Interleave Detection Manual

A guide to InterleaveDetection_nii.m

1. Installation

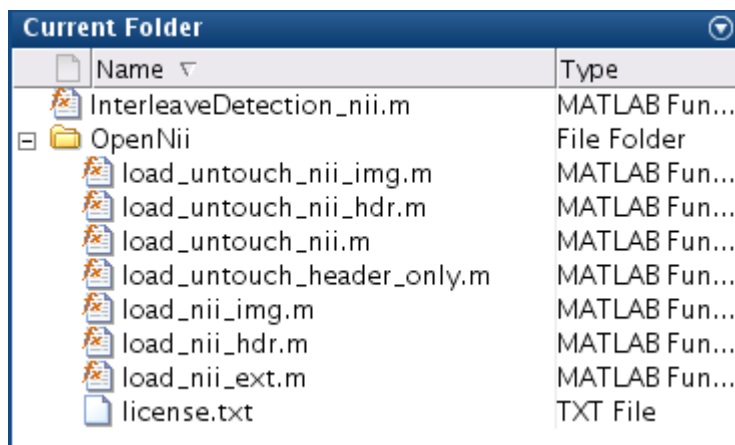Download the zip file from our website and follow these instructions:

a. Unzip

Create a new directory to unzip the files into. Then unzip everything from "InterleaveDetection_nii.zip" into that directory.

Note: Leave all internal directories as they are. Do not move files from the "OpenNii" Folder.

As long as you leave the "OpenNii" folder in the same directory as the "InterleaveDetection_nii.m" file, the program should run normally.

b. Files

Once you finish unzipping the files, change your matlab directory to that location. Your "current directory" window should look like this:

This is the complete list of files included in the zip file. If you are missing any, it's likely that something went wrong during the unzip, or a file was missed when transferring to a new directory. Check the zip file to ensure that all files are present, and unzip again.

c. Modifying The Directory

If you move the "OpenNii" folder to any location other than this, you must add that directory to matlab before the interleave detection program will run.

For example, if "InterleaveDetection_nii.m" is in:
```
/home/USER/matlab/Interleave
```

and you've moved the "OpenNii" folder to:
```
/home/USER/matlab/SupportFunctions
```

you will need to run the following code before the interleave detection program will work:

```
addpath('/home/USER/matlab/SupportFunctions/OpenNii');
```

2. Running the code

Note: this code only works on images acquired in the Z direction (with x/y slices acquired sequentially or with interleave)
To run the code, you only need two inputs: The nii file you wish to analyze, and the directory you want to save information to. For example, if I want to run the file:
```
'/home/USER/fMRI_Data/Subject1/Rest_Bold.nii'
```

And I wanted to save the results of the analysis in the folder:
```
'/home/USER/fMRI_Data/Subject1/Interleave_Results'
```

I would run the following command in matlab:

```
FilePath='/home/USER/fMRI_Data/Subject1/Rest_Bold.nii';
SaveDir='/home/USER/fMRI_Data/Subject1/Interleave_Results';

[Inter,pInt]=InterleaveDetection_nii(FilePath,SaveDir);
```

Of course, you can always just enter the directories directly as the function arguments, as long as you include single quotes around it.

Inter is the interleave value detected by the program.
pInt is the statistical significance of the interleave value.

These are returned so you can use them for building your own output files if running a script to analyze multiple images. These outputs can be ignored if you do not wish to use them.

3. Code Output

a. Saving The Output Files

The code will generate two files: first, a "*FILENAME*_stats.txt" which is merely a text file including the filename, the detected interleave value, and the significance of that value in a tab separated file. Second, a file named "*FILENAME*.png", which is a visual guide to the analysis. *FILENAME* is taken from the name of the file automatically.

NOTE: If you process two images with the same name, you must choose different save directories or the information will be overwritten.

For example, if you have the following data:
/home/USER/fMRI_Data/Subject01/REST_BOLD.nii
/home/USER/fMRI_Data/Subject02/REST_BOLD.nii
/home/USER/fMRI_Data/Subject03/REST_BOLD.nii

And you attempt to run the following code:

```
FilePath1='/home/USER/fMRI_Data/Subject01/REST_BOLD.nii';
FilePath2='/home/USER/fMRI_Data/Subject02/REST_BOLD.nii';
FilePath3='/home/USER/fMRI_Data/Subject03/REST_BOLD.nii';
SaveDir='/home/USER/fMRI_Data/Interleave_Results';

InterleaveDetection_nii(FilePath1,SaveDir);
InterleaveDetection_nii(FilePath2,SaveDir);
InterleaveDetection_nii(FilePath3,SaveDir);
```


You will find the following files in the directory */home/USER/fMRI_Data/Interleave_Results/:*
  REST_BOLD.nii.png
  REST_BOLD_Stats.txt

Even though you ran the code three times, because the nii images are all named the same, they will be overwritten in the results directory. The program does not look for existing files before writing.
However, if you rename the files to indicate which subject they come from, multiple files will be saved in the results directory.

