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A simple program to automate folder creation, organization, 3D NifTi conversion of fMRI data, preprocessing and analysis in MATLAB.

Once setup, you will never have to manually do it. ©

#### **DISCLAIMER**

I shall not be held responsible for fake activations, MATLAB crashes, thermonuclear war, or you getting fired by your boss because you lost the acquired fMRI data. Please do some research if you have any concerns about features included in the script! YOU are choosing to make modifications, and if you point the finger at me for messing up your data, I will laugh at you.

#### Introduction

Generally, we create a pair of folders for each run; a data folder and an analysis folder. T1 scans will go to another folder. MATLAB jobs are saved to a 'job' folder. All other files can be saved into a 'junk' folder. The 4D nii files in each data folder are then converted to 3D NifTi using MRICRON. The 3D NifTi files are then processed in MATLAB (pre-processing and statistical analysis)

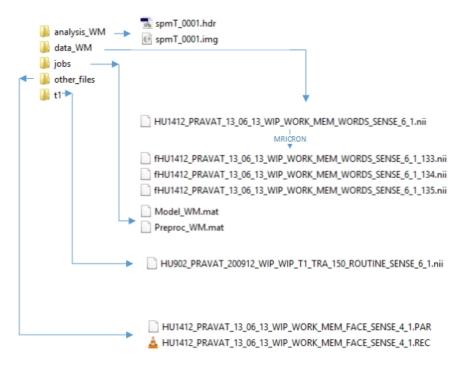


Figure 1. General folder structure

### What does the program do?

This program does the following

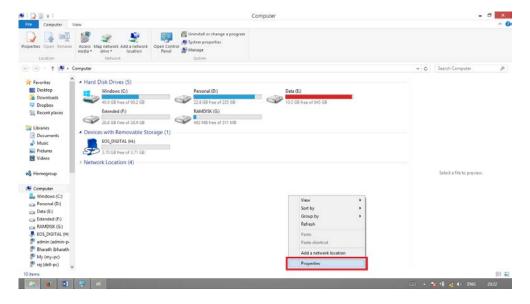
- 1. Creates data and analysis folders for each run.
- 2. Moves T1 file to T1 folder.
- 3. Moves all unwanted files to a junk folder.
- 4. Moves 4D NifTi file to data folder for each run.
- 5. Converts the 4D NifTi file 3D NifTi files
- 6. Calls MATLAB batch script to pre-process and analyse the 3D NifTi files. In short, it does everything. ©

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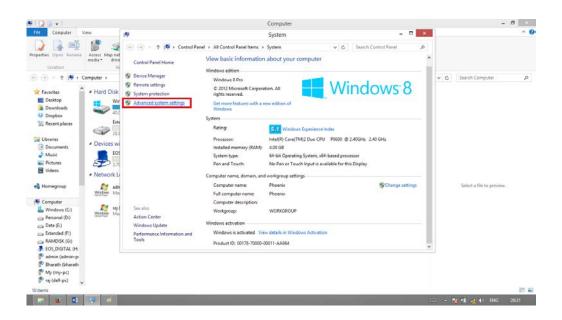
#### How to use?

Save the file makemylifeeasier.exe in C:\Scripts folder.

Now open 'My Computer'. Right click and click Properties.

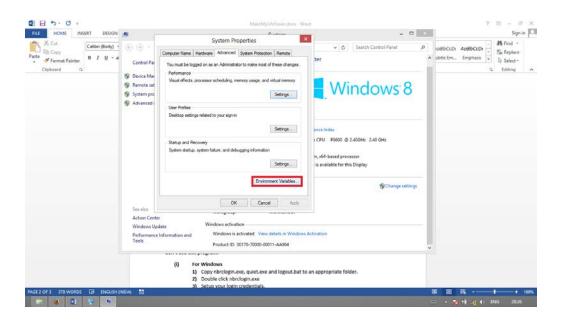


### **Click Advanced System Settings**

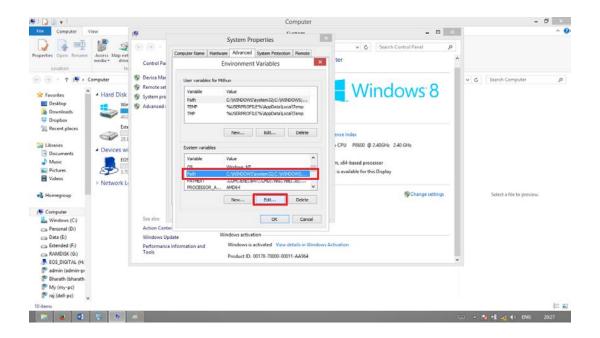


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Click Environment Variables.

