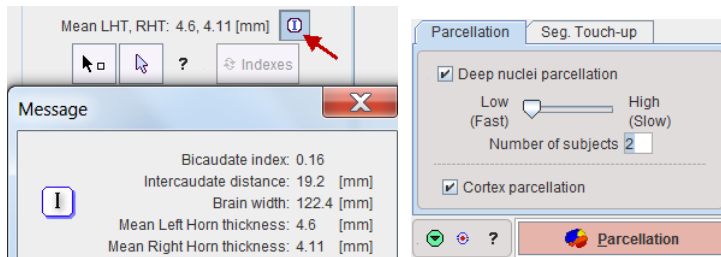

The number of selected references is defined by the **Number of subjects** parameter in the **Parcellation** tab. According to a study the optimal number to use is 8. As the calculation time for the corresponding 16 hemispheres is quite substantial, please set the number of subjects to **2**. Make sure that the **Deep nuclei parcellation** box is checked, as these are the results of interest. Because the derivation of the cortical VOIs doesn't involve major calculations, also check the **Cortex parcellation** box.

Finally, with the parameters set as illustrated above, initiate **Parcellation** by the corresponding action button. With the setting of 2 subjects the program has to process 4 hemispheres and will try to do this in parallel. Therefore, a system with 4 processing cores will only take 50% calculation time compared to a 2 core system. Most likely, processing will take about 10-15 minutes while you can monitor the progress in the status bar.

Brain Segments and PET-MR Matching
The parcellation results are presented as label map which is fused with the MR image on the **BRAIN SEGMENTS** page. Please inspect the parcellation quality by dragging the fusion slider left/right.
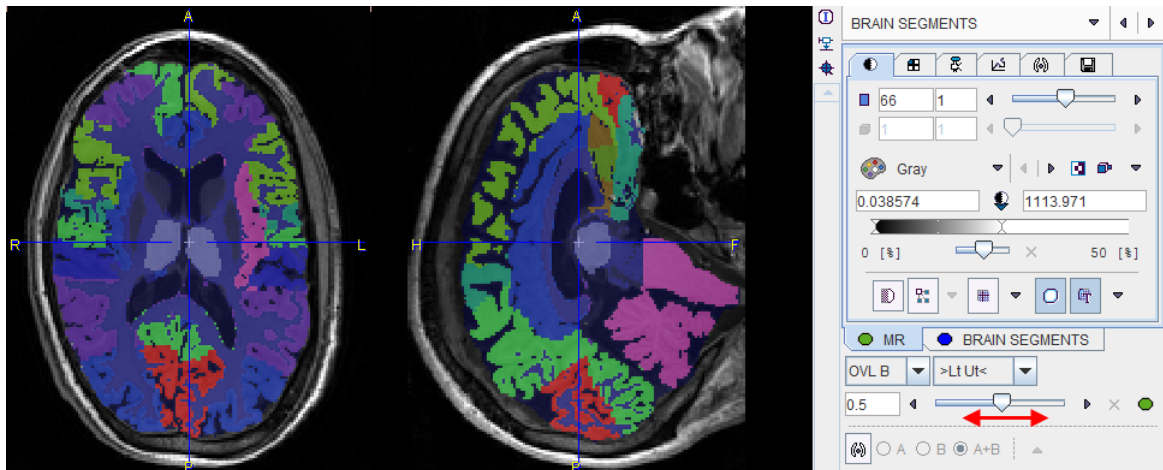

In the next step, PET will be rigidly matched to the MRI. Set the default parameter configuration by clicking the *default* button indicated below. The **Matching sampling** becomes **3 pix**els.
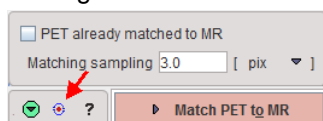

