

Introduction to Brain Science and
fMRI (3)

Miscellaneous: FSL, MRICron,
or Matlab

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Other software packages

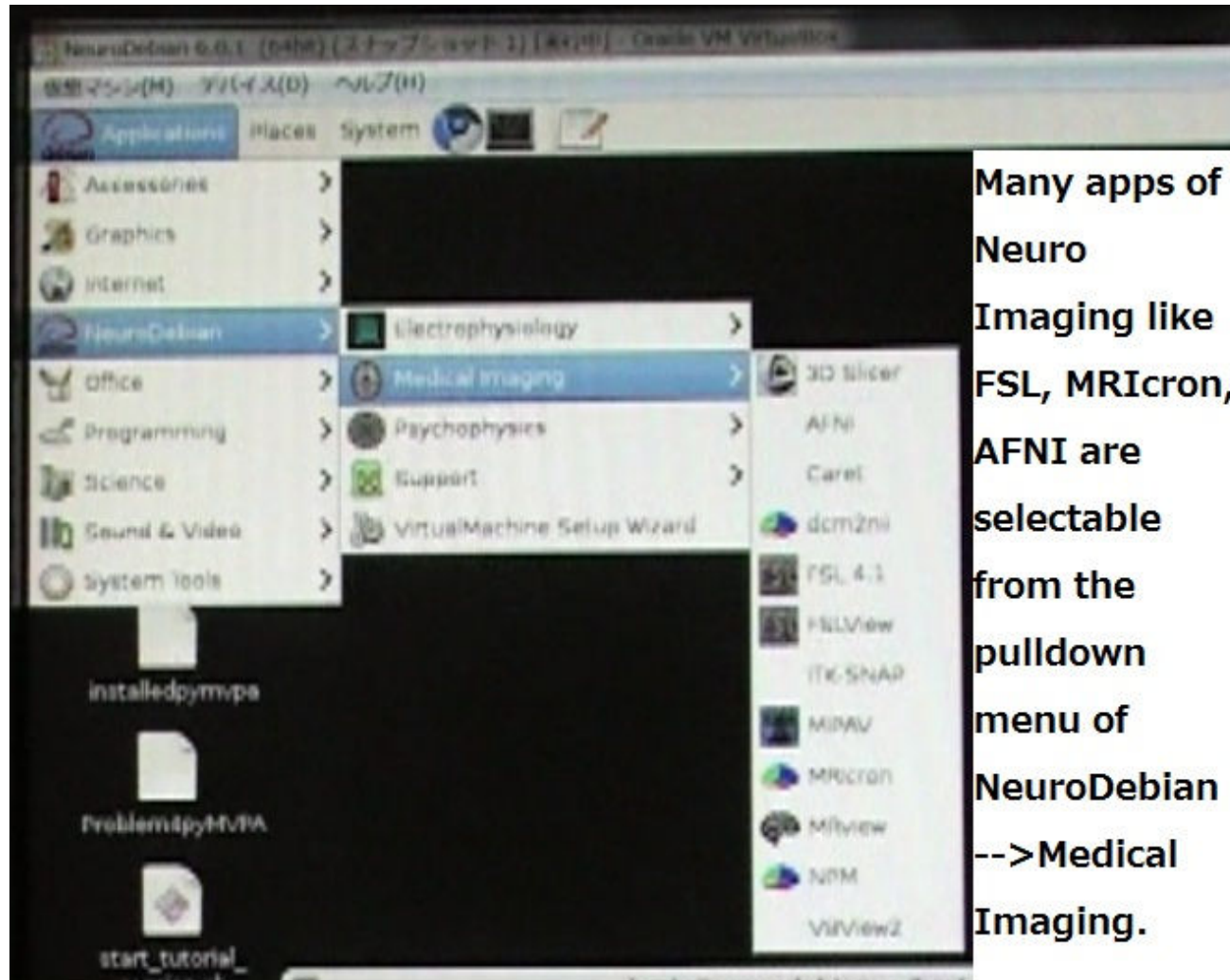
NeuroDebian Virtual Machine

- Operation system for brain researchers
- <http://neuro.debian.net/>
- <http://neuro.debian.net/vm.html>
- To be recommended in your own laboratory

NeuroDebian Virtual machine

- The merits of NeuroDebian Virtual machine are:
- many applications for the neuroimaging are already preinstalled: FSL, AFNI, MRICron..,
- using Synaptic Package Manager, you can add some fonts (Asian CJK--indispensable for our works), additional applications like dcm2nii, GNU R etc.