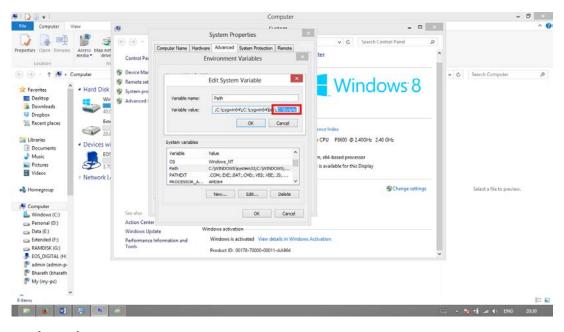


In 'System Variables' select Path and click Edit



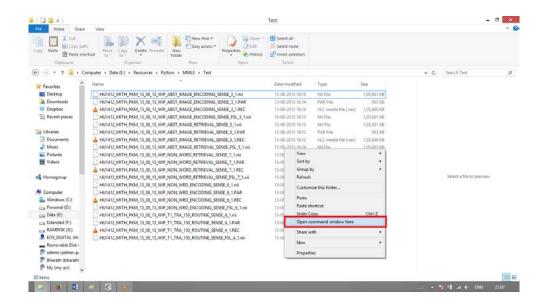
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Add C:\Scripts after a semicolon.



#### Click OK $\rightarrow$ OK $\rightarrow$ OK.

Go the folder where scan data is located. Right Click with 'SHIFT' key held down. Click Open command window here.



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In the command line that opens write *makemylifeeasier* and press enter.

```
E:\Resources\Python\MMLE\Test>makemylifeeasier
Hello Mithun,
This is a simple script to automate folder creation, organization and 3D NifTi c
onversion
Written in Python & Compiled using PyInstaller

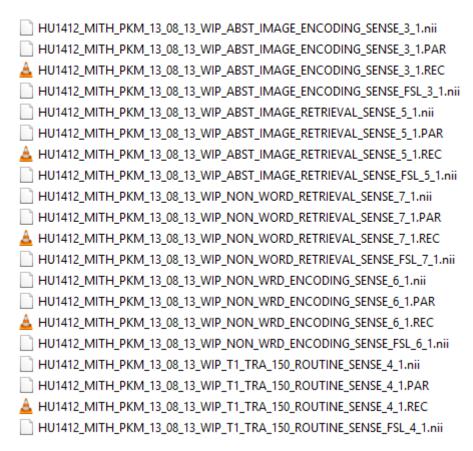
Configuration file does not exist
First run? Lets configure your data and analysis folders
This will create a configuration file(pairs.conf)
in the C:\Scripts folder

Enter the number of data and analysis folder pairs:
```

An example scenario is dealt with below.

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### Following is a list of files.



#### There are 4 runs

- 1) Abstract Image Encoding
- 2) Abstract Image Retrieval
- 3) Non Word Encoding
- 4) Non Word Retrieval

Enter the number of runs.

### Enter the number of data and analysis folder pairs :4

For run one ie Abstract Image Encoding, a pair of folders should to be created.

- 1) data\_aie
- 2) analysis aie

Enter the data and analysis folder names

```
Enter details for pair number 1
Please enter the name of data folder (eg:-data_working_memory) :data_aie
Please enter the name of analysis folder (eg:-analysis_working_memory) :analysis
_aie
```

The file HU1412\_MITH\_PKM\_13\_08\_13\_WIP\_ABST\_IMAGE\_ENCODING\_SENSE\_3\_1.nii should be moved to data aie folder. It should then be converted to 3D NifTi format.

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#### Each run has

- 1) A nii file
- 2) A FSL nii file
- 3) PAR file
- 4) REC file

The files have the string ABST\_IMAGE\_ENCODING in common. Enter it as the kind of parameter.

