Robert C. Welsh
rcwelsh@med.umich.edu
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SPM8 Batch Processing

These commands are run from the terminal window and work under bash. The commands will allow you to do the following:

- Slice timing correction of data (actually uses FSL slicetimer)
- Realignment of data (actually users FSL mcflirt)
- Coregistation of overlay (or high-resolution) image to functional image.
- Coregistation of high-resolution image to overlay image.
- Warping of high-resolution image to MNI (e.g. T1) template
- Warping of time-series data to MNI template via the high-resolution image.
- Smoothing of time-series data.
- Segmentation of high-resolution image.

All of the commands expect your data organization to adhere to the following structure:

```
[High level experiment directory]/
    Subjects/
        YYMMDDAB/
            anatomy/
            func/
                run_XX/
```

The commands will do one process at a time, but you can specify an unlimited number of subjects (assuming they all have the same directory structure and generic file names, i.e. ht1overlay, raprun_XX, etc). Additionally, these commands are launched from a terminal window and will execute in the background, thus you can log out after submitting the commands. Additionally, when the process ends it will exit gracefully, produce a log file for any debugging issues and release any matlab licenses that it consumes.

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Until we retire the old spm2 batch processing scripts you will need to type "**spm8**" at the terminal if you want to enable these commands.

All of the commands have built in help (which will not be repeated here). If you issue the command without any command line arguments you will be presented with the help.

The commands (capitalization is important) are:

```
sliceTime
realignfMRI
coregOverlay
coregHiRes
warpHiRes
warpfMRI
smoothfMRI
segHiRes
```

Additionally, these commands use the `nifti` format for all files (`nii`). This will save on space as well as result in a higher throughput for your preprocessing.

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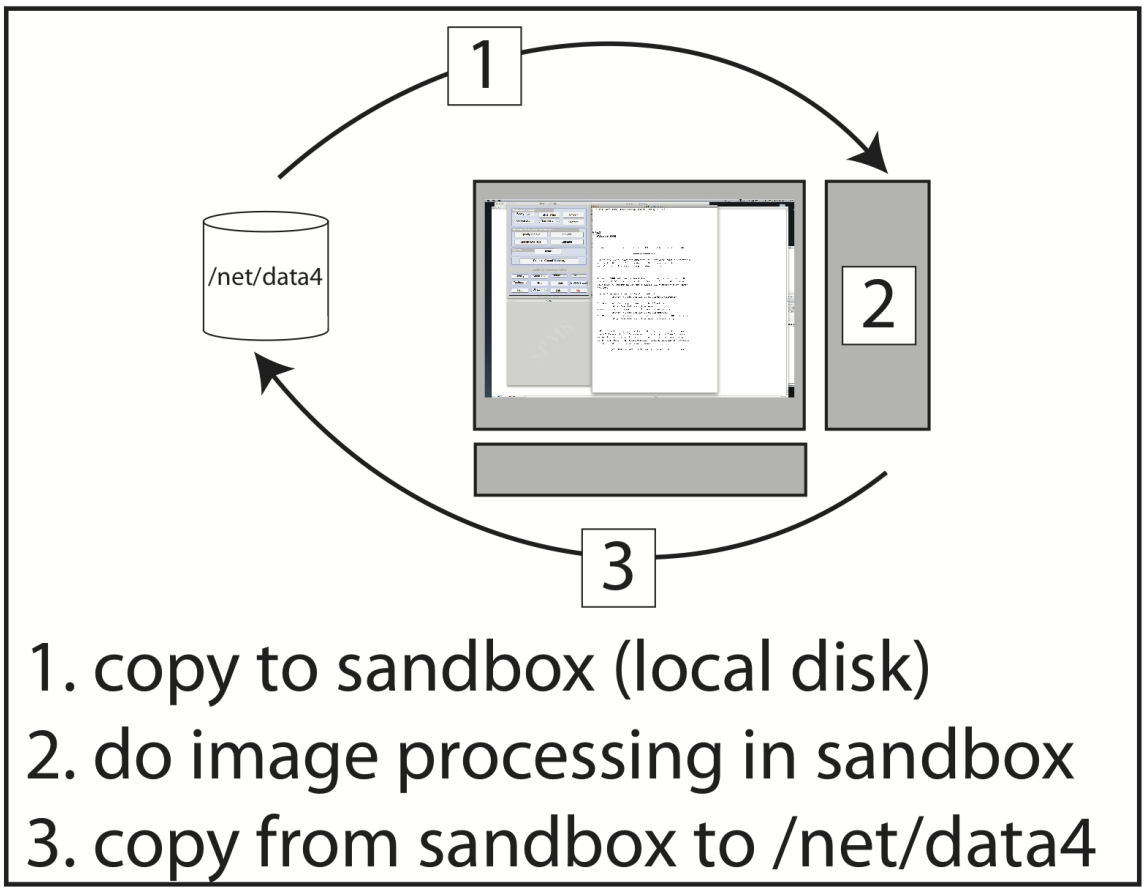
Sandbox

To facilitate processing of time-series data for the warping and smoothing I have implemented the concept of a sandbox. The basic idea is that if the data resides on /net/data4, it is first copied over to the **sandbox** (a local disk), worked up, and then sent back to /net/data4.



I've performed speed comparison tests, and running data processing directly on /net/data4 5-10 slower versus utilizing a sandbox. The scripts will automatically determine if your data resides on /net/data4 and will utilize the sandbox accordingly.