Screenshot of NeuroDebian (1)



Many apps of
Neuro
Imaging like
FSL, MRICron,
AFNI are
selectable
from the
pulldown
menu of
NeuroDebian
--> Medical
Imaging.

Screenshot of NeuroDebian (2)

The screenshot displays the NeuroDebian desktop environment. On the left is a sidebar with icons for 'Computer', 'brain's Home', 'tutorial_data', 'installedpymvpa', 'Problem4pyMVPA', 'start_tutorial_session.sh', 'trouble_old', 'Tsubame2.txt', 'Tutorial commands', 'u2w', 'w2u', and 'Trash'. The main area contains two windows:

Terminal Window (brain@neurodebian: ~/host)

```
brain@neurodebian:~$ ls
data      linal.txt  misc      Slicer3brain  u2w
Desktop   lina2.txt  Problem4pyMVPA  trouble20110320
Downloads linall.txt Screenshots.png trouble_old
host      mipav      screenshots    Tutorial commands

brain@neurodebian:~$ pwd
/home/brain

brain@neurodebian:~$ cd host
brain@neurodebian:~/host$ whoami
bash: whoami: command not found
brain@neurodebian:~/host$ whoami
brain

brain@neurodebian:~/host$ free
              total        used        free      shared    buffers     cached
Mem:      4060996      514452      3546544           0          14856      262476
-/+ buffers/cache:      235416      3825580
Swap:      4022672           0      4022672
```

Synaptic Package Manager (as superuser)

Quick search: Search

S	Package	Installed Version	Latest Version	Description
<input type="checkbox"/>	python-cdb		0.34-0.1	Python CDB (constant database) library
<input type="checkbox"/>	python-cg		0.14.1-2+b1	nVidia Cg driver binding for Python
<input type="checkbox"/>	python-ifeffit		2:1.2.11d-6	Python GUI interface and extensions for IFEFFIT
<input type="checkbox"/>	python-pygpu		0.2.0a-629-2	embedded language for programming GPU usi
<input type="checkbox"/>	python-pyopencl		0.92-1	module to access OpenCL parallel computatio

No package is selected.

Synaptic Package Manager is quite useful and easy for installing many programs at one time without running any command.

6 packages listed, 1205 installed, 0 broken. 0 to install/upgrade, 0 to remove

Annotations:

- An arrow points from the 'free' command output in the terminal to the text: "It is better to set a virtual memory swapping in addition to the native memory allocated to the D drive (more than 8 G bytes recommended), if you want to process a machine learning of the brain data, for instance."
- Another arrow points from the same output to the text: "Synaptic Package Manager is quite useful and easy for installing many programs at one time without running any command."

Recommendation of NeuroDebian Virtual Machine

- Prof.Akama is a heavy user of **NeuroDebian-Virtual Machine on Windows 64-bit platform**. As NeuroDebian was installed in D drive (not C), it is quite easy to make a mount point to Windows file system. The virtual and native OSs are thus quasi-seamless, to the extent to which natural drag and drop of files don't make us realize we are using two different OSs, and we can open files in NeuroDebian using software working on the side of Windows (like Office.) Even if a sudden business matter (sometimes Windows is mandatory for it) interrupted my research on neural science to move back from NeuroDebian to the Windows, this parallel usage to switch from one OS to another doesn't frustrate me at all.
- In short, I strongly recommend to any researchers of the neuroscience a NeuroDebian-Virtual Machine on Windows7-64bit.

Another software: FSL

- “FSL is a comprehensive library of analysis tools for FMRI, MRI and DTI brain imaging data. FSL is written mainly by members of the [Analysis Group, FMRI, Oxford, UK](#). FSL runs on Apple and PCs (Linux and Windows), and is very easy to install. “

FSL

- <http://www.fmrib.ox.ac.uk/fsl/>
- Developed by [Analysis Group, FMRI, Oxford, UK](#).
- Preprocessing, Statistical Analysis, Good 3D, 4D (movie) views, conversion between voxel coordinates and MNI.
- Available on Windows (needs virtual machine) and Linux.
- Unfortunately not available on the Educational Computer System, but we can use a part of this package here: `/etc/matlab`.