### Enter the kind of file that goes to the data folder :ABST\_IMAGE\_ENCODING

Enter the names for MATLAB batch files. The extension .m is not required. *Creation of MATLAB* batch files is dealt with, at the end of this manual.

```
Enter the name of MATLAB preprocess batch file :data_process
Enter the name of MATLAB analysis batch file :analysis_encode
```

This applies to each and every run.

```
Enter details for pair number 2
Please enter the name of data folder (eg:-data_working_memory) :data_air
Please enter the name of analysis folder (eg:-analysis_working_memory) :analysis_air
Enter the kind of file that goes to the data folder :ABST_IMAGE_RETRIEVAL
Enter the name of MATLAB preprocess batch file :data_process
Enter the name of MATLAB analysis batch file :analysis_retrieval
Enter details for pair number 3
Please enter the name of data folder (eg:-data_working_memory) :data_nwe
Please enter the name of analysis folder (eg:-analysis_working_memory) :analysis_nwe
Enter the kind of file that goes to the data folder :NON_WRD_ENCODING
Enter the name of MATLAB preprocess batch file :data_process
Enter the name of MATLAB analysis batch file :analysis_encode
Enter details for pair number 4
Please enter the name of data folder (eg:-data_working_memory) :data_nwr
Please enter the name of analysis folder (eg:-analysis_working_memory) :analysis_nwr
Enter the kind of file that goes to the data folder :NON_WORD_RETRIEUAL
Enter the name of MATLAB preprocess batch file :data_process
Enter the name of MATLAB analysis batch file :analysis_retrieval
```

Finally T1 image, HU1412\_MITH\_PKM\_13\_08\_13\_WIP\_T1\_TRA\_150\_ROUTINE\_SENSE\_4\_1.nii will be moved to t1 folder.

```
Enter the T1 folder name :t1
Enter the kind of file that goes to T1 folder :T1
```

Similarly enter the folder to which all other types of files (FSL, PAR, REC) will be moved.

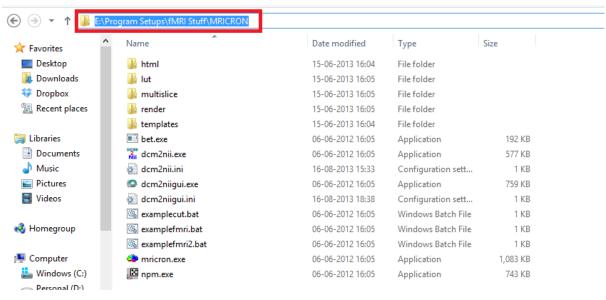
```
Enter the folder for all other files :other_files
```

Then enter the folder for SPM8 Batch jobs. To skip creation of jobs folder, leave the field blank.

Enter the jobs folder name :jobs

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Finally enter the folder where dcm2nii.exe (MRICRON) is located



Enter the folder where dcm2nii.exe is located. Your MRICRON folder :E:\Program S etups\fMRI Stuff\MRICRON

#### Done!

Configuration file created. Run program again Press Enter to continue

#### !IMPORTANT

Open MRICRON folder. Make a new file **dcm2nii.ini** if not present. If present remove the content and add the following.

### [BOOL]

DebugMode=0 UntestedFeatures=0 UINT16toFLOAT32=1 Verbose=0 Anonymize=1 AnonymizeSourceDICOM=0 AppendAcqSeries=1 AppendDate=1 AppendFilename=0 AppendPatientName=0 AppendProtocolName=1 AutoCrop=0 CollapseFolders=1 createoutputfolder=0 CustomRename=0 enablereorient=1 OrthoFlipXDim=0 EveryFile=1 fourD=0 Gzip=0 ManualNIfTIConv=0 PhilipsPrecise=0 RecursiveUseNameAppend=0 SingleNIIFile=1 SPM2=0Stack3DImagesWithSameAcqNum=0

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Swizzle4D=1 UseGE 0021\_104F=0

[INT]
MaxReorientMatrix=1023
MinReorientMatrix=200
RecursiveFolderDepth=5
OutDirMode=0
SiemensDTIUse0019If00181020atleast=15
SiemensDTINoAngulationCorrectionIf00181020atleast=1000
SiemensDTIStackIf00181020atleast=15

[STR]

OutDir=C:\Users\Mithun\Documents

You might want to edit the last line. Save the file.

Now run the program again.

- 1) Right click holding down SHIFT key
- 2) Click Open Command Window here
- 3) Type makemylifeeasier and press Enter

See the magic ☺

NOTE: Before running the program make sure you have created MATLAB batch job file.

