PETPVE12-Toolbox Manual

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The toolbox authors:

Gabriel González-Escamilla

Catharina Lange

Ralph Buchert

Michel J. Grothe

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INTRODUCTION AND OVERVIEW

This manual is intended to help any user to perform a partial volume effects (PVE) correction of PET data using the PETPVE12 Toolbox. It covers different aspects of this type of image processing – starting with the very basics and ending up with additional information on how to deal with different types of data. Basically it may be divided into three main sections.

1) Download and installation. This also includes a quick-start guide on how to start the toolbox as well as a short overview of the toolbox´s principle workflow.

2) A detailed description of how to perform different types of PVE correction with the toolbox. At the end, the user should know about the common steps to create ready-to-use PVE corrected PET data for uptake quantification, and how to apply these steps with the toolbox.

3) Variations in the principle processing pipeline for some specific settings.

DOWNLOAD AND INSTALLATION

The PETPVE toolbox runs within SPM12 (http://www.fil.ion.ucl.ac.uk/spm/software/spm12/). This means that SPM12 needs to be installed and added to your Matlab path before the PETPVE toolbox can be installed. See instruction on the web for windows (http://en.wikibooks.org/wiki/SPM/Installation_on_Windows), Linux (http://en.wikibooks.org/wiki/SPM/Installation_on_Linux) or Mac OS (http://en.wikibooks.org/wiki/SPM/Installation_on_Mac_OS_%28Intel%29).

Download (https://github.com/GGonEsc/petpve12) and unzip the PETPVE toolbox (petpve12.zip) within the folder of your choice. You will get a folder called “petpve12”, which contains several matlab functions, subfolders, compiled scripts and image files. Finally, place the folder “petpve12” into the SPM12 “toolbox” folder.

The toolbox has been tested under Windows7 and Ubuntu-14.04 OS. It was tested under SPM12 running in Matlab R2013a, although it may also work with SPM8 and previous Matlab versions.

STARTING THE TOOLBOX

Start Matlab and launch SPM12 (i.e., type “spm pet” on the Matlab command window).

Select “petpve12” from the toolbox dropdown options on the SPM menu (see Fig 1).

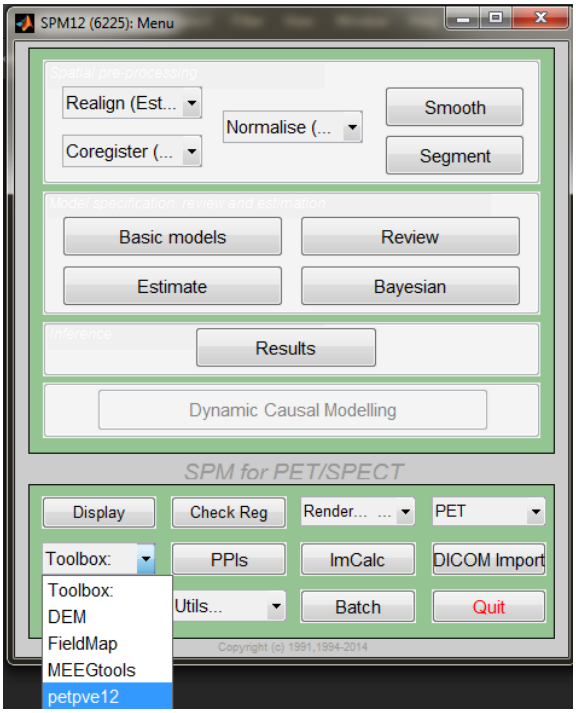

Figure 1. SPM menu, and petpve12 toolbox selection.

