ABACI

Automated Brain Anatomy for Cohort Imaging

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USER GUIDE

Automated Brain Analysis for Cohort Imaging
GIN, CEA-CNRS-Bordeaux University
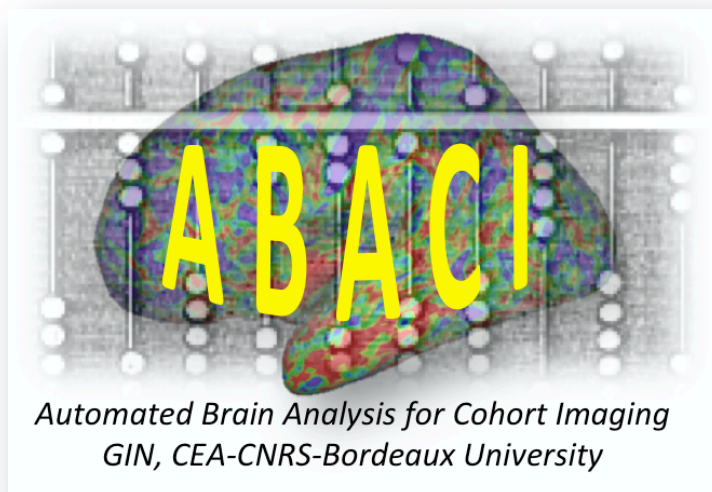
Groupe d'Imagerie Neurofonctionnelle

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LabEx TRAIL ANR-10-LABX-57

Contents

1 Introduction

The Automated Brain Anatomy for Cohort Imaging (ABACI) project provides an environment for storing, managing, and processing neuro-imaging sessions. For this end all the necessary software as well as a set of pipelines (sequential image processing in a "batch mode") for automated processing of structural MRI, acquired in the framework of cohort studies, are provided.

ABACI is released as a virtual machine (VM) running on Ubuntu (http://www.ubuntu.com/) operating system. It also includes the Extensible Neuroimaging Archive Toolkit (XNAT) (http://www.xnat.org) as well as the pipelines mentioned above. Together they offer a standardized, modular, extensible and community driven platform for storage and processing MRI data.

1.1 Installation & setup

ABACI is released as a virtual machine, meaning that it can be run on any system or platform by installing any virtualization software on your host system. We strongly advice using VirtualBox (https://www.virtualbox.org) which is an open-source virtualization product by Oracle.

This section will assume you already have installed the latest version of VirtualBox (https://www.virtualbox.org/wiki/Downloads).

1) Open the file ABACI.ova and VirtualBox will automatically open a dialog to import the VM:
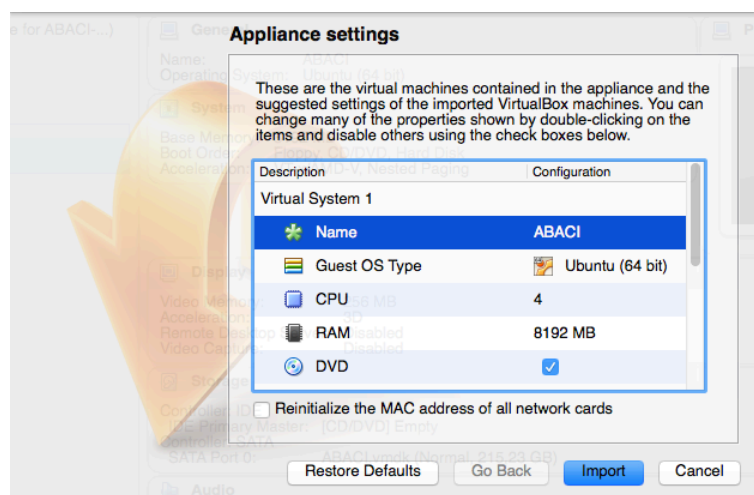
2)   At this stage you can configure all the necessary settings, like CPU number and RAM, accordingly to your host system. We strongly advice not to exceed the half of your CPU number and the half of your total RAM.

3)   Click "Import". You will see a dialog showing the process of the deployment, this could take up to several hours depending on your host system.

4)   After importing the VM, you will find ABACI on the left panel of VirtualBox.

From there you can launch ABACI VM by double clicking on it or with the button "Start" on the top panel of VirtualBox.

