Recipes for MAP18

by Hans-Jürgen Huppertz

Swiss Epilepsy Clinic, Zurich

(still in development)

Introduction

The Morphometric Analysis Program v2018 (short: MAP18) is intended to facilitate the detection and visualization of epileptogenic pathologies. A major part of the program is dedicated to morphometric MRI analysis, which compares the individual brain anatomy with a normal database and highlights deviations in terms of gyration, cortical thickness and grey-white matter differentiation. This shall improve the recognition and delineation of focal cortical dysplasias (FCD) and other cortical malformations. Furthermore, the software allows creating serial curved surfaces in different depths parallel to the cortical surface. This resembles the method of Curvilinear Reformatting as proposed by Bastos et al. (1999) but requires no manual input (e.g., no marking of supporting points on the cortical surface). Moreover, the software includes SISCOM analysis (i.e. subtraction ictal single-photon emission computed tomography (=SPECT) coregistered to MRI), whole brain FLAIR analysis as proposed by Focke N et al. (Epilepsia 2008 and 2009), quantitative FLAIR analysis of temporo-mesial structures (Huppertz HJ et al., Epilepsy Res 2011), automated detection of periventricular nodular heterotopia (PNH) (Pascher B et al., Epilepsia 2013), and tools for visualization of implanted subdural electrodes (Kovalev D et al., AJNR 2005). Recently, a simple volumetric MRI evaluation was added for structures important in epileptology such as hippocampi, cerebral hemispheres, etc.

MAP18 is based on algorithms of the free and open source software for Statistical Parametric Mapping (SPM; cf. https://www.fil.ion.ucl.ac.uk/spm) of the Wellcome Centre for Human Neuroimaging, UCL Queen Square Institute of Neurology, London, UK, in its current version (SPM12; cf. https://www.fil.ion.ucl.ac.uk/spm/software/spm12).

Officially, MAP18 is intended for research purposes only and has not been reviewed or approved by the European Medicine Agency (EMA) or by any other agency. Any clinical application of the software is at the sole risk of the party engaged in such application. There is no warranty of any kind that the software will produce useful results in any way. Use of the software is at the recipient's own risk.

Compared to the previous version (i.e. MAP07), MAP18 includes the following improvements and new features:

- usage of SPM 12 algorithms for normalization and segmentation
- improved segmentation of SPM12 (into 6 instead of 3 compartments)
- new large normal database of > 3000 averaged T1 images
- FCD detection by artificial neural networks
- conversion of result images back to DICOM format
- volumetric MRI analysis

The whole program roughly consists of the following files:

- map18.p (main program)
- map18.m and map18_welcome.txt (explanatory texts)
- several MATLAB mex files precompiled for Windows 32bit and 64bit
- several template and masking images
- several normal databases
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The program requires:

- SPM12 software
- bet_for_map18.exe (renamed version of the FSL brain extraction tool)

To present result images, the program uses 'MRIcro 1.37' and 'MRIcron' (by Chris Rorden; http://www.mccauslandcenter.sc.edu/crnl/tools) and can invoke the Mango viewer (http://ric.uthscsa.edu/mango) if it is present in the MATLAB path or in the subdirectory 'c:\Program Files\Mango'). 'MRIcroGL' is used for volume rendering of results from curvilinear reformatting, and 'Surf Ice' to display the cortical surface (both programs by Chris Rorden; http://www.mccauslandcenter.sc.edu/crnl/tools).

MAP18 expects one or more T1- or T2-weighted MRI volume data sets in ANALYZE or NIFTI format with axial and radiological orientation as input. The origin should be approximately at the anterior commissure. Alternatively, instead of images in ANALYZE or NIFTI format, the program can also import DICOM images, convert them to ANALYZE format and then process them. In this case, the program expects the path and name of the directory containing the DICOM images as input.

There are three possibilities for calling and executing MAP18:

- Using the graphical user interface (GUI mode): When calling 'map18' without input arguments, the program will ask for one or more input files and additional input arguments using a graphical user interface (GUI). The input image(s) can be offered in NIFTI, ANALYZE or DICOM format.
- From command line: The function 'map18' can be executed from the command line with name and path of one image volume ('*.img' or '*.nii') and additional input arguments. The format is:
  `map18(image,mode,norm,space,sensitivity,ROI_mode,viewer,age,email)`
  The variables `'image','mode','norm'` etc. have to be filled / replaced by the appropriate content (cf. appendices). The second last item (i.e. `'age'`) is optional and must only be used when volumetric analysis is desired. The last item (i.e. `'email'`) is also optional and can be omitted.
- Using the automatic processing pipeline: A call to the function 'automatic_MAP18.m' invokes this pipeline. It is necessary to edit the parameter file

'automatic_MAP18.ini' beforehand to adjust the program to local conditions (i.e. site-specific names for institution and sequences etc.). For further explantions cf. the PDF named 'Editing the automatic_MAP07.ini file.pdf' or the Appendix 'Editing the 'automatic_MAP18.ini' - File'. It is strongly recommended to rename the parameter file mentioned above with a site-specific filename in order to avoid overwriting by future updates.

The following chapters present a collection of 'recipes' for use of MAP18. In these recipes, various tasks and types of image processing are explained step by step. Text passages in blue colour inserted in between provide further explanations and recommendations.

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Installation of MAP18

MAP18 is based on algorithms of the SPM software (statistical parametric mapping, Wellcome Trust Centre for Neuroimaging, London, UK) and additional procedures developed in house. It runs on MATLAB (Mathworks, US) which is available for diverse operating systems. So far, no additional MATLAB toolbox is necessary. Even the internal use of artificial neural networks (ANN) for FCD detection does not require MATLAB's Neural Network Toolbox (the toolbox is only necessary for the training process). However, the use of ANNs is the reason why MAP18 will only run on MATLAB versions that are not older than the R2011b release of MATLAB®. In addition, since several external Windows programs are invoked by MAP18 (e.g. for brain extraction or presenting result images), the software is only meant to run on a PC with Windows operating system.

An installation file named `'install_MAP18.p'` allows installing MAP18 on any Windows PC where the earlier version MAP07 was already registered and where a MATLAB version higher than release R2011a is running. On new PCs never used with any previous MAP version run `'diagnose.p'` or call `map18('diagnose')` from MATLAB command line and return the output to the author of MAP18.

The installation (and later updates as well) requires an internet connection to the FTP server of the Swiss Epilepsy Clinic ('share.swissepi.ch') to download all necessary data including scanner- and site-specific normal databases. All parameters for the connection to our FTP server (i.e. FTP address, username, password) are already integrated in the installation file. However, it may be necessary to adjust the local firewall settings with the help of IT staff (e.g. open the firewall for address 'share.swissepi.ch' and port 21). The connection to the FTP server is only necessary for installation and updates, not for normal operation of MAP18.

To start the installation, copy the file `'install_MAP18.p'` to the folder where MAP18 and all additional programs shall be installed. Then run `'install_MAP18.p'` in MATLAB and follow the instructions in the installation routine. At the end of installation, a hyperlink named `'update_MAP18'` allows to download the most recent program files, while another hyperlink named `'test_MAP18'` starts a first test run on the MRI data of an example case included in the installation download.

Alternatively, the participants of the Summer School on Imaging (SuSIE, http://www.imaging-in-epilepsy.org) should install MAP18 from the distributed USB stick. To this end, start MATLAB, switch to the subfolder `'…\MATLAB-Programs\MAP18_for_SPM12\MAP18_Program'` on this USB stick and call the tool `'transfer_MAP18.p'` from MATLAB command line. When asked for a new location of

MAP18, enter `'c:\'` or – for example, in case of missing writing permissions at this level of the system disk - choose another appropriate destination.

For the rest of this document, it is assumed that MAP18, SPM12 and all other programs and example data sets have been installed or copied below `'c:\MATLAB-Programs'`. Otherwise, the paths given in the subsequent recipes have to be changed accordingly. Please make sure, that this path (including all subfolders) is integrated in the MATLAB path (via "Menu" > "Set path…" or by calling the command `addpath(genpath('c:\MATLAB-Programs'))` from MATLAB command line).

1 Start image processing by GUI

Step by step explanations how to start processing of an example case using the graphical user interface (GUI):

1. Switch to subfolder containing the image (optional):

   In the MATLAB command window type `cd c:\MATLAB-Programs\Testcase` or `cd('c:\MATLAB-Programs\Testcase')` and press `<RETURN>`.
   Note that for this example the path to the input image may have to be edited.
   It is recommended that each subfolder for image processing contains only one input image (T1- or T2-weighted volume data set), albeit accompanied by images of other modalities of the same patient.

2. Call MAP18:

   In the MATLAB command window type `map18` and press <RETURN>
   In the subsequently upcoming MAP18 welcome window press button `'Proceed…'`.

   The second button `'Bail out…'` would end the program at this point. Later, processing can only be stopped by pressing `Ctrl+C` which is the usual way of stopping the execution of a MATLAB program.

2. Select input image:

   In the window `'Select ANALYZE or NIFTI input images…'` navigate in the left subwindow to the subdirectory `'…\MATLAB-Programs\Testcase'` (*only necessary when step 1 has been skipped*), select `'Testcase_ZUR_3T_T1_29Feb2017.img'` in the right subwindow and press `'Done'`.

   The program expects T1- or T2-weighted MRI volume data sets in ANALYZE or NIFTI format with axial and radiological orientation as input. The origin should be approximately at the anterior commissure. It is possible to select more than one file as input images. The predefined filter `'(^[A-Z]\w*)(_T1_)…'` causes that files of this subfolder are only displayed when the filename starts with a capital letter and contains the phrase `'_T1_'`. The filter can be changed by editing its content and pressing `<RETURN>` or reset to 'no filter' by pressing the button `'Reset'`.

3. Select other images for coregistration:

   In the window `'Select other images to coregister with the input image…'` select `'Testcase_ZUR_3T_FLAIR_WBA_29Feb2017.img'` and press `'Done'`.

   This menu appears only when exactly one input image has been selected and when this image has not yet been processed before. Otherwise, this menu is skipped.

However, even without this menu or when no other images are selected at this point, the program itself tries to identify images of other modalities within the subdirectory of the input image. For example, when a T1-weighted image has been selected as input and T2-, FLAIR-, PET-, SPECT-, DWI-, T2*-, MP2RAGE- or inversion recovery images with almost the same filename (i.e., first letters equivalent) and the filename suffix `'_T2TSE'`, `'_FLAIR'`, `'_PET'`, `'_DWI'`, `'_Hemoflash'`, `'_MP2'` or `'_IR'`, somewhere in the filename exist in the same directory, then these T2, FLAIR, PET, DWI, T2*, MP2RAGE and/or IR images will be coregistered with the T1 image and subsequently normalized with the same normalization parameters as the input image.

Example: A FLAIR image called `'Testcase_ZUR_3T_FLAIR_29Feb2017.img'` would automatically be coregistered with a T1 volume data set named `'Testcase_ZUR_3T_T1_29Feb2017.img'`.

The same is true for post-operative images with the suffix `'_postOP'`, e.g. `'Testcase_ZUR_3T_T1_29Feb2017_postOP.img'`.

If the FLAIR image has the suffix `'_FLAIR_WBA'`, it will not only be coregistered and normalized but also subject to an additional whole brain FLAIR analysis according to the method of Focke et al., Epilepsia 2008 and 2009 (with small modifications) and to regional / hippocampal FLAIR analysis according to the method of Huppertz et al, Epilepsy Research 2011.

4. Select other images for normalization:

   In the window `'Select already coregistered images to normalize with the input image…'` select nothing and press `'Done'`.

   This is meant for normalizing images which are already in register with the input image, e.g. region of interest (ROI) images, and shall only be normalized with the same normalization parameters as the input image. However, this menu appears only when exactly one input image has been selected and when this input image has not yet been processed before. Otherwise, this menu is skipped. Nevertheless, even without this menu or when no other images are selected at this point, the program itself tries to identify ROI images created with MRIcro by searching for the typical prefix `'l'`, e.g. `'lTestcase_ZUR_3T_T1_29Feb2017.img'`.

5. Select mode of action:

   In the pull-down menu `'Which mode?…'` select `'Full processing, i.e. morphometric and volumetric analysis'`.

   For other possible modes of action cf. list in Appendix A: Modes of action

6. Select normal database:

   In the pull-down menu `'Which normal database (according to scanner / sequence /age)?…'` select `'Large average from all 1.5 and 3T scanners / T1 / children & adults'`.

   Other normal databases are listed in Appendix B: Normal databases

7. Select space:

   In the pull-down menu `'Select stereotactic space for result images:'` select `'Standard space (i.e. all result images normalized)'`.

   The two other possibilities are `'native space (i.e. all result images transformed to native space by inverse normalization)'` and `'both possibilities (i.e. all result images stored both in standard and native space)'`. If `'native'` or `'both'` are selected, the resulting z score images in native space can also be saved as bitmap (*.bmp) images in separate subdirectories which allows to import them in some DICOM viewers (e.g. KPACS). In addition, by help of the DICOM toolkit (DCMTK) the z score images in native space can be transferred to DICOM format which allows to import them in most DICOM viewers, e.g. as additional sequence in the original MRI. However, this step requires that the input image has been generated by the MAP18 processing pipeline which includes storing of one DICOM example file with all necessary DICOM information of the original MRI in the patient/study directory.

8. Select sensitivity for FCD detection:

   In the pull-down menu `'Select sensitivity for FCD detection:…'` select `'medium (i.e. medium sensitivity and specificity)'`.

   The menu 'sensitivity' relates to the sensitivity of FCD and PNH detection (using the old method based on z score criteria) and offers the following possibilities:

   `'high'` >> high sensitivity and lower specificity
   `'medium'` >> medium sensitivity and specificity
   `'low'` >> low sensitivity and higher specificity

9. Select visualization of suspect regions:

   In the pull-down menu `'Select visualization of suspect regions:…'` select `'closed (i.e. closed border of ROI)'`.

   The menu relates to the visualization of suspect regions as regions of interest (ROIs) in MRIcro format and offers the following possibilities:

   `'full'` >> full painting of ROI
   `'closed'` >> closed border of ROI
   `'dotted'` >> dotted border of ROI

10. Enter age of patient:

    In the input field `'Age of selected patient(s):'` enter a number for the age (e.g. `42.1243` without quotation marks) and press `<RETURN>`.

    If this input is left to be zero MAP18 tries to determine the age of the patient from the DICOM example file (created by during 'pipeline' processing) or from a subfolder with an age entry (cf. directory of test case).

11. Select viewer:

    In the pull-down menu `'Select viewer for presentation of morphometric maps:…'` select `'MRIcro (best for morphometric maps)'`.

    The menu offers 5 possibilities:

`'MRIcro'`	>> call MRIcro 1.37 with all morphometric maps (best option for displaying morphometric maps although the contrast has to be adjusted manually; however the white point is set most precisely)
`'MRIcroN'`	>> call MRIcroN with all morphometric maps (with intensity window already set)
`'MRIcroGL'`	>> call MRIcroGL (best for visualization of implanted electrodes, not so much for morphometric maps)
`'Mango'`	>> call Mango viewer (but only if it is present in the MATLAB path or in the subdirectory 'c:\Program Files\Mango\Mango.exe')
`'None'`	>> no viewer; no presentation of the result maps (might be wise if more than one input image has been chosen for processing)

12. Enter address for email notification (optionally):

    In the input field `'Email address for notification:…'` keep the default content `'none@nowhere'` and press `<RETURN>`.

    This item is optional and allows to hand over an email address for notification. When image processing has successfully finished, an email will be sent to this address. However, this functionality depends on the local / site-specific properties of internet access and firewall and cannot be guaranteed. Leave the default content `'none@nowhere'` if no notification is desired.

After this last selection the processing of the example case starts. The MATLAB command window repeats the selected starting parameters and subsequently shows all processing steps with corresponding comments. Processing ends with the output `'All done!'` in the MATLAB command window. By the way, the same kind of image processing can also be invoked from command line or by a shortcut.

Since MRIcro has been selected as viewer, the most important result images show up automatically in separate MRIcro windows after image processing. This includes the

normalized input image, the resulting morphometric maps (i.e. Extension, Junction and Thickness Image), the FCD probability map and – if available – the coregistered FLAIR image with the FLAIR z score image resulting from whole brain FLAIR analysis. Scrolling through the MRIcro images can be paired. Adjusting signal intensities and contrast in MRIcro are described in another recipe named 'Adjusting contrasts in MRIcro'.

In addition, one or two IrfanView windows appear which allow scrolling through the scatter plots resulting from volumetric MRI analysis and regional FLAIR analysis. To this end, `*.jpg` and `*.tif` files have to be associated with IrfanView. The program itself is located in `'c:\MATLAB-Programs\OtherSoftware\IrfanView'`.

Apart from these main result files, the subfolder of the input image contains much more intermediate files and results at the end of image processing. The Appendix D: Result images gives an overview and explains the meaning of these files.

