

Version 3.0

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## **Export**

If planning to use the fMRI program, the data will need to be run through the export script.

1. Open a new terminal to create the export script:

```
[user@solaris:/home/user] ./export [experiment] [#runs] [#slices/run] [#imgs/run] [exam#1] [series#]2
```

When the reconstruction has finished, run the export script:

```
[user@solaris:/home/ user] pvwave3  
[user@solaris:/home/user] waveadv  
Select the task: align, analyze or export: export  
WAVE> exp_[experiment]
```

## **Export Contingencies**

### **2. Inconsistent Experiment Design**

If an experiment does not have the same number of slices or images throughout, each section will have to be exported separately. To begin, create and run the script as usual for the first section of the experiment. For each successive section, modify the export script created for the previous section.

```
export_off_rec_stim, '/export/data/reconstruction/[experiment]/r1/', '/export/data/preal  
ignment/[experiment]/', '[experiment]r1s', 25, 36  
export_off_rec_stim, '/export/data/reconstruction/[experiment]/r2/', '/export/data/preal  
ignment/[experiment]/', '[experiment]r2s', 25, 36  
export_off_rec_stim, '/export/data/reconstruction/[experiment]/r3/', '/export/data/preal  
ignment/[experiment]/', '[experiment]r3s', 25, 36
```

In the above lines, the run number and number of slices and images, in bold, are the only areas that may need to be changed to fit the second section. A new script cannot be created because otherwise, the experiment name will not be preserved in the resulting files.

Exporting a six-run experiment with 25 slices and 36 images in the first three runs and 25 slices and 102 images in the last three runs follows:

```
[user@solaris:/home/user] ./export [experiment] 3 25 36 [exam#] [series#]  
[user@solaris:/home/user] waveadv  
Select the application: fmri, export, or custom: export  
WAVE> exp_[experiment]
```

When the above has finished running, quit out of wave by typing ctrl + d, and modify the export script:

```
[user@solaris:/home/user] cd /export/data/scripts  
[user@solaris:/export/data/scripts] textedit4 exp_[experiment].pro
```

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<sup>1</sup> Omit the “e” and the “s”

<sup>2</sup> This number is usually “3” for the axial series, but this information can be verified with the scanner technician.

<sup>3</sup> If working on a pc, type “pvwave-pc” instead.

<sup>4</sup> Any text editor may be used.

A new window with the export script will open. The run numbers should be changed from 1-3 to 4-6 and the number of images from 32 to 102:

```
export_off_rec_stim,'/export/data/reconstruction/[experiment]/r4/','/export/d
ata/prealignment/[experiment]/','[experiment]r4s',25,102
export_off_rec_stim,'/export/data/reconstruction/[experiment]/r5/','/export/d
ata/prealignment/[experiment]/','[experiment]r5s',25,102
export_off_rec_stim,'/export/data/reconstruction/[experiment]/r6/','/export/d
ata/prealignment/[experiment]/','[experiment]r6s',25,102
```

Restart wave and run the newly edited script:

```
[user@solaris:/home/user] waveadv
Select the application: fmri, export, or custom: export
WAVE> exp_[experiment]
```

### 3. Online Reconstruction

To export data which has been reconstructed on the scanner, two different export scripts must be created. These two scripts can be copied and modified from previous experiments. Using tmf2 as a template for the first script needed is best. In terminal 4:

```
[user@solaris:/home/user] cd /export/data/scripts
[user@solaris:/export/data/scripts] cp exp_on_tmf2.pro exp_[experiment].pro
[user@solaris:/export/data/scripts] textedit exp_[experiment].pro
```

A new window with the following script will open:

```
pro exp_on_tmf2

; this file needs to be modified each time off-line recon is done.
; for batch jobs, arguments are as follows
; export_on_recon,source_dir,dest_dir,exam num,exp name,num slices,num
images,num runs,offset

export_on_recon,'/export/data/scanner/tmf2/s2/','/export/data/prealignment/tm
f2','E16955S2','tmf2',16,32,1,0
export_on_recon,'/export/data/scanner/tmf2/s3/','/export/data/prealignment/tm
f2','E16955S3','tmf2',16,32,1,1
export_on_recon,'/export/data/scanner/tmf2/s4/','/export/data/prealignment/tm
f2','E16955S4','tmf2',16,32,1,2
export_on_recon,'/export/data/scanner/tmf2/s5/','/export/data/prealignment/tm
f2','E16955S5','tmf2',16,32,1,3
export_on_recon,'/export/data/scanner/tmf2/s9/','/export/data/prealignment/tm
f2','E16955S9','tmf2',16,32,1,4
export_on_recon,'/export/data/scanner/tmf2/s10/','/export/data/prealignment/t
mf2','E16955S10','tmf2',16,32,1,5

end
```

Change all instances of tmf2 to the experiment name by selecting **Find → Find and Replace** and typing tmf2 in the **Find** field and experiment name in the **Replace** field. The following must also be changed accordingly: exam num, exp name, num slices, num images, num runs, and offset. Notice that an "s" directory for each series is inside the experiment directory and that the series number is also appended to the end of the exam number. Make sure that the s directories and series number correspond for each line. When all the changes have been made, save the file and exit.