5)   When you open your ABACI VM, the Firefox browser will open automatically and a blank page will show while loading the ABACI page. You should see "waiting for localhost" on the lower left corner. Please don't manually reload the page until it finishes loading.

6)   The first time you log in you must use:
user: admin
password: admin
Then click on "Login".

7)   To modify the administrator password, you should go to Administer/Users then click on "admin" (on the Username column) and then click on "edit".
From Administer/Users you can also modify other users as well as adding new ones.

8)   IMPORTANT: In order to be able to use the FreeSurfer pipeline, you need to register FreeSurfer on (http://surfer.nmr.mgh.harvard.edu/fswiki/Registration) and

follow the instructions. The licence key file must be placed in the FreeSurfer install location $FREESURFER_HOME: /usr/local/freesurfer. To do so, open a terminal:

And type:

```
cp license.txt /usr/local/freesurfer
```

2 Basic usage

After everything is correctly initialized, you will be able to access ABACI application via the Firefox browser already installed in Ubuntu. ABACI is configured to run Firefox automatically on start-up and it can also be run by typing (http://localhost:8080/xnat) on Firefox.

2.1 Add a project

After logging in (user: admin, password: admin), you can start by creating a project by clicking in "new / project" (on the gray toolbar at the top of the website). Fill the project information (just make sure that "Alias(es)", in case you define one, is different than the Running ID and Project ID) and click on "Submit".

New Project

Step 1: Enter project details

Project Title

REQUIRED: Enter the full name of your project here. This will show up on project listings.

Running Title

REQUIRED: Create a simple abbreviation of your project name, using 24 characters or less. Spaces are allowed. This will be commonly used in menus and UI elements.

Project ID

REQUIRED: Create a one word project identifier. This is used in the database and **cannot be changed**.

Project Description

Optional: Provide a description of your project. This is for reference only and is not searchable.

Keywords

Optional: Enter searchable keywords. Each word, separated by a space, can be used independently as a search string.

Alias(es)

Optional: Enter alternate aliases (for example: charge codes) that this project can be identified by.

Investigator(s)

PI [SELECT ▼] ⊘ [More Investigators] [Create Investigator]

Optional: List investigators associated with this project. This is for reference only and **does not provide access** to this project for the listed investigators.

Step 2: Define Project Accessibility

Select the accessibility of your project.

- ⦿ Private — Only you and study members will be able to access study data.
- ◯ Protected
- ◯ Public

[Submit]

2.2 Add a subject

Once you have created your first project it's time to add a subject to it. Go back to "home" and click on "New / Subject". Select the project it will belong to, fill its information and click on "Submit".

Enter a new subject

Primary Project:	(SELECT) ⇕
Subject's ID within this project:	
Subject's research group within this project:	

Demographics

YOB/DOB/Age	Please Select One ⦿ Date Of Birth _____ [>] ◯ Year Of Birth ◯ Age
Gender	(SELECT) ⇕
Handedness	(SELECT) ⇕
Education	
Race	
Ethnicity	
Height (inches)	
Weight (lbs)	
Recruitment Source	

[Submit]

2.3 Add an imaging session

After creating a subject, you will be directed automatically to its details page, where you will see the list of experiments and sessions associated with this subject and from you can also share the subject to other projects.

There are two ways to upload an imaging session: whether clicking "Upload / Images" on the upper grey toolbar or by clicking "Upload Images" on the right action panel.

Note: you have to click on "Activate IcedTea-Web.", then on "allow and remember", and finally allow the applet to run.

You can leave the date empty (it will take the date information from the DICOM headers if you do so) and click on "Launch Uploader". Select the location of the images to upload and click on "Next", it will automatically detect all imaging sessions in that folder and list the scan types. After selecting which scans to upload click on "Next", enter the session name and click on "Finish".


After uploading the session, click on "click here to finish archiving the session", or you can finish archiving later by clicking on "Upload / Go to prearchive", then select the session you left on pre-archive and click on "Archive" at the right actions panel.

Once the session has been archived, you will be directed to the subject details page, where you see the uploaded scans corresponding to the session.