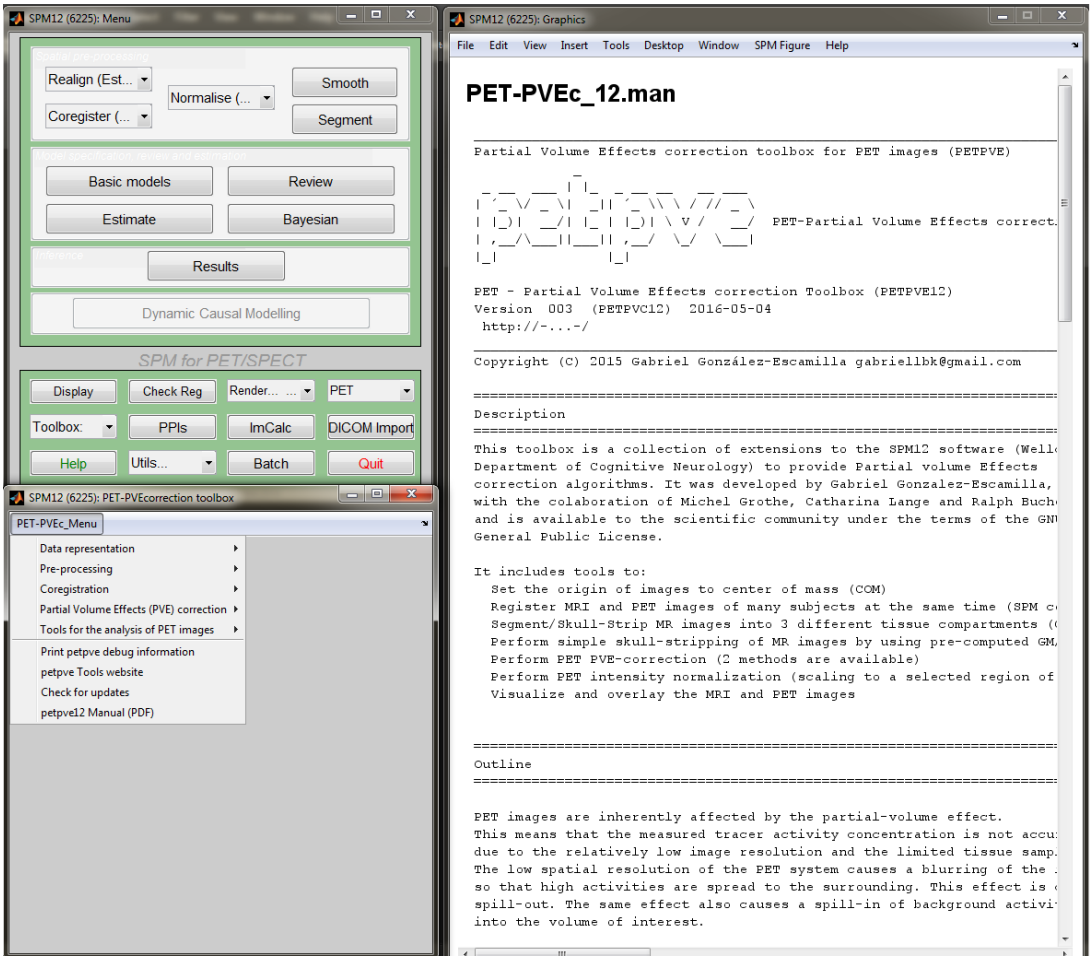

Figure 2. PETPVE12 menu and welcome page.

OVERVIEW OF PETPVE12 FUNCTIONALITY

The PETPVE12 toolbox comes with different modules suitable for PVE-correction and quantitative analysis of PET data. The different steps mainly fall into the following categories:

1) Pre-processing: Segmentation of the anatomical (T1-weighted) MRI data into gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF) tissue compartments and creation of a skull-stripped version of the original anatomical scan that may be used for PET-MRI co-registration.

2) PET-MRI co-registration: matching the spatial orientation of the PET and MRI images from the same subject using rigid-body transformations (rotations and translations).

3) Partial Volume Effects (PVE) correction of PET images: The toolbox offers principally two different possibilities:

I. Voxel-based correction using the Müller-Gärtner method (MG – Müller-Gärtner et al., 1992), including its later modifications ("modified Müller-Gärtner" [mMG] – Rousset et al., 1998b);
II. ROI-based correction using the geometric transfer matrix method (GTM - Rousset et al., 1998a).

4) Tools for the analysis of PET images:

I. Extraction of regional uptake values (in standard or native space);
II. Intensity normalization of (PVE-corrected) PET images. Intensity normalization is a post-processing step that utilizes a reference region to standardize the regional PET signal and allows for the direct inter-subject comparison of preprocessed PET data.
III. Creation of white matter ROIs according to a grey matter Atlas.

Main modules are available in the SPM12 Batch Editor environment. General information on the SPM Batch Editor Window (Batch GUI) can be found at: http://en.wikibooks.org/wiki/Neuroimaging_Data_Processing/SPM.

Note: Useful information about each module and specific parameter explanations are listed at the bottom of the Batch Editor Window.

PARTIAL VOLUME EFFECTS CORRECTION OF PET DATA (modules & how-to)

1) Anatomical MRI (T1) preprocessing

The segmentation routine implemented in the PETPVE12 toolbox is adopted from the segmentation function of the VBM8 toolbox (http://dbm.neuro.uni-jena.de/vbm/), as described in Gaser et al., (2009) and the VBM8 manual. The function has been slightly modified to allow for brain mask determination and skull-stripping. The complete function segments, bias corrects, and creates the spatial normalization parameters that map to MNI standard space (based on a DARTEL transformation to VBM8's MNI-IXI template).

Note: In order to apply the deformations from MNI to subject's space, you will need to write iy_*.nii images.

PET-PVEc_Menu → Preprocessing → Segment & Skull-Strip T1 images

Parameters:

Volumes <- X

Select one anatomical image volume for each subject.

Writing options

- Gray matter

  Produce grey matter images in native space (is in alignment with the original MRI): c1*

- White matter

  Produce white matter images in native space (is in alignment with the original MRI): c2*

Cerebrospinal fluid (CSF)

  Produce CSF images in native space (is in alignment with the original MRI): c3*

- Bias Corrected

  This is the option to produce a bias corrected version of your image. MR images are usually corrupted by a smooth, spatially varying artifact that modulates the intensity of the image (bias). These artifacts, although not usually a problem for visual inspection, can impede automated processing of the images. The bias corrected version should have more uniform intensities within the different types of tissues.

