

Running spiral BOLD scans

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Motivation

Spiral readout for T2*-weighed functional imaging has certain advantages over traditional EPI readout:

1. **Speed:** Spiral acquisition of k-space tends to be faster as compared to EPI. For example given TR=2000 and slice thickness of 4mm one can obtain full-head coverage (40 slices as compared to 32 for low bandwidth EPI).

2. **Flexibility in selecting echo time TE.** With spirals short TEs are possible. Spiral acquisition may start either at the center of k-space (*spiral out*), or in the periphery (*spiral in*), thus emphasizing BOLD modulation either in high or low spatial frequencies. The *spiral in* sequence is still under development and currently does not give comparable image quality to the *spiral out*.

3. Spiral images may exhibit **lesser susceptibility artifacts** (due to isotropic sampling of k-space and shorter acquisition window).

Disadvantage: a spiral equivalent for EPI ghosting is image blurring in radial direction. This may result in larger point-spread function and, thus, coarser effective spatial resolution as compared to EPI acquired using the same grid (e.g. of 64x64 voxels).

Setting up a protocol for spiral acquisition

A protocol called *spiral fMRI* exists in “head” selection of protocol list. The protocol calls a pulse sequence developed at the Center: *spep_product*.

The default protocol parameters are: TR=2000ms, TE=25ms (or 30 ms), spiral out, #reps = 10.

Just like with a standard EPI fMRI protocol, slice prescription can be done using the graphical prescription tool (Rx button). However, spiral protocol is not coupled to the **BrainWave Real Time** option therefore, paradigm manager cannot be used for setting TR and #reps. In fact, #reps are set by pressing the **user CVs** button, and entering desired values in CVs page. Likewise, the direction of spiral acquisition is also set via user CVs, second CVs page.

NB: For co-registration of spiral functionals with structural scans, it is critical to write down Start and End positions of **both** functional and structural scan prescriptions (for S-I, L-R, and A-P directions). Co-registration is performed using a Matlab script, and these values serve as input to the co-registration program.

Data reconstruction and transfer

Unlike data acquired with GE product sequences, data produced by **spep** pulse sequence are stored as raw data in P-files in directory **/usr/g/mrraw**. Image reconstruction into AFNI bricks is done automatically offline after the scan. **Please allow time for reconstruction to finish** (~5 minutes after the scan finishes) before transferring your data. Open a command tool and follow the instructions below:

1. **cd /usr/g/mrraw**
2. **ls -ltr P*** to find the latest P-files.
3. To transfer the P-file and reconstructed brick:
aslgecopy -s server -r raid# -d datadir Pfilename brikgname username
(EXAMPLE: aslgecopy -s cfmri -r raid3 -d 060601Pilot P01208.7 scan1 guest)

The program will produce an afni brick brikgname+orig.{HEAD, BRIK}.

NB: the reconstruction process may be rather lengthy depending on # images to be reconstructed. If a dual (or multiple) echo option is used, one brick per echo will be created with a suffix eN, where N stands for echo number.