How to extract the value of voxels by using FSL (1)

- The ***etc/matlab*** subdirectory of **FSL** contains a number of functions for reading/writing Nifti and Analyze files.
- **Uncompress matlab-fsl.zip**
- Copy all the hdr/img files and these FSL-based scripts (all the m files of which the names include the character strings of “avw”) in the same directory accessible from Matlab.

How to extract the value of voxels by using FSL (2)

- Using FSL (needs all the m files in /fsl/matlab but don't needs Matlab)
- **>>read_avw_img('lrs20110223-0004-00001-000001-01');**
- %This will output the 3-dimensional array (so called tensor) for all the intensity values.
- %You must not sepcify the file extension (hdr, img) in the string for the argument of read_avw_img command.
- **>> size(read_avw_img('lrs20110223-0004-00001-000001-01'))**
- ans =
- 53 63 23
- %This command will provide the dimension size of the data: [53 63 23].

How to extract the value of voxels by using FSL (3)

- Use the script of **fcmrnew2.m** (by Prof. Akama and Prof. Wakita)
- This Matlab script allows us to automatically
 - 1)detect all the Analyze files in the current directory and
 - 2)produce
 - a csv file representing the matrix for the time course values of the selected voxels whose coordinates are to be read from a csv file OR of all the voxels included in the Analyze files.
 - a csv file for the correlation matrix among the time course values
 - a csv file for the adjacency matrix for fcMRI (explained later)
- You have only to type
 - fcmrnew2('csv file name where the interesting voxels are enumerated under the form of voxel coordinates', threshold value for pruning the edges in functional connectivity)
 - %for example, **fcmrnew2('coord.csv', 0.2)**
 - or fcmrnew('ALL',threshold value for pruning)
 - %for example, **fcmrnew2('ALL', 0.2)**
 - and press Enter.
- Requirement: you need to use in the same directory the files in /etc/matlab of FSL package.

Cf. How to extract the value of voxels by using SPM

- Using SPM
- i)Specify one "img" file.
- **>>vol=spm_vol('lrs20110223-0004-00001-000001-01.img')**
- vol =
 - fname: 'lrs20110223-0004-00001-000001-01.img'
 - mat: [4x4 double]
 - dim: [53 63 23]
 - dt: [4 0]
 - pinfo: [3x1 double]
 - n: [1 1]
 - descrip: 'spm - 3D normalized'
 - private: [1x1 nifti]
- %This command will give you the information about the selected img file.
- %vol.dim will provide the dimension size of the data: [53 63 23].
- %So vol.dim(1)*vol.dim(2)*vol.dim(3) let you know the total number of the voxels included in the data: 76797.
- **>>array=spm_read_vols(vol);**
- %This will output the 3-dimensional array (so called tensor) for all the intensity values.

Bits of knowledge about Matlab with FSL (1)

- Matlab is very useful for dealing with three dimensional arrays (tensor) which can stand for the series of a voxel index (voxel coordinate) represented by an element of (x, y, z).
- A voxel can be identified by specifying a tensor value such as [35 56 22].
- If the tensor space for all the voxels in the image data is specified as
 - `p=read_avw_img('lrs20110223-0004-00001-000001-01');`
- then the intensity of the voxel above can be known by
 - `p(35,56,22)`
- But also by a sequential serial number as
 - `p(2678)`

Bits of knowledge about Matlab with FSL (2)

- Run on Matlab
 - `a=rand(6,7,8)`
- to produce a random tensor with the dimension of $6 \times 7 \times 8$ (so `size(a)` returns 6 7 8 and `size(a, 1)` 6.)
- So what is the 3D index `[p q r]` for `a(101)` so that `a(p,q,r)==a(101)` returns 1 (meaning TRUE for Matlab)?
- And what is the sequential number `s` for the 3D index `[l,m,n]` so that `a(s)==a(l,m,n)` returns 1?
- Use **`sub2ind(size(a),l,m,n)`** and **`[l,m,n]=ind2sub(size(a),[s])`**
- Or use **`coord2index.m`** and **`index2coord.m`** (by Prof. Akama).