- Skull-Striped (SS)

  Skull-stripped image: ss*. Here you can select which image is going to be skull-stripped. Two options are allowed: the original structural MRI image or the bias corrected image (m0*). A skull-stripped version of the bias corrected image is output (m1*).

  Save binary Brain Mask. Produces an image volume of the binary brain mask that was used for skull-stripping: bm*

- Tissue-labeled image

The Tissue-labeled images are single files containing binary non-overlapping tissue segments, obtained via majority rule, based on the probability of a specific tissue type at each voxel and taking into account partial volume effects of mixing different tissue classes within a single image voxel**.** This image can be used in the PET PVE correction modules.

- Deformation Fields

This option is useful to apply the normalization parameters to other images or particular regions of interest. Note that the deformation field is based on "DARTEL normalization" of the MRI scan to MNI space.

Estimation options

Various options that can be adjusted in order to improve the performance of the algorithm with your data. Knowing what works best should be a matter of empirical exploration. For example, if your data has very little intensity non-uniformity artifact, then the bias regularization should be increased. This effectively tells the algorithm that there is very little bias in your data, so it does not try to model it.

Extended options

By default, the high-dimensional DARTEL spatial normalization is used. Remaining non-brain tissue can be removed more thoroughly by setting the option "Clean up any partitions" to "Thorough Cleanup". Parameters for two de-nosing methods can also be changed. The optimal weighting for the SANLM filter is internally estimated. The MRF weighting is not necessary to change, because the SANLM filter will have a much larger de-nosing effect. Values of "0" will deselect both filters.

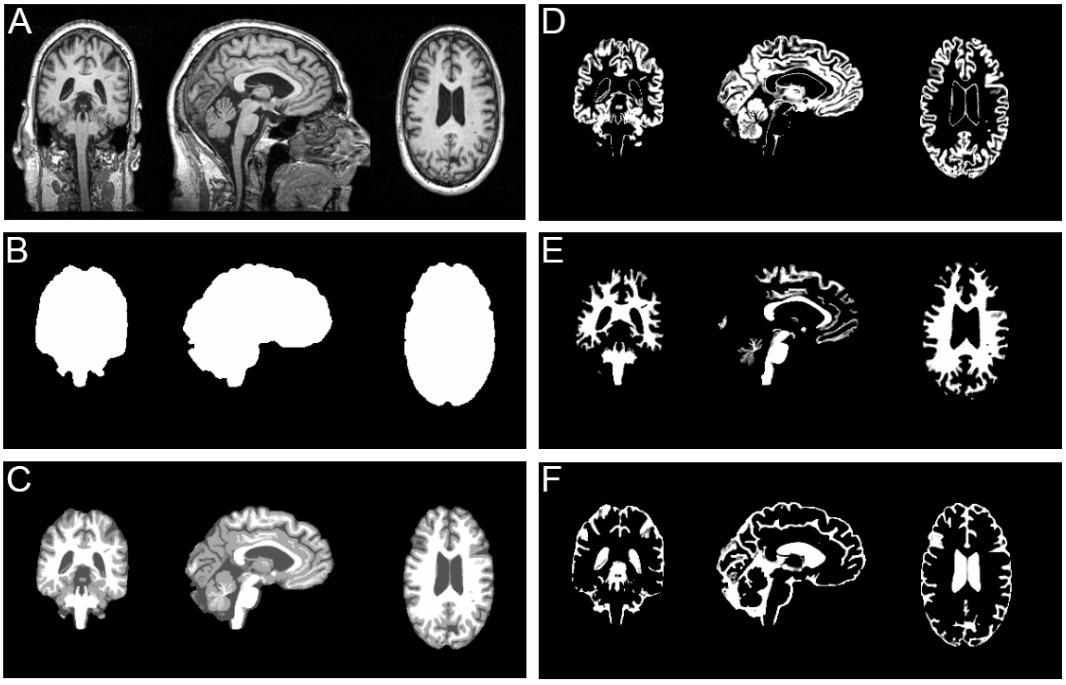

Figure 3. Example of output images from the Segmentation module. A is the original MRI (T1w); B is the brain mask; C is the tissue-labeled image; D, E and F are the probabilistic tissue segments.

Note: The segmentation function will also produce a deformation field (iy_*.nii) that may be used to deform masks and atlases from MNI to native space. Alternatively, DARTEL flow fields may be used within the toolbox.

2) PET-MRI coregistration

The first step here is to check whether the structural MRI and the PET images are in the same orientation. If the images do not approximate MNI space orientation and origin (for reference see e.g. SPM templates) they should be manually re-oriented before co-registration (see ***TECHNICAL DETAILS*** for more info).