Activate **Match PET to MR** to start rigid matching. The result is shown on the **MATCHED PET** page for inspection and correction. As the result is fine, don't interfere with the matching at this time. In order to

compare the parcellation quality with that of the MPA choose **MR** as the **Result space** and start contour creation with the **Outline** button.
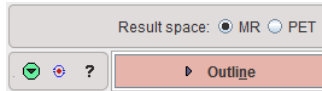
Volume of Interest Exploration

The resulting VOI outlines are shown on **VOIs** page. Note that the VOI tree arrangement is somewhat different as for the MPA. The parcellation results appear at the top, followed by the cortical VOIs which are derived by intersecting the Maximum Probability Atlas with the GM segment (p≥0.3). Configure the axial single-slice layout, set the fusion weighting to **100% MR**, select slice **61** and then compare the basal nuclei segmentation quality. It is superior to the MPA result, and it can be further improved by using more knowledge base subjects than 2. The illustration below demonstrates a slight improvement of the caudate definition when using 8 subjects.
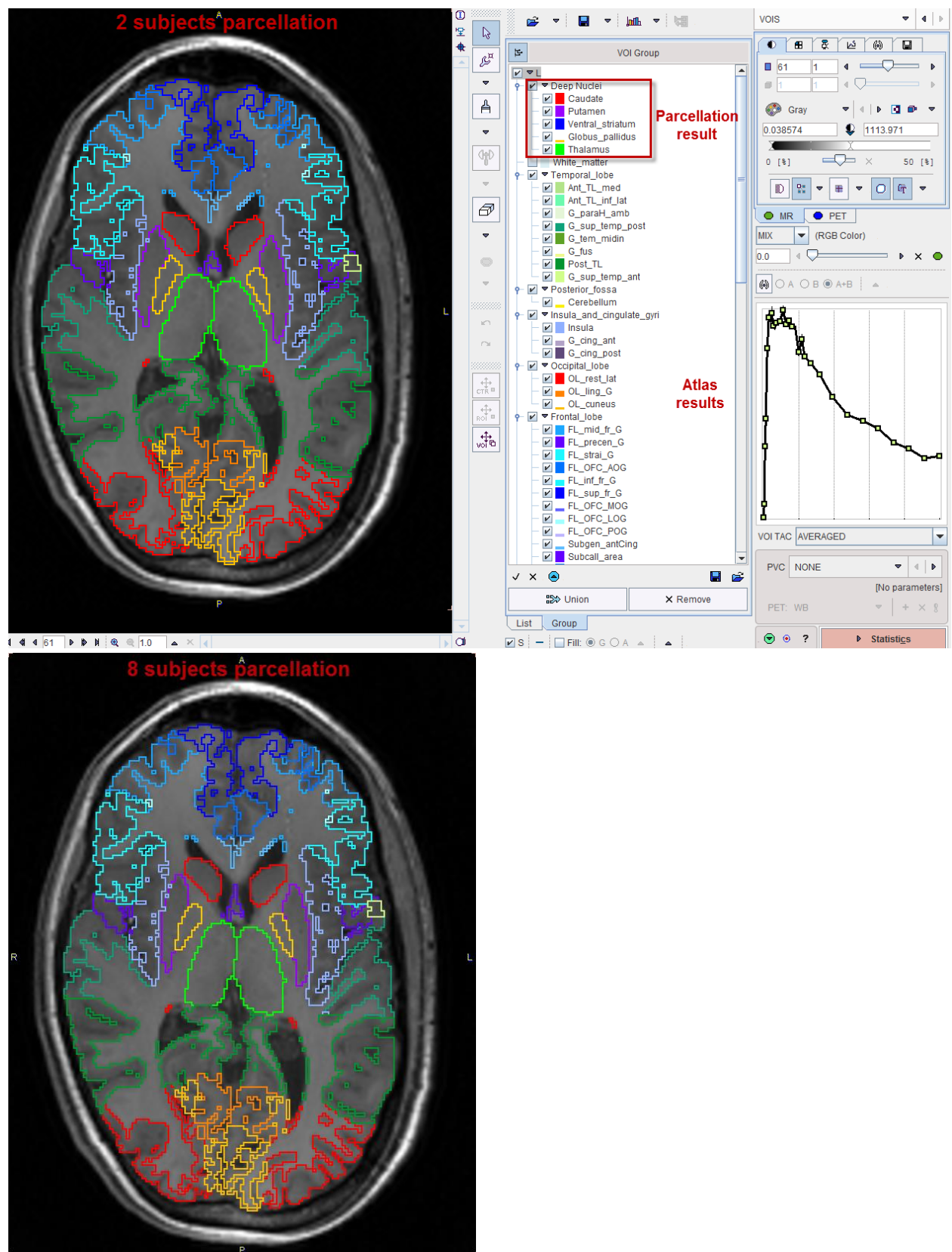
From this stage on processing is identical to that described for the MPA exercise. Please **Save** the **Protocol** under the name **Parcellation-MR-PET (2subj)** and the VOIs under **Parcellation MR space (2 subj).**