Bits of knowledge about Matlab with FSL (3)

- “**voxelvalvec**”: Matlab script written by Prof. Akama for transferring all the voxel values from Analyze images into flat CSV files.
- Run voxelvalvec.
 - `>> voxelvalvec`
- Open *.csv (don't use Excel, they are too big!).
- Compare the series of the activation values between ***slrs*.hdr/img*** [realigned, coregistered, normalized and **smoothed**] and ***lrs*.hdr/img*** [realigned, coregistered, and normalized] to check the **smoothing** effects.
- Exercise: Compute the variances of Δ (the delta: difference between the value of each cell and that of the adjacent one)

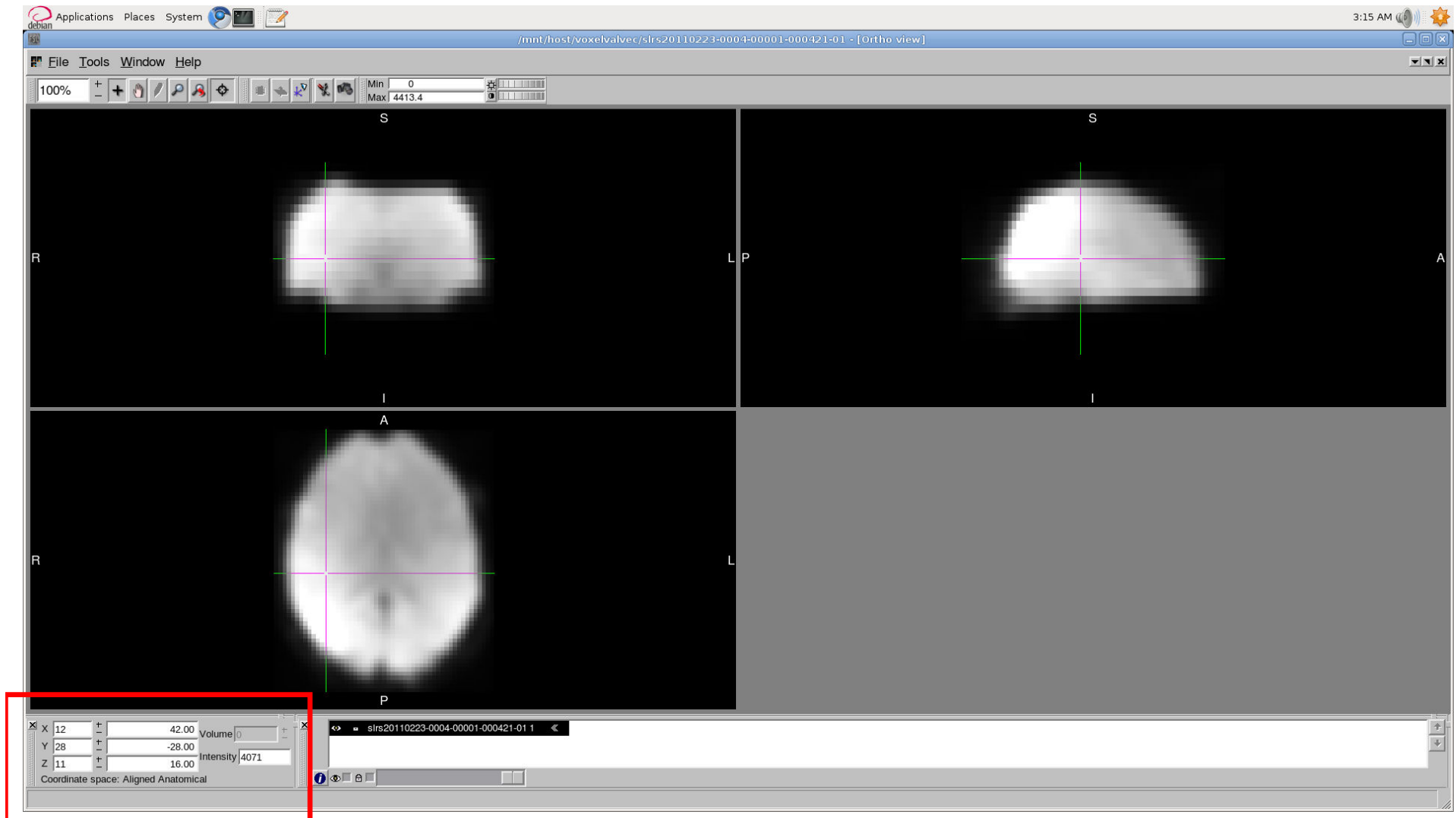
Check the variable list in “Workspace”