For example, if you have the following data:
/home/USER/fMRI_Data/Subject01/REST_BOLD_Sub01.nii
/home/USER/fMRI_Data/Subject02/REST_BOLD_Sub02.nii
/home/USER/fMRI_Data/Subject03/REST_BOLD_Sub03.nii

And you run the following code:

```
FilePath1='/home/USER/fMRI_Data/Subject01/REST_BOLD_Sub01.nii';
FilePath2='/home/USER/fMRI_Data/Subject02/REST_BOLD_Sub02.nii';
```

```
FilePath3='/home/USER/fMRI_Data/Subject03/REST_BOLD_Sub03.nii';
SaveDir='/home/USER/fMRI_Data/Interleave_Results';

InterleaveDetection_nii(FilePath1,SaveDir);
InterleaveDetection_nii(FilePath2,SaveDir);
InterleaveDetection_nii(FilePath3,SaveDir);
```
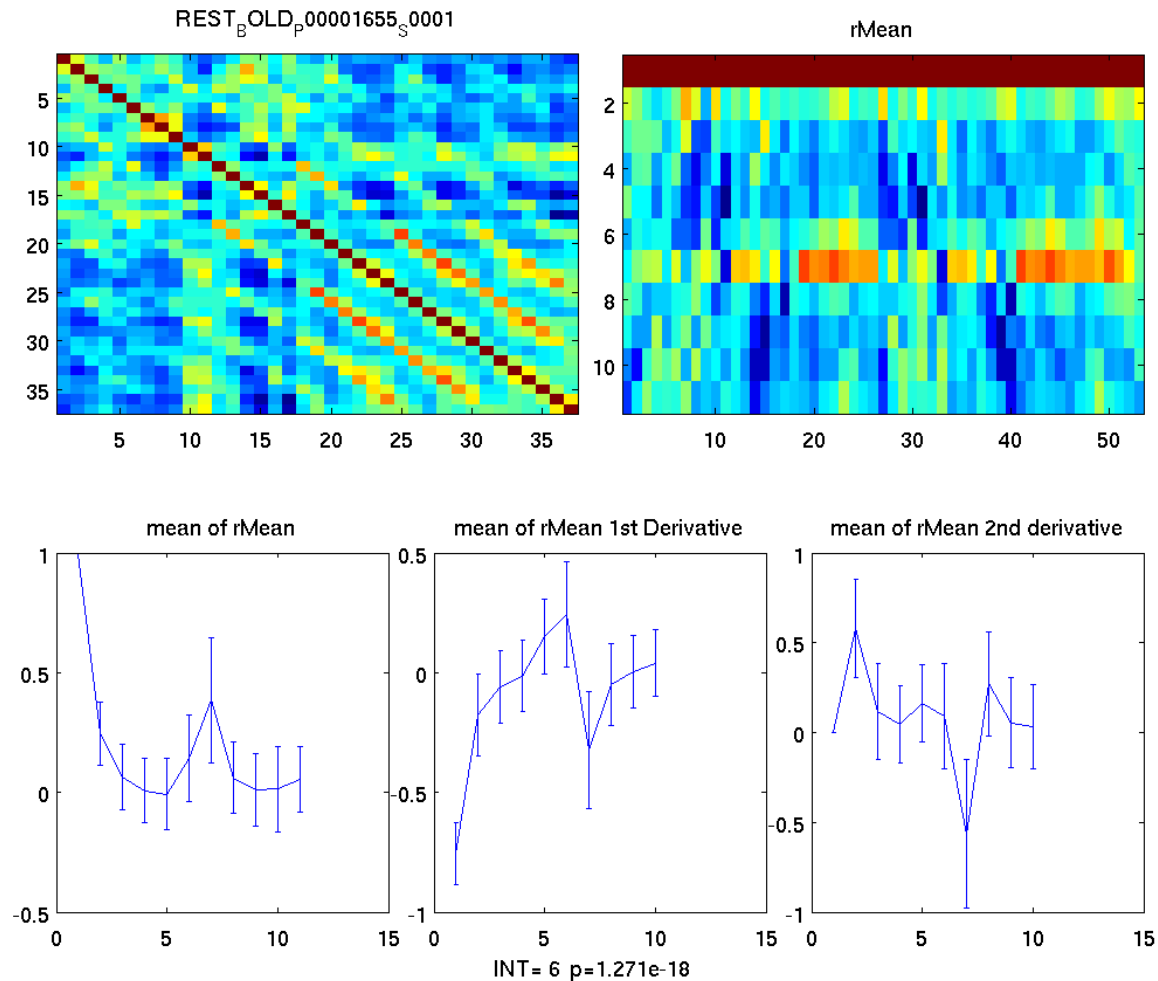
You will find the following files in the directory */home/USER/fMRI_Data/Interleave_Results/:*