2. MRI and Dynamic ^{11}C-PIB PET

The data set of "patient" **MRI-PIB Dynamic** includes a dynamic PET acquisition of ^{11}C-PIB during 70 minutes as well as a resampled T_1-weighted MRI. The patient was classified as MCI with MMSE 27 at the time of the PIB scan and had converted to AD one year later.

The data can be processed in exactly the same way as described for Raclopride. The only difference is the PET uptake pattern, which however makes no difference for the MR-based VOI-finding. The illustrations below show the VOI outcome in the MR space on slice 60. These results can be reproduced using the protocols available in the **Neuro** DB.

MR-based Maximum Probability Atlas Result
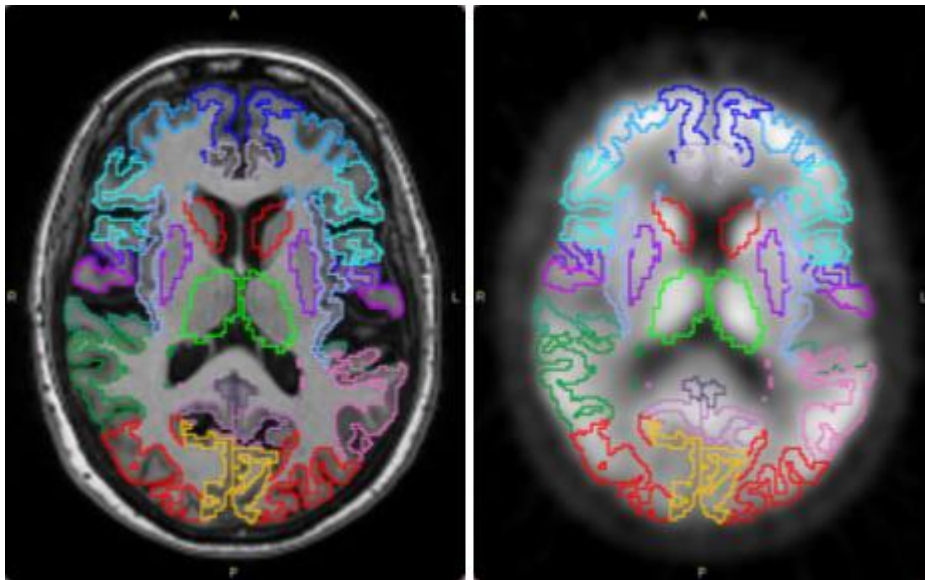
T1-Parcellation Result
Parcellation using 8 knowledge base subjects.
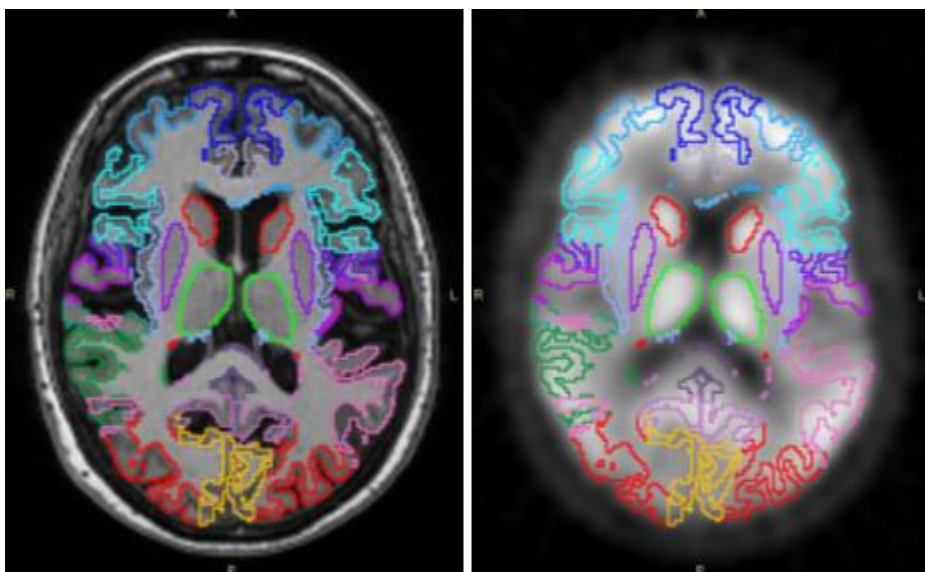
3. MRI and Static FDG PET