- `num [53,63,23]`: there are 53, 63, 23 voxels along x, y, and z axis respectively.
- `voxelnum 76797`: there are 76797 voxels in total in this image file (there remain some empty cells).
- `read_avw_img_result` : allows us to know the activation values from Voxel Coordinate.
 - `>>read_avw_img_result` [All the values are displayed in a sweep.]
 - `>>read_avw_img_result(13,34,9)`
- By a right click, you can save this array as a mat file to be loaded once again.
 - `>>load hoge.mat`
 - `>>read_avw_img_result(44,24,4)`

Relationship between the Voxel Coordinate System and the standard MNI System

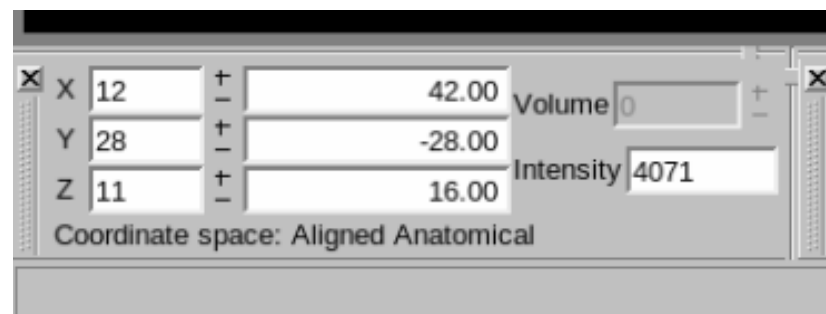
- Voxel Index (Coordinate) System:
 - Relative system
 - Specific to each set of brain images (dependent on the spatial resolution after the reslice.)
 - The numbers (x,y,z) are all integers larger than 0.
 - Needed to know activation values and the HRF.
- MNI (Montreal Neurological Institute) Coordinate System
 - One of the most representative brain atlas (with Talairach)
 - Absolute System; independent of any particular image
 - "mm mm mm" values in SPM8 are based on MNI.
- FSL-View (Interactive display tool for 3D and 4D data) has a very useful window to convert voxel coordinates to MNI vice versa.

Screenshot of FSL-View



Coordinate Space

- Let's know the activation value of the voxel (13,29,12) from Matlab.
 - `>> read_avw_img_result(13,29,12)`
 - `ans =`
 - `4071`
- Input (12,28,11)—minus one from each value—in the Coordinate space of FSL-View, and you will know the MNI coordinate of this voxel
- (42, -28, 16)
- Check the intensity values are the same.



Talairach versus MNI

- Talairach Atlas
- http://en.wikipedia.org/wiki/Jean_Talairach
- MNI Brain
- <http://imaging.mrc-cbu.cam.ac.uk/imaging/MniTalairach>
- Scripts to convert from one to another
 - mni2tal.m
 - tal2mni.m

Conversion

- Copy these 2 m files to your Matlab directory.
- **>> mni2tal(13,29,12)**
- ans =
- 13 29 10

- **>> tal2mni(13,29,10)**
- ans =
- 13 29 12

Information about a particular coordinate

- Brede Database

- <http://neuro.imm.dtu.dk/services/brededatabase/>

- The values must be entered using Talairach.

Brede Database - Talairach coordinate search

brede_loc_query — Search after locations (Talairach coordinates) in the Brede Database

13 29 10

Location search (one coordinate) e.g., 14 -9 -15

13 29 10

Experiment search (several coordinates)

13 29 10

Visualize in INC Talairach atlas

Click to read the literature.