2 Start image processing from command line

Instead of using the graphical user interface (GUI), image processing can also be started from MATLAB command line. To this end, the command `'map18'` is executed with path and name of one input image in ANALYZE or NIFTI format (ending `'*.img'` or `'*.nii'`) and additional input arguments. The general format for this is:

```
map18(image,mode,norm,space,sensitivity,ROI_mode,viewer,age,email)
```

The variables `'image','mode','norm'` etc. have to be filled / replaced by the appropriate content (cf. appendices). The second last item (i.e. `'age'`) is optional and must only be used when mode of action is `'vol'` or `'full'`. The last item (i.e. `'email'`) is also optional and can be omitted. When filled with a valid email address, it can be used for automatic notification when the image processing has come to an end.

As an example, all parameters selected manually for the test case of the preceding recipe ('Start image processing by GUI') can be handed over with just one command line as shown below:

1. Command line input:

   Type `map18('c:\MATLAB-Programs\Testcase\Testcase_ZUR_3T_T1_29Feb2017.img', 'full','AVG_T1_Large','standard','medium','closed','MRIcro',40.1243, 'none@nowhere')` and press `<RETURN>`.

   Note that in this example the path to the input image may have to be edited.

   It is recommended that each subfolder for image processing contains only one input image (T1- or T2-weighted volume data set), albeit accompanied by images of other modalities of the same patient. All images should be either in ANALYZE or NIFTI format.

   Please note that for all kinds of analysis (i.e. modes of action) the starting point is always the T1 (or T2) input image. Thus, even for a FLAIR analysis the first input parameter (i.e. `'image'`) is always the corresponding T1 (or T2) image. And for the third input parameter (i.e. `'norm'`) the desired T1 (or T2) normal database should be selected. If for example a FLAIR normal database is required, the correct NDB will be deduced from the name of the T1 normal database and then selected automatically by the program itself.

As a result the MAP18 welcome windows shows up for 10 seconds and then image processing starts.

3 Start image processing by shortcut

Image processing can also be started by shortcuts from MATLAB command line. In this case, MAP18 would process all 3D T1 or T2 images in the current directory with default parameters. For example, the image processing started by GUI or from command line described in the previous recipes could also be invoked in the following way:

1. Switch to subfolder containing the image:

   In the MATLAB command window type `cd c:\MATLAB-Programs\Testcase` or `cd('c:\MATLAB-Programs\Testcase')` and press `<RETURN>`.

   Note that for this example the path to the input image may have to be edited.

   It is recommended that each subfolder for image processing contains only one input image (T1- or T2-weighted volume data set), albeit accompanied by images of other modalities of the same patient.

2. Shortcut at command line:

   Type `map18('full')` and press `<RETURN>`.

   Note that no age information is transferred by this shortcut. However, volumetric analysis requires the age of the patient at the time of MRI measurement. Otherwise, the age is set to zero in the resulting scatter plots. Therefore, in order to hand over this information, create a subfolder named `'age xxxx'` before invoking the shortcut. The term `'xxxx'` should be replaced by the precise age information (e.g. `'age 40.1243'`). However, this method works only if the subfolder contains exactly one input image. If a volumetric analysis has already been done before, the age information is stored in the file `'*_volume_results.mat'`, and a subfolder with age information is not required any more.
   By the way, the same shortcut (i.e. `map18('full')`) is used internally when calling `'test_MAP18'` to execute MAP18 on the test case included in the installation.

   Alternative shortcut:

   Type `map18('all')` and press `<RETURN>`.

   This does the same image processing as the shortcut above, except for volumetric MRI analysis. Thus, no age information is required.

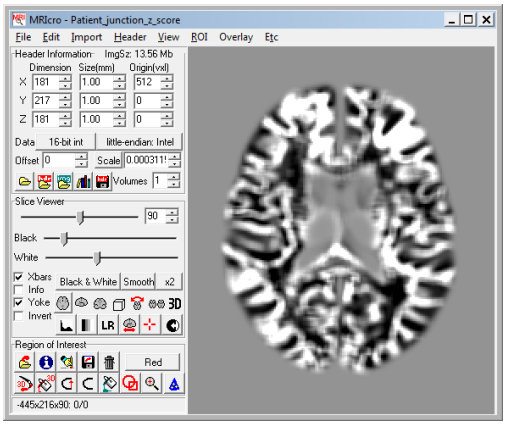
   For a complete list of shortcuts, cf. list in Appendix C: Shortcuts and hyperlinks.
   In addition, the command `map18('hyperlinks')` lists all available shortcuts and presents them as hyperlinks so that they can be invoked by just one mouse click.

4 Adjust contrasts in MRIcro

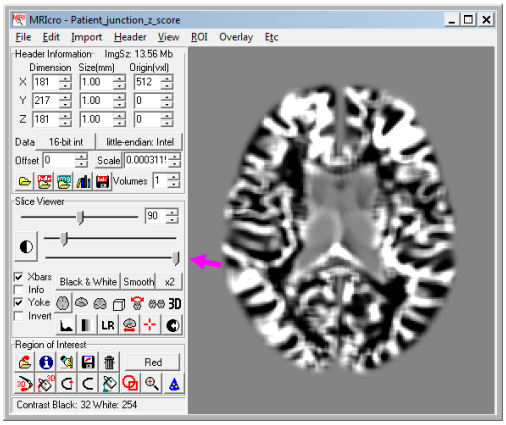
Displaying the z score maps resulting from morphometric or FLAIR analysis with MRIcro requires that the contrast is adjusted manually. The best method is to set the white point of the entire data set to the highest value, i.e. the highest z score. All local maxima also receive the appropriate signal intensities (grayscales) in gradation. At the same time, the sensitivity for the detection of possible abnormalities is handled dynamically. If a region with high z scores due to a clear dysplasia is present, it will appear bright, while the rest of the image data set is rather dark. If clear dysplastic tissue and thus high z scores are missing, the white point will be automatically set to a lower level which increases the sensitivity for more subtle lesions. This means, however, that more regions in the image data set may appear bright, without necessarily corresponding to dysplastic tissue. The following steps describe how to adjust the white point in MRIcro:

1. Load morphometric map into MRIcro

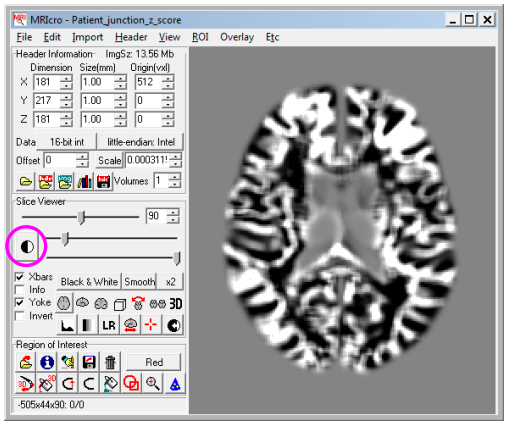
   Try these steps with the Junction Image resulting from processing the test case.

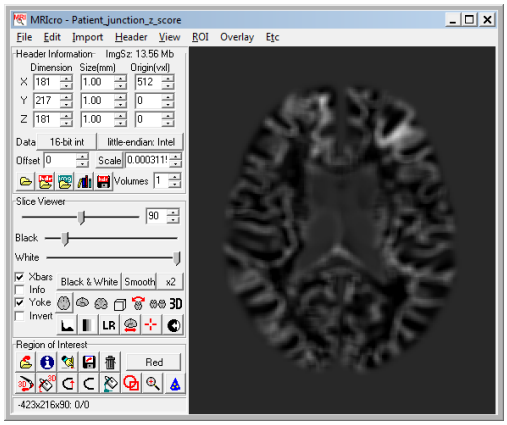


2. Drag 'white' slider to the right end



3. Press button 'Optimize contrast'





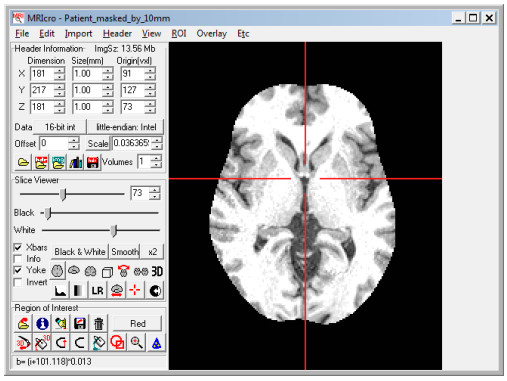
Contrasts are now optimal for viewing and analyzing the morphometric map

5 Display results of curvilinear reformatting

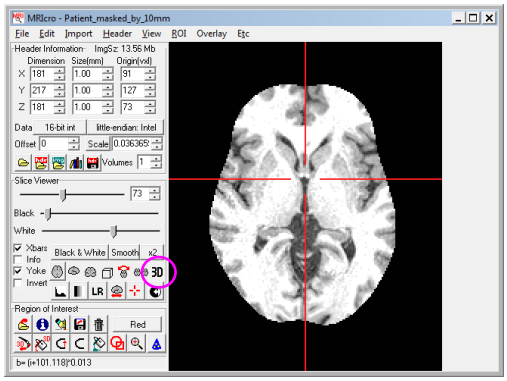
5.1 Volume rendering with MRIcro

1. Load image into MRIcro

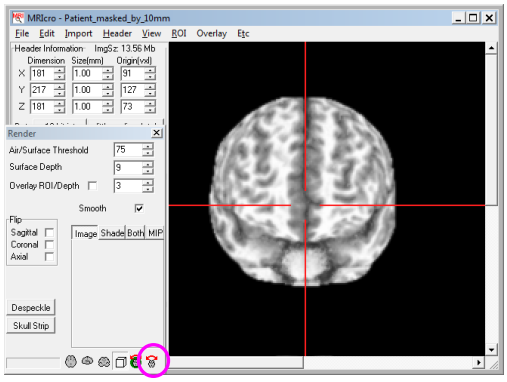
   Instead of the example shown here, try `'wmTestcase_ZUR_3T_T1_29Feb2017_masked_by_18mm.img'` resulting from curvilinear reformatting of the test case.



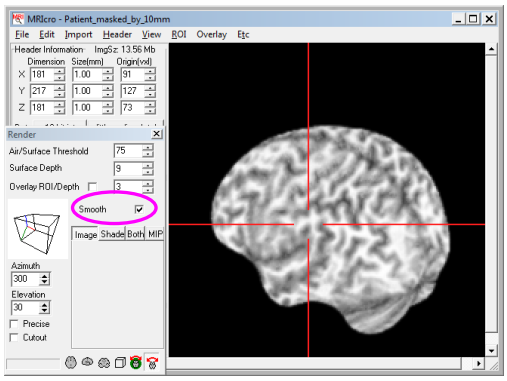
2. Select 3D view



3. In the 'Render' window select 'Free rotate'

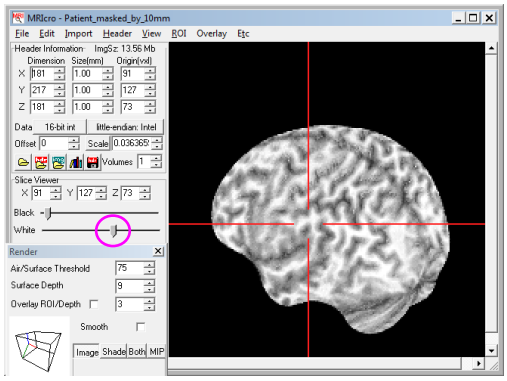


4. Deselect 'Smooth'

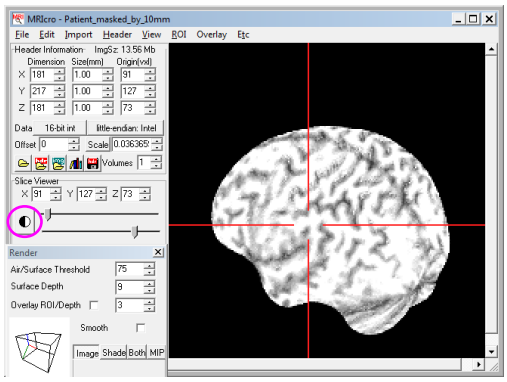


5. Set white point

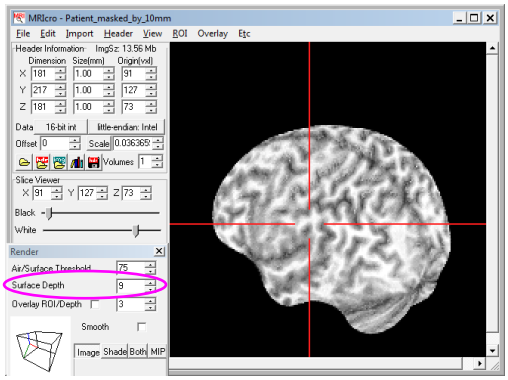
   Drag 'white' slider somewhat to the right but not fully to the right end



6. Press button 'Optimize contrast'

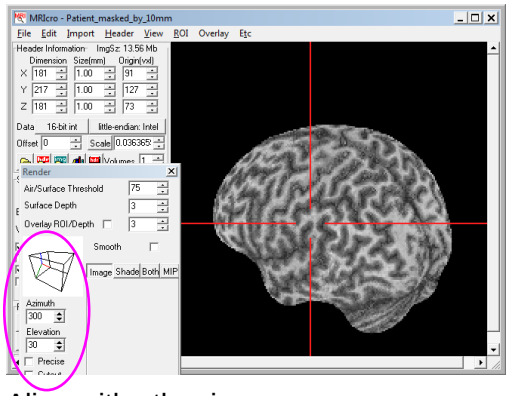


7. Set 'Surface Depth' to 2 or 3 mm



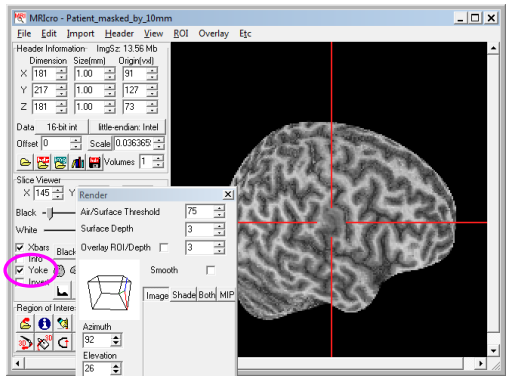
8. Rotate model to set viewing angle

Alternatively, directly select desired 'Azimuth' and 'Elevation' by entering values.



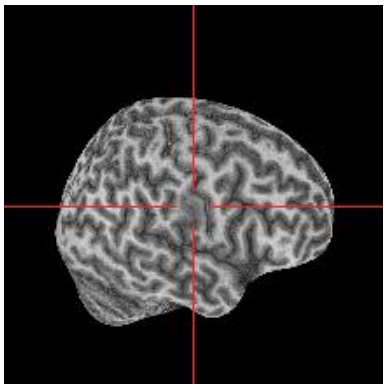
9. Align with other images

Set crosshairs to the lesion and set the 'Yoke' flag to align the crosshairs with those in other images (for example morphometric maps)



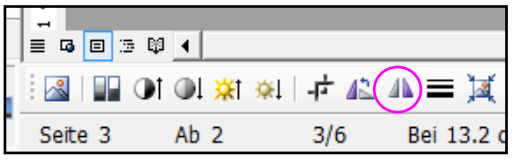
10. Copy image

Copy image by pressing 'Ctrl' + 'C', then paste the image into a Word file by pressing 'Ctrl' + 'V'



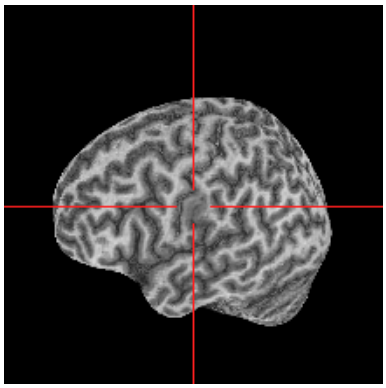
11. Do a left-right flip of the 3D image in the Word file:

This is necessary because MRIcro expects MRI data sets in neurological orientation (R=R) while the output of MAP18 is in radiological orientation (R=L).



12. Finish:

It is now clearly recognizable that the lesion in this example is located behind the left central sulcus.



5.2 Volume rendering with MRIcroGL

The results of curvilinear reformatting can also be displayed using MRIcroGL (http://www.cabiatl.com/mricrogl), an excellent viewer for medical images authored by Chris Rorden who has also written MRIcro and MRIcroN. The viewer provides tools for 2D and 3D display of images but requires a graphics card that supports volume rendering, with the appropriate driver installed. Most modern discrete graphics cards from ATI and Nvidia are acceptable, while several integrated Intel chipsets do not support volume rendering (please cf. MRIcroGL user guide for further information).

The following steps describe how to invoke MRIcroGL from MAP18 or SPM12, respectively, together with the results of curvilinear reformatting (provided that the MRI data of the patient to investigate has already been processed by MAP18):

1. Switch to subfolder containing the image:

   In the MATLAB command window type `cd c:\MATLAB-Programs\Testcase` or `cd('c:\MATLAB-Programs\Testcase')` and press `<RETURN>`.
   Note that the results of morphometry and curvilinear reformatting must already be present in the patient folder.

2. Shortcut at command line:

   Type `map18('show3D')` and press `<RETURN>`.

   This loads the normalized T1 image and the corresponding Junction Image of this patient into the SPM graphics window.