You can view the scans directly from the site by clicking "View / Images" and selecting the session you want to display, then click "Go".
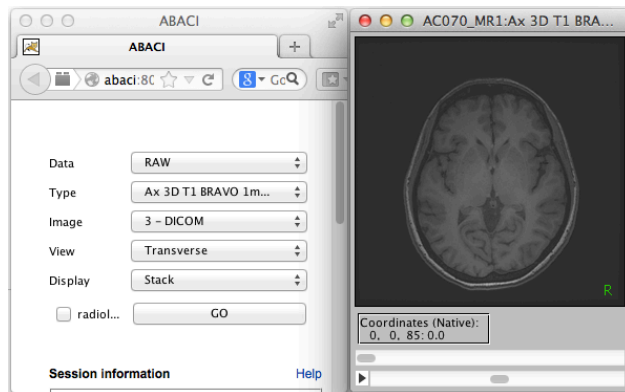
To copy files from the host computer to the VM you must use its "Shared folder". To do so, you must configure the Shared folder from the settings of your ABACI instance in VirtualBox:
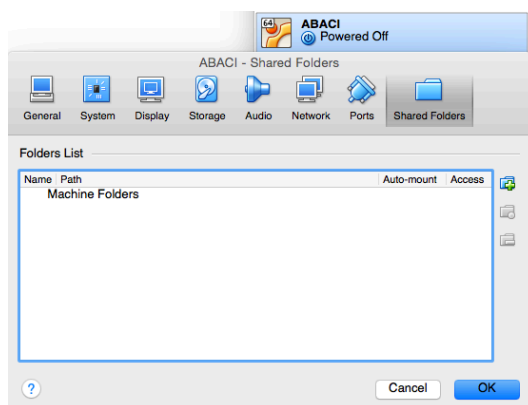
Click on the folder with a green plus icon on the right. Then choose the folder you will use to share files from the host computer to the VM.
From the VM, the files on the Shared folder are accessible at:

```
/media/sf_shared/
```

The files must be copied out from that folder and change the owner (for example):

```
sudo cp –r /media/sf_shared/example_folder /home/abaci/
sudo chown –r abaci:abaci /home/abaci/example_folder
```

By doing so, you will be able to access these files or folders from the ABACI web application and upload the files

3 Pipelines

Before having the pipelines available to be run at each subject in the project you must add them to the project. To do so, go to your project details page and click on "Pipelines" tab (next to "Manage"). A list of the pipelines available to the project will be shown, for the moment it is empty. Click on "Add more pipelines" and select the pipelines that you want to add to your project. For each pipeline a popup will open offering the default values. Please refer to the Developer Documentation on how to add new pipelines to ABACI.

Once you have added all the pipelines you need, you can launch them on every subject by going to the session details page (e.g. MR Session) and clicking on "Build" at the right actions panel.

Most of the pipelines create new information on the session (e.g. assessments or resources). An assessor is information that is indexed into the database and therefore searchable, on the other hand resources are usually output files from the pipelines that can be directly downloaded from the subjects page.

Under the tag "History" you will find all the pipelines and modifications on the session, as well as the status, the date and the user which created the subject. This item is very useful for tractability.

3.1 Manual Quality Control

The second pipeline you will usually run is the manual QC. This pipeline allows you to score the imaging session on several criteria such as Position, Contrast, etc.

To run this pipeline click on "Build", select "ManualQC" and click "Submit". To score each criteria you just have to select a value ranging from 0 to 5 or "Failed / Passed" for others. Please remember to score or fill every criterion. Then click "Submit". Note that you can view the images using the XNAT viewer.

Once the pipeline has finished running, you will see a new assessment (on the bottom of the subject details page), which contains the scores for each criterion.

3.2 Dicom to Nifti

To convert the uploaded DICOM files into NIFTI (needed for all the pipelines except the QC ones) you need to run this pipeline.

In order to do so, click on "Build", select "DicomToNifti", "Submit", select the scans that you want to convert to NIFTI in "scanids" and then select "Y" in "create_nii".

When the pipeline ends you will not see new information on the session page except for when you place your mouse over the "Files" tag on every scan, you should see:

These NIFTI files are not downloadable, to do so click on "Manage files" on the left menu. Then select only the nifti files you want to download on each sequence.

3.3 Voxel Based Morphometry

The Voxel Based Morphometry (VBM) pipeline runs a series of preprocessing on T1 sequence nifti files such as normalisation or segmentation using SPM12 (http://www.fil.ion.ucl.ac.uk/spm).