The data set of "patient" **MRI-FDG Static** includes a static FDG PET acquisition as well as a resampled T$_1$-weighted MRI. This data set can be processed using the MRI and PET workflows as described for the Raclopride study above. However, for the exercise described in this section, we will neglect the MRI and directly apply the MPA methodology to the FDG image. This illustrates the PET-only case where the information in the PET image is sufficiently close to the MNI PET template for a direct normalization.

PET-based Analysis using the Maximum Probability Atlas Method

PET Image Loading and Cropping

Please restart PMOD, launch the **Neuro** tool from the ToolBox and select the **Maximum Probability Atlas** tab. Activate the **Load PET** button, select the **MRI-FDG Static** patient, and load the **FDG Brain PET** series. **Crop** the image, and at this time use the **Norm** action button to start the PET-only workflow.
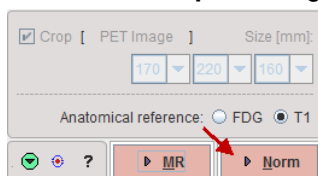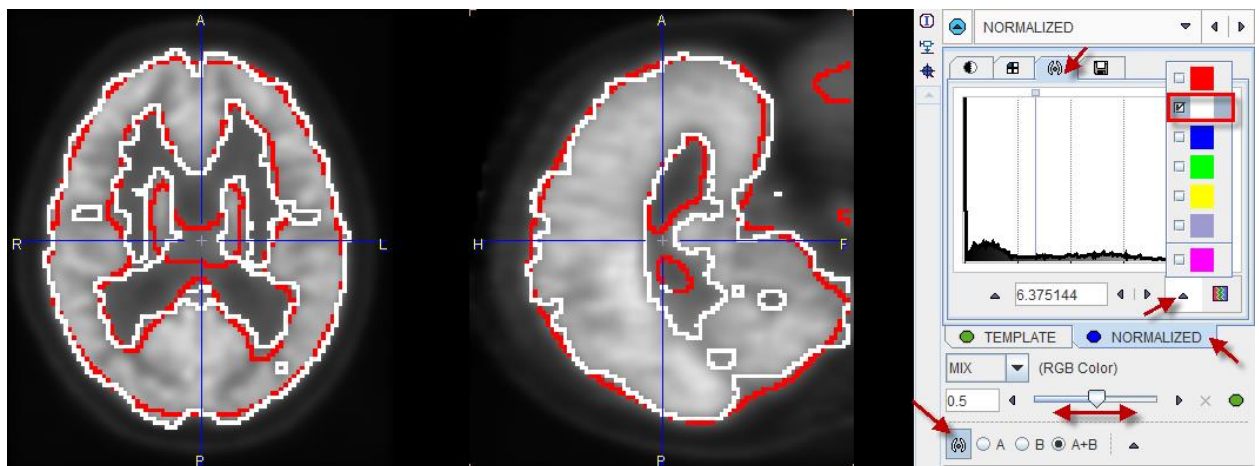
PET Normalization