3. Place crosshairs:

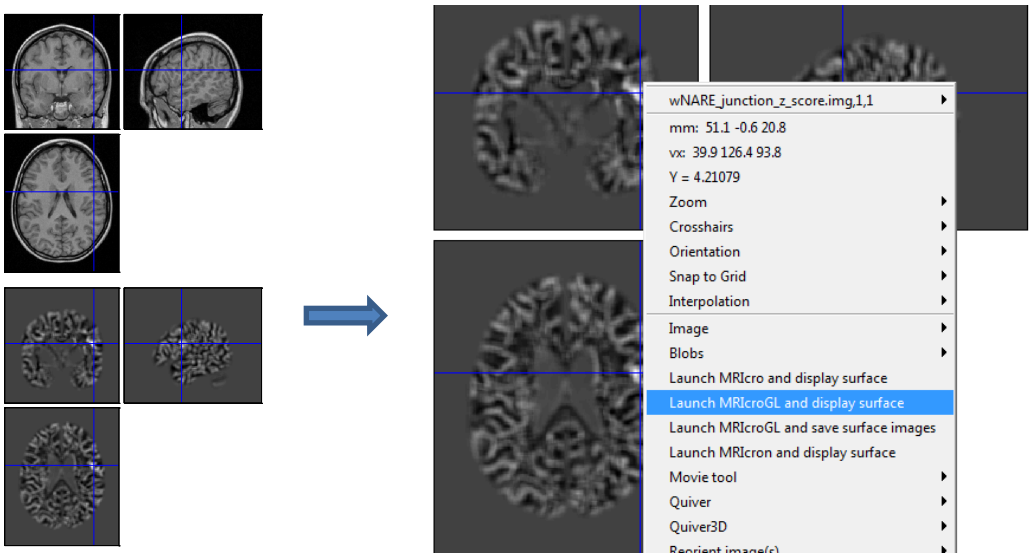
   In the SPM graphics window set the crosshairs on the position in the brain for which you want to display a curved surface.

   When the lesion is highlighted in the Junction Image, it may be used to guide the placing of the crosshairs.

4. Launch MRIcroGL and display surface:

   Press the right mouse button, and from the menu
   choose the function `'Launch MRIcroGL and display surface'`.

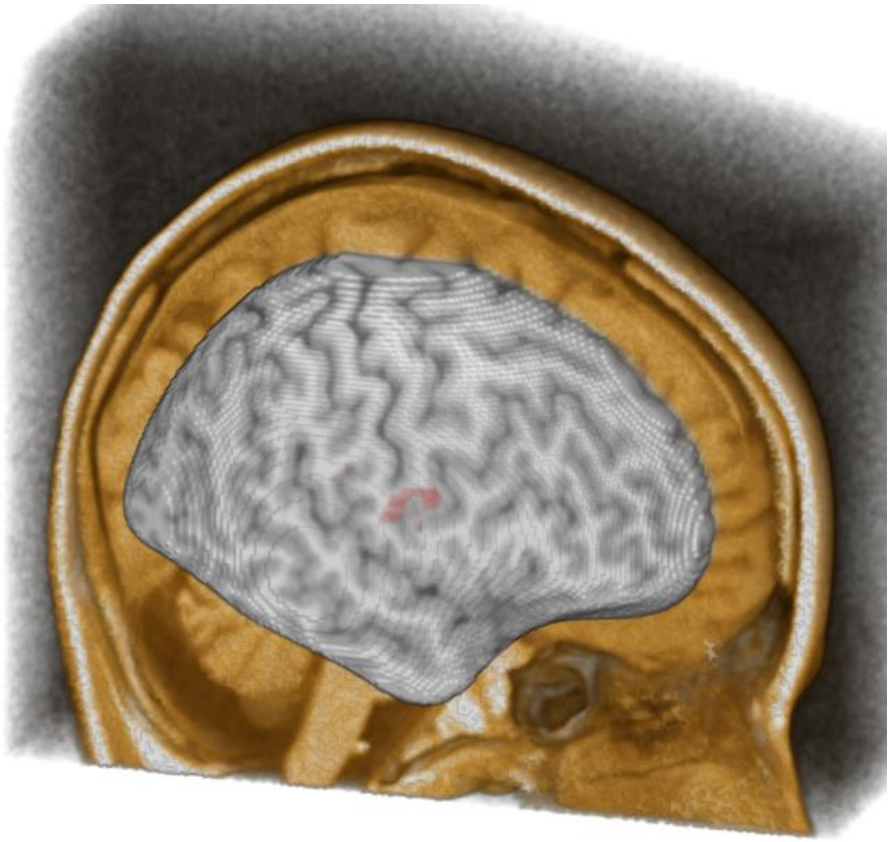
   This invokes MRIcroGL together with a startup script which is created on the fly and contains all the necessary information (i.e. which curvilinearly reformatted image is loaded, which viewing angle is chosen, which viewing depth). The startup script loads the curvilinearly reformatted image of the chosen depth and displays the surface from the correct viewing angle (as determined from the trajectory between crosshair position and centre of the brain).



Note that the screenshots shown here are taken from another example patient.

5. Optimize display in MRIcroGL:

   From this point on, the whole functionality of MRIcroGL is available: e.g., the brain can be freely rotated, cutouts can be defined and additional overlays can be loaded (for example the results of morphometric analysis as in the example below)



Alternatively, MRIcroGL can load sequentially all curvilinear reformatted images with depths from 0 to 30 mm and make snapshots from the chosen viewing angle:

1. - 3. Same steps as before

4. Launch MRIcroGL and save surface images:

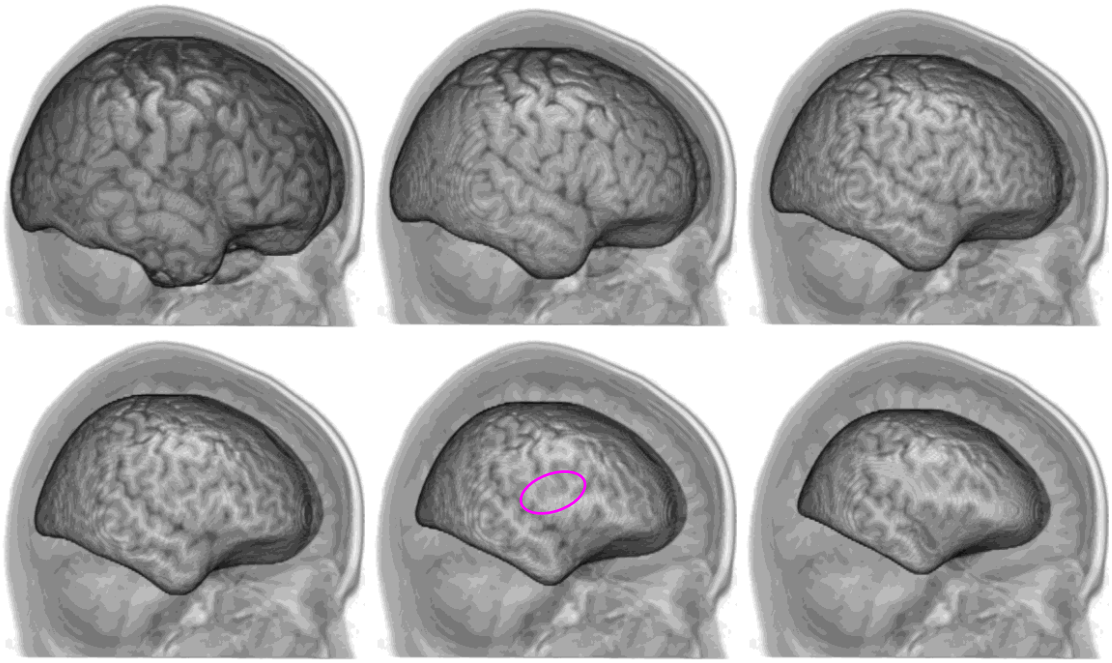
   Press the right mouse button, and from the menu
   choose the function `'Launch MRIcroGL and save surface images'`.

   The resulting PNG image files are saved in a new subfolder named `'3D-xxx-yyy'`. The expressions `'xxx'` and 'yyy' are numbers which code azimuth and elevation of the chosen viewing angle.

5. Display surface images in IrfanView:

   When the last surface image (with 30 mm depth) has been created and saved, close the MRIcroGL window manually.

   This automatically opens the new surface images in IrfanView which can then be used to scroll through these images.



Note that the screenshots shown here are taken from another example patient.

6 Average input images

If more than one MRI of the same patient is available, it might be worth to average these MRIs in order to increase signal-to-noise ratio (SNR). This might be advantageous for subsequent postprocessing and morphometric analysis. The following steps describe how to average three 3D T1 data sets of the same patient.

1. Switch to subfolder containing the example images:

   In the MATLAB command window
   type `cd c:\MATLAB-Programs\Examples\Example_Average`
   or `cd('c:\MATLAB-Programs\ExampleData\Example_Average')`
   and press `<RETURN>`

   Note that the path to the input image may have to be edited.

2. Call MAP18:

   In the MATLAB command window type `map18` and press <RETURN>.
   In the subsequently upcoming MAP18 welcome window press button `'Proceed…'`.

3. Select input image:

   In the window `'Select ANALYZE or NIFTI input images…'`
   navigate in the left subwindow to the subdirectory `'…\MATLAB-Programs\Example Data\Example_Average'` (*only necessary when step 1 has been skipped*),
   select `'ExampleAverage_KK_1T_T1_01Jan2005.img'` in the right subwindow
   and press `'Done'`.

4. Select other images for coregistration:

   In the window `'Select other images to coregister with the input image…'` select `'ExampleAverage_HU_3T_T1_07Dec2008.img'` and `'ExampleAverage_HU_3T_T1_05Jun2009.img'` press `'Done'`.

5. Select other images for normalization:

   In the window `'Select already coregistered images to normalize with the input image…'` select nothing and press `'Done'`.

6. Select mode of action:

   In the pull-down menu `'Which mode?…'` select `'Coregister other images with the input image & average all images'`.

7. Decide about cropping of images:

   In the pull-down menu `'Crop input images…'` select `'No'`.

   With the alternative selection (i.e. `'Yes'`), MAP18 would try to crop the image areas around the head in all images (i.e. input images and images selected for coregistration and averaging). Subsequent processing would be continued with the cropped images. The original images would be stored in zip files named `'xxx_before_cropping.zip'`.

Subsequently MAP18 coregisters both images with the input image, adjusts the intensities to a common mean value and then averages all images. The resulting mean image is called `'ExampleAverage_AVG_T1.img'` and has the same dimensions as the input image.

By the way, the same kind of image processing could be invoked by a shortcut:

1. Shortcut at command line:

   Type `map18('average')` and press `<RETURN>`.

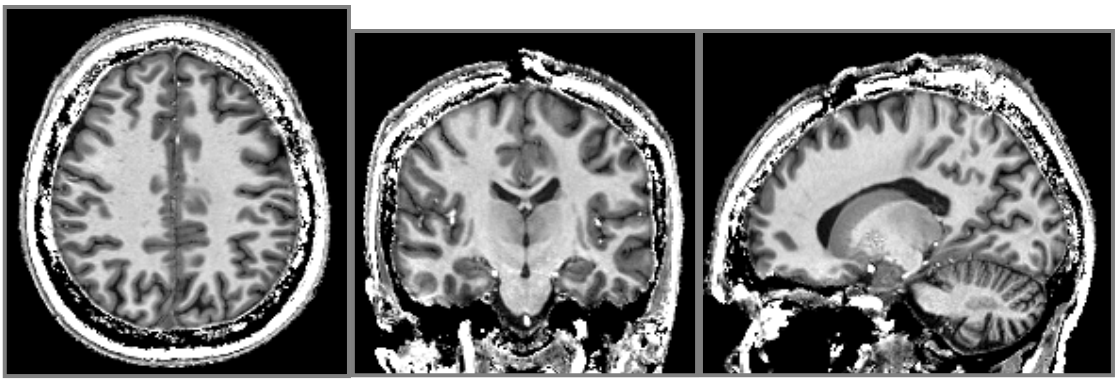
   Map18 will ask for the input image (select the MRI of 2009) and then automatically coregister the other images found in the subfolder of the input image.

7 High resolution analysis

Normally, all normalized images resulting from morphometric analysis and curvilinear reformatting have an isotropic voxel resolution of 1 mm. However, it is possible to increase the spatial resolution by interpolation and to create high-resolution result images with 0.5 mm voxel length. So far, this option only exists for two modes of action (i.e. the creation of the 'Junction Image' and curvilinear reformatting) and only appears when MAP18 is started manually using the GUI. When then one of these two modes is selected (i.e., 'junction' = 'Calculate junction image', or 'curv' = 'Create curved surfaces'), an additional menu appears asking for the spatial resolution of the resulting images.

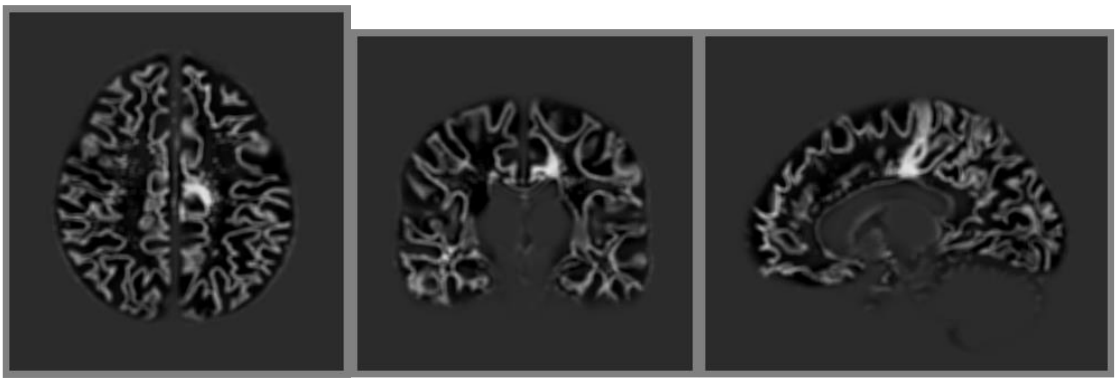
Please, note that the calculation of high resolution images requires a lot of memory (about 2 GB) since these images occupy 8-fold space in the internal memory compared to normal resolution images. With insufficient memory, the program will crash. In addition, these images occupy very much disk space (> 100 MB per image). However, the results may be worth the additional investment in time, memory and disk space.

Here is an example of high-resolution analysis (shown in a patient with a cortical dysplasia in the left medial central region):

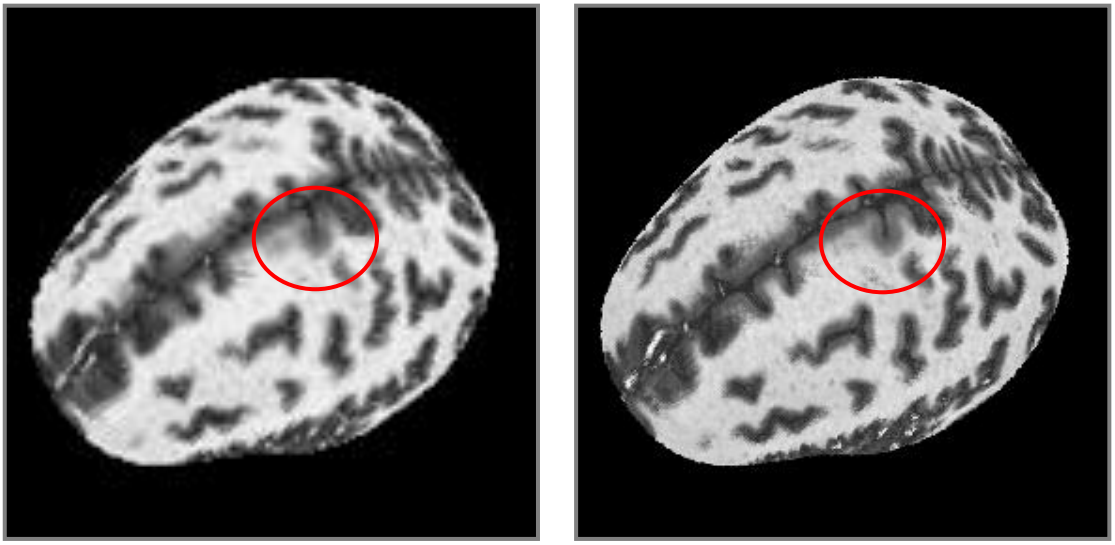


T1 input image (7T scanner, Magdeburg)

Junction Image with 1 mm voxel resolution



Junction Image with 0.5 mm voxel resolution



Curvilinear Reformatting with **1 mm** and **0.5 mm** voxel resolution

The following steps describe how to create a high resolution Junction Image:

1. Switch to subfolder containing the example images:

   In the MATLAB command window
   type `cd c:\MATLAB-Programs\Examples\Example_Average`
   or `cd('c:\MATLAB-Programs\ExampleData\Example_Average')`
   and press `<RETURN>`.

   Note that the path to the input image may have to be edited.

2. Call MAP18:

   In the MATLAB command window type `map18` and press <RETURN>.
   In the subsequently upcoming MAP18 welcome window press button `'Proceed…'`.