REST_BOLD_Sub01.nii.png
REST_BOLD_Sub01_Stats.txt
REST_BOLD_Sub02.nii.png
REST_BOLD_Sub02_Stats.txt
REST_BOLD_Sub02.nii.png
REST_BOLD_Sub02_Stats.txt

b. Understanding The PNG Image
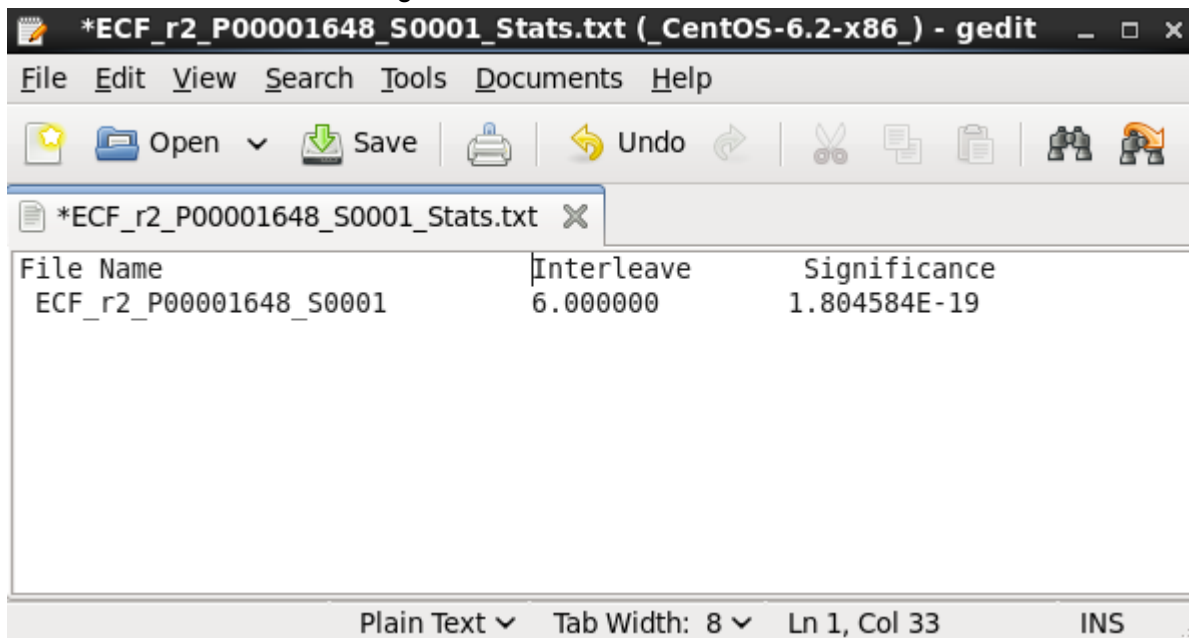
The png file will look like this:

1. **Top Left:** The cross correlogram of each slice-average signal (over the z axis). Indices indicate which slices are being compared.
2. **Top Right:** The temporal distance correlation function. Essentially, the correlogram is folded in half along the diagonal and cropped to obtain a rectangular area
3. **Bottom Left:** The average of the temporal distance correlation function (top right) across each row. The Y axis in this figure corresponds to the X axis in the top right image. Notice that the first value is "1" in both images. This is because the correlation of a slice with itself is the maximum possible value.
4. **Bottom Center:** The derivative of the bottom left plot.
5. **Bottom Right:** The second derivative of the bottom left plot. Notice the global minimum at the interleave value..

6. **INT & p:** At the very bottom of the image, you see two values: INT and p. INT is the detected Interleave value, and p is the significance (or certainty) of that value.

NOTE: Due to the nature of these signals, a p value of anything larger than $1x10^{-3}$ is considered a weak correlation. Even p values in the range of 10^{-4} - 10^{-5} should be manually inspected to verify results.

c. Understanding The Text File

The text file will look something like this:

This file is fairly straightforward. The name of the file is in the first column, followed by the detected interleave value, followed by the significance of that value. This file has been formatted to look better to the viewer. Depending on the length of the file name, the columns may not match up as nicely. However, the intention of this file is to be read by matlab, excel, or any other data processing tool. The tab separation makes it easy for these programs to extract the necessary information, and we recommend not reformatting the raw text file for viewing.

If you wish to view the data, import it into excel or a similar data processing program.