The controls on the **MATCHED PET** page are appropriately set for the PET-based normalization.
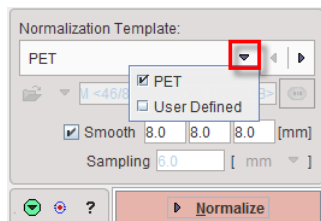
Ideally, one would use an FDG template in the MNI space which could be selected by the **User Defined** choice in the **Normalization Template** menu. However, as no FDG template is available, please select the **PET** choice. Keep the **8mm** Gaussian filtering definition and proceed with the **Normalize** button to start the calculation of the stereotactic normalization.

Normalization Validation

The resulting **NORMALIZED** FDG image is shown together with the PET template. Please use the iso-contours and the fusion slider for verifying that the normalization was indeed successful.

Proceed with the **Segment Brain** button to apply the normalization transform to the Maximum Probability Atlas.

Brain Segment Validation

The **BRAIN SEGMENTS** page shows the FDG image together with the transformed atlas image in a fusion display. As the PNEURO settings are serialized, the fusion image seen will depend on the last configuration settings of this page. Because the MRI has not been considered for the normalization, the only **Result space** options are **Atlas** and **Input/PET**, and the GM probability threshold is evaluated using an *a-priori* GM map.
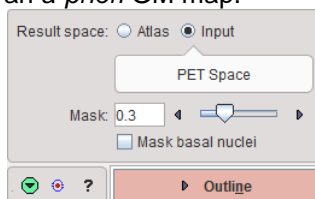
With the configuration settings above the following result is seen. Please try out how the result changes when selecting the **Atlas** result space and when shifting the GM probability **Mask** threshold.
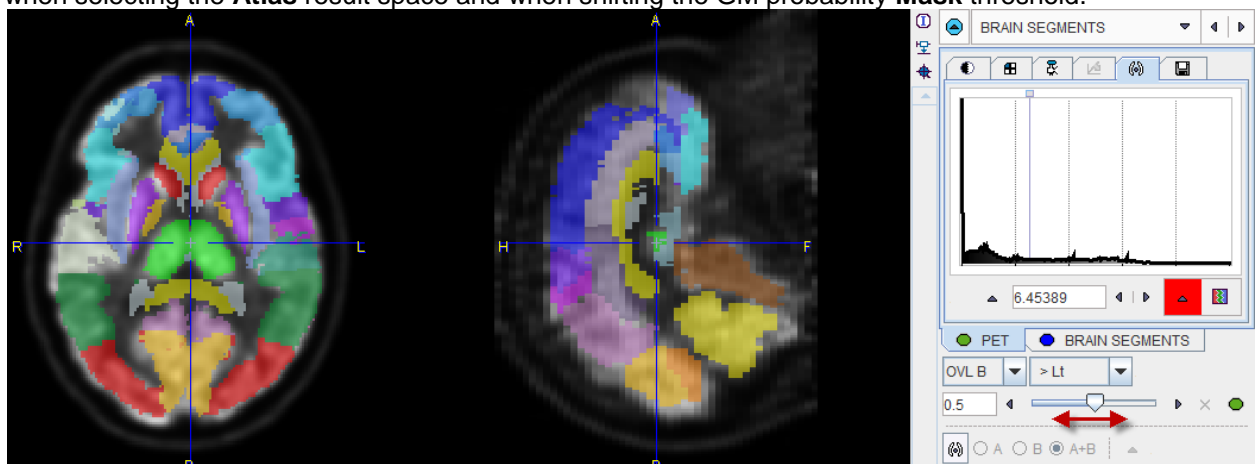
Finally, proceed with the **Outline** button to obtain the outline contour definition of the brain structures.