3. Select input image:

   In the window `'Select ANALYZE or NIFTI input images…'` select `'ExampleAverage_AVG_T1.img'` in the right subwindow and press `'Done'`.

4. Select other images for coregistration:

   In the window `'Select other images to coregister with the input image…'` select nothing and press `'Done'`.

5. Select other images for normalization:

   In the window `'Select already coregistered images to normalize with the input image…'` select nothing and press `'Done'`.

6. Select mode of action:

   In the pull-down menu `'Which mode?…'` select `'Calculate Junction Image'`.

   Alternatively, select `'Create curved surfaces'` to perform curvilinear reformatting with interpolated high resolution. Please note that for Extension and Thickness Image, higher resolution is not offered because due to methodological reasons this would not really change the result maps.

7. Select normal database:

   In the pull-down menu `'Which normal database (according to scanner / sequence /age)?…'` select `'Large average from all 1.5 and 3T scanners / T1 / children & adults'`.

8. Select space:

   In the pull-down menu `'Select stereotactic space for result images:'` select `'Standard space (i.e. all result images normalized)'`.

9. Select voxel resolution:

   In the pull-down menu `'Voxel resolution of normalized result images: …'` select `'High (0.5 mm) – Cave: Requires 8fold RAM and disk space!'`.

10. Input address for email notification:

    In the input field `'Email address for notification:…'` keep the default content `'none@nowhere'` and press `<RETURN>`.

At the end of image processing, the subfolder of the input image contains the result maps (i.e. the normalized T1 image and the 'Junction Image', both interpolated to 0.5 mm voxel resolution). They are named `'wmPatient_AVG_T1_highRes.img'` and `'wPatient_AVG_T1_highRes_junction_z_score.img'`, respectively.

By the way, the same kind of image processing could also be invoked by a shortcut:

1. Shortcut at command line:

   Type `map18('highRes')` and press `<RETURN>`.

   However, at the end of image processing, the result maps (i.e. the normalized T1 image and the 'Junction Image', both interpolated to 0.5 mm voxel resolution) do not show up automatically in MRIcro but have to be opened manually. Both are easily recognizable by the suffix `'_highRes'` in the filenames.

8 Subtract images to create a difference image

This is a method to compare two images of the same patient by coregistration and subtraction. As a result, we get a 'difference image' which highlights disparities between both input images. However, before subtracting one image from the other, it is necessary to rescale and normalize the voxel intensities in both images to a common level. Usually, this is done by calculating a scaling factor for the whole brain. However, due to diverse acquisition parameters or use of different scanners, a single scaling factor for the whole brain may not be sufficient to transfer all tissue compartments to a common and comparable level. Therefore, if necessary the tool in MAP18 calculates individual scaling factors for GM and WM. Since the two images which are to compare may not offer the necessary contrast for segmentation of grey and white matter (e.g. T2* images as in the example below) the segmentation is standardly based on a separate T1 input image of the same patient. In principle, this approach (i.e. with separate rescaling of grey and white matter) would even allow to compare two images of different modalities, e.g. T1 and T2 images. However, there are also limitations. The overall quality of results depends very much on the segmentation of the T1 image, and with separate rescaling for grey and white matter there are always edge artefacts at the border of these tissue compartments. Nevertheless, the tool may be useful, for example in patients with multiple lesions in whom a potential change between two MRI acquisitions shall be determined or excluded.

The following steps describe how to do subtraction analysis for T2* (hemoflash) images in an example patient with multiple cavernoma. Due to the large number of lesions it is difficult to assess if there is any change between the MRI acquisitions of 2007 and 2011. However, the 'difference image' resulting from subtraction analysis highlights several newly developed cavernoma which could be easily missed when only evaluating the standard / original T2 * images.

1. Switch to subfolder containing the example images:

   In the MATLAB command window
   type `cd c:\MATLAB-Programs\Examples\Example_Difference`
   or `cd('c:\MATLAB-Programs\ExampleData\Example_ Difference')`
   and press `<RETURN>`.

   Note that the path to the input image may have to be edited.

2. Call MAP18:

   In the MATLAB command window type `map18` and press <RETURN>.
   In the subsequently upcoming MAP18 welcome window press button `'Proceed…'`.

3. Select input image:

   In the window `'Select ANALYZE or NIFTI input images…'` select `'ExampleDiff_ZUR_T1_11Jul2007.img'` in the right subwindow and press `'Done'`.

4. Select other images for coregistration:

   In the window `'Select other images to coregister with the input image…'` select nothing and press `'Done'`.

   Note that the choice of the two images to subtract follows later.

5. Select other images for normalization:

   In the window `'Select already coregistered images to normalize with the input image…'` select nothing and press `'Done'`.

6. Select mode of action:

   In the pull-down menu `'Which mode?…'` select `'Calculate difference of 2 images coregistered to the input images'`.

7. Select normal database:

   In the pull-down menu `'Which normal database (according to scanner / sequence /age)?…'` select `'Large average from all 1.5 and 3T scanners / T1 / children & adults'`.

8. Select space:

   In the pull-down menu `'Select stereotactic space for result images:'` select `'Standard space (i.e. all result images normalized)'`.

9. Select two subtraction images:

   In the window `'Select two subtraction images for ExampleDiff_ZUR_T1_11Jul2007.img …'` select `'ExampleDiff_ZUR_Hemoflash_11Jul2007_sub1.img'` and `' ExampleDiff_ZUR_Hemoflash_11Apr2011_sub2.img'` and press `'Done'`.

10. Select viewer:

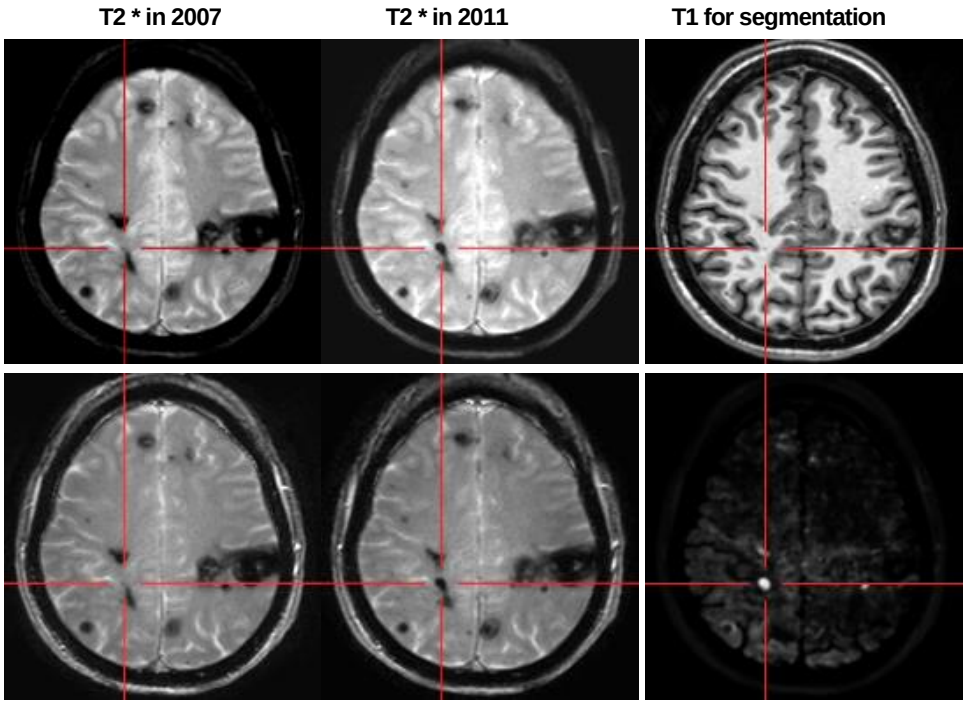
    In the pull-down menu `'Select viewer for presentation of morphometric maps:…'` select `'MRIcro (best for morphometric maps)'`.

13. Input address for email notification:

    In the input field `'Email address for notification:…'` keep the default content `'none@nowhere'` and press `<RETURN>`.

After the end of image processing, several MRIcro windows show up which present the normalized T1 input image, both coregistered and normalized T2* (hemoflash) images,

again these T2* (hemoflash) images after rescaling to a common signal intensity, and finally the so-called 'difference image' where disparities between both T2* images appear bright (cf. figure below). Please not that it might be necessary to adjust brightness and contrasts for the difference image. Explanations and result images for this example patient can also be found in the PDF `'Updates for MAP07 - Oct 2012.pdf'`.



By the way, the same kind of image processing can be invoked from command line:

1. Alternative command line input:

   Type `map18('c:\MATLAB-Programs\Examples\Example_Difference\Example Diff_ZUR_T1_11Jul2007.img','subtract','AVG_T1_Large','standard','none', 'none','MRIcro')` and press `<RETURN>`.

Alternatively, it can be started from within the patient subfolder by the following shortcut, then using default parameters.

1. Shortcut at command line:

   Type `map18('subtract')` and press `<RETURN>`.

   In both cases, Map18 will automatically identify the two images for subtraction analysis by the suffix `'_sub1'` and `'_sub2'` in the filenames. However, the first parts of the filenames (i.e. the patient name) have to match the filename of the input image.

9 Quantitative FLAIR Analysis

The following steps describe how to invoke selectively quantitative FLAIR analysis. The method consists of the *whole brain FLAIR analysis* as described by N. Focke and colleagues in Epilepsia 2008 and 2009, and of the *regional FLAIR analysis* of temporomesial structures as described in Huppertz HJ et al., Epilepsy Res 2011. For further information please cf. descriptions of previous updates (i.e. `'Updates for MAP07 - Jan 2010.pdf'` and `'Updates for MAP07 - Jan 2010.pdf'`) which can be downloaded using the command `download_additional_data_for_MAP18` on the MATLAB command line.

1. Switch to subfolder containing the example images:

   In the MATLAB command window type `cd c:\MATLAB-Programs\Examples\Example_HS` or `cd('c:\MATLAB-Programs\ExampleData\Example_ HS')` and press `<RETURN>`

   Note that the path to the input image may have to be edited.

2. Call MAP18:

   In the MATLAB command window type `map18` and press <RETURN>.
   In the subsequently upcoming MAP18 welcome window press button `'Proceed…'`.

3. Select input image:

   In the window `'Select ANALYZE or NIFTI input images…'` select `'ExampleHS_HU_3T_T1_14Aug2017.img'` in the right subwindow and press `'Done'`.

4. Select other images for coregistration:

   In the window `'Select other images to coregister with the input image…'` select `'ExampleHS_HU_3T_T1_16Jun2018_postOP.img'` and press `'Done'`.

   Note that the choice of the FLAIR image follows later.

5. Select other images for normalization:

   In the window `'Select already coregistered images to normalize with the input image…'` select nothing and press `'Done'`.

6. Select mode of action:

   In the pull-down menu `'Which mode?…'` select `'Whole brain FLAIR analysis'`.

7. Select normal database:

   In the pull-down menu `'Which normal database (according to scanner / sequence /age)?…'` select `'Large average from all 1.5 and 3T scanners / T1 / children & adults'`.

8. Select space:

   In the pull-down menu `'Select stereotactic space for result images:'` select `'Standard space (i.e. all result images normalized)'`.

9. Select FLAIR images:

   In the window `'Select corresponding FLAIR image for ExampleHS_HU_T1_14Aug2017.img …'` select `'ExampleHS_HU_3T_FLAIR_WBA_14Aug2017.img'`.

10. Select normal database for FLAIR analysis:

    In the pull-down menu `'Which normal database for FLAIR:…'` select `'Average FLAIR NDB'`.

11. Select viewer:

    In the pull-down menu `'Select viewer for presentation of morphometric maps:…'` select `'MRIcro (best for morphometric maps)'`.

14. Input address for email notification:

    In the input field `'Email address for notification:…'` keep the default content `'none@nowhere'` and press `<RETURN>`.

Alternatively, the whole brain FLAIR analysis could be invoked from command line:

1. Command line input:

   Type `map18('c:\MATLAB-Programs\ExampleData\Example_ HS\ExampleHS_HU_3T_T1_14Aug2017.img','FLAIR','AVG_T1_Large', 'standard','medium','closed','MRIcro')` and press `<RETURN>`.

   Note that in this example the path to the input image may have to be edited.

   Furthermore, please note that the starting point for each kind of analysis (i.e. mode of action) is always the T1 (or T2) input image. Thus, even for a FLAIR analysis the first input parameter (i.e. 'image') is always the corresponding T1 (or T2) image but not the FLAIR image. The FLAIR image to work on will be found by the program itself, by deducing the name from the name of the T1 (or T2) input image (i.e. the program searches for files named like the input image, but with the phrase '_T1_' replaced by '_FLAIR_WBA_'). And for the third input parameter (i.e. 'norm') the desired T1 (or T2) normal database should be selected. The additionally required FLAIR normal database is selected internally by the program itself. If there are site-

specific FLAIR normal databases available, the correct one will be deduced from the name of the selected T1 normal database; otherwise the average FLAIR normal database named `'Average FLAIR NDB'` will be chosen automatically.

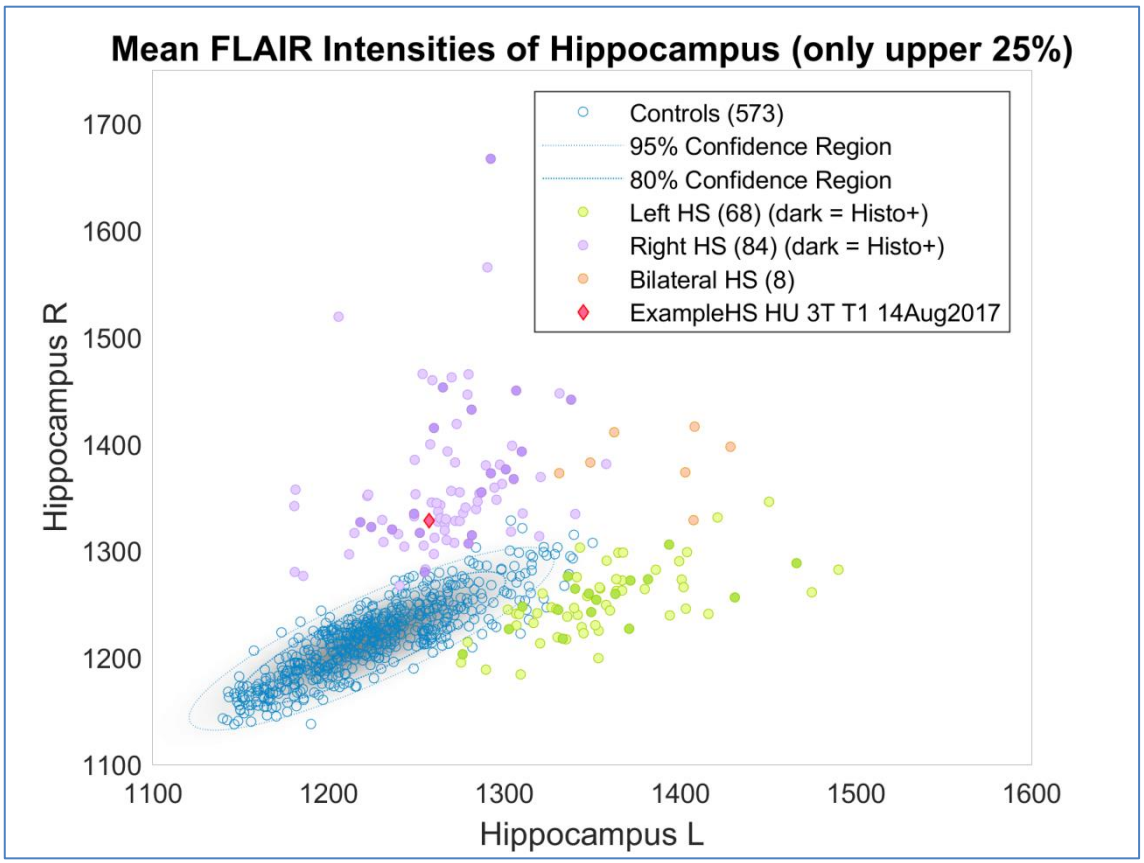
The same kind of image processing could be invoked by a shortcut from command line:

1. Shortcut at command line:

   Type `map18('FLAIR')` and press `<RETURN>`.

   Map18 will automatically identify the FLAIR image by the phrase `'_FLAIR_WBA'` in the filename. However, the first part of the filenames (i.e. the patient name) has to match the filename of the input image. Furthermore, the program will select automatically the average T1 normal database (i.e. `'AVG_T1_Large'`) and the average FLAIR normal database (i.e. `'Average FLAIR NDB'`) for processing of the T1 and FLAIR image.

At the end of image processing the following result image (named `'ExampleHS_HU_3T_FLAIR_WBA_14Aug2017_flair_analysis_Hippocampus_upper25.tif'`) can be found in the patient subfolder, indicating that this example patient has a hyperintensity of the right hippocampus due to hippocampal sclerosis:



10 Volumetric MRI Analysis

The following steps describe how to invoke selectively volumetric MRI analysis.