By default this pipeline uses SPM's tissue probability maps (TPM) to compute the resulting volumetries. The TPM used is entered as an input argument (template) when you run the pipeline, so you can choose your own TPM in case you have computed one:

To run this pipeline, click on "Build", select "VBM", "Submit" and then select the scan number corresponding to the T1 sequence in "scanids".
 This pipeline generates an assessor containing Grey and White Matter (GM, WM) and Cerebrospinal fluid (CSF) volumetries, as well as left and right hippocampal volumes:

VBM Details

MRSession	MRi_ShareDB_E00128
ID	MRi_ShareDB_E00128_VBM
Project	mrishare
Base Scan Number	7
VBM Volumetry Results (mm3)	
GM Volume	879295.56
WM Volume	537682.5
CSF Volume	344574.53
Left Hippocampus Volume	5104.77
Right Hippocampus Volume	4961.06
Algorithm parameters	
Stereotaxic Space	MNI
SPM Version	/bin/bash
Atlas used for hippocampus volume	AAL for SPM 12 (http://www.gin.cnrs.fr/AAL-216)

Hippocampal volumes are computed using AAL atlas (http://www.gin.cnrs.fr/AAL-216).

To download the generated output files click on "Manage Files" on the action box (left panel), and then select "VBM", under "Resources":
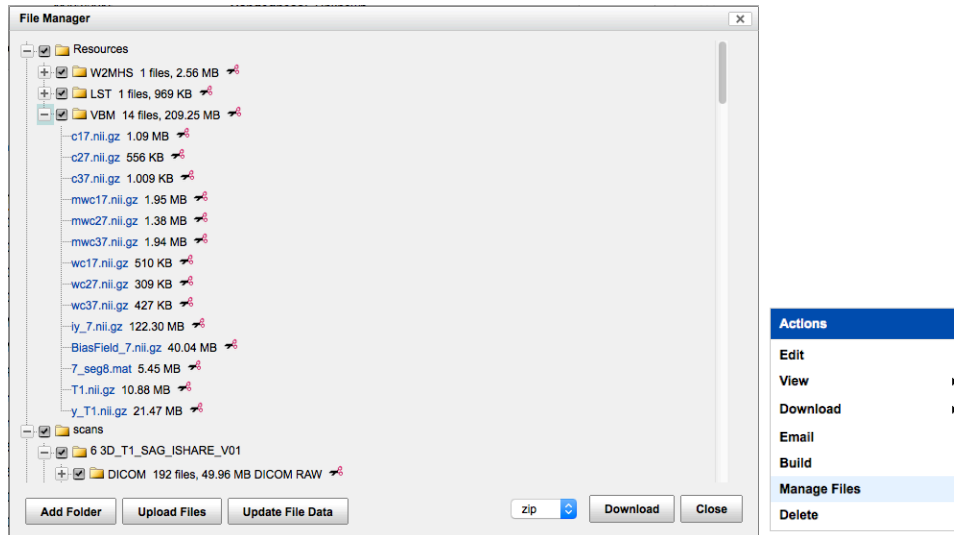
The generated output files are the following:

- c1(series number).nii.gz – Grey matter probability map
- c2(series number).nii.gz – White matter probability map
- c3(series number).nii.gz – CSF probability map
- mwc1(series number).nii.gz – Modulated and warped Grey Matter probability map
- mwc2(series number).nii.gz – Modulated and warped White Matter probability map
- mwc3(series number).nii.gz – Modulated and warped CSF probability map
- wc1(series number).nii.gz – Warped (stereotaxic space) Grey Matter probability map
- wc2(series number).nii.gz – Warped (stereotaxic space) White Matter probability map
- wc3(series number).nii.gz – Warped (stereotaxic space) CSF probability map
- iy_(series number).nii.gz – Inverse 3D deformation field
- y_(series number).nii.gz – 3D deformation field
- BiasField_(series number).nii.gz – 3D inhomogeneity field
- (series number)_seg8.mat – Deformation matrix in Matlab format

3.4 FreeSurfer

The pipeline implemented to perform a FreeSurfer analysis runs a standard "recon-all" procedure with the following arguments:

```
-qcache -all -hippo-subfields -cubic -3T
```

While another recon-all argument (-target) is added as an input argument in the pipeline, its default value is `-target fsaverage`, which allows specifying a common-space target other than fsaverage (the default):

Pipeline for building Freesurfer data for 15_11_04-08_46_17-STD-1_3_12_2_1107_5_2_43_66056

Name	Value
scanids	○6 ○7 ○8 ○9 ○10 ○11 ○12 ○13 ○14 ○15 ○16 ○17 ○18 ○19 ○20 ○21 ○22 ○23 ○24 ○25 ○26 ○27 ○28 ○29 ○30
target	-target fsaverage
sessionId	
xnat_id	
project	
subject	

☐ Run pipeline in-process?
☐ Suppress workflow entries for pipeline execution?