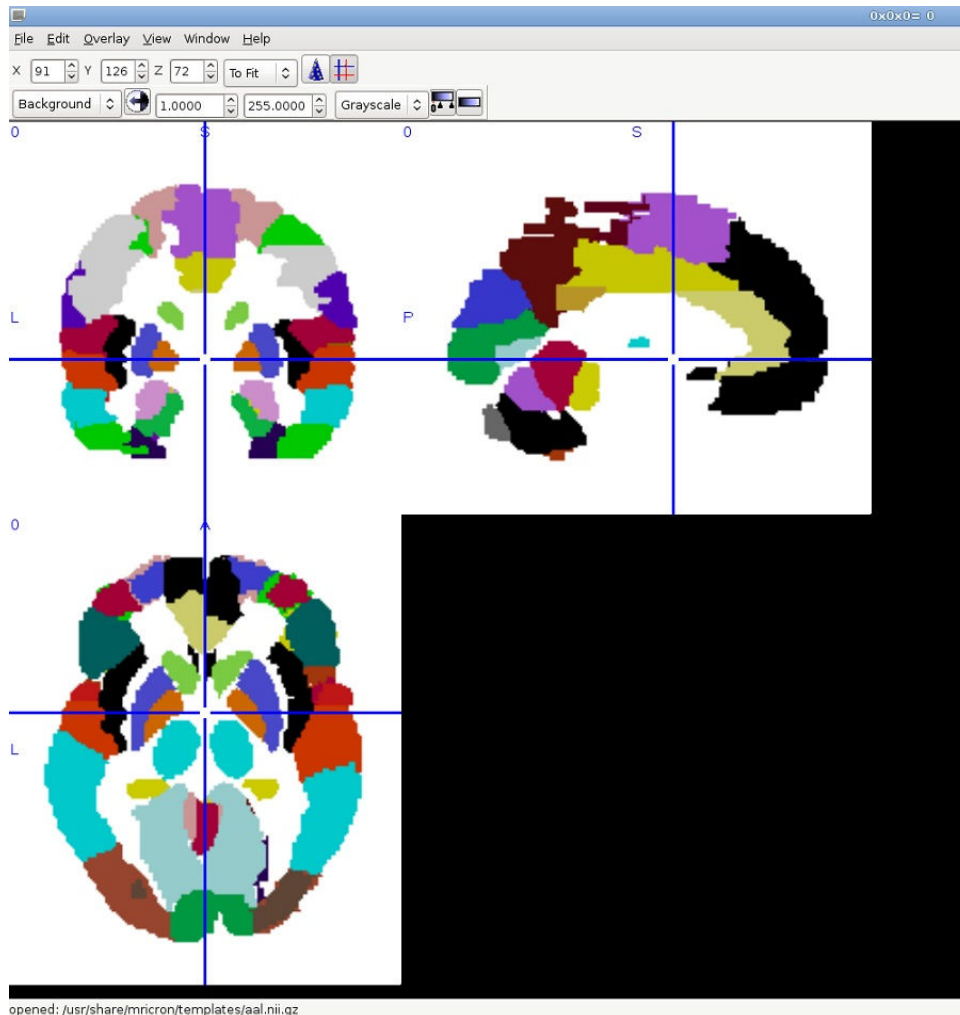
#	Distance	x	y	z	WOBIB	Description
1	4.6	9	31	7	161	Anterior cingulus — Harm avoidance and D2 5HT2A negative correlation (WOEXP: 493)
2	8.3	9	26	17	83	Anterior cingulate gyrus — Cold pain on right foot masked by silent word reading (WOEXP: 264)
3	9.0	11	28	18	83	Anterior cingulate cortex — Cold pain on right foot (WOEXP: 263)
4	9.0	5	33	13	54	Right anterior cingulate — Romantic love (WOEXP: 176)
5	9.0	7	33	3	76	Right anterior cingulate cortex — Increase due to hypnosis versus rest and mental imagery (WOEXP: 239)
6	9.1	11	37	12	152	Right anterior cingulate — Nonconscious encoding of face-word associations (WOEXP: 467)
7	9.4	15	35	3	178	Corpus callosum — Syllable counting versus semantic judgment (WOEXP: 555)
8	10.6	13	21	2	76	Right caudate nucleus — Increase due to hypnosis versus rest and mental imagery (WOEXP: 239)
9	10.8	17	39	9	71	Right medial frontal cortex — 75% disgusted faces versus neutral faces (WOEXP: 222)
10	11.0	9	35	18	176	Right cingulate gyrus — Verbal fluency (WOEXP: 539)
11	11.7	3	31	16	171	Anterior cingulate — Increases in rapid auditory processing (WOEXP: 524)
12	11.8	7	33	0	76	Right anterior cingulate cortex — Hypnosis (WOEXP: 236)
13	12.4	8	22	1	116	Right caudate nucleus — Visuospatial 0-back, Pittsburgh site (WOEXP: 359)
14	12.5	11	30	22	83	Anterior cingulate gyrus — Cold pain with silent word reading versus cold pain (WOEXP: 267)
15	12.6	16	22	20	101	Anterior cingulate — Fentanyl during heat and warm stimulus on left arm (WOEXP: 316)
16	13.0	0	29	9	98	Medial frontal cortex, right/left — Happy face viewing (WOEXP: 307)
17	13.5	22	28	0	130	Opercular region — Coprolalia during Tourette's syndrome (WOEXP: 403)
18	13.6	6	19	16	118	Thalamus — Heat pain - female (WOEXP: 368)
19	14.0	0	29	15	122	Anterior cingulate cortex — Migraine headache (WOEXP: 380)
20	14.1	5	23	20	47	Anterior cingulate — Probabilistic reasoning versus deductive (WOEXP: 152)
21	14.2	1	28	18	76	Anterior cingulate cortex — Hot pain on right hand during hypnosis (WOEXP: 235)