1. Switch to subfolder containing the example images:

   In the MATLAB command window type `cd c:\MATLAB-Programs\Examples\Example_HS` or `cd('c:\MATLAB-Programs\ExampleData\Example_ HS')` and press `<RETURN>`

   Note that the path to the input image may have to be edited.

2. Call MAP18:

   In the MATLAB command window type `map18` and press <RETURN>.
   In the subsequently upcoming MAP18 welcome window press button `'Proceed…'`.

3. Select input image:

   In the window `'Select ANALYZE or NIFTI input images…'` select `'ExampleHS_HU_3T_T1_14Aug2017.img'` in the right subwindow and press `'Done'`.

4. Select other images for coregistration:

5. In the window `'Select other images to coregister with the input image…'` select `'ExampleHS_HU_3T_T1_16Jun2018_postOP.img'` and press `'Done'`.

6. Select other images for normalization:

   In the window `'Select already coregistered images to normalize with the input image…'` select nothing and press `'Done'`.

7. Select mode of action:

   In the pull-down menu `'Which mode?…'` select `'Determine Volumes'`.

8. Enter age of patient:

   In the input field `'Age of selected patient(s):'` enter a number for the age (for this case `32.6`, without quotation marks) and press `<RETURN>`.

   If the default input (i.e. zero) is left MAP18 tries to determine the age of the patient from the DICOM example file (created by during 'pipeline' processing) or from a subfolder with an age entry. This last method would work for this example case because the patient/study directory already contains a subfolder named `'age 32.6'`.

After this last entry, volumetric analysis starts.

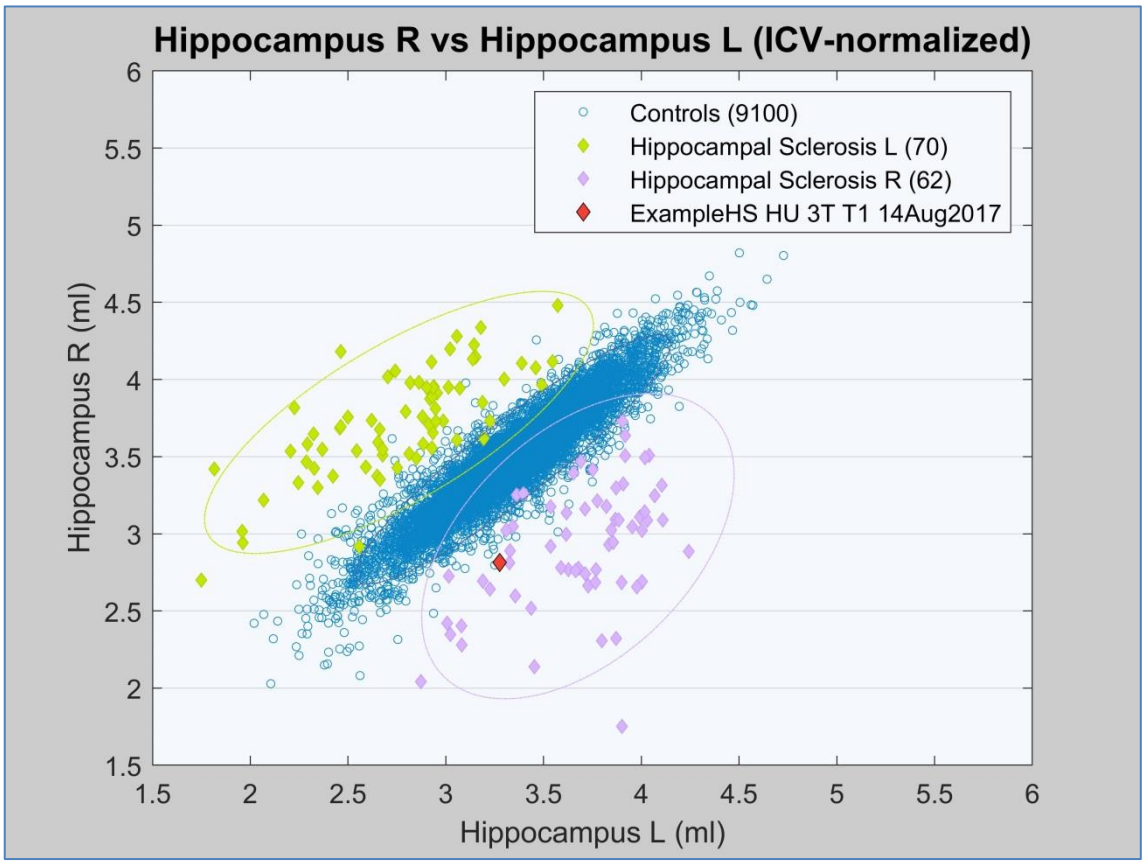
The same kind of image processing could be invoked by a shortcut from command line:

1. Shortcut at command line:

   Type `map18('vol')` and press `<RETURN>`.

   In this case Map18 will determine the age of the patient from a subfolder with age information included already in the directory of this example case.

At the end of image processing several scatter plots showing volumetric results can be found in the patient/study directory, among them the following result image (named `'ExampleHS_HU_3T_T1_14Aug2017_Hippocampus R vs Hippocampus L (ICV-normalized) for DD HS.jpg'`). The results indicate that this example patient has an atrophy of the right hippocampus due to hippocampal sclerosis:



Since November 2018, there is also a scatter plot for comparing amygdala volumes of both sides. However, please note that the sensitivity for detection of amygdala enlargement is quite low due to high measurement variability of this structure. In addition, not all cases of limbic encephalitis are accompanied by visible changes of temporomesial structures.

11 Inverse normalization

The result images of morphometric analysis, curvilinear reformatting or FLAIR analysis are primarily calculated in MNI space, which is recognizable by the prefix `'w'` in the file-names. Generally, it is recommended to use these 'normalized' images when screening for epileptogenic lesions or other pathologies. It is easier to recognize pathologies and deviations from normal anatomy when using a standardized reference space. In addition, the window size of MRIcro can be kept stable this way.

However, sometimes (e.g. for intraoperative neuronavigation) it is required to transform these result images back into native space. This is done by 'inverse normalization' which applies the parameters of previous normalization in opposite direction. The following steps describe how to do this using the test case already known from the first chapters as an example. It is assumed that the image processing of the test case has already taken place and the results of the analysis are available in the patient folder.

1. Switch to subfolder containing the image (optional):

   In the MATLAB command window type `cd c:\MATLAB-Programs\Testcase` or `cd('c:\MATLAB-Programs\Testcase')` and press `<RETURN>`.

2. Call MAP18:

   In the MATLAB command window type `map18` and press <RETURN>
   In the subsequently upcoming MAP18 welcome window press button `'Proceed…'`.

3. Select input image:

   In the window `'Select ANALYZE or NIFTI input images…'` navigate in the left subwindow to the subdirectory `'…\MATLAB-Programs\Testcase'` (*only necessary when step 1 has been skipped*), select `'Testcase_ZUR_3T_T1_29Feb2017.img'` in the right subwindow and press `'Done'`.

4. Select mode of action:

   In the pull-down menu `'Which mode?…'` select `'Inverse normalization to native space of input image'`.

5. Decide about conversion to DICOM format:

   In the pull-down menu `'Export result images in native space also as DICOM files:…'` select `'No'`.

   The export to DICOM format is described in another chapter. Here, we skip this option because conversion to DICOM would require a so-called 'DICOM example file'

containing the DICOM information from the original MRI of this patient. This is usually created automatically during pipeline processing (cf. Image processing using the automated pipeline) but is not available for this test case since his input image has been converted to NIFTI format outside of pipeline processing.

6. Decide about conversion to Bitmap format:

   In the pull-down menu `'Export result images in native space also as *.bmp images:…'` select `'No'`.

   Bitmap (i.e. *.bmp) images can be imported in some DICOM viewers. However, this is only useful when import of result images in DICOM format is not possible, for example due to missing information in some of the DICOM fields.

7. Select images to transform back to native space:

   In the window `'Select image(s) to transform back to native space of …'` select in the right subwindow one result of morphometric analysis (i.e. the Junction Image, here called `'wTestcase_ZUR_3T_T1_29Feb2017_junction_z_score'`) and the FCD probability map (named `'wTestcase_ZUR_3T_T1_29Feb2017_probFCD'`).

   Afterwards, press `'Done'`.

   The choice of Junction Image and FCD probability map is only an example. You are free to choose other or more result images. The filter `'^w[A-Z]\w*'` ensures that only 'normalized' result images of this patient subfolder are presented.

After this last selection, MAP18 starts with inverse normalization of the chosen result images. The whole process should take only a few minutes.

At the end of image processing, the patient folder contains two new files: `'Testcase_ZUR_3T_T1_29Feb2017_junction_z_score'` and `'Testcase_ZUR_3T_T1_29Feb2017_probFCD'`, representing the Junction Image and the FCD probability map in the original native space of the T1-weighted input image `'Testcase_ZUR_3T_T1_29Feb2017.img'`. The removal of the prefix `'w'` indicates that these images are no longer in 'normalized' (i.e. MNI) space (cf. Appendix D: Result images).

By the way, inverse normalization can also be invoked by a shortcut:

1. Shortcut at command line:

   Type `map18('inverse')` and press `<RETURN>`.

   This will bring all available result images of morphometric analysis, curvilinear reformatting or FLAIR analysis in the current directory back to native space.

12 Convert to and from DICOM format

MAP18 has two commands to transform images either from DICOM to ANALYZE format or from ANALYZE format back to DICOM format: `map18('convert')` and `map18('DICOM')`. ´The following steps show how to apply them.

12.1 Convert from DICOM to ANALYZE or NIFTI format

As an example, we use the DICOM data of a patient with known FCD. The subfolder '`c:\MATLAB-Programs\ExampleData\Example_DICOM`' contains 6 sequences of his MRI.

1. Switch to directory containing DICOM subfolders:

   In the MATLAB command window
   type `cd c:\MATLAB-Programs\ExampleData\Example_DICOM`
   or `cd('c:\MATLAB-Programs\ExampleData\Example_DICOM')`
   and press `<RETURN>`.

2. Shortcut at command line:

   Type `map18('convert')` and press `<RETURN>`.

3. Select input data:

   In the window `'Select one or more DICOM directories…'` navigate in the left subwindow to the subdirectory `'…\MATLAB-Programs\ExampleData\Example_DICOM'` (*only necessary when step 1 has been skipped*), select all 6 subfolders listed in the right subwindow and press `'Done'`.

   Each of these 6 subfolders corresponds to one MR sequence (i.e. T1, T2 …). It I not necessary to enter these subfolders; the selection is done on folder level.

4. Decide about reorientation of images:

   In the selection menu `'Reorientate images axially?'` select `'yes'`.

   The alternative selection `'no'` would leave the images in their original orientation during acquisition. However, it is strongly recommend to bring the converted images into *axial* orientation in order to have them correctly presented in SPM or MRIcro.

5. Decide about voxel size:

   In the selection menu `'Voxel size?'` select `'1 mm'`.

   The alternative selection `'0.5 mm'` can be useful when the chosen MR sequence has a resolution higher than 1 mm and shall be for subsequent high resolution analysis. Otherwise, '1 mm' is sufficient because this is the default resolution within SPM12.

6. Decide about format:

   In the selection menu `'Format?'` select `'.img'`.

   The resulting images will be in ANALYZE format. The alternative selection `'.nii'` would create NIFTI images. MAP18 can process both formats, but the result images of morphometric analysis etc. will be in ANALYZE format. This allows to open them in MRIcro 1.37 which among the available viewers has still the best options for setting contrasts and white point in morphometric maps (cf. Adjust contrasts in MRIcro).

After this last selection conversion of images starts. At the end, there will be 6 new images in ANALYZE format (with .img and .hdr file) in the folder where MAP18 has been started:

- NobodyAnonymus_ Princeton_T1W_3D_TFE_01Jan2000.img
- NobodyAnonymus_ Princeton_T1W_FFE__KM_01Jan2000.img
- NobodyAnonymus_ Princeton_T2W_FLAIR_01Jan2000.img
- NobodyAnonymus_ Princeton_T2W_FLAIR_c_01Jan2000.img
- NobodyAnonymus_ Princeton_T2W_Haemo_SENSE_01Jan2000.img
- NobodyAnonymus_ Princeton_T2W_TSE_SENSE_01Jan2000.img

The conversion tool tries to determine patient name, institution name, sequence name and date of MRI from the corresponding fields in the DICOM header and to use this information for naming of the new images.

12.2 Convert from ANALYZE or NIFTI to DICOM format

Here, the results of the previous chapter are employed to show how images in ANALYZE or NIFTI format can be converted back to DICOM format.

1. Switch to subfolder containing the image:

   In the MATLAB command window
   type `cd c:\MATLAB-Programs\ExampleData\Example_DICOM`
   or `cd('c:\MATLAB-Programs\ExampleData\Example_DICOM')`
   and press `<RETURN>`.

2. Shortcut at command line:

   Type `map18('DICOM')` and press `<RETURN>`.

3. Select input data:

   In the window `'Select one or more images…'` navigate in the left subwindow to the subdirectory `'…\MATLAB-Programs\ExampleData\Example_ DICOM'` (*only*

necessary when step 1 has been skipped), select the ANALYZE file `'NobodyAnonymus_Princeton_Zürich_T1W_3D_TFE_01Jan2000.img'` created in the previous chapter and press `'Done'`.

4. Select orientation:

   In the pull-down menu `'Which orientation for resulting output images in DICOM format?…'` select `'Original'` and press `'Done'`.

   Optionally, during conversion to DICOM format, the orientation of the resulting output images can be changed. The corresponding menu offers 4 possibilities: 'axial', 'coronar', 'sagittal' and 'original'.

5. Decide about anonymization:

   In the pull-down menu `'Shall the resulting output images in DICOM format be anonymized ?…'` select `'No'` and press `'Done'`.

   As a further option, the images can also be anonymized. This means that several DICOM fields (cf. explanations in Appendix C: Shortcuts and hyperlinks) are filled with other information. The corresponding menu offers two possibilities for anonymization: 'yes' or 'no'.

6. Select DICOM example file:

   In the window `'Select DICOM example file…'` navigate in the left subwindow to the subdirectory `'1.3.46.670589.11.17286.5.0.5424.2012030215390075560'` and from the right subwindow select the first available DICOM file (i.e. `'1.3.46.670589.11.17286.5.0.5424.2012030215453029573.dcm'`) and press `'Done'`.

   The so-called 'DICOM example file' contains the DICOM information from the original MRI of this patient. It is usually created automatically during pipeline processing (cf. Image processing using the automated pipeline). In this example case, however, the conversion from DICOM to ANALYZE format was done directly, not by means of the automated pipeline. Therefore, the DICOM example file is missing. As a substitute, one of the DICOM files of the original T1 sequence is selected in this step.

After this last selection the conversion to DICOM format starts. The black point of signal intensities is set to the minimum of all voxel values, and the image is saved slice by slice as DICOM files in a new subfolder named `'DICOM_xxx'` with `xxx` replaced by the filename of the chosen ANALYZE or NIFTI file. In this example, the new subfolder is named:

- DICOM_NobodyAnonymus_Princeton_T1W_3D_TFE_01Jan2000

By the way, if the dysplastic lesion in this example patient has not been found so far, the following shortcut might help (given that the ANALYZE images according to the description in the first chapter have already been created):

1. Shortcut at command line:

   Type `map18('mapFCD')` and press `<RETURN>`.

2. Select input image:

   In the window `'Select ANALYZE or NIFTI input images…'` select `'NobodyAnonymus_Princeton_T1W_3D_TFE_01Jan2000'` in the right subwindow and press `'Done'`.

After the end of image processing, open the normalized T1 image and the FCD probability map in MRIcro.

13 Image processing using the automated pipeline

As an alternative to manual operation MAP18 includes an automated pipeline for image processing. When set up correctly, this pipeline automatically recognizes new incoming DICOM images in the local PACS and controls the conversion of these DICOM images into ANALYZE format, the detection of different MR sequences, the naming rules for image files, and the subsequent image processing with MAP18.

To demonstrate this functionality, we will use the freeware K-PACS to read in DICOM data of an example patient. The installation software is available at www.k-pacs.net; alternatively use the command `download_additional_data_for_MAP18` on the MATLAB command line to get the program.

Then, follow the steps below:

1. Install K-PACS:

   Preferably, install this program in the recommended destination folder (i.e. `'c:\KPacs'`).

2. Read in the example data:

   Open KPACS and read in the example data using the button `'Filesystem'` in the upper right corner. The example data is located in `'c:\MATLAB-Programs\ExampleData\Example_DICOM'`.

   For those, who are not familiar with KPACS: After selecting the whole subfolder `'Example_DICOM'` KPACS reads the DICOM information of the selected MRI but not yet the MR images. At the end, the most important information found in the DICOM header of the MRI data (i.e. patient name, modality, date of birth, study date etc.) is displayed in the first line of the 'Filesystem' content table. For this example case, the line will read: `'MR Nobody Anonymus 404844 19800101 20120302 House^Dr Neurokranium etc.'` In order to read in the actual MRI data, you have to check the box at the beginning of this line and then double-click on the line. After KPACS has imported the imaging data, switch back from 'Filesystem' to 'Imagebox'. Now, the MRI is also listed in the content table of the 'Imagebox'.