[Close] [Submit]

This pipeline produces a set of output files and some variables (measures). Like in the VBM pipeline, this measures will be available as assessments, being indexed to the database and searchable:

Freesurfer Assessor Details

MRSession	MRi_ShareDB_E00128
ID	MRi_ShareDB_E00128_FS
Project	mrishare
Freesurfer version	freesurfer-Linux-centos4_x86_64-stable-pub-v5.3.0

Freesurfer Results (mm3)

Estimated Total Intracranial Volume	1868006.22937

Grey matter:

Left cortical volume	304412.391137
Right cortical volume	298138.529665
Total cortical volume	602550.920802
Left cerebellum volume	57151.1
Right cerebellum volume	63718.0
Total cerebellum volume	120869.1
Left nucleus volume	26093.2
Right nucleus volume	25403.2
Total nucleus volume	51496.4
Left hemispheric volume	330505.591137
Right hemispheric volume	323541.729665
Total hemispheric volume	654047.320802
Left volume	387656.691137
Right volume	387259.729665
Total volume	774916.420802
Left hippocampus volume	4592.7
Right hippocampus volume	4729.2
Total hippocampus volume	9321.9
Left surface area (mm2)	103799.0
Right surface area (mm2)	102733.0
Total surface area (mm2)	206532.0
Left cortical thickness (mm)	2.59474
Right cortical thickness (mm)	2.56809
Mean cortical thickness (mm)	2.581415

White matter:

Left cortical volume	276635.384476
Right cortical volume	275047.312073
Total cortical volume	551682.696549
Left cerebellum volume	15072.2
Right cerebellum volume	16589.9
Total cerebellum volume	31662.1
Left volume	291707.584476
Right volume	291637.212073
Total volume	583344.796549
Corpus callosum volume	3446.9

Cerebrospinal fluid:

Ventricle volume	25273.7

To download the generated output files click on "Manage Files" on the action box (left panel), and then select "Freesurfer", under "Resources":
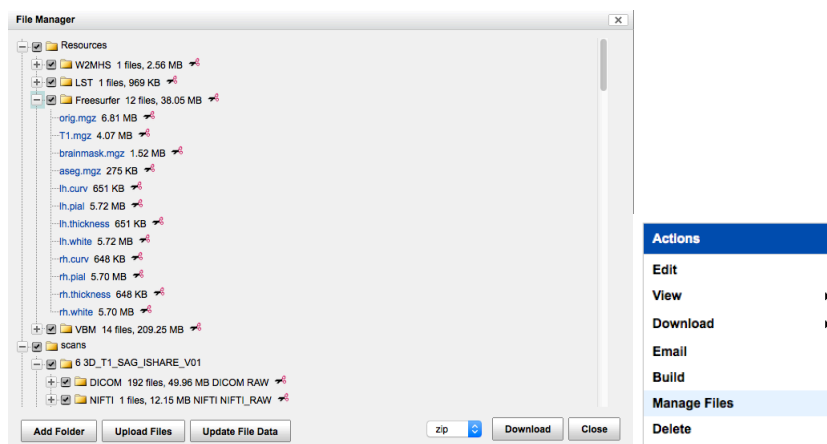
The generated output files are the following (.mgz files are in FreeSurfer format):

- orig.mgz – Raw T1
- T1.mgz – Intensity-normalised T1
- brainmask.mgz – Skull-stripped, intensity-normalised T1
- aseg.mgz – Segmentation output
- *h.curv – Curvature values
- *h.pial – 3D PIAL surface model
- *h.thickness – Cortical thickness
- *h.white – 3D white surface model

3.5 DTI Preprocessing

This pipeline implements standard FSL pre-processing methods for diffusion weighted imaging such as eddy current correction (http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/EDDY/UsersGuide), BET (http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/BET) and DTIFIT (http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FDT/UserGuide#DTIFIT).