Two options are available: "Estimate" (Recommended) and "Estimate & Reslice". Both use the standard SPM12 functions to coregister the two images

i) Align PET-MRI images (Estimate): coregistration parameters are estimated and stored into the image header without changing the actual image.

ii) Align PET-MRI images (Estimate & Reslice): the estimated transformation stored in the header will be applied to the data, generating a new dataset with the prefix 'r' (as a default; can be changed to any string).

PET-PVEc_Menu → Coregistration → "*Align PET-MRI images (Estimate)*":

Parameters:

Define the reference images by highlighting on "*Reference*" *Image* row, then click on the button *Select Files* in the bottom. Here you should select at once for all your subjects the image files (typically the structural MRI; one per subject) you want to coregister to, and click *done*.

Now do the same for the "*Source Image*" parameter, this time choosing the files (one per subject) you want to coregister to your reference images (typically the PET images).

The "*other images*" option may be used when you have another PET image from the same subject that is in alignment with the source (MR) image (it only accepts one image per subject).

There are four adaptable parameters of the coregistration function. Defaults should work best in most cases (see the SPM12 manual for more detailed information).

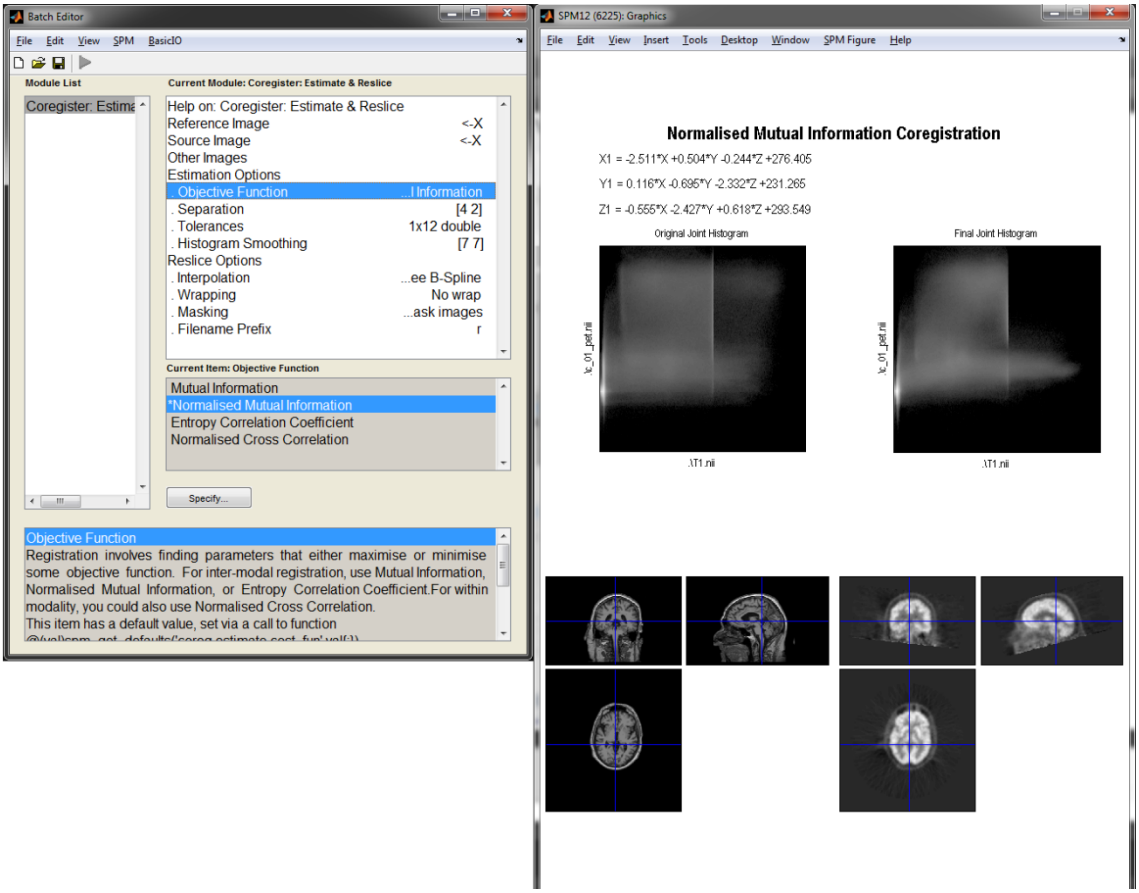

Figure 4. SPM Graphics window after coregistration process, showing successful PET to MRI coregistration.

*NOTE: "Estimate & Reslice", apart from estimating the parameters, will also create a new version of the PET image, with an 'r' prepended to the filename and with the same voxel/matrix size as the structural. This is not usually necessary when the final goal is to normalize the images to a standard template, as "estimate" parameters are encoded in the image header and SPM/the toolbox will take account of the these coregistration parameters in the subsequent steps.

