

# Digital Brain Perfusion Phantom Documentation

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## Introduction

The Digital Brain Perfusion Phantom package provides data and Matlab tools to create a realistic digital 4D brain phantom, in particular for reproducible evaluation of reconstruction algorithms using non-linear regularization for perfusion CT and perfusion C-arm CT. It is based on the Realistic Digital Brain Perfusion Phantom originally published by Riordan et al. [1]. Since classical digital CT phantoms usually consist of homogeneous structures and have a very sparse representation in transformations like total variation or wavelets, they highly favor non-linear reconstruction algorithms. This phantom allows for a more authentic evaluation by providing a brain model based on real physiological data and avoiding sparsity by continuously varying perfusion parameters and anatomical structures using MR data.

The phantom was created by segmenting brain MRI scans from a human volunteer into white and gray matter, cerebrospinal fluid (CSF), skull and arteries. White/gray matter and CSF segmentation was done from T1 weighted MRI data using the Freesurfer software [2]. The skull was segmented from a sequence of MRI scans using a dedicated algorithm [3]. Arteries were segmented from a time-of-flight acquisition by thresholding and manual post-processing.

The package includes a tool to annotate areas with reduced and severely reduced perfusion inside the segmented brain and a tool to create a 4D volume consisting of time attenuation curves (TACs) corresponding to the annotated tissue areas. The TACs inside the brain tissue are simulated by convolution of an arterial input function (AIF) measured with clinical perfusion CT [1] with residual functions, which correspond to the stroke annotation. The TACs of vessel structures are simulated by the real measured AIF. Anatomic tissue structures are incorporated into the phantom by adding appropriate constants to the TACs.

To reduce the sparsity of the brain phantom, the MR data is used to vary the perfusion parameters assigned to the tissue voxels by the annotation. Therefore each tissue voxel is associated with a normalized value of its T1 weighted MR value. The MR values are normalized to interval  $[-1, 1]$  in each slice by first computing the mean and the standard deviation  $\sigma$  of all MR values inside the slice associated to a segmented tissue voxel. Then the mean is subtracted

from the MR values and the values are limited to  $[-2*\sigma, +2*\sigma]$  by setting all values  $< -2*\sigma$  to  $-2*\sigma$  resp. all values  $> 2*\sigma$  to  $2*\sigma$ . Finally all values are divided by  $2*\sigma$ . The perfusion parameters of each tissue voxel are varied by:

$$PV(x) = P(x) + NMR(x) * DP(X)$$

$PV(x)$  denotes the varied perfusion parameter of voxel  $x$  (CBF or MTT, CBV is defined as  $CBF*MTT$ ),  $P(x)$  the default perfusion parameter of voxel  $x$  according to annotation,  $NMR(x)$  the normalized MR value and  $DP(x)$  the maximal deviation of the perfusion parameter. The HU values of the anatomic structures are varied similarly to reduce sparsity.

For an overview of computational methods to calculate perfusion parameters from reconstructed TACs see [4].

[1] A. J. Riordan, M. Prokop, M. A. Viergever, J. W. Dankbaar, E. J. Smit, and H.W. A. M. de Jong, "Validation of ct brain perfusion methods using a realistic dynamic head phantom," *Medical Physics*, vol. 38, no. 6, pp. 3212–3221, 2011.

[2] Freesurfer image analysis suite. [Online]. Available: <http://surfer.nmr.mgh.harvard.edu/>

[3] Navalpakkam BK, Braun H, Kuwert T, et al., Magnetic Resonance-based attenuation correction for PET/MR hybrid imaging using continuous valued attenuation maps. *Invest Radiol*. 2013, 48:323-332.

[4] A. Fieselmann, M. Kowarschik, A. Ganguly, J. Hornegger, and R. Fahrig, "Deconvolution-based ct and mr brain perfusion measurement: Theoretical model revisited and practical implementation details," *International Journal of Biomedical Imaging*, 2011, article ID 467563.