There are two possible ways this pipeline executes. If the VBM pipeline was launched before, it will take the corregistration matrix generated by VBM (**with the parameters used when launching it**) and corregister the output files over the T1, and in this case it will also generate the corregistered and warped files (their names start with 'r' and 'w' respectively). If the VBM pipeline wasn't launched, it will just generate the output files and not corregister them.

This pipeline generates a set of files, including FA, coloured FA, etc. To download the generated output files click on "Manage Files" on the action box (left panel), and then select "DTI", under "Resources":
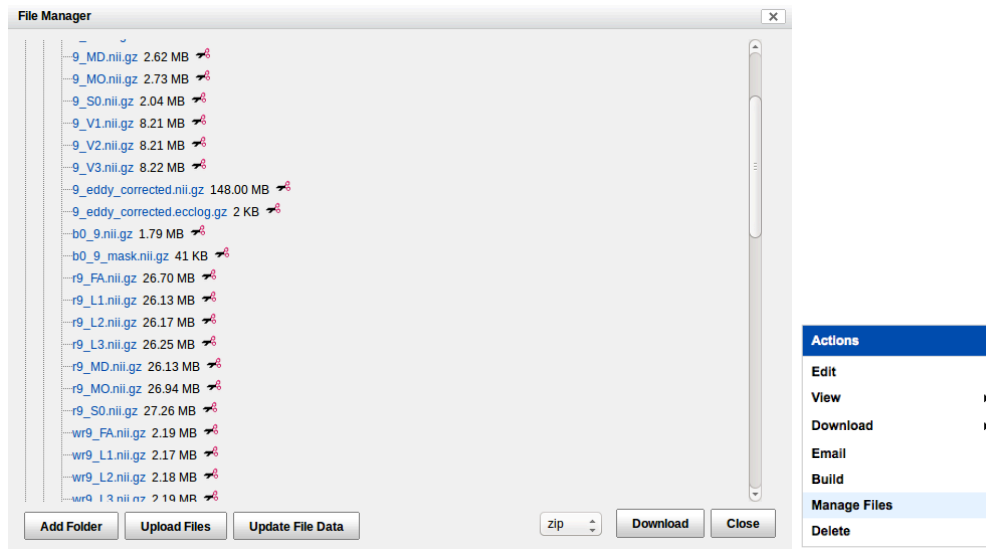
The following files are generated:

- (series number)_FA.nii.gz – Fractional anisotropy map
- (series number)_L*.nii.gz – Eigenvalues
- (series number)_V*.nii.gz – Eigenvectors

    The eigenvectors and eigenvalues of the 3×3 matrix D reflect the diffusivity of water in each direction. This can be used to quantify the diffusivity by the so-called fractional anisotropy (FA) maps on a voxel-wise analysis.

- (series number)_MD.nii.gz – Mean diffusivity map
- (series number)_eddy_corrected.nii.gz – Raw eddy current corrected nifti image
- bo_(series number).nii.gz – bo map
- bo_(series number)_mask.nii.gz – bo map mask
- r* - Same list as above but coregistered to the T1 scan (if VBM was launched before)
- w* - Same list as above but warped (if VBM was launched before)

3.6 White Matter Hyperintensities (LST)

The first pipeline for automatic detection of White Matter Hyperintensities (WMH) is based on the Lesion Segmentation Tool (LST) for SPM - http://www.applied-statistics.de/lst.html.

This pipeline runs an automatic segmentation on WMH and computes the total volume of WMH over several thresholds. These total volumes are available as an assessor:

Manual Quality Control Details

MRSession	MRi_ShareDB_E00128
ID	MRi_ShareDB_E00128_LST
Project	mrishare

Algorithm parameters

Build files location   /Library/ISHAREDB/build/mrishare/20151118_173356/15_11_03-15_11_18-STD-1_3_12_2_1107_5_2_43_66056

Initial threshold	WMH total volume (mm3)
0.05	2384.0
0.10	98.0
0.15	0.0
0.20	0.0
0.25	0.0
0.30	**0.0**
0.35	0.0
0.40	0.0
0.45	0.0
0.50	0.0
0.55	0.0
0.60	0.0
0.65	0.0
0.70	0.0
0.75	0.0
0.80	0.0
0.85	0.0
0.90	0.0
0.95	0.0
1.00	0.0

LST outputs a nifti lesion probability map for each threshold value. These maps give a total volume of WMH on each threshold.