3) Partial Volume Effects (PVE) correction of PET images

This is the module that performs PVE correction of the PET images. Two different types of PVE-correction (PVEc) strategies are provided by the toolbox: a voxel-based method using the 3-compartmental algorithm described by Müller-Gärtner et al. (1992) (MG) including its modifications proposed by Rousset et al. (1998b; "modified Müller-Gärtner" – mMG); and a ROI-based method using the geometric transfer matrix (GTM) correction (Rousset et al. (1998a). Detailed information on these methods and their implementation are described in the ***toolbox manuscript***. Briefly, the MG method uses the three segmented tissue compartments (GM, WM, CSF) to correct the PET GM signal for spill-in effects from the surrounding tissue (typically WM signal) as well as spill-out effects of GM PET signal into adjacent WM and CSF compartments. The GTM method is based on the estimation of signal spill-over between each pair of a pre-specified set of non-overlapping brain regions, typically a parcellation of the brain's gray matter according to some structural atlas, in addition to the WM and CSF compartments. The GTM method thus also considers signal differences, and hence spill-over, between different GM structures. In the mMG approach, the WM PET

signal used for correcting spill-in effects within the MG approach is estimated using the GTM method. Thus, to select the mMG option in the MG settings, the ROI-based correction needs to be computed first.

3.1) PVE using the MG method

Upon completion this module a PVE-corrected PET image (prefixed by pve*) will be written in the same directory as the entered PET scans.

PET-PVEc_Menu → Partial Volume Effects (PVE) correction → Partial Volume Effects (PVE) correction (MG)

Parameters:

Coregistered PET data <- X

Select one PET image volume for each subject (must be coregistered with the structural MRI). If image dimension and voxel size of the PET image do not match the MRI (such as when using "*Align PET-MRI images (Estimate)"* in the coregister step*)*, the PET image will be automatically resliced.

Tissue segments

Enter the type of input segments: 'Probabilistic maps' or 'Tissue-labeled image'

- Probabilistic maps (Default)

  Can be any tissue probability map, independent of the segmentation algorithm (i.e. output from segmentation routines in SPM 5/8/12 or VBM8/PETPVE12 toolboxes. Although segmentation maps from other software packages such as FSL may also work, here the names of tissue maps must contain the corresponding prefixes: c1* or p1* for GM; c2* or p2* for WM; and c3* or p3* for CSF).

  • GM segments

    Enter gray matter tissue segment maps (c1* or p1*)

  • WM segments

    Enter white matter tissue segment maps (c2* or p2*)

- Tissue-labeled image

  • Tissue-labeled image

    Enter the tissue labeled image as output from VBM8 "Est&Write" or PETPVE12 "Segment & Skull-Strip".

PVE-correction options

- PET PSF (FWHM in mm)

  Enter the Point Spread Function (PSF) of the PET scanner, can be a single number (for isotropic PSFs) or a 1 by 3 vector (for non-isotropic PSFs).

- Gray matter threshold

  Threshold to binarize the probabilistic GM tissue segments.

Optimal threshold may depend on the quality and acquisition parameters of the structural MRI scan as well as on the particular segmentation algorithm used to define the different tissue types. Default setting is 0.5. This threshold resulted in reasonably sized GM segments when segmenting our test MRI data (from ADNI) with the VBM8 segmentation routine as implemented in the toolbox - segmentation module.

- CSF Signal

For most commonly used radiotracers the CSF signal can be assumed to be zero, and spill-in effects are typically neglected in the PVE correction procedure. Default is false, by setting this parameter to true, the PVE correction will also estimate and correct CSF spill-in effects.

• Zero CSF signal

• Estimate CSF segments

- From tissue-labeled image

- From CSF segments

Enter cerebrospinal fluid segment maps (c3* or p3*)

- Save convolved tissue maps

The PSF-convolved tissue segments can be written to disk. Default is false.

Estimation of WM (and CSF) signal

Select a method to compute the WM (and, if specified, the CSF signal). Five methods are provided: “From WM tissue segments” (default), “Eroded WM tissue segments”, “Using values from GTM (mMG)”, “From MNI deep-WM mask”, “User specified values”:

- User specified values

Enter a vector with the WM signal of every subject.

Enter a vector with the CSF signal of every subject. Only available when “CSF Signal” is set to true.

- From deep-WM mask in a (standard space) template

• Deep WM binary mask

Select the mask for deep white matter in the template. It will be deformed to match subject’s native space (dimensions and voxel size) using the DARTEL flow field (u_*) or the deformation field (iy_*) specified in the next step.

• Deformation Input

File that describes the mapping from the template to the individual’s anatomy. Two options are allowed for input:

- “DARTEL flow field” (u_*.nii) or “Inverse deformation field” (iy_*.nii). A deformed version of the WM label to subject’s native space is written to disk (prefixed by w*).

· Dartel flow field

· Inverse deformation field

- From WM tissue segments (Default)

  If probabilistic maps are selected as tissue segments, PET signal will be averaged across all voxels that surpass the specified threshold value (default is 0.5 as for the GM).

