

# Acquiring Field Maps on the 3T Scanners at UCSD CFMRI

Revision date: 08/19/2014

## Overview

This document describes the procedure of acquiring field maps on the 3T scanners at CFMRI 3T West (MR750) currently has two field map protocols available: Protocol 1 and Protocol 2. Both protocols can be found under /adult/head/fMRI\_Basic on the scanner. Below are the step-by-step directions on how to run the field map protocols.

## Protocol 1

The directions below assume that you are using the 8ch head coil for EPI/DTI acquisitions. The field map scans use BODY coil by default. If you are using the split head coil (quadrature birdcage) then you should change the field map protocol to use the split head coil. If you are using any other coils, please consult with us before using this fieldmap protocol.

### Step by step instructions:

1. Make sure that you are in research mode.
2. Perform a localizer scan.
3. Load the protocols fm\_TE1\_NFS and fm\_TE2\_NFS.
4. View edit fm\_TE1\_NFS. Note the system will indicate that you are switching to the body coil. Accept this (unless you are using the split head coil). The body coil will be used for the field map acquisition, while EPIs will typically use the 8-channel head coil.
5. Prescribe the slices that you will be using for the EPI. Verify that auto-shim is checked. Save and run fm\_TE1\_NFS.
6. View edit fm\_TE2\_NFS. Copy the graphical prescription from fm\_TE1\_NFS (use original loc option). Verify that auto-shim is not checked. Save and run the series.
7. It is good practice to visually inspect the field map images for motion or operator errors (e.g. different prescription for TE1 and TE2). The TE1 and TE2 images are acquired as magnitude, phase, real, and imaginary for each slice. In particular, if there is a significant motion or physical between the TE1 and TE2 images (most easily seen in the magnitude images), the field map computations will not work. Warning: if the TE1 and TE2 prescriptions are not identical, the correction algorithm will not work!
8. Prescribe your EPI run. Typically, this will use the 8 channel head coil. Copy the graphical prescription from fm\_TE1\_NFS. (NOTE: in order to copy the prescription, the FOV, slice thickness, slice spacing, and matrix size must match that of the TE1 and TE2 images. Also make sure to use the original loc option). Also make sure to turn off auto-shim.
9. Run the EPI.

### Post Processing:

The post processing tool for data acquired with this protocol is **ppge4**. The following files are required run ppge4:

1. ppge4 (a Cshell script)
2. epidewarp4.ucsd (a Cshell script)

3. dicomrx (a compiled executable for Linux)

All the above files can be downloaded from the CFMRI website:

<http://cfmriweb.ucsd.edu/Howto/3T/fieldmap.html>

System requirements and instructions on how to use ppge4 can be obtained by typing ppge4 in a Linux command window without any arguments.

## **Protocol 2**

The directions below assume that you are using the 8 channel head coil for EPI/DTI acquisitions. If you are using a different coil, please consult with us before using this field map protocol.

### Step by step instructions:

1. Make sure that you are in research mode.
2. Perform a localizer scan.
3. Load the protocol *AssetCal*, prescribe slices to cover the entire brain, and run it.
4. Load the protocol *fm\_grass\_64x64* (or *fm\_grass\_128x128* if it is for a DTI scan).
5. Prescribe the slices that you will be using for the functional run. Verify that auto-shim **is** checked. Save the series.
6. Run *fm\_grass\_64x64* (or *fm\_grass\_128x128*).
7. Prescribe your EPI (or DTI). Copy the graphical prescription from the *fm\_grass* scan. (NOTE: in order to copy the prescription, the FOV, slice thickness, slice spacing, and matrix size must match that of the field map prescription. Also make sure to turn off auto-shim.
8. Run the EPI.

### Post Processing:

The post processing tool for data acquired with this protocol is **ggfm**. The following files are required run ggfm:

4. ggfm (a Cshell script)
5. epidewarp4.ucsd (a Cshell script)
6. dicomrx (a compiled executable for Linux)

All the above files can be downloaded from the CFMRI website:

<http://cfmriweb.ucsd.edu/Howto/3T/fieldmap.html>

System requirements and instructions on how to use ggfm can be obtained by typing ggfm in a Linux command window without any arguments.

Please contact Kun Lu ([kunlu@ucsd.edu](mailto:kunlu@ucsd.edu)) for questions.