→
Nearest locations treated
in previous researches

Another software: MRlcron

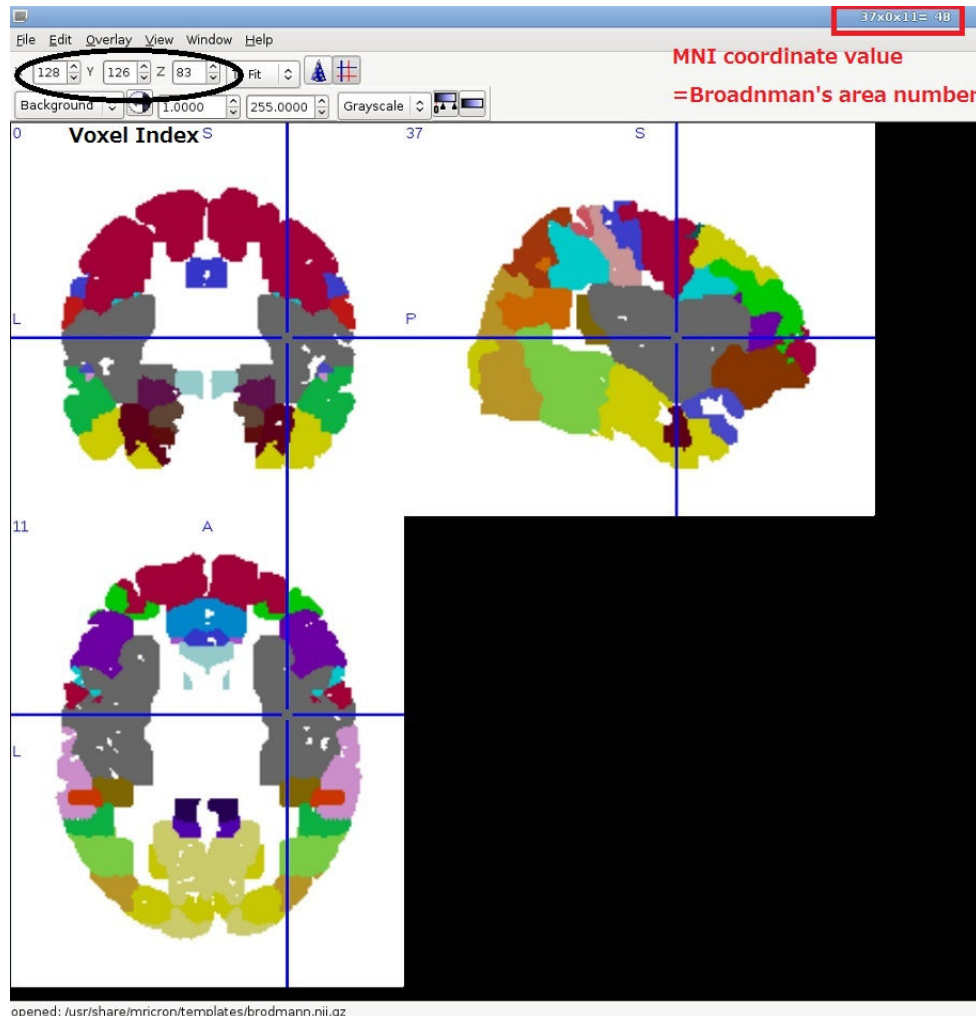
- “MRlcron is a cross-platform NIfTI format image viewer. It can load multiple layers of images, generate volume renderings and draw volumes of interest. It also provides dcm2nii for converting DICOM images to NIfTI format and NPM for statistics. MRlcroGL is a variant of MRlcron that uses OpenGL for very fast rendering, but requires a modern NVidia or ATI graphics card. ”
- <http://www.cabiatl.com/mricro/mricron/>
- <http://www.nitrc.org/projects/mricron>
- Available on the Educational Computer System here.