To download the probability maps (lst.tar.gz) click on "Manage Files" on the action box (left panel), and then select "LST", under "Resources":
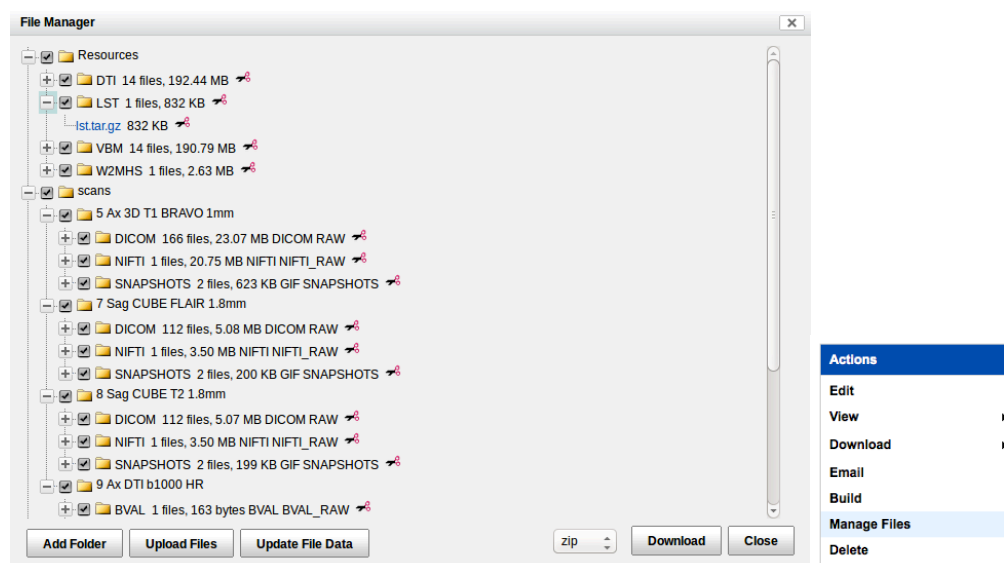
4 Scripts

In order to overcome two major limitations that XNAT has, two important scripts are added to ABACI.

The first of these limitations is XNAT not being able to upload an entire project (or study) already present physically in the local disks, instead of uploading images individually for each subject.

Another limitation is XNAT not being able to launch the same pipeline for all subjects in the same project, instead of manually launching the same pipeline on each subject.

4.1 importDcm

To tackle the first limitation, a script that uploads an entire project, or series of images/subjects, is provided. This script will read and upload to XNAT the images found in the folder provided by the user via the command line. **In order for this script to work, the target project has to exist in XNAT, if it does not; you have to manually create it before launching the script.**

To use this script you need to open a new terminal window (on the left panel):

On the terminal type: importDcm

```
abaci@abaci:~$ importDcm
usage: importDcm.sh <site> <user> <password> <project> <directory>
<site>        : Site to be used (e.g.: http://localhost:8080/xnat).
<user>        : Site username (e.g.: admin).
<password>    : Site password (e.g.: admin).
<project>     : Project to import images on.
<directory>   : Directory where raw images are on.
abaci@abaci:~$
```

As you can see from the command line output, its usage is importDcm.sh
<site> <user> <password> <project> <directory>.

So in order to upload an study located in "/home/abaci/tmp" to a project
named "test" you should type:

importDcm http://localhost:8080/xnat admin admin test /home/abaci/tmp

you should see an output like the following:

```
abaci@abaci:/usr/local/ABACI/scripts$ importDcm http://localhost:8080/xnat admin admin test /home/abaci/tmp
Subject cd (1/2)
Uploading session A (1/1) of subject cd.
done
  % Total    % Received % Xferd  Average Speed   Time    Time     Time  Current
                                 Dload  Upload   Total   Spent    Left  Speed
100    32  100    32    0     0    517       0 --:--:-- --:--:-- --:--:--   524
Session ID is: 296E3382E32D0C8B8CF70F1A4E09967F
create subject
  % Total    % Received % Xferd  Average Speed   Time    Time     Time  Current
                                 Dload  Upload   Total   Spent    Left  Speed
100    12  100    12    0     0     31       0 --:--:-- --:--:-- --:--:--    31
create session ABACI_S00002
  % Total    % Received % Xferd  Average Speed   Time    Time     Time  Current
                                 Dload  Upload   Total   Spent    Left  Speed
100    12  100    12    0     0     30       0 --:--:-- --:--:-- --:--:--    30
.found a new series 20151204_140002333
```

It must be noted that **this script will only upload the images if they are
properly organized in sub directories.** The way this script reads the images
from the root folder you provided via the command line: Subject/Session.