Volume of Interest Exploration

The resulting VOI outlines are shown on the **VOIS** page. Change the layout to show a single axial slice and select the **Gray** color table. The following result is shown.
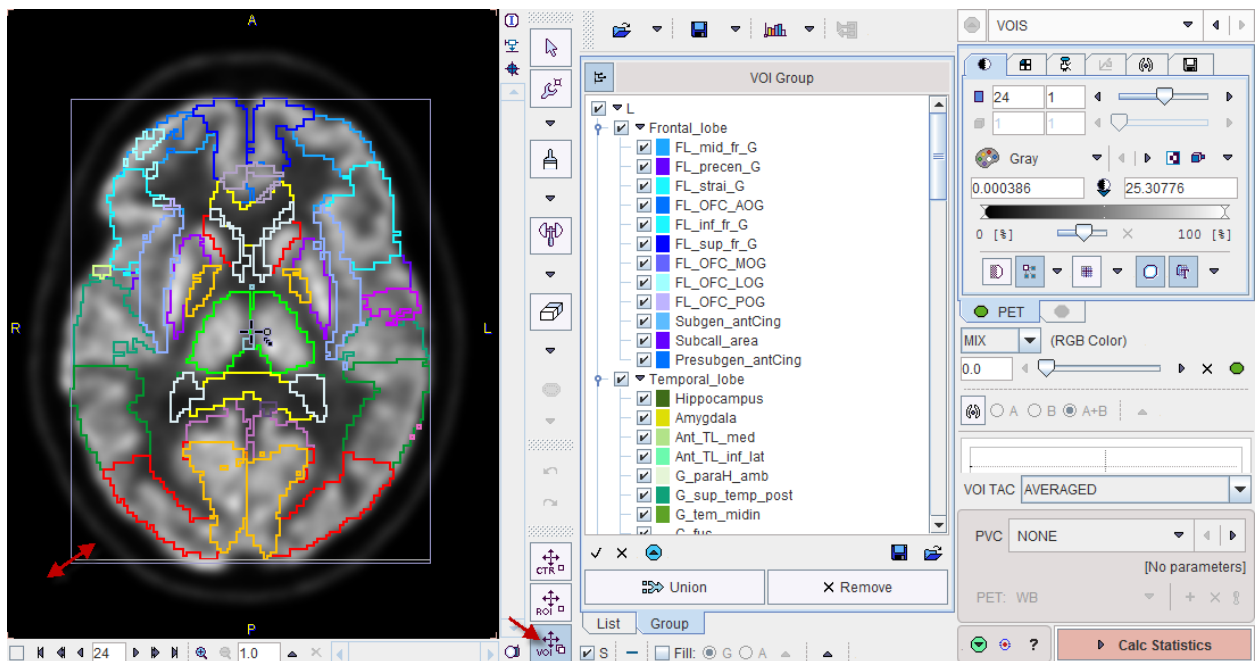
Apparently the caudate/putamen VOIs don't fit too well, while the cortical VOIs seem to be positioned too much to the inner of the brain at the left and lower side in the image. A global scaling of all selected VOIs can easily be applied by dragging the left lower corner of the bounding box with the VOI action button active.

Statistics Calculation

Finally, calculate the regional PET uptake with the **Calc. Statistics** button. The result on the **Statistics** page shows the average uptake in the 83 structures of the MPA together with their volumes.

