SPIRAL IN/OUT PULSE SEQUENCE/RECON FOR FMRI

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1. Pulse sequence

General notes on characteristics and usage:

The spiral package includes the pulse sequence and reconstruction software that installs and runs on the scanner, and off-line postprocessing software that can be used to obtain Analyze-format images (e.g. for use in SPM or Melodic) or AFNI BRIKs.

The k-space trajectory can be chosen as spiral-out, spiral-in, or spiral in-out (both), controlled by a user CV. In the later case, two separate sets of images are obtained having a common TE (defined as the center of k-space), and they may be combined after reconstruction as desired. See ref. 5 for discussion of the philosophy of the spiral-in approach, as well as methods of combining the two sets of images.

The sequence has a 1.25 kHz sinc2 RF pulse that is not spectrally selective and which allows contiguous slice acquisition. A fat saturation RF pulse and crusher gradient is used to suppress the lipid signal to avoid ringing of the off-resonant signals into the high spatial frequency portion of the spiral-in acquisition. The spiral gradient waveforms depend on the desired matrix size, field of view and number of interleaves. As the matrix size is increased the resolution is increased, but the readout duration increases as well, and there is greater potential for off-resonance blurring. This can be reduced by increasing the number of interleaves. The acquisition matrix size is controlled by setting the 'freq' acquisition matrix size during scan prescription or by modifying the CV `opxres` (see below).

Optional dummy acquisitions (a TR period in which the sequence runs but no data are acquired) can be played out before actual data acquisition commences, in order to diminish non-equilibrium NMR effects. This is controlled by another user CV as described below.

The sequence runs in a conventional interleaved fashion, whereby each slice plane is excited once every TR period, in straight numerical sequence. The acquisition time/frame is nint*TR, where nint is the number of interleaves.

If there are 2 or more time frames collected, the first time frame has a TE that is 2 msec longer than what is called for. During reconstruction, frames 1 and 2 are used to create a field map. Note, therefore that the first time frame will have different signal amplitude than all others, and should not be used in any postprocessing analysis.

The sequence can be started with an external TTL pulse. In the standard mode, if the appropriate CV is set (to 1, see below), the scan will begin approximately 20 µs after the rising edge of a 1 µs or longer signal applied to the AUX_TRIG port, located in the back of the systems cabinet on the MGD chassis,

jack J7. Autoprescan and Autoshim function as usual, but when the scan button is pushed, the scanner will become ready and wait until receipt of the trigger. Alternatively, press prep for scan, and when the scan ready lights come on, you may arm the scanner by pressing start scan. The scan will start when the trigger is received. There is a watchdog timer which will abort the scan if a trigger is not received within about 24 seconds. The ability to start the sequence externally has been found useful for synchronizing the scan with the stimulation computer. A second mode (external trig set to 2) will cause the scanner to wait for a trigger for each frame.

A "cluster slice" acquisition mode is controlled by a user CV. If selected, the sequence eliminates dead time between slice acquisitions, so that all slices are acquired as rapidly as possible and then it will wait (silently) until time TR runs out. This method of acquisition may be beneficial in certain paradigms where dead time in the sequence allows more effective auditory stimulus presentation. The amount of dead time depends on the duration of each slice acquisition and TR.

The sequence is compatible with phased array mode and will collect as many channels as the coil config tells it to. Note, that the Pfiles get correspondingly larger. This is a nontrivial amount of data, e.g. if the coil is 8 or more channels. The sequence will check to see if the memory and Pfile size are within range of the scanner hardware.

Raw data files of the form Pxxxxx.7 are created in /usr/g/mrraw. There must be adequate disk space to contain the resulting scan. The size of the scan depends on the resolution chosen. For example, with 8 slices and 100 time frames rhrawsize is about 30 MB. The user should be aware that besides creating the raw file, the scanner also generates useless (for our purposes) link files in mrraw that should be periodically removed to avoid clogging linux's file system. There is one link for each slice collected, i.e. opslquant.

The bandwidth is controlled on the scan prescription page. 125 kHz is recommended for most fMRI applications.

The PSD can generate output pulses to control external equipment in synchrony with the scan. A TTL pulse is generated at J12 (DABOUT6) on the MGD front panel (a BNC connector). The pulse length, placement in the sequence and frequency can be controlled. The default is to produce a 5ms pulse, 5ms after the end of the RF pulse, once every TR period. The maximum frequency is one pulse per slice, and the minimum is one per scan. The first pulse only occurs after the nextra disdaqs have played out (which is different from the scope trig). For further information, email gary.