For example, if you have two subjects named subject1 and subject2 located in
/home/abaci/tmp, and each subject has two imaging sessions namely session1
and session2 for each subject, the folders should be organized as follows:

```
/home/abaci/tmp/

          ->subject1/
                  ->session1/
                  ->session2/

          ->subject2/
                  ->session1/
                  ->session2/
```

4.2 pipelineprojectlauncher

To address the second limitation described earlier, a script is made available for you to launch one pipeline over all the subjects present in a project. This script will only launch the pipelines **available on the project** (see section 3).

There are two ways of running this script; one way interactively and other way as one command line with arguments. Both ways have to be launched from the terminal.

In a new terminal window type `pipelineprojectlauncher,` then you should see an output similar to the next one:

```
abaci@abaci:~$ pipelineprojectlauncher
ABACI pipeline launcher
   Launchs a pipeline over all the subjects in one project. Be carefull since the input arguments (e.g. scan number of the T1 sequen
ce) must be the same for ALL subjects in the project.

The site you are using is: http://localhost:8080/xnat
Please enter your username: admin
Password:
Available projects in the site: test,
Please select a project: test
Available pipelines in the project: DicomToNifti,VBM,LST,PreprocDTI,W2MHS,
Please select a pipeline: DicomToNifti
Set the input parameters for the pipeline (leave blank to use DEFAULT VALUES):
   scanids: 4
   xnat_id:
   sessionId:
   project:
   subject:
###
Confirm launch [y/N]: y
Launching DicomToNifti on experiment ABACI_E00001
Launching DicomToNifti on experiment ABACI_E00005
Launching DicomToNifti on experiment ABACI_E00006
abaci@abaci:~$
```

As you can see, this script is *interactive*, meaning that it will show you options and ask you to choose from those options. First you will be asked to input your username and password (admin/admin by default). Then you will be shown the available projects in XNAT (in this example there is only one project named test), so you should type its name. Then it will show you the list of available pipelines in the project (in this example you have: DicomToNifti, VBM, LST, PreprocDTI and W2MHS), so you should type the name of the chosen pipeline (for this example DicomToNifti was chosen). Finally it will ask you to input the pipeline's parameters (or leave blank to use pipeline's default values). It must be noted that these parameters are exactly the same as when you launch the pipeline from the web-application (by clicking on "build").

Alternatively, this pipeline can be launch in one command line:

```
abaci@abaci:~$
abaci@abaci:~$ pipelineprojectlauncher -s http://localhost:8080/xnat -u admin -p admin -j test -i DicomToNifti -a scanids=4
```

Here, the information is passed as command line arguments instead of interactively. If you type pipelineprojectlauncher –h in the command line, you will see a description of each argument.

This example command line runs the pipeline with exactly the same arguments as the previous example.

5 Installed software

Here you will find the complete list of software's installed (and therefore distributed within ABACI) as well as their versions:

- **Ubuntu 14.04 LTS** - http://www.ubuntu.com/

- **XNAT 1.6.5** – http://www.xnat.org/

- **PostgreSQL 9.3.9** - http://www.postgresql.org/

- **Apache Tomcat 7.0.64** - http://tomcat.apache.org/

- **Matlab Compiler Runtime 7.1.3 & 7.1.41**- http://www.mathworks.com/products/compiler/mcr/

- **SPM12** - http://www.fil.ion.ucl.ac.uk/spm/software/spm12/

- **SPM8** - http://www.fil.ion.ucl.ac.uk/spm/software/spm8/

- **LST 1.2.3** - http://www.applied-statistics.de/lst.html

- **MRICRON 4/08/2014** - http://www.mccauslandcenter.sc.edu/mricro/mricron/

- **FSL 5.0** - http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/

- **FreeSurfer 5.3** - https://surfer.nmr.mgh.harvard.edu/