Name	AVERAGED	Volume [ccm]	Unit
FL_mid_fr_G_l	12.907862564538233	28.363018798828126	kBq/cc
FL_mid_fr_G_r	13.85341367131928	29.198281860351564	kBq/cc
FL_precen_G_l	12.476676433419309	17.913249206542968	kBq/cc
FL_precen_G_r	12.718356858886409	17.51807098388672	kBq/cc
FL_strai_G_l	12.781398316522575	3.2916549682617187	kBq/cc
FL_strai_G_r	12.617151853840822	3.5251693725585938	kBq/cc
FL_OFC_AOG_l	13.048120870716332	4.414320373535157	kBq/cc
FL_OFC_AOG_r	12.953480692617322	4.297563171386718	kBq/cc
FL_inf_fr_G_l	12.866653638336627	13.211526489257812	kBq/cc
FL_inf_fr_G_r	13.514716793948274	12.906161499023437	kBq/cc
FL_sup_fr_G_l	13.047412515859456	32.86266174316406	kBq/cc
FL_sup_fr_G_r	12.903999167746449	33.81019134521485	kBq/cc
FL_OFC_MOG_l	12.833450755322506	4.679269409179687	kBq/cc
FL_OFC_MOG_r	12.623492265522595	4.697232055664062	kBq/cc
FL_OFC_LOG_l	12.351266994051738	2.62254638671875	kBq/cc
FL_OFC_LOG_r	13.290542751789859	2.797682189941406	kBq/cc
FL_OFC_POG_l	12.110909567096016	3.9517822265625	kBq/cc
FL_OFC_POG_r	12.072080552366359	3.7946090698242188	kBq/cc
Subgen_antCing_l	9.823736906051636	0.772393798828125	kBq/cc
Subgen_antCing_r	11.030342561442678	0.736468505859375	kBq/cc
Subcall_area_l	11.12760681576199	0.2424957275390625	kBq/cc
Subcall_area_r	8.358735611564235	0.1706451416015625	kBq/cc
Presubgen_antCing_l	12.315061128461684	0.8307723999023438	kBq/cc
Presubgen_antCing_r	12.923197110493978	0.5254074096679687	kBq/cc
Hippocampus_r	8.733252322035176	2.01181640625	kBq/cc
Hippocampus_l	8.986514400889856	1.7648300170898437	kBq/cc
Amygdala_r	8.646436798897234	1.1541000366210938	kBq/cc
Amygdala_l	9.756265306967766	1.2978012084960937	kBq/cc
Ant_TL_med_r	8.484884775519102	5.968089294433594	kBq/cc
Ant_TL_med_l	9.473763534103531	5.9635986328125	kBq/cc
Ant_TL_inf_lat_r	11.0004737991117623	3.2781829833984375	kBq/cc
Ant_TL_inf_lat_l	11.31561884141693	3.103047180175781	kBq/cc
G_paraH_amb_r	10.274733780058428	3.812571716308594	kBq/cc

Copy the results to the clipboard and paste them to Excel. Return to the **BRAIN SEGMENTS** page, change the **Result Space** to **Atlas**, outline, calculate the statistics and copy them also to the Excel. Compare the **Atlas** and the **PET** space results by calculating their % difference in Excel.