3. Edit the 'automatic_MAP18.ini' - file:

   Edit this file following the instructions given in Appendix E: Editing the 'automatic_MAP18.ini' – File.

   It is prudent to create a copy of this file in order to save the original version. Later, you may also consider to create different `'*.ini'` files for different modes of action.

To open the `'automatic_MAP18.ini'` file within the MATLAB editor type `open('automatic_MAP18.m')` in the MATLAB command window and press `<RETURN>`. Alternatively, you may also use any other text editor. When editing the `'automatic_MAP18.ini'` file, be careful not to induce any frame shift, for example by forgetting commas or apostrophes.

Editing the 'automatic_MAP18.ini' – file should at least cover the following aspects:

a) Define the correct path to the local `'DICOMDirectory'`. Here, this should be the path to the imagebox of the newly installed KPACS program, i.e. `'c:\KPacs\Imagebox'`.

b) Choose a `'Destination'`, where the results of MRI postprocessing shall be stored, e.g. `'c:\MAP18_Results'`.

c) Define a `'StartingTime'` which is prior to reading in the example data, e.g. `'24-Jan-2018 11:12:19'`. This item controls the time point from which on images imported into KPACS are regarded as new and will be analysed by MAP18.

d) Check that the name of the institution where the MRI has been acquired (`'Princeton'` in this example case) appears in the paragraphs `'[InstitutionNames]'`, `'[Tokens]'` and `'[MAP18 Parameters]'`.

e) Check that the name of native 3D T1 sequence (`'T1W_3D_TFE'` in this example case) appears in the paragraph `'[SeriesDescriptions]'`.

f) Check that the name of the thin-sliced FLAIR sequence (`'T2W_FLAIR_c'` in this example case) appears in the paragraph `'[SeriesDescriptions for Images to Coregister]'` in the first line (i.e. `'FLAIR_WBA = …'`).

g) Check that the remaining MR sequences of this example patient are also listed in the paragraph `'[SeriesDescriptions for Images to Coregister]'`.

Actually, this should be true already. The items d) to g) were only meant to make you aware of these naming definitions ☺.

4. <u>Call the automated pipeline:</u>

In the MATLAB command line type `automatic_MAP18('automatic_MAP18.ini')` and press `<RETURN>`. When the prompt `'Press Enter to proceed...'` appears in the MATLAB command window, press again `<RETURN>`.

It is recommended to create a MATLAB shortcut (called `'Favorite Commands'` since MATLAB version 2018a) with the content `automatic_MAP18('automatic_MAP18.ini')`. This allows starting MAP18's automated image processing pipeline with one mouse click. Alternatively, a shortcut with content `map18('automatic')` would allow to switch between different `'*.ini'` files.

At the end of image processing for this example case, all results can be found in the subfolder `'c:\MAP18_Results\NobodyAnonymus\Morphometry_PRI_3T_T1_01Jan2000'`.

Appendix A: Modes of action

The table below lists all modes of action available in MAP18. The abbreviations can be used as input for the variable `'mode'` when starting image processing from command line by `map18(image,mode,norm,space,sensitivity,ROI_mode,viewer,age,email)`. They also correspond to the choices offered in the pull-down menu `'Which mode?…'` presented when starting image processing by GUI.

In general, these 'modes of action' build on each other and comprise necessary preprocessing steps contained in the preceding modes of action. For example, mode `'map'` causes - if not done before - a normalization and segmentation of the input image with subsequent calculation of all morphometric maps. Mode `'FCD'` also invokes these processing steps before starting the automated FCD detection algorithm. If these preprocessing steps have already been performed before, however, only the detection of FCDs is repeated (which might be interesting for testing different thresholds). Mode `'all'` comprises all steps mentioned before and additionally PNH detection and curvilinear reformatting. Finally, mode `'full'` encompasses everything that mode `'all'` involves, as well as volumetric analysis.

However, some methods (i.e. `'FLAIR', 'PNH', 'curv', 'SISCOM', 'uncover', 'visualize', 'inverse', 'vol'`) refer to circumscribed types of image processing and do not include all the preceding modes of action, but only the preprocessing required for the specific task (usually normalization and segmentation).

Abbreviation	Meaning
'coregister'	coregister other images with the input image (do nothing else, i.e. no normalization or segmentation)
'average'	coregister other images with the input image, adjust intensities to common mean and then average all images
'subtract'	coregister two other images with the input image, normalize the input image and both coregistered images to MNI space, rescale and normalize the intensities of the coregistered images to a common level (compartmentwise!) and calculate a difference image of the two coregistered images
'normalize'	normalize the input image to MNI space
'extension'	create only the 'Extension Image'
'junction'	create only the 'Junction Image'

'thickness'	create only the 'Thickness Image'
'map'	create all morphometric maps
'FLAIR'	whole brain FLAIR analysis according to the method of Focke N et al., Epilepsia 2008 and 2009, and *regional* FLAIR analysis of amygdala and hippocampus according to Huppertz HJ et al., Epilepsy Res 2011
'FCD'	detect FCD by searching for z score maxima (old method)
'mapFCD'	create FCD probability map using an artificial neural network pretrained by images with labelled FCD lesions (new method)
'PNH'	detect periventricular nodular heterotopia (PNH) according to Pascher B et al., Epilepsia 2013. If the results of a whole brain FLAIR analysis are available, they are used to exclude false-positive findings where the FLAIR signal is too high for a PNH lesion.
'curv'	create curved surfaces (i.e. curvilinear reformatting)
'all'	create morphometric maps & curved surfaces and detect FCD & PNH
'SISCOM'	SISCOM, i.e. subtraction of ictal and interictal SPECT and subsequent coregistration to MRI
'uncover'	uncover implanted subdural electrodes according to the method described by D. Kovalev et al., Am J Neuroradiol 2005 (requires pre- and post-implantation MRI data)
'visualize'	visualize implanted subdural and depth electrodes by segmentation of metal artefacts in the cranial CT scan (CCT) (requires pre-implantation MRI data and post-implantation CCT)
'deface'	deface MRI, i.e. remove facial details in MNI space and transform back 'defaced' input image(s) to native space
'inverse'	inverse normalization, i.e. transform result images to native stereotactic space by inverse normalization, including optional conversion to BMP images and DICOM files
'vol'	volumetric MRI analysis (limited to structures relevant in epileptology)
'full'	create morphometric maps & curved surfaces, detect FCD & PNH, and perform (small) volumetric MRI analysis

Appendix B: Normal databases

MAP18 contains the following *general* normal databases:

Abbreviation	Description of normal database
'AVG_T1_Large'	Average from 61 1.5 & 3T scanners with 3716 T1 images (children & adults). This NDB is meant for MRI data for which no scanner-specific NDB is available.
'AVG_T1'	Average from 5 different 1.5 & 3T scanners with 5x30 T1 images (adults). This NDB for T1 images is included for backwards compatibility. It is the only NDB which has been described in former publications.
'AVG_T2'	Average from 5 different 1.5 & 3T scanners with 228 T2 images (adults)

Currently existing *scanner-specific* normal databases are listed below. However, the selection within MAP18 is limited to those normal databases actually delivered together with this program for the site of implementation. Please, check the subdirectory `'…\Map15_for_SPM12\Norm_Databases'` for available normal databases.

'FR_Vision_T1'	SIEMENS Magnetom Vision 1.5T (Freiburg) with 45 T1 images (adults)
'BE_Symphony_T1'	SIEMENS Magnetom Symphony 1.5T (Bethel) with 38 T1 images (adults)
'MZ_Vision_T1'	SIEMENS Magnetom Vision 1.5T (Mainz) with 37 T1 images (adults)
'BO_Intera_T1'	PHILIPS Gyroscan Intera 1.5T (Bonn) with 46 T1 images (adults)
'BO_Avanto_T1'	SIEMENS AVANTO 1.5T (Bonn) with 30 T1 images (adults)
'BO_Avanto_T2'	SIEMENS AVANTO 1.5T (Bonn) with 30 T2 images (adults)
'BO_Trio_T1'	SIEMENS TRIO 3T (Bonn) with 255 T1 images (adults)
'BO_Trio_T2'	SIEMENS TRIO 3T (Bonn) with 64 T2 images (adults)
'HL_Sonata_T1'	SIEMENS Sonata 1.5T (Zurich Hirslanden) with 51 T1 images (adults)
'HL_Intera_T1'	PHILIPS Intera 3T (Zurich Hirslanden) with 30 T1 images (adults)
'DD_Sonata_T1'	SIEMENS Sonata 1.5T (Dresden) with 30 T1 images (adults)
'S_Vision_T1_5-9'	SIEMENS Magnetom Vision 1.5T (Stuttgart) with 32 T1 images (5-9 ys)
'S_Vision_T1_9-13'	SIEMENS Magnetom Vision 1.5T (Stuttgart) with 29 T1 images (9-13 ys)
'S_Vision_T1_13-18'	SIEMENS Magnetom Vision 1.5T (Stuttgart) with 18 T1 images (13-18 ys)
'KISPI_GE_T1_10-12'	GENERAL ELECTRICS 3T (Zurich Kispi) with T1 images (10-12 ys)
'KISPI_GE_T1_8-10'	GENERAL ELECTRICS 3T (Zurich Kispi) with 10 T1 images (8-10 ys)
'ER_Trio_T1'	SIEMENS TRIO 3T (Erlangen) with 43 T1 images (adults)
'HH_Sonata_T1'	SIEMENS Sonata 1.5T (Hamburg) with 33 T1 images (adults)
'Leuven_Vision_T1'	SIEMENS Magnetom Vision 1.5T (Leuven) with T1 images (adults)
'Maastricht_Achieva_T1'	PHILIPS Achieva 3T (Maastricht) with T1 images (adults)
'INN_Sonata_T1'	SIEMENS Sonata 1.5T (Innsbruck) with 31 T1 images (adults)
'MR_Trio_T1'	SIEMENS TRIO 3T (Marburg) with 51 T1 images (adults)
'MR_Sonata_T1'	SIEMENS Sonata 1.5T (Marburg) with 24 T1 images (adults)
'KI_Achieva_T1'	PHILIPS Achieva 3T (Kiel) with 128 T1 images (adults)
'B_Symphony_T1'	SIEMENS Magnetom Symphony 1.5T (Berlin) with 33 T1 images (adults)
'BRU_Achieva_T1'	PHILIPS Achieva 3T (Brussels) with 85 T1 images (adults)
'BRU_Achieva_T1_05-	PHILIPS Achieva 3T (Brussels) with 50 T1 images (05-18 ys)
'KI_NP_Achieva_T1'	PHILIPS Achieva 3T (Kiel Neuropaed) with 67 T1 images (7-18 ys)
'CC_Trio_T1'	SIEMENS TRIO 3T (Cleveland Clinic) with T1 images (adults)
'CC_T1_3-5'	SIEMENS &PHILIPS (Cleveland Clinic) with 46 T1 images (3-5 ys)
'CC_T1_5-10'	SIEMENS &PHILIPS (Cleveland Clinic) with 110 T1 images (5-10 ys)
'CC_T1_10-15'	SIEMENS &PHILIPS (Cleveland Clinic) with 109 T1 images (10-15 ys)
'CC_T1_15-21'	SIEMENS &PHILIPS (Cleveland Clinic) with 105 T1 images (15-21 ys)
'CC_Terra_T1'	SIEMENS Magnetom Terra 7T (Cleveland Clinic) with T1 images (adults)

'HH_Skyra_T1'	SIEMENS Skyra 3T (Hamburg) with 50 T1 images (adults)
'HH_Skyra_T2'	SIEMENS Skyra 3T (Hamburg) with 50 T2 images (adults)
'HU_Achieva_T1'	PHILIPS Achieva 3T (Zurich, Dr. Huber) with T1 images (adults)
'ZG_Trio_T1'	SIEMENS TRIO 3T (Zagreb) with T1 images (adults)
'UL_Symphony_T1'	SIEMENS Magnetom Symphony 1.5T (Ulm) with 50 T1 images (adults)
'Whisgott_Achieva_T1'	PHILIPS Achieva 3T (Dresden, Dr. Whisgott) with T1 images (adults)
'W_Achieva_T1'	PHILIPS Achieva 3T (Wien) with 43 T1 images (adults)
'W_Achieva_T2'	PHILIPS Achieva 3T (Wien) with T2 images (adults)
'VO_Symphony_T1'	SIEMENS Magnetom Symphony 1.5T (Vogtareuth) with 27 T1 images (5-17 ys)
'BP_Achieva_T1'	PHILIPS Achieva 3T (Budapest) with T1 images (adults)
'FR_Trio_T1'	SIEMENS TRIO 3T (Freiburg) with 77 T1 images (adults)
'FR_Trio_T1_4-6'	SIEMENS TRIO 3T (Freiburg) with 100 T1 images (4-6 ys)
'FR_Trio_T1_6-14'	SIEMENS TRIO 3T (Freiburg) with 77 T1 images (6-14 ys)
'HGW_Verio_T1'	SIEMENS Verio 3T (Greifswald) with 100 T1 images (adults)
'ATL_Trio_T1'	SIEMENS TRIO 3T (Atlanta) with 66 T1 images (8-22 ys)
'BARC_Achieva_T1'	PHILIPS Achieva 3T (Barcelona) with 37 T1 images (adults)
'PHI_Achieva_T1'	PHILIPS Achieva 3T (Philadelphia) with 92 T1 images (adults)
'SAN_Skyra_T1'	SIEMENS Skyra 3T (Santiago de Chile) with 55 T1 images (adults)
'MS_Intera_T1'	PHILIPS Intera 3T (Muenster) with 48 T1 images (adults)
'UAB_Achieva_T1'	PHILIPS Achieva 3T (Birmingham, Alabama) with 36 T1 images (adults)
'LR_Achieva_T1'	PHILIPS Achieva 3T (Little Rock, Arkansas) with 58 T1 images (adults)
'LZ_Verio_T1'	SIEMENS Verio 3T (Linz, Austria) with 40 T1 images (adults)
'LZ_Verio_T2'	SIEMENS Verio 3T (Linz, Austria) with 40 T2 images (adults)
'BRI_Discovery_T1'	GENERAL ELECTRICS Discovery 3T (Brisbane) with 45 T1 images (adults)
'KP_Biograph_T1'	SIEMENS Biograph 3T (Kaposvar) with 50 T1 images (adults)
'KP_Biograph_T2'	SIEMENS Biograph 3T (Kaposvar) with 50 T2 images (adults)
'SD_Achieva_T1'	PHILIPS Achieva 3T (Santo Domingo) with 75 T1 images (adults)
'PTE_Trio_T1'	SIEMENS TRIO 3T (Pecs) with 44 T1 images (adults)
'THR_Avanto_T1'	SIEMENS AVANTO 1.5T (Teheran) with 52 T1 images (adults)
'FR_Prisma_T1'	SIEMENS PRISMA 3T (Freiburg) with 158 T1 images (adults)
'FR_Prisma_T1MP2'	SIEMENS PRISMA 3T (Freiburg) with 153 T1 MP2RAGE images (adults)
'SOF_Signa_T1'	GE Signa 1.5T (Sofia) with 69 T1 images (adults)
'RIX_Ingenia_T1_1-5'	PHILIPS Ingenia 1.5T (Riga) with 25 T1 images (1-5 ys)
'RIX_Ingenia_T1_2-11'	PHILIPS Ingenia 1.5T (Riga) with 52 T1 images (2-11 ys)
'RIX_Ingenia_T1_11-18'	PHILIPS Ingenia 1.5T (Riga) with 53 T1 images (11-18 ys)
'ROW_Skyra_T1'	SIEMENS Skyra 3T (Rotenburg, Wümme) with 74 T1 images (adults)
'ROW_Skyra_T2'	SIEMENS Skyra 3T (Rotenburg, Wümme) with T2 images (adults)
'MDLN_Essenza_T1'	SIEMENS Essenza 1.5T (Medellin) with 150 T1 images (adults)
'MYS_Signa_T1'	GE Signa 3T (Malaysia) with 52 T1 images (adults)
'SIN_Ingenia_T1'	PHILIPS Ingenia 3T (Singapore) with T1 images (adults)
'MD_Terra_T1'	SIEMENS Magnetom Terra 7T (Magdeburg) with 32 T1 images (adults)
'MD_Terra_T2'	SIEMENS Magnetom Terra 7T (Magdeburg) with 32 T2 images (adults)
'MIL_Achieva_T1'	PHILIPS Achieva 1.5T (Milan) with 151 T1 images (adults)
'MIL_Achieva_T1_old'	PHILIPS Achieva 1.5T (Milan) with 56 T1 images (adults), before scanner adjustments
'MIL_Achieva_T1_new'	PHILIPS Achieva 1.5T (Milan) with 95 T1 images (adults), after scanner adjustments
'PA_Signa_T1'	GE Signa 3T (Porto Alegre) with 154 T1 images (5-58 ys)
'MUC_Signa_T1	GE Signa 3T (Munich) with 73 T1 images (adults)
'UAB_Ingenia_T1_2-6'	PHILIPS Ingenia 3T (Birmingham, Alabama) with 20 T1 images (2-6 ys)
'UAB_Ingenia_T1_6-14'	PHILIPS Ingenia 3T (Birmingham, Alabama) with 20 T1 images (6-14 ys)
'CTU_Trio_T1'	SIEMENS TRIO 3T (Chengdu) with 189 T1 images (adults)
'CTU_Trio_T1_06-16'	SIEMENS TRIO 3T (Chengdu) with 41 T1 images (6-16 ys)
'MAD_Prisma_T1'	SIEMENS Prisma 3T (Madrid) with 56 T1 images (adolescents & adults)
'MAD_Prisma_T1_02-12'	SIEMENS Prisma 3T (Madrid) with 21 T1 images (2-12 ys)
'PNI_Skyra_T1'	SIEMENS Skyra 3T (PNI, Bangkok) with 42 T1 images (adults)
'HGH_Prisma_T1'	SIEMENS Prisma 3T (Hangzhou, First Hospital) with 106 T1 images (adults)
'BUE_Achieva_T1'	PHILIPS Achieva 3T (Buenos Aires) with 42 T1 images (adults)
'IIS_Verio_T1'	SIEMENS Verio 3T (Madrid IIS) with 31 T1 images (adults)
'NYC_Achieva_T1'	PHILIPS Achieva 3T (New York, Columbia) with 30 T1 images (adults)
'BUS_Achieva_T1'	PHILIPS Achieva 3T (Busan, South Korea) with 62 T1 images (adults)