- Eroding WM tissue segments

  Tissue compartment images, either probabilistic or tissue-labeled, can be eroded (voxels at the edge are removed) based on a Gaussian weighting function. This is helpful when you do not have a standard mask for the deep WM (and CSF) signal spill-in calculation, and/or you do not want to draw a mask on every subject. Erosion can be increased modifying the value 'PVEopts.EroThresh' on "geg_petpve12_get_defaults.m". It saves to disk the eroded versions with the prefix: e*.

- Using values from GTM (mMG)

  This is the option to create the modified-MG (mMG) corrected images by using the WM (and CSF) signal from the ROI-based GTM mehod.

  Select the *.txt file output from the GTM method.

3.2) PVE using the GTM method

The primary output from this module is a .txt file containing the raw and PVE-corrected average PET signals of all specified regions (pvc*_labels.txt). Optionally, an image volume can be written to disk, which contains all regions, labeled with their average PVE-corrected PET signal (pvc*_labels.nii).

PET-PVEc_Menu → Partial Volume Effects (PVE) correction → Partial Volume Effects (PVE) correction (GTM)

Parameters:

Coregistered PET data <- X

Select one PET image volume for each subject (already coregistered with its structural MRI). If image dimension and voxel size of the PET image do not match the MRI (such as when using "*Align PET-MRI images (Estimate)"* in the coregister step*)*, the PET image will be automatically resliced.

Tissue segments

Enter the type of input segments: 'Probabilistic maps' or 'Tissue-labeled image'

- Probabilistic maps

  Can principally be any tissue probability map, independent of the segmentation algorithm (i.e. output from segmentation routines in SPM 5/8/12 or VBM8/PETPVE12 toolboxes, although segmentation outputs of other software packages such as FSL may also work when prefixing accordingly).

  • GM segments

    Enter gray matter tissue segment maps (c1* or p1*)

  • WM segments

    Enter white matter tissue segment maps (c2* or p2*)

- Tissue-labeled image

• Tissue-labeled image

Enter the tissue labeled image as output from VBM8 “Est&Write” or PETPVE12 “Segment & Skull-Strip”.

PVE-correction options

- PET PSF (FWHM in mm)

Enter the Point Spread Function (PSF) of the PET scanner, can be a single number (for isotropic PSFs) or a 1 by 3 vector (for non-isotropic PSFs).

- CSF signal options

For most commonly used radiotracers the CSF signal is assumed to be zero, and spill-over effects are typically neglected during the PVE correction procedure in most PET studies.

However, the GTM method is aimed at controlling for partial volume effects in small regions, where the CSF spill-over can be appreciable. Accordingly, the toolbox will always include the CSF into the GTM algorithm.

- CSF signal

• Atlas-defined CSF ROIs

Predefined CSF ROIs in the input atlas (Default).

• Single CSF ROI

A single CSF ROI, created with from the tissue map.

- GTM inclusion of CSF

• From CSF segments

Enter cerebrospinal fluid segment maps (c3* or p3*)

• From tissue-labeled image

Use the CSF map inside the tissue-labeled image

White matter (CSF) options for GTM inclusion

- Tissue threshold (Default)

Threshold for WM/CSF tissue segments to avoid overlapping with GM (necessary for GTM). Default is to use the same as for GM (0.5). *This option has no effect on the tissue-labeled image.
This can be changed via the geg_petpve12_defaults.m

- Tissue erosion

Erode the mask (probabilistic or tissue-labeled) to remove edge voxels.

GTM creation options

Select a method to define labels of the different brain structures to be used in the Geometric Transfer Matrix (GTM) method. Individual ROIs can be obtained by manually delineating an individual’s structural

MRI scan or by automatically propagating the labels of some standard anatomical atlas onto the individual's anatomy. (Note that the WM and CSF ROIs must be defined in the corresponding atlas).

Two options are available:

(i) "Atlas in (standard) template" (default)

(ii) "Atlas in subject's native space"

• Atlas in standard template

- Template Atlas <- X

Select the *.nii volume image containing all brain ROIs labeled with unique numbers. This atlas is propagated to the individual MRI, and masked with the tissue compartments to avoid ROI overlapping and reduce misalignments due to inaccuracies of the registration process. Default choice is the Desikan-Killiany structural atlas in the "Atlases" folder of the toolbox.

- Deformation Input

Two options are allowed for input: "DARTEL flow field" (u_*.nii) or "Inverse deformation field" (iy_*.nii). A deformed version of the atlas volume image to the subject's individual space is written to disk (prefixed by w*)

· DARTEL flow field (Default)

· Inverse deformation field

- Deformation Options

Defaults should be OK.

• Atlas in subject's native space

- Parcellation Atlas <- X

Select the *.nii volume image containing all ROIs (labeled with unique numbers) in the same space as the MRI scan.

Atlas descriptor file

A .txt file containing the names (1st column) and numbers of the atlas ROIs (2nd column). Default is the atlas descriptor of the Desikan-Killiany atlas (in the "Atlases" folder of the toolbox).