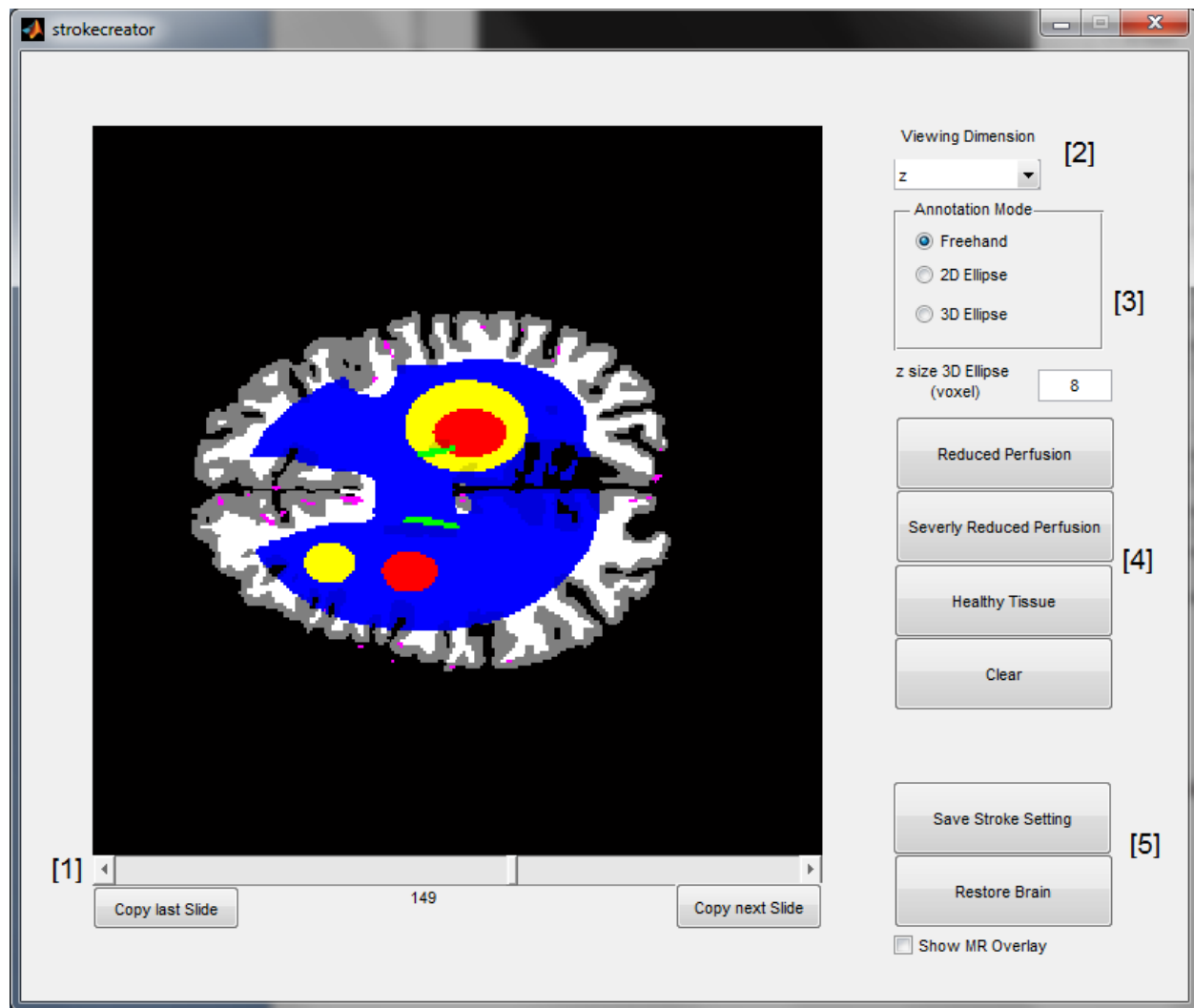


Figure 1: Stroke Annotation Tool

## Stroke Annotation Tool

To create a 4D perfusion brain phantom, first start the stroke annotation tool by calling `strokecreator` from the Matlab command prompt.

Scroll through the segmented brain slices using slider [1].

Select viewing dimension in popup box [2].

Select annotation mode “Freehand”, “2D Ellipse” or “3D Ellipse” [2]. For “3D Ellipse” mode set length of z axis of the 3D ellipse in corresponding text box.

Annotate areas with reduced (yellow) and severely reduced (red) perfusion by clicking on corresponding buttons [4] and drawing the area into segmented brain.

There is also possibility to annotate areas with healthy tissue. These areas will be marked in the saved annotation file for later evaluation purposes. Tissue that was not annotated will also be simulated as healthy tissue.

To clear annotated structures, click “Clear” button and draw the area to clear into the segmented brain.

To save the current annotation, press the “Save Stroke Setting” button [5] to save the annotation in the “brain.mat” file. A previously existing file in the directory will be overwritten. The annotation saved in the “brain.mat” file will be automatically loaded when starting `strokecreator`. To clear all annotations press the “Restore Brain” button. To show the T1 weighted MR overlay, which is used to vary the perfusion parameters and anatomical structures, activate the “Show MR Overlay” checkbox.

Click “Copy last slide”/“Copy next slide” buttons [1] to copy annotated areas from the previous respectively following slice.

## 4D Phantom Creation Tool

After finishing annotation and saving the annotation in the “brain.mat” file, the `create_phantom` function creates the 4D volume describing the anatomical structures and the dynamic TACs of the digital brain according to the annotated stroke structures.

To modify the perfusion parameters, the static HU units of the anatomical structures and their variation, open the `create_phantom.m` file and change the corresponding constants in the beginning of the Matlab code. CBF values are given in ml/100 ml/min, CBV values in ml/100ml and MTT values in seconds. The MTT values are always defined as CBV/CBF.

Start `create_phantom(phantompath, dt, addskull)` function to create 4D phantom data files. The `phantompath` parameter defines the output directory for the raw phantom data files. The 4D volume will be written as 3D volumes sampled in with the temporal distance defined by parameter `dt` in the temporal interval [0...49] s. The parameter `addskull` indicates if a skull is added to the brain phantom. Each 3D volume is written as raw data file in 32 bit floating point precision and is of size 256x256x256. The file name of each written 3D volume is an integer number defining its time sample index starting with 1, e.g. if `dt` was set to 0.5 s the 3D volume with filename `i = 21` is the time sample at  $t = (i-1)*dt = 10$  s.