Display the brain atlas of AAL



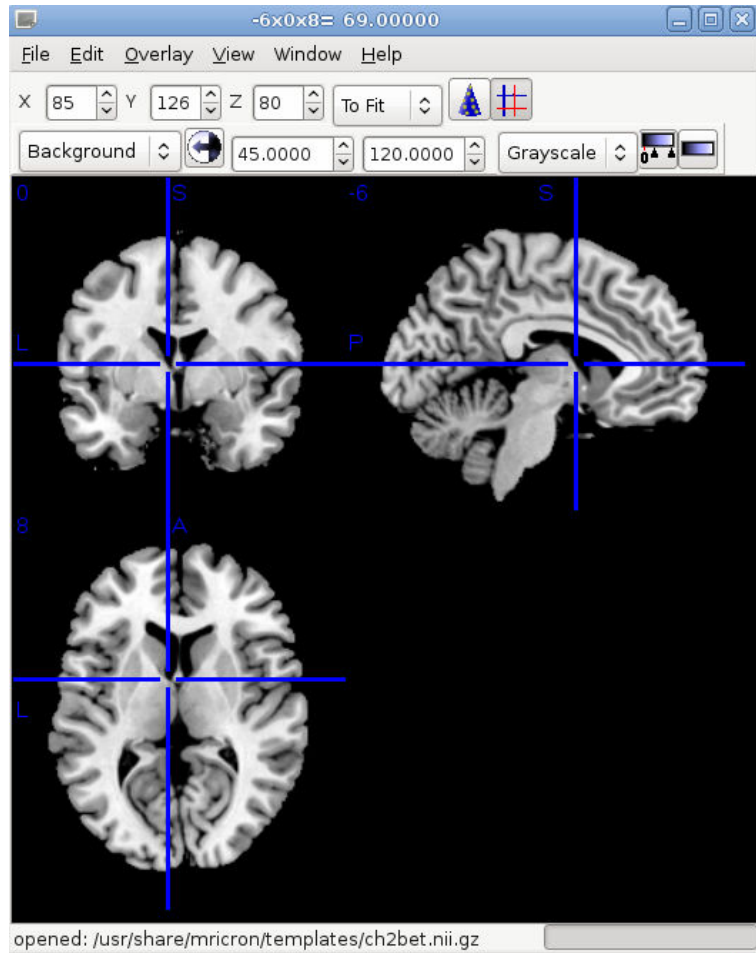
- Automated Anatomical Labeling (AAL) is a software package and digital atlas of the human brain, dependent on SPM. (ref.N. Tzourio-Mazoyer et al, 2001)(Wikipedia)
- File->Open templates->aal.nii.gz
- Move the crosshair and know its location through the MNI coordinate system (and the voxel index) and the name of the region.

Display the Brodmann's map



- A **Brodmann area** is a region of the cerebral cortex defined based on its cytoarchitectonics, or organization of cells. (Wikipedia)
- http://en.wikipedia.org/wiki/Brodmann_area
- If you want to specify MNI values, choose the pulldown menu of
- View→MNI coordinates→MNI positions
- and continue to click the marks of up and down, so the crosshair moves automatically.

Display the rendered images



- MR images without skull
- File->Open templates->ch2bet.nii.gz
- Move the crosshair and know its location through the MNI coordinate system (and the voxel index) and the depth of the crosshair from the surface.

Difference in voxel coordinates between FSL and MRICron

- $\text{MRICron}(x) = 53 - \text{FSLView}(x)$: left-right reversal
- $\text{MRICron}(y) = \text{FSLView}(y) + 2$
- $\text{MRICron}(z) = \text{FSLView}(z) + 1$ (rarely 2?)
- Exercise
 - Open an brain image (**lrs20110223-0004-00001-000001-01.hdr/img**, for example) by using MRICron.

- END