4) Tools for the analysis of PET images

4.1) Create binary masks from template atlas

This function allows the user to extract single ROIs from an atlas image, or to create a single composite mask from series of ROIs contained in an atlas; e.g. create a mask of the cerebellum to perform intensity normalization, or create a cortical composite ROI typically used in amyloid PET studies.

PET-PVEc_Menu → Analysis → Create mask/composite from atlas

This is not part of the SPM batch. Inputs: the atlas image and a txt file (tab separated) containing the ROI names (1st column) and their respective numerical ID (2nd column) of regions used to form the binary new mask.

4.2) Mean value extraction from ROIs/Atlas

4.2.1) Mean values within ROIs (calculation in standard space)

This function displays on screen the mean signal values within one or several binary masks extracted from the spatially normalized PET data The binary mask and the subjects must be in the same standard anatomical space (e.g. DARTEL warped images).

PET-PVEc_Menu → Analysis → ROI/Atlas estimations → single ROIs mean (standard space)

This is not part of the SPM batch. Inputs: one or more binary masks; warped PET images.

4.2.2) Mean values within all regions defined by an atlas (calculation in standard space)

This function estimates mean values of each ROI (atlas label) in a template atlas for all selected subjects. Both atlas and subjects should be in the same standard anatomical space (e.g. DARTEL warped images).

This function creates an excel file containing the subject values (rows) of every ROI (columns).

PET-PVEc_Menu → Analysis → ROI/Atlas estimations → Atlas means (standard space)

This is not part of the SPM batch. Inputs: Template atlas, a txt file (tab separated) containing the names (1st column) and ID numbers (2nd column) of regions, warped PET images, and an output directory to save the excel file named: wName_of_atlas.nii

4.2.3) Mean values within ROIs (calculation in native space)

This is basically the same as the function ***4.2.1***, but it first propagates the ROI mask from template space to the subjects' native space and performs the signal averaging there. The function requires deformation fields (u_* or iy_*) to be specified that map from template space to the individuals' native space.

PET-PVEc_Menu → Analysis → ROI/Atlas estimations → single ROIs mean (native space)

This is not part of the SPM batch. Inputs: one or more binary masks, native space PET images. The function will ask you whether you want to use SPM inverse deformation fields (iy_*) or the DARTEL flow fields (u_*) to map from template to native space.

4.2.4) Mean values within all regions defined by an atlas (calculation in native space)

This is basically the same as the function ***4.2.2***, but it first propagates the atlas file from template space to the subjects' space and performs the signal averaging there. This function requires the deformation fields (u_* or iy_*) to be specified that map from template space to the individual's' native space.

This function creates an excel file containing the subject values (rows) of every atlas label (columns).

PET-PVEc_Menu → Analysis → ROI/Atlas estimations → Atlas means (native space)

This is not part of the SPM batch. Inputs: Template atlas, a txt file (tab separated) containing the names (1st column) and ID numbers (2nd column) of regions, native space PET images, and an output directory to save the excel file named: Name_of_atlas.xls. It will ask you whether you want to use SPM inverse deformation fields (iy_*) or the DARTEL flow fields (u_*) to map from template to native space.

4.3) PET intensity normalization

In order to interpret the (PVE-corrected or uncorrected) PET signal in a (semi-)quantitative way, the values are typically rescaled or "intensity normalized" to a reference value from a brain region that is considered to reflect only unspecific tracer binding and/or is believed not to be affected by the entity that is being studied.

The module can perform this step directly on voxel-wise PET images. The user can use pre-estimated values or use provided masks for this purpose (whole cerebellum, cerebellar gray matter, and brain stem). These masks are provided within the "Atlases" folder of the toolbox.

PET-PVEc_Menu → Analysis → PET intensity normalization

Parameters:

PET-data <-X

Select PET data for intensity normalization, e.g. the pve* output from the PVE-correction step

Reference activity

Three options are available: "From mask in MNI space", "From mask in subject's space" and "using pre-estimated values".

From mask in MNI space

From mask in subject's space

- Individual masks of reference region

  Select a binary mask of the reference region for each subject.

- Standard space mask of reference region

  Select one binary mask in MNI space. This mask will be deformed to each subject's individual space based on the deformation input that has to be specified below.

- Deformation Input

  Two options are allowed for input: "DARTEL flow field" (u_*.nii) or "Inverse deformation field" (iy_*.nii). A deformed version of the reference region's label to subject's native space is written to disk (prefixed by w*).

  · DARTEL flow field

  · Inverse deformation field

- Deformation Options

  Default options should be OK for most situations.

Using pre-estimated values

Enter a vector with the 'reference' signal of every subject.

*NOTE: This step is not mandatory, since the user can also introduce the mean values of the reference region as a scaling value into the statistical model. Although, it can be performed for statistical simplicity.