Usage

The user CV's are the following:

```
# of interleaves                              Number of "shots"/image
number of temporal frames                     Number of repetitions of the scan
ext trig: (0) none, (1) start scan, (2) start frame        If set, wait for trigger
                                                    on AUX_TRIG port
data xfer script or not(0)                    If set, initiates automatic data transfer/recon using
                                                    "son of recon" shell script
cluster slice acquisition (1) or not (0)   If set, puts dead time at the end of the slice
                                                    acquisition
Number of extra shots before data acq      Number of disdaqs (dummy acquisitions)
```

```
gtype: (0) spiral out, (1) spiral in, (2) both        Set to 2 for spiral in-out
Record physio data (1) or not(0)        If set, cardiac and respiratory data are saved in /usr/g/service
```

After scan prescription, the sequence parameters can be modified using Display CVs. Some useful CVs:

```
opfov           FOV, mm
opxres          Actual resolution, equivalent matrix size
nl              Number of interleaves
nframes         Number of temporal frames
opuser2         Controls external trigger (as above)
optr            TR, usec
opte            TE, usec
oprbw           Bandwidth, kHz
nextra          Number of disdaqs (dummy acquisitions, default 2)
```

2. Recon

General description
The reconstruction program grids the raw data into a 2x k-space matrix, performs a 2D FFT and writes the output images in either a single image file per slice/frame or as one large file (the 'onefile' format).

There are several important features which work in concert with the psd when more than one time frame is gathered. The first is that a B_O map is generated from the first two acquisitions. The echo time is made TE + 2 ms for the first frame. This does not deter using the first frame in fMRI post processing since the echo time difference is small compared to TE, but allows the calculation of the field map. The resulting map is used to make a first order shim correction to the reconstruction by building it into the gridding process, free of charge. This occurs on an individual slice basis, which is advantageous over Autoshim, in that the latter only corrects the average shim at the center of the volume. Note, therefore, that the first time frame will have a different signal contrast than all others and it might be useful to ignore it in postprocessinh

The second feature of grecons is that a correction is made for phase fluctuations in the data, using the first several points of the spiral acquisition (at the k-space origin) [2]. The second time frame is used to generate a reference phase value which in turn is used to correct all other views. This navigator correction has been found beneficial in reducing frame-to-frame variation from brain pulsatility, and typically results in a 50% reduction in rms fluctuation in multi-interleave acquisitions. It has no effect in single-shot acquisitions.

Another feature of the grecons program is that a correction is made for off resonance effects that derive from concomitant field ('Maxwell field') terms. The program derives the direction cosines for the slice being reconstructed from header information and calculates a time dependent phase correction that is applied to the raw data before gridding. The effect is to reduce off-resonance blurring for slices off-axis [4].

The program is multi-threaded, with up to 4 threads used to take advantage of the multiple processors on the host and speed up reconstruction.

Usage: Automatic reconstruction

The sequence can initiate an automatic reconstruction that results in generation of an image file in /usr/g/mrraw. Simply set the xfer data User CV to 30. When the scan is completed the shell script recon30 is started. The following actions ensue:

A. grecons12 is started on the host with the –O option, i.e., it generates a single output file, /usr/g/mrraw/Pxxxxx.7.mag, containing the concatenated image files in the same order as for the multiple file convention.

B. The program writeihdr12 extracts useful header information and places it in a text file, /usr/g/mrraw/EeeeeeSsssPxxxxx.7, where eeeee is the exam number, sss is the series number. All pertinent scan parameters are saved.

C. A log file, /usr/g/bin/recon30.log, is updated with a record of the event.

D. If physio data was collected, recon45 script is invoked to write /usr/g/mrraw/Pfile.physio. A matlab script (readphys11.m is included to transform this file to sampled cardiac and respiratory data at a desired TR for later use.

The recon program usually runs faster than data can be acquired, and thus will normally finish before the end of the next scan. After completion, two files remain: the image file and the header file. The image file will be less than half the size of the original Pfile because 1) it contains magnitude data (not complex) and 2) the k-space data are oversampled somewhat. This speeds the ftp transfer of data off the scanner.

Usage: Offline reconstruction
If you wish to reconstruct off line, type `grecons12` to get a list of switches and options. It is recommended that the Onefile option be used for reconstruction, because of the large number of images that are generated when the in-out trajectory is employed. If not, the output images are headerless flat files of short ints, either 64x64, 128x128 or 256x256, with a separate file for each image in the default mode. They are created as Pxxxxx.7.yyy, where yyy is defined by the pseudocode

```
yyy = 1;
for (slc = 0; slc < opslquant; slc++)   {
    for (traj = 0;traj < ntraj; traj++)    {
        for (frm = 0; frm < nframes; frm++)   {
            reconstruct_image(yyy++)
        }
    }
}
```

Here ntraj = 2 for spiral in-out, and the files are grouped by trajectory, with the spiral-in data preceding the spiral-out data for each slice. Thus, the time frames for a given slice are grouped together and numbered sequentially.