### Instructions for Linux.

The Linux binary is attached. Save it to ~/Scripts.

Add  $^/$ Scripts to your PATH by editing .bash\_profile. Alternatively, you can add a file to /etc/profile.d;

Eg:- fmri.sh with

export PATH = /home/<username>/Scripts:\$PATH

as the content.

Configure the program in the same way mentioned above.

Take extra care while adding path to dcm2nii binary. (Folder names with spaces and / in Linux) dcm2nii.ini file is to be added to .dcm2nii folder in your home folder Run by opening terminal in the scan data folder.

Note: The binary is compiled for x64 systems. If you have x86, either run it with Python (edit paths in source code if necessary) or compile it yourself.

#### Creation of MATLAB Batch files

The program processes data in two steps

- 1. Pre-processing
- 2. Statistical Analysis
- I. Preprocessing Batch file

Open pre-processing SPM batch you have created. In menu click 'Save Batch and Script' and save your SPM batch. SPM saves two .m files.

1. <filenameyougave>.m

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2. <filenameyougave>\_job.m

Lets say, you gave the name data\_process.

Now, there are two files; data\_process.m and data\_process\_job.m

Open data process job.m in a text editor and make the following modifications.

1. Add the following to the start.

```
function [] = data_process(scan_folder,t_one)
folder = scan_folder;
spm fmri;
scan_files=spm_select('FPlist',folder, 'f.*nii');
scan_files=cellstr(scan_files);
spm_jobman('initcfg');
```

2. Find the line

```
matlabbatch{1}.spm.temporal.st.scans = <FILES>
and change it to

matlabbatch{1}.spm.temporal.st.scans{1,1} = scan_files;
```

3. Find the line

```
matlabbatch{3}.spm.spatial.coreg.estwrite.source
And change it to
matlabbatch{3}.spm.spatial.coreg.estwrite.source{1,1} = t_one;
```

4. Add the following line to the end of the file.

```
spm_jobman('run', matlabbatch);
```

### Now, save the file in C:\Scripts (Windows) or ~/Scripts (Linux).

```
IMPORTANT NOTE : The function name (data_process here) should be
same as the name of the file.
ie. data_process.m, saved in C:\Scripts or ~/Scripts will have first
line as
function [] = data_process(scan_folder,t_one)
Also, 'data_process' is the name of MATLAB file, that will be
specified during creation of configuration file for this program.
```

## II. Analysis Batch file

Open analysis SPM batch you have created. In menu click 'Save Batch and Script' and save your SPM batch. SPM saves two .m files.

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- 3. <filenameyougave>.m
- 4. <filenameyougave>\_job.m

Lets say, you gave the name analysis.

Now, there are two files; analysis.m and analysis\_job.m

Open analysis\_job.m in a text editor and make the following modifications.

5. Add the following to the start.

```
function [] = analysis(analysis_folder,scan_folder)
scan_files=spm_select('FPlist',scan_folder, 'swraf.*nii');
spm('Defaults','fMRI');
spm_jobman('initcfg');
rp_file = spm_select('FPlist',scan_folder, '^rp.*txt');
```

6. Find the line

```
matlabbatch{1}.spm.stats.fmri_spec.dir = <FOLDER>
and change it to

matlabbatch{1}.spm.stats.fmri_spec.dir{1,1} = analysis_folder;
```

7. Find the line

```
matlabbatch{1}.spm.stats.fmri_spec.sess.multi_reg
And change it to
matlabbatch{1}.spm.stats.fmri_spec.sess.multi_reg{1,1} = rp_file;
```

8. Add the following line to the end of the file.

```
spm_jobman('run', matlabbatch);
```

### Now, save the file in C:\Scripts (Windows) or ~/Scripts (Linux).

```
IMPORTANT NOTE : The function name (analysis here) should be same as
the name of the file.
ie. analysis.m, saved in C:\Scripts or ~/Scripts will have first
line as
function [] = analysis(scan_folder,t_one)
Also, 'analysis' is the name of MATLAB file, that will be specified
during creation of configuration file for this program.
```

Now add C:\Scripts (Windows) or ~/Scripts (Linux) to MATLAB Path.

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The Source Code is attached. Feel free to edit @ Written in Python. Compiled using Pylnstaller.