4.4) Creation of WM ROIs according to a GM template atlas

Tissue segments

Enter the type of input segments: 'Probabilistic maps' or 'Tissue-labeled image'

- Probabilistic maps

Can principally be any tissue probability map, independent of the segmentation algorithm (i.e. output from segmentation routines in SPM 5/8/12 or VBM8/PETPVE12 toolboxes, although segmentation outputs of other software packages such as FSL may also work when prefixing accordingly).

• GM segments

Enter gray matter tissue segment maps (c1* or p1*)

• WM segments

Enter white matter tissue segment maps (c2* or p2*)

- Tissue-labeled image

• Tissue-labeled image

Enter the tissue labeled image as output from VBM8 "Est&Write" or PETPVE12 "Segment & Skull-Strip".

Options to avoid tissue overlapping

• Threshold WM/CSF tissue segments (Default).

Uses a threshold to binarize the WM/CSF tissue segments used to limit the WM/CSF atlas regions. Default is 0.5.

• Tissue erosion

Erodes tissue segments using a Gaussian weighting function to limit the WM/CSF atlas regions.

CSF options for atlas inclusion

• Single CSF ROI

If your atlas does not contain any CSF ROI this option adds the one CSF, according with the subject tissue map. If your template atlas already contains CSF regions, this option is not for you.

• Multiple CSF ROIs (default)

If your template atlas already contains CSF regions, this options allows you to keep them.

Template Atlas options

- Template Atlas in standard space

  - Template Atlas <- X

    Select the *.nii volume image containing all brain ROIs labeled with unique numbers. This atlas is propagated to the individual MRI, and masked with the tissue compartments to avoid ROI overlapping and reduce misalignments due to inaccuracies of the registration process. Default choice is the AAL structural atlas in the “Atlases” folder of the toolbox.

  - Deformation Input

    Two options are allowed for input: “DARTEL flow field” (u_*.nii) or “Inverse deformation field” (iy_*.nii). A deformed version of the atlas volume image to the subject’s individual space is written to disk (prefixed by w*)

    · DARTEL flow field

    · Inverse deformation field

Atlas descriptor file

A .txt file containing the names (1st column) and numbers of the atlas ROIs (2nd column). Default is the atlas descriptor of the AAL atlas (in the “Atlases” folder of the toolbox).

TECHNICAL INFORMATION

Standard SPM (templates) orientation

SPM and the toolbox assumes the following image positions:

The top-left image is coronal with the top (superior) of the head displayed at the top and the left shown on the left. This is as if the subject is viewed from behind (See Figure 5).

The bottom-left image is axial with the front (anterior) of the head at the top and the left shown on the left. This is as if the subject is viewed from above (See Figure 5).

The top-right image is sagittal with the front (anterior) of the head at the left and the top of the head shown at the top. This is as if the subject is viewed from the left (See Figure 5).

If your images do not match this orientation you can use SPM's display functions to reorient your image.

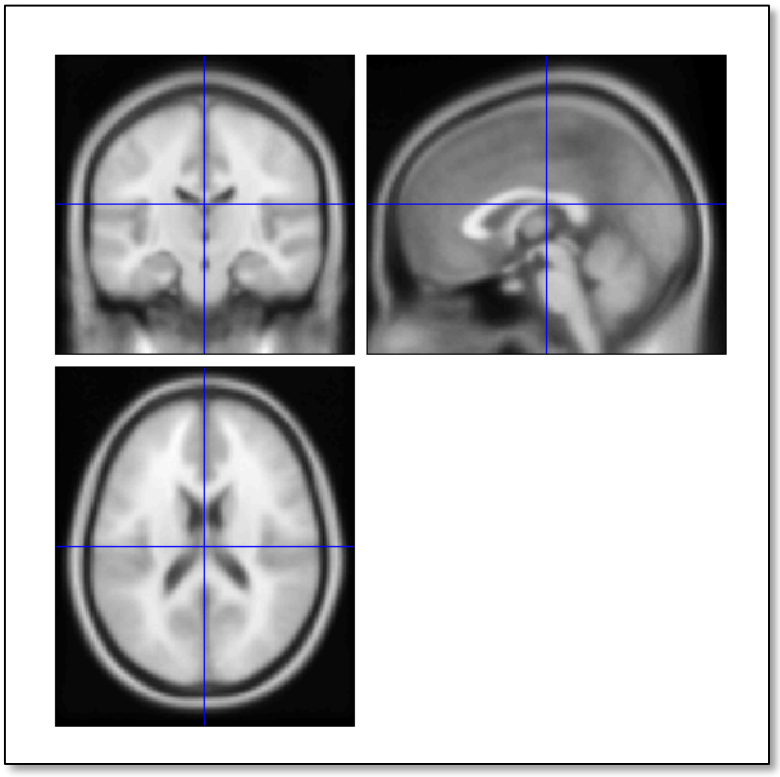

Figure 5. SPM standard orientation (avg152T1).

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Authors: **Gabriel González-Escamilla, Catharina Lange, Ralph Buchert** and **Michel Grothe**.