By using the –O switch on the command line of grecons, a single output file is generated with all images concatenated in the same order. The file is named Pxxxxx.7.mag.

3. Typical Parameters for fMRI, 3T

2D GRE sprlio

```
# interleaves   = 1
# frames        = 100
external trig   = 0          /*  auxiliary trigger not used to initiate scan  */
xfer data       = 30         /* to use automatic recon process (see above)  */
gtype           = 2          /* use spiralio
nextra          = 2          /* 2 dummy frames before acquisition begins */
record physio   = 1          /* will acquire physio data, beginning with dummy frames */
```

psd name sprlio
FA/TE/TR/BW   77/30/2000/ 125 kHz
22cm FOV, 30 slices, 4 mm skip 1
freq encoding 64   /* equivalent matrix size */

This example will scan for 200 s, producing 6000 images with 3.44 mm pixel size. This is a single shot protocol, so the temporal resolution in this case is 2000 ms/frame. The first 100 images will correspond to slice 1 spiral-in, the second 100 to slice 1 spiral-out, etc. for slices 2- 30. Thus, there are two images for every slice and time frame.

4. Postprocessing

There are two scripts that can automatically create Analyze volumes or AFNI BRIKs, makevols and makebricks, respectively.

```
>makevols E12345S005P01024.7 outfoo
```

will create a set of files outfoo.Vnnn.img and outfoo.Vnnn.hdr, where nnn = 001 to nframes. Similarly,

```
>makebrick E12345S005P01024.7 outfoo
```

will create the two AFNI brik files. Other options for including retroicor or rvhrcor in the processing can be seen by typing the script name without arguments.

The programs that are run during these script executions are:

A) sprlioadd: Required if spiral in/out data are obtained (5). After reconstruction using grecons, sprlioadd can be used to combine the in-out images or to simply extract the in- or the out- images from the concatenated file(s). Consult the help menu obtained by typing the name of the program without arguments:

```
>sprlioadd
Usage: sprlioadd [-B] [-N npix] [-O] [-m mode] infile outfile nframes
nslc
  -B for Big Endian input format (applies only for little Endian
platform)
```

```
  npix default is 64
  -O for single input file ('onefile') format
  mode = 0: wtd average [default]; 1: simple ave
          2: extract spiral-in;     3: extract spiral-out
```

An example is

```
sprlioadd -O P01024.7.mag p01024 280 24
```

This will generate a new Onefile output, p01024, which combines the spiral-in/out data using weighting.

B) expandonefile: Images can be extracted from the Onefile format.

```
>expandonefile
Usage: expandonefile [-s isl1] [-e isl2] [-f nfr2do] [-l] [-V] [-r]
[-o orient] infile outfile nslc nframes npix
  infile in grecons Onefile format
  outfile pathname
  nslc: num slices in infile
  nframes: num frames in infile
  npix: reconstructed matrix size
  isl1,2: start, end slice to do [all]
  nfr2do: num frames to do [all]
  -l: input is in Little Endian format (else Big Endian)
  -V: output is in Volumes, one file/frame
      default is one file per image
  -r: reverse slice order in Volume
  orient: input is 0 = axial, 1 = sag, 2 = cor [0]
```

An example is

```
expandonefile p01024 I 24 280 64
```

which will generate I.??? Images in the usual flat file format.

The figure below shows examples of images combined or not.

5. Questions?

Send me a note.

References

1. Glover, GH; Law, CS. Spiral-in/out BOLD fMRI for increased SNR and reduced suspectbility artifacts. Magn. Reson. Med. 46:515-522 (2001).

2. G. H. Glover, S. Lai, Self-Navigated Spiral fMRI: Interleaved versus Single-shot, Mag. Reson. Med. 39:361-368 (1998).

3. Glover, GH. Simple analytic spiral k-space algorithm. Magn. Reson. Med., 42:412-415 (1999).

4. King KF, Ganin A, Zhou XJ, Bernstein M, Concomitant field effects in spiral scans, Magn. Reson. Med. 41:103-112 (1999).