'Gent_PrismaFit_T1'	SIEMENS Prisma 3T (Gent, Belgium) with 62 T1 images (adults)
'LL_TrioTim_T1'	SIEMENS TrioTim 3T (Loma Linda) with 68 T1 images (adults)
'AUR_Ingenia_T1_3-18'	PHILIPS Ingenia 3T (Aurora, Colorado) with 50 T1 images (3-18 ys)
'Rome_Skyra_T1_6-16'	SIEMENS Skyra 3T (Rome) with 30 T1 images (6-16 ys)
"HGH_Terra_T1'	SIEMENS Terra 7T (Hangzhou, Second Hospital) with 30 T1 images (adults)
'BE_Verio_T1'	SIEMENS Verio 3T (Bethel) with 102 T1 images (adults)
'MO_Intera_T1'	PHILIPS Intera 3T (Modena) with 68 T1 images (adults)
'CHAR_Skyra_T1_2-6'	SIEMENS Skyra 3T (Berlin Charite) with 37 T1 images (2-6 ys)
'CHAR_Skyra_T1_6-18'	SIEMENS Skyra 3T (Berlin Charite) with 57 T1 images (6-18 ys)
'BBI_Signa_OPT_T1'	GE Signa Optima 1.5T (Brain Institute, Bucharest, Romania) with 364 T1 images (adults)
'BBI_Signa_VOY_T1'	GE Signa Voyager 1.5T (Brain Institute, Bucharest, Romania) with 186 T1 images (adults)
'BBI_Signa_OPT_T2'	GE Signa Optima 1.5T (Brain Institute, Bucharest, Romania) with 130 T2 images (adults)
'BBI_Signa_VOY_T2'	GE Signa Voyager 1.5T (Brain Institute, Bucharest, Romania) with 63 T2 images (adults)

Appendix C: Shortcuts and hyperlinks

MAP18 offers a series of shortcuts that allow the most frequently used actions and types of image processing to be called very quickly from command line without having to specify additional parameters. The command `map18('hyperlinks')` lists all these shortcuts as hyperlinks, so that they can be called by a simple mouse click from the MATLAB command window. The following table shows all available shortcuts and their meaning. Text passages in blue colour provide further explanations.

General commands:	
map18('help')	display help and explanations for MAP18
map18('diagnose')	determine current environment for MAP18
map18('version')	display date of MAP18 compilation
map18('hyperlinks')	list hyperlinks for useful shortcuts
Command for pipeline processing:	
map18('automatic')	start 'automatic_MAP18.m' after asking for *.ini file This is useful for automating image analysis with MAP18 in a processing pipeline. It might be necessary to edit the 'automatic_MAP18.ini' file in order to adjust the program to local conditions (Appendix E: Editing the 'automatic_MAP18.ini' - File).
Shortcuts for various analyses:	
Note that MAP18 will use default parameters with these shortcuts and typically will only ask for input image(s) if there is either no or more than one source image in the current directory.	
map18('coregister')	coregister other images with the input image MAP18 expects one T1 input image (with '_T1_' in the filename) in the current folder, and then automatically coregisters other images found in the same folder, given that the first parts of the filenames (i.e. the patient name) match the filename of the input image.
map18('average')	coregister other images with the input image, adjust intensities to common mean level and then average all images MAP18 will ask for one input image and then automatically coregister other images found in the subfolder of the input image.
map18('subtract')	coregister two other images with the input image, normalize the input image and both coregistered images to MNI space, rescale and normalize the intensities of the coregistered images to a common level (compartmentwise!) and calculate a difference image of the two coregistered images MAP18 expects one T1 input image (with '_T1_' in the filename) in the current folder, and two other images with suffix '_sub1' and '_sub2', respectively, in the filenames. The first parts of the filenames (i.e. the patient name) have to match the filename of the input image.
map18('highRes')	calculate 'Junction Image' with interpolated high resolution (0.5 mm)

map18('FCD')	detect FCD in morphometric maps (with medium sensitivity and specificity)
map18('mapFCD')	create FCD probability map using a pretrained artificial neural network
map18('PNH')	detect PNH in the Extension Image (with medium sensitivity and specificity)
map18('FLAIR')	perform whole brain and regional FLAIR analysis MAP18 will process all images with suffix '_FLAIR_WBA' within the directory of input image(s).
map18(all)	perform morphometric (incl. curvilinear reformatting & lesion detection)
map18('vol')	determine volumes (limited to structures relevant in epileptology)
map18('volExample')	show examples of full volumetric MRI analysis (for neurodegenerative diseases)
map18('full')	perform morphometric and volumetric MRI analysis with default parameters
Commands for displaying results:	
map18('MRIcro')	display normalized input image, coregistered images & result maps with MRIcro This viewer is best for displaying and adjusting contrasts in morphometric maps.
map18('MRIcroN')	display normalized input image, coregistered images & result maps with MRIcroN
map07('Mango')	display morphometric maps with Mango viewer (http://ric.uthscsa.edu/mango) However, the program has to be present in the MATLAB path or in the Windows program folder (i.e. 'c:\Program Files\Mango\Mango.exe').
map18('show3D')	load normalized input image & 'Junction Image' with function 'Check Reg' of SPM. To show a 3D image of curved surfaces, set crosshairs to the desired position in the brain, press right mouse button and select 'Launch MRIcroGL and display surface' or 'Launch MRIcroGL and save surface images' from the menu.
map18('surface')	load native & normalized GM image with function 'Check Reg' of SPM and start up renderer 'Surf Ice' with the normalized GM image to inspect the cortical surface To show the surface in native space, set crosshairs into native GM image, press right mouse button & select 'Launch SurfIce and display cortical surface'.
Commands for format conversions and anonymizing, checking, cropping and defacing of images:	
map18('check')	check image(s), i.e. try reading ANALYZE or NIFTI image(s) and create snapshots
map18('crop')	crop image(s), i.e. try clipping of neck and borders of image cube
map18('deface')	deface MRI, i.e. normalize input image(s) to MNI space (by 'unified segmentation' incl. bias correction), remove facial details of the input image(s), and then transform back 'defaced' input image(s) to native space
map18('defaceSPM')	deface MRI using the method by John Ashburner included in SPM (i.e. 'spm_deface') which is much faster and works directly in native space after affine registration of the input image(s) to a template
map18('inverse')	transform result maps back to native space of input image
map18('convert')	convert DICOM files to ANALYZE or NIFTI format Optionally, the images can be axially reorientated and resliced to 1mm resolution.
map18('DICOM')	convert to DICOM format; optionally, change orientation and anonymize MAP18 uses a DICOM example file to extract information about patient, study, orientation etc. Usually, this DICOM example file is created automatically in the patient/study directory when using the automated pipeline processing. Otherwise, the program will ask for a DICOM example file which then has to be chosen from the imagebox of the

	PACS, preferably from the original MRI of the patient. Optionally, during conversion to DICOM format, the orientation of the resulting output images can be changed. The corresponding menu offers 4 possibilities: 'axial', 'coronar', 'sagittal' and 'original' (i.e. original orientation of input image). As a second option, the images can also be anonymized: please cf. shortcut map18('anonymize'). The corresponding menu offers two possibilities for anonymization: 'yes' or 'no'. Note: If the conversion to ANALYZE format was done using automated pipeline processing, not only one single DICOM example file is stored but all DICOM files of the input image are copied to a subfolder named `'DICOM_Files_of_input_image'` within the patient/study directory. This allows more precise conversion back to DICOM format (e.g. with correct table position etc.). Previously, this only worked when the original orientation and dimensions of the input image were preserved (i.e. no cropping, no reorientation / reslicing to 1 mm axial slices during pipeline processing). However, since the parameters of cropping, reorientation and reslicing are now stored in *.mat-files, the original orientation and dimensions of the input image can be restored, no matter how the parameters 'ResliceImage' and 'CropImage' are set in the automatic_MAP18.ini – file.
map18('anonymize')	anonymize DICOM files, i.e. fill the DICOM fields 'StudyDate' 'SeriesDate', 'AcquisitionDate', 'ContentDate', 'PatientName', 'PatientID', 'PatientBirthDate', 'PatientSex', 'InstitutionName', 'InstitutionalDepartmentName', 'ReferringPhysicianName' and 'RequestingPhysician' with other predefined information.
Command for cleaning up:	
map18('delete')	delete majority of files from MAP18 analysis & keep only most important ones

Some additional tools and more general shortcuts are presented as hyperlinks when calling `map18('help')`, but can also be called directly from MATLAB command line:

Command	**Meaning**
install_MAP18	install MAP18 and all belonging programs and tools from scratch by downloading all necessary files from the FTP server of the Swiss Epilepsy Clinic Installation is only permitted on computers which have already been activated for MAP18. Microsoft Windows operating system is required.
update_MAP18	download updates for MAP18 from the FTP server of the Swiss Epilepsy Clinic
transfer_MAP18	copy MAP18 and all belonging programs and tools to a new location Afterwards, all corresponding MATLAB paths are automatically updated.
test_MAP18	execute MAP18 with default settings on a test case When called a second time, the same command deletes all existing result files and restores the initial state of the test case.

Appendix D: Result images

After image processing, the patient folder contains a lot of result files with partially similar file names, which can be confusing. The following overview shall help to distinguish the result files by file names and their prefixes and suffixes.

Generally, SPM employs the following file prefixes (cf. SPM12 manual):

Prefix	Example	Meaning / Explanation
'r'	rTestcase_ZUR_3T_FLAIR_WBA_29Feb2017.img	coregistered image (usually with the input image)
'm'	mTestcase_ZUR_3T_T1_29Feb2017.img	bias corrected image (i.e. corrected for signal inhomogeneities)
'w'	wTestcase_ZUR_3T_T1_29Feb2017_probFCD.img	normalized image (normalized to MNI space by SPM12's 'unified segmentation' algorithm, known as 'New Segment' in SPM8)
'wm'	wmTestcase_ZUR_3T_T1_29Feb2017.img	normalized & bias corrected image

For the following table the example case used in the first recipes serves as a basis. The listing corresponds to the order in which the files are created during image processing. You should see the same order when you sort the folder contents in Windows Explorer by 'change date'. The most important files & results are highlighted by orange colour. Please note that the header files (*.hdr) which ordinarily accompany images in ANALYZE format (*.img) have been omitted in the list below.

Filenames	Meaning / Explanation
Testcase_ZUR_3T_T1_29Feb2017.img	input image (in ANALYZE format)
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017_orig.img	Original FLAIR image (before bias correction during FLARI analysis)
Testcase_ZUR_3T_T1_29Feb2017_no_alignment_required.tif	tiff image showing the alignment of input image and SPM T1 template
wmTestcase_ZUR_3T_T1_29Feb2017_DARTELized.img	input image normalized to MNI space by DARTEL algorithm (only used internally for volumetric analysis)
Testcase_ZUR_3T_T1_29Feb2017_Normalization_with_DARTEL.tif	tiff image showing the DARTEL normalization of the input image to the SPM T1 template
wmTestcase_ZUR_3T_T1_29Feb2017.img	input image normalized to MNI space by SPM12's 'unified segmentation' algorithm (used for morphometric analysis)
Testcase_ZUR_3T_T1_29Feb2017_Segmentation.tif	tiff image showing the results of input image segmentation
Testcase_ZUR_3T_T1_29Feb2017_Means.mat	MATLAB mat-file containing means of tissue intensities (i.e. for GM, WM and CSF) in the normalized input image
Testcase_ZUR_3T_T1_29Feb2017_Normalization.tif	tiff image showing the results of input image normalization to MNI space by SPM's 'unified segmentation' algorithm
Testcase_ZUR_3T_T1_29Feb2017_Ns.mat	MATLAB mat-file containing the number of

	voxels for the different tissue classes (in the normalized image)
wTestcase_ZUR_3T_T1_29Feb2017_extension_z_score.img	normalized 'Extension Image' (highlighting abnormally located grey matter / abnormally deep sulci); the degree of deviation to the selected normal database is expressed as z scores in the voxel values
wTestcase_ZUR_3T_T1_29Feb2017_junction_z_score.img	normalized 'Junction Image' (highlighting blurring of the grey-white matter junction); the degree of deviation to the selected normal database is expressed as z scores in the voxel values
wTestcase_ZUR_3T_T1_29Feb2017_thickness_z_score.img	normalized 'Thickness Image' (highlighting abnormally thick cortex); the degree of deviation to the selected normal database is expressed as z scores in the voxel values
wTestcase_ZUR_3T_T1_29Feb2017_combined_z_score.img	normalized and combined z score image = combination of all three morphometric maps (i.e. Extension, Junction and Thickness Image); each voxel contains the highest z score off all three maps at the respective location
wmTestcase_ZUR_3T_T1_29Feb2017_masked_by_00mm.img	normalized images & corresponding headers resulting from curvilinear reformatting at different depth as measured in millimetres from the cortical surface (for 3D volume rendering with MRIcro or MRIcroGL by Chris Rorden; http://www.mccauslandcenter.sc.edu/crnl/tools)
wmTestcase_ZUR_3T_T1_29Feb2017_masked_by_02mm.img	
wmTestcase_ZUR_3T_T1_29Feb2017_masked_by_04mm.img	
wmTestcase_ZUR_3T_T1_29Feb2017_masked_by_06mm.img	
wmTestcase_ZUR_3T_T1_29Feb2017_masked_by_08mm.img	
…	
wmTestcase_ZUR_3T_T1_29Feb2017_masked_by_30mm.img	
wmTestcase_ZUR_3T_T1_29Feb2017_skull_stripped.img	normalized and skull-stripped image (with skull-stripping by means of bet.exe) for 3D volume rendering by means of MRIcro, MRIcroGL or SurfIce)
wmTestcase_ZUR_3T_T1_29Feb2017_right_hemisphere.img	normalized image (with left half of the brain masked out)
wmTestcase_ZUR_3T_T1_29Feb2017_right_hemisphere _skull_stripped.img	normalized and skull-stripped input image (with left half of the brain masked out)
wmTestcase_ZUR_3T_T1_29Feb2017_left_hemisphere.img	normalized image (with right half of the brain masked out)
wmTestcase_ZUR_3T_T1_29Feb2017_left_hemisphere _skull_stripped.img	normalized and skull-stripped input image (with right half of the brain masked out)
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017_no_alignment _required.tif	tiff image showing the alignment of the FLAIR image with the input image
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017_seg8.mat	MATLAB mat-file derived from 'unified segmentation' algorithm ('New Segment' in SPM8)
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017.img	FLAIR image in original native space, after bias correction during whole brain FLAIR analysis
rTestcase_ZUR_3T_FLAIR_WBA_29Feb2017.hdr	coregistered FLAIR image (to input image)
Testcase_ZUR_3T_T1_29Feb2017_Coregistration_of_Testcase _ZUR_3T_FLAIR_WBA_29Feb2017.tif	tiff image showing the coregistration of the FLAIR image with the input image
wrTestcase_ZUR_3T_FLAIR_WBA_29Feb2017_flair_scaled.img	coregistered & normalized FLAIR image after rescaling of intensities to a common mean level
wrTestcase_ZUR_3T_FLAIR_WBA_29Feb2017_flair_z_score.img	coregistered & normalized FLAIR z score image