Comparison of Outcome using the Different Methodologies

For your convenience the VOIs resulting from the MR-based approaches was also calculated. The illustration below shows a side-by-side comparison of slice 24 in the PET space. The left outlines were obtained with the T_1-parcellation using 8 subjects, the middle outlines with the MPA method applied to the MRI, and the right outlines with the MPA method directly applied to the FDG PET as descriubed above.
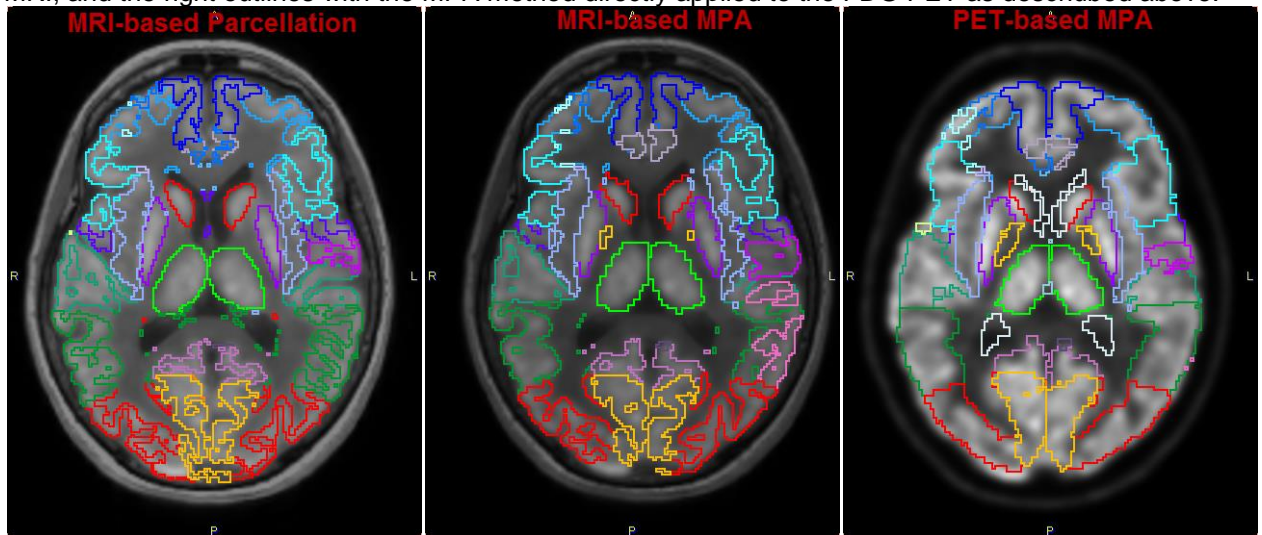
The quality of the VOI definition seems to decrease from left to right. This is in line with the recommendation of employing the anatomical MRI whenever it is available, and applying the T_1-parcellation if the basal nuclei are relevant.

Note that protocols for reproducing these results are available in the **Neuro** database.

PNEURO Hints

Computer System:

For the effective use of PNEURO with original high-resolution data workstation systems with 8 cores and 16GB RAM (or better) are highly recommended. The availability of multiple cores will speed up denoising as well as parcellation, because all hemispheres of the subjects selected in the knowledge base can potentially be processed in parallel. Note that the number of cores can effectively be doubled be enabling hyper-threading on processor chips like the Intel core i7.

When to Apply Parcellation:

The T_1-MR-based parcellation is preferable for questions related to the deep nuclei because of the construction of an individual maximum probability atlas in this area. If only cortical structures are relevant, the Maximum Probability Atlas might be preferable because the cortical outcome is very similar for both methods, but it is faster and additionally allows evaluating the results in the MNI space.

Waiting Time Reduction:

While the step-wise workflow with inspection of intermediate results is aimed at robust results, it involves some waiting time during the different processing steps. One approach to partially circumvent this problem is using the *Run all* button in the lateral taskbar:

The procedure for the MPA is:

- Load PET image and Crop
- Load MR image and Crop
- Apply default parameter button ⊙ in the lateral taskbar
- Run all

The procedure for the T_1-parcellation requires an additional step for defining the 4 landmarks:

- Load PET image and Crop
- Load MR image and Crop
- Set Denoising to None and proceed. Define the landmarks.
- Apply the default parameter button ⊙ in the lateral taskbar
- Run all

Saving of Information:

There are different ways of saving the intermediate and final results of PNEURO. Generally it is recommended saving a protocol, so that any time later the details of the analysis configuration as well as the manually edited VOIs may be inspected. If you would like to use intermediate results such as spatial transformations and/or transformed images, the most convenient procedure is to open the *Save all* window with the lateral ▣ button, check all items of interest and save, optionally with replacing the patient name by a new string.