A. Spiral-out

B. Spiral-in

C. Spiral -in/out,
Simple average

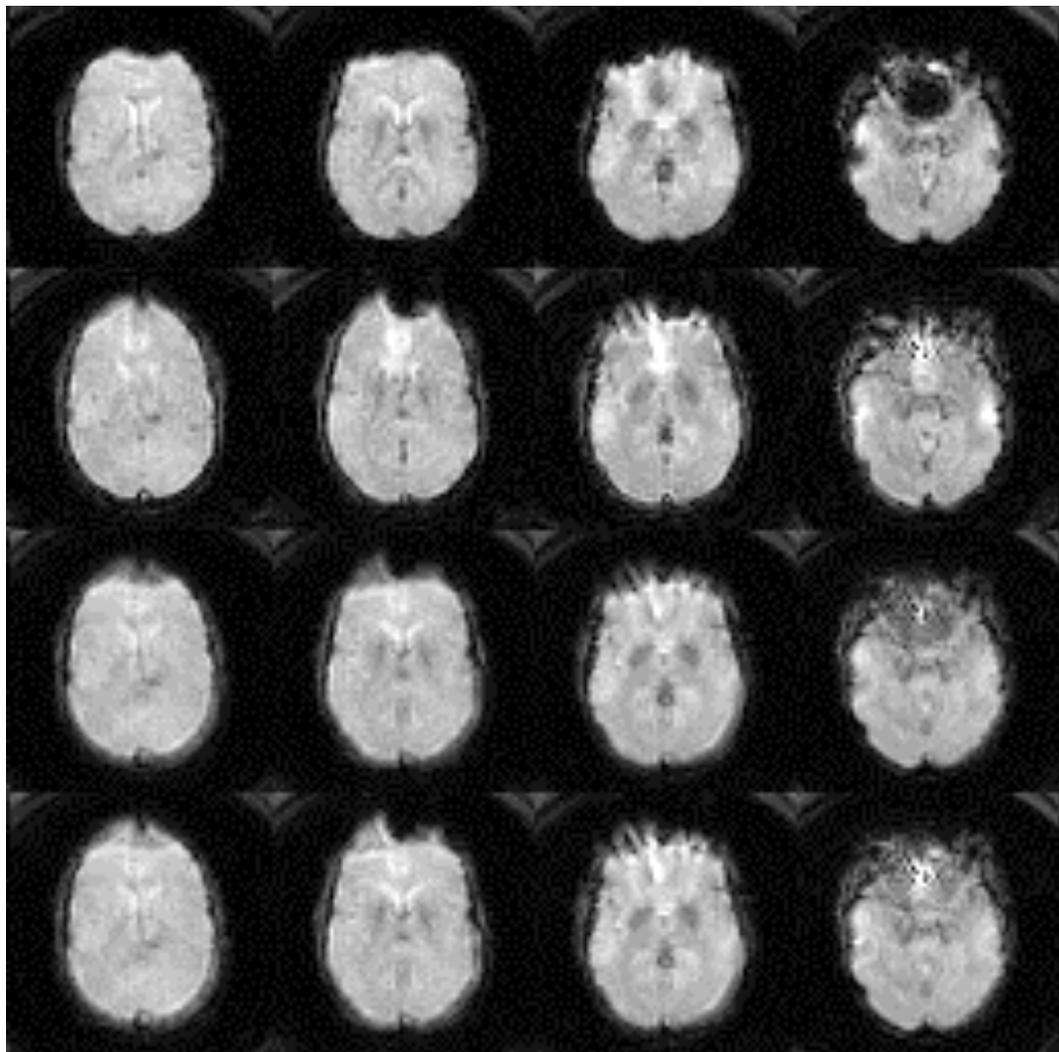D. Spiral -in/out,
Weighted average

Figure 1. Example of results using various options. The combination of images in C and D is performed using spiral-in/out acquisition data using a post-processing program, `sprlioadd`. This program operates on the images produced by `grecons`, the reconstruction program, and produces a new timeseries. Options in the program allow extraction of any of the images in A-D from simultaneously acquired spiral-in/out data.

Installation instructions

The tar file contains files that should be loaded on the scanner (`scanner.tar`) and postprocessing programs `fmriutil.lnx, fmriutil.osx` that can be loaded on a linux or mac workstation, arranged in corresponding directories.

1. Scanner

In `/usr/g/research`, do the following.

```
>mkdir spiral
>cd spiral
[load scanner.tar]
>tar xvf scanner.tar
sprlio1252
sprlio1252.psd.o
grecons12
writeihdr12
recon30
recon45.
>cd /usr/g/bin
>ln -s /usr/g/research/spiral/sprlio1252 sprlio
>ln -s /usr/g/research/spiral/sprlio1252.psd.o sprlio.psd.o
>ln -s /usr/g/research/spiral/grecons12 .
>ln -s /usr/g/research/spiral/writeihdr12 .
>ln -s /usr/g/research/spiral/recon* .
```

The psd can then be accessed by typing `sprlio` as its name on the scan prescription page.

The `grecons12` and `writeihdr` programs can be installed on any Linux platform as well as the scanner, if desired for offline reconstruction (which is not recommended).

2. Postprocessing

Load the appropriate tarfile directory on your workstation in some suitable place and make accessible to user. Make sure all files are executable. Files are scripts `makevols, makebrick`, and programs `spriioadd, expandonefile, makeaheader`