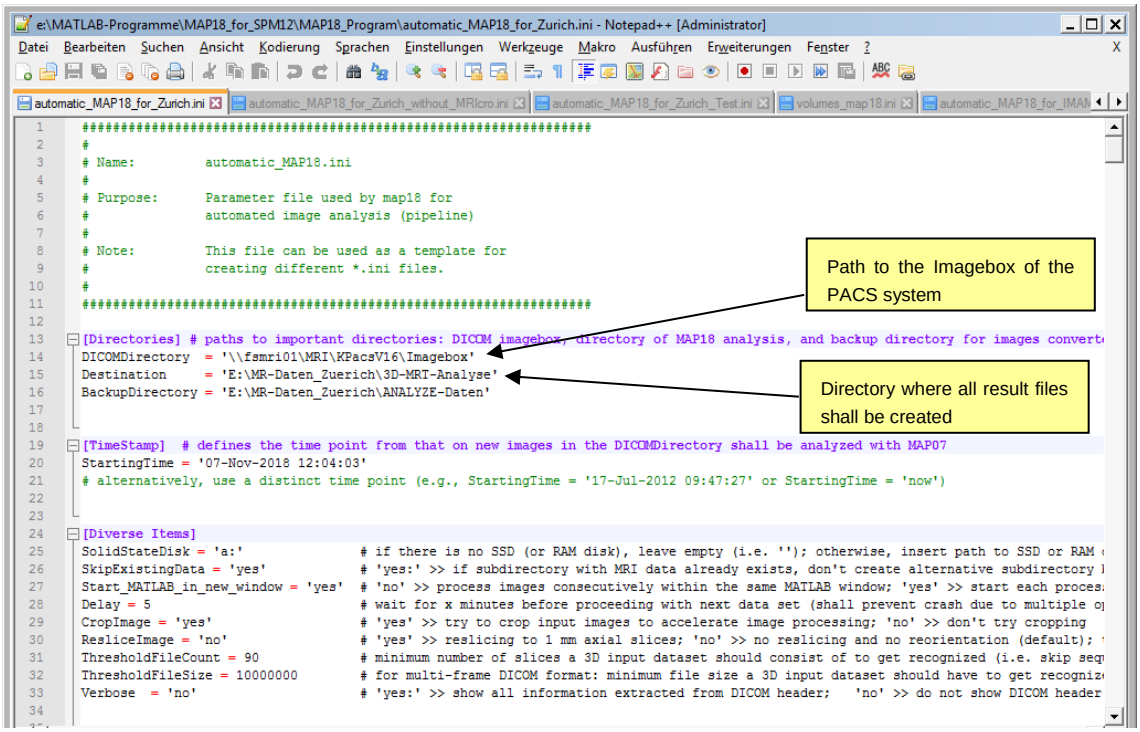
	resulting from FLAIR analysis (highlighting abnormally high FLAIR signal); the degree of deviation to the FLAIR normal database is expressed as z scores in the voxel values
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017_flair_analysis.mat	MATLAB mat-file containing mean FLAIR intensities of regional structures (i.e. hippocampus and amygdala of left and right side)
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017_flair_analysis.txt	text file containing mean FLAIR intensities of regional structures (i.e. hippocampus and amygdala of left and right side)
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017_flair_analysis_Amygdala_upper25.tif	tiff image showing scatter plot with mean amygdalar FLAIR intensities of current patient compared to healthy controls and patients with limbic encephalitis
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017_flair_analysis_Hippocampus_upper25.tif	tiff image showing scatter plot with mean hippocampal FLAIR intensities of current patient compared to healthy controls and patients with hippocampal sclerosis
Testcase_ZUR_3T_FLAIR_WBA_29Feb2017_further_FLAIR_results.zip	zip file with further / intermediate results of whole brain FLAIR analysis
wTestcase_ZUR_3T_T1_29Feb2017_junction_z_score4.img	normalized ROI image derived from 'Junction Image' by searching for z score maxima exceeding a threshold of 4 (i.e. result of the old FCD detection algorithm; similar maps are created from Extension and Thickness Image when the chosen threshold is exceeded).
wTestcase_ZUR_3T_T1_29Feb2017_junction_z_score4.roi	normalized ROI derived from 'Junction Image' (in MRIcro *.roi format)
wTestcase_ZUR_3T_T1_29Feb2017_junction_z_score4 – Center1 – Size 1930 – zScoreMax 6.6 - 79 104 135 Paracentral_Robul_R.tif	tiff image showing the highest z score maximum in the Junction Image and the corresponding location in the normalized input image; the filename encodes the chosen z score threshold, the number of the center, the size of the region, the highest z score within this region, the coordinates of the voxel with the highest z score and the approximate anatomical location
wTestcase_ZUR_3T_T1_29Feb2017_combined_z_score4 - Center1 – Size1167 – zScoreMax 6.6 – 79 104 135 Paracentral_Robul_R.tif	tiff image showing the highest z score maximum in the combined z score image and the corresponding location in the normalized input image; the filename encodes the chosen z score threshold, the number of the center, the size of the region, the highest z score within this region, the coordinates of the voxel with the highest z score and the approximate anatomical location
wTestcase_ZUR_3T_T1_29Feb2017_combined_z_score4.img	normalized ROI image derived from combined z score image by searching for z score maxima exceeding a threshold of 4 (i.e. result of the old FCD detection algorithm; similar maps are created from Extension and Thickness Image when the chosen threshold is exceeded).
wTestcase_ZUR_3T_T1_29Feb2017_combined_z_score4.roi	normalized ROI derived from combined z score image (in MRIcro *.roi format)
wTestcase_ZUR_3T_T1_29Feb2017_probFCD.img	FCD probability map (results from new FCD detection algorithm based on artificial neural networks and encodes probability for dysplastic

	tissue in graded voxel values between 0 and 1)
wTestcase_ZUR_3T_T1_29Feb2017_PNH.img	intermediate image used by the PNH detection algorithm
Testcase_ZUR_3T_T1_29Feb2017_Segmentation_for_volumetry .tif	tiff image showing the results of input image segmentation for volumetric analysis
wTestcase_ZUR_3T_T1_29Feb2017_Gray_Matter.roi	normalized ROI of the grey matter compartment resulting from segmentation for volumetric analysis (in MRIcro *.roi format)
wTestcase_ZUR_3T_T1_29Feb2017_White_Matter.roi	normalized ROI of the white matter compartment (in MRIcro *.roi format)
wTestcase_ZUR_3T_T1_29Feb2017_CSF.roi	normalized ROI of the CSF compartment (in MRIcro *.roi format)
Testcase_ZUR_3T_T1_29Feb2017_volume_results.mat	MATLAB mat-file containing the results of volumetric MRI analysis
Testcase_ZUR_3T_T1_29Feb2017_segmentation_results.zip	zip file with further / intermediate results of normalization and segmentation
Testcase_ZUR_3T_T1_29Feb2017_all_results.mat	MATLAB mat-file containing input parameters and result values & paths and names of input and result images (for debugging purposes)
Testcase_ZUR_3T_T1_29Feb2017_further_morphometric_results .zip	zip file with further / intermediate results of morphometric analysis
Testcase_ZUR_3T_T1_29Feb2017 – Intracranial Volume vs Age .jpg	jpg images showing scatter plot with results of volumetric MRI analysis for intracranial volume, brain, cerebrum, cerebellum and hippocampus (compared to healthy controls)
Testcase_ZUR_3T_T1_29Feb2017 – Brain vs Age (ICV-normalized).jpg	
Testcase_ZUR_3T_T1_29Feb2017 – Cerebrum vs Age (ICV-normalized).jpg	
Testcase_ZUR_3T_T1_29Feb2017 – Cerebellum vs Age (ICV-normalized).jpg	
Testcase_ZUR_3T_T1_29Feb2017 – Cerebrum R vs Cerebrum L (ICV-normalized age-adjusted).jpg	
Testcase_ZUR_3T_T1_29Feb2017 – Hippocampus R vs Hippocampus L (ICV-normalized) for DD HS.jpg	

Appendix E: Editing the 'automatic_MAP18.ini' - File

This text file can be found in the directory `'…\MAP18_for_SPM12\MAP18_Program'`. It controls the automated 'pipeline processing' included in MAP18 and described in the recipe 'Image processing using the automated pipeline'. The pipeline comprises the automated conversion of DICOM images into ANALYZE format, the detection of different MR sequences, the naming rules for image files, and the subsequent image processing with MAP18.

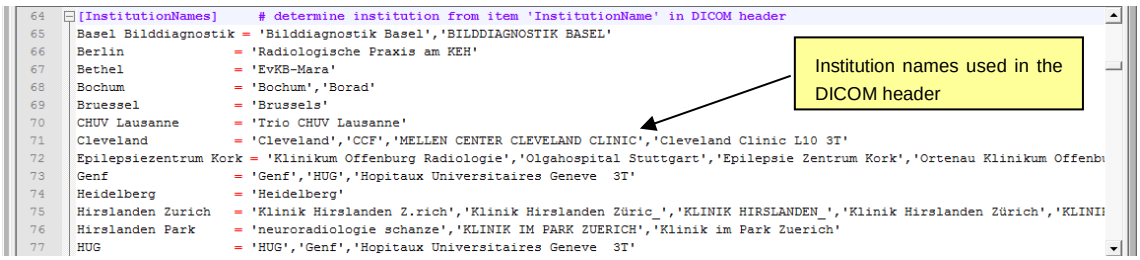
The following overview shall explain which items have to be at least adjusted for each user site. Other parameters are explained in the commentary parts of this text file.



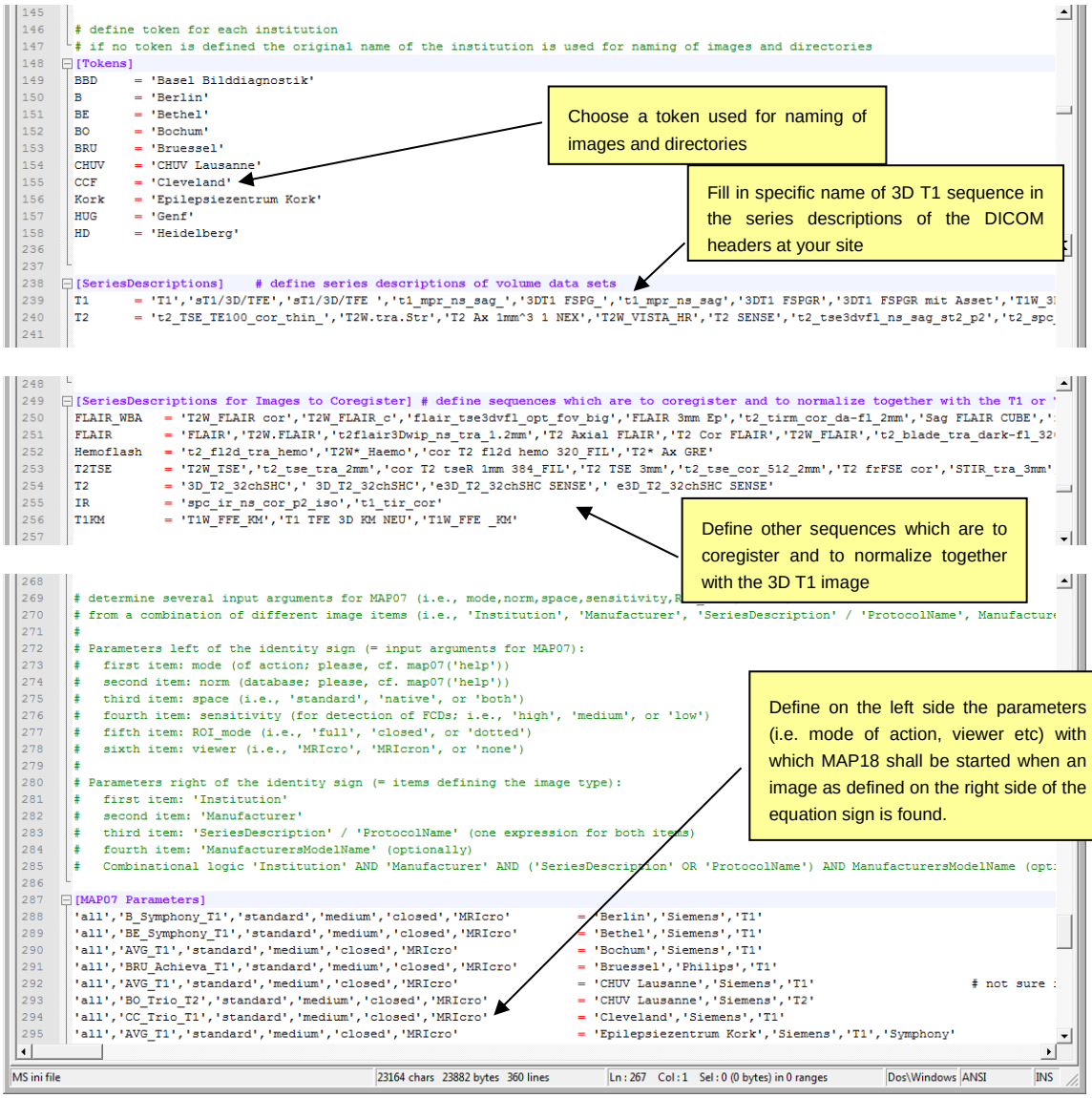

```
[Directories] # paths to important directories: DICOM imagebox, directory of MAP18 analysis, and backup directory for images convert
DICOMDirectory  = '\\fsmri01\MRI\KPacsV16\Imagebox'
Destination     = 'E:\MR-Daten_Zuerich\3D-MRT-Analyse'
BackupDirectory = 'E:\MR-Daten_Zuerich\ANALYZE-Daten'

[TimeStamp]  # defines the time point from that on new images in the DICOMDirectory shall be analyzed with MAP07
StartingTime = '07-Nov-2018 12:04:03'
# alternatively, use a distinct time point (e.g., StartingTime = '17-Jul-2012 09:47:27' or StartingTime = 'now')

[Diverse Items]
SolidStateDisk = 'a:'                # if there is no SSD (or RAM disk), leave empty (i.e. ''); otherwise, insert path to SSD or RAM
SkipExistingData = 'yes'             # 'yes:' >> if subdirectory with MRI data already exists, don't create alternative subdirectory
Start_MATLAB_in_new_window = 'yes'   # 'no' >> process images consecutively within the same MATLAB window; 'yes' >> start each proces
Delay = 5                            # wait for x minutes before proceeding with next data set (shall prevent crash due to multiple o
CropImage = 'yes'                    # 'yes' >> try to crop input images to accelerate image processing; 'no' >> don't try cropping
ResliceImage = 'no'                  # 'yes' >> reslicing to 1 mm axial slices; 'no' >> no reslicing and no reorientation (default);
ThresholdFileCount = 90              # minimum number of slices a 3D input dataset should consist of to get recognized (i.e. skip seq
ThresholdFileSize = 10000000         # for multi-frame DICOM format: minimum file size a 3D input dataset should have to get recogniz
Verbose  = 'no'                      # 'yes:' >> show all information extracted from DICOM header;   'no' >> do not show DICOM header
```




```
[InstitutionNames]     # determine institution from item 'InstitutionName' in DICOM header
Basel Bilddiagnostik = 'Bilddiagnostik Basel','BILDDIAGNOSTIK BASEL'
Berlin               = 'Radiologische Praxis am KEH'
Bethel               = 'EvKB-Mara'
Bochum               = 'Bochum','Borad'
Bruessel             = 'Brussels'
CHUV Lausanne        = 'Trio CHUV Lausanne'
Cleveland            = 'Cleveland','CCF','MELLEN CENTER CLEVELAND CLINIC','Cleveland Clinic L10 3T'
Epilepsiezentrum Kork = 'Klinikum Offenburg Radiologie','Olgahospital Stuttgart','Epilepsie Zentrum Kork','Ortenau Klinikum Offenb
Genf                 = 'Genf','HUG','Hopitaux Universitaires Geneve  3T'
Heidelberg           = 'Heidelberg'
Hirslanden Zurich    = 'Klinik Hirslanden Z.rich','Klinik Hirslanden Züric_','KLINIK HIRSLANDEN_','Klinik Hirslanden Zürich','KLINI
Hirslanden Park      = 'neuroradiologie schanze','KLINIK IM PARK ZUERICH','Klinik im Park Zuerich'
HUG                  = 'HUG','Genf','Hopitaux Universitaires Geneve  3T'
```



To start 'pipeline processing' call `automatic_MAP18('automatic_MAP18.ini')` from MATLAB command line. You may define different `'*.ini'` files for different modes of action. In this case the command `map18('automatic')` opens a menu for selection of the desired `'*.ini'` file.

After initializing pipeline processing the program waits for the arrival of new images in the image directory of the local PACS system. If an appropriate MRI with a 3D T1 image arrives, the DICOM images are converted to ANALYZE format and transferred to the destination directory. Then, MAP18 is automatically started with the parameters defined in the last paragraph of the 'automated_MAP18.ini' - file and executes the analysis on the new image(s).

Appendix F: Abbreviations

Abbreviation	Meaning
ANN	artificial neural network Used for novel method of automated FCD detection implemented in MAP18.
FCD	focal cortical dysplasia
GUI	graphical user interface
PNH	periventricular nodular heterotopia
MAP	Morphometric Analysis Program
MNI	Montreal Neurological Institute During image processing individual brain images are often transformed into a common coordinate space. The two most widely used spaces in the neuro-science community are the Talairach space and the Montreal Neurological Institute (MNI) space.
ROI	region of interest The (old) FCD detection algorithm in MAP18 creates ROI images displaying suspicious regions where the z score in the morphometric maps exceeds a certain predefined threshold.