

Howto: Correcting Surface Coil Bias Using *BC*

Overview

Images collected with a surface coil may have an artifact called bias, a change in intensity from part of the image to another that depends on the distance from the receive surface coil. *BC* is a program that corrects this bias artifact. To use *BC*, data should be accompanied by a reference scan with minimum anatomical contrast (“mincon”). This scan is part of some protocols that involve collection with a surface coil.

Requirements

Minimum Contrast Image

You should have a mincon image from the same data acquisition with a prescription that is similar to the image you want to correct. It is acceptable to collect a mincon image with a lower spatial resolution than the image to be corrected. At this time, both the Bruker and DICOM data must be available to run *BC*.

Image to Be Corrected

You will need the image to be corrected in both the Bruker format and DICOM format data.

Installation

BC uses MATLAB and runs on a Linux operating system. You must have MATLAB installed on your computer to run *BC*. You should have the *BC* files which can be downloaded from the center website. Download *BC.tar* from the website, untar the files and put them in their own directory.

afni

afni will need to be installed on your system for *BC* to work.

Running *BC*

Create a Study Directory and Select a Study Name

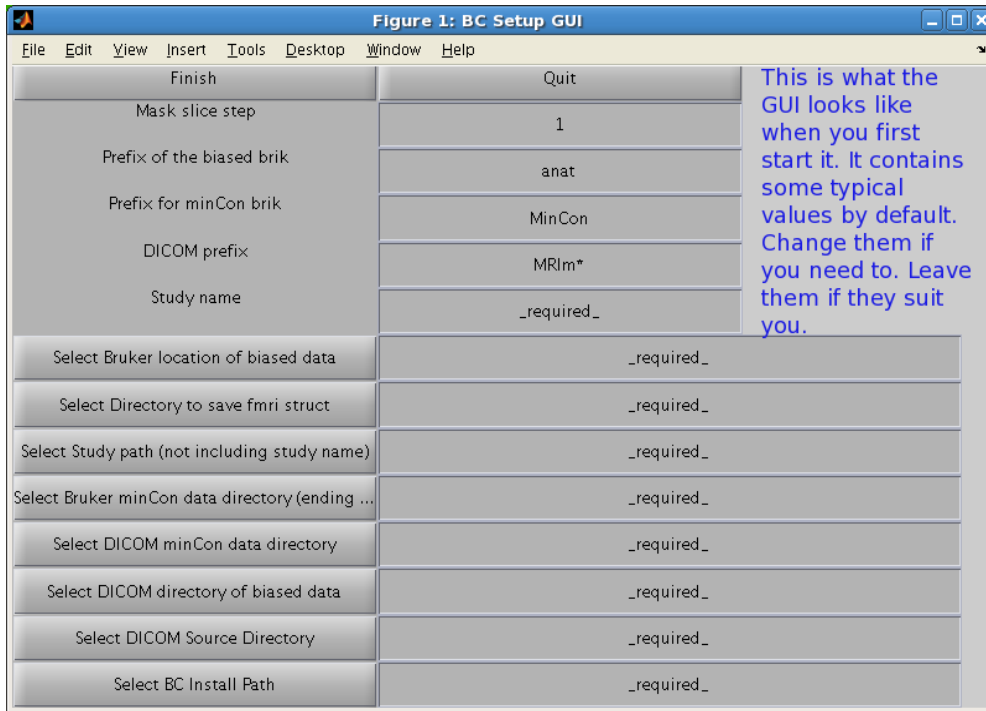
Choose a “study directory” where the output files of your study will be located and create a directory with the “study name” that you select. Later, you will enter these locations into the *BC* GUI. For example, I want my **study directory** to be `/mnt/raid9/rbussell/data/tmarc` and I chose the **study name** `gp120_912dTestBCGui`. So I created a directory with this command (in a linux terminal):

```
mkdir /mnt/raid9/rbussell/data/tmarc/gp120_912dTestBCGui
```

When you want to view the corrected files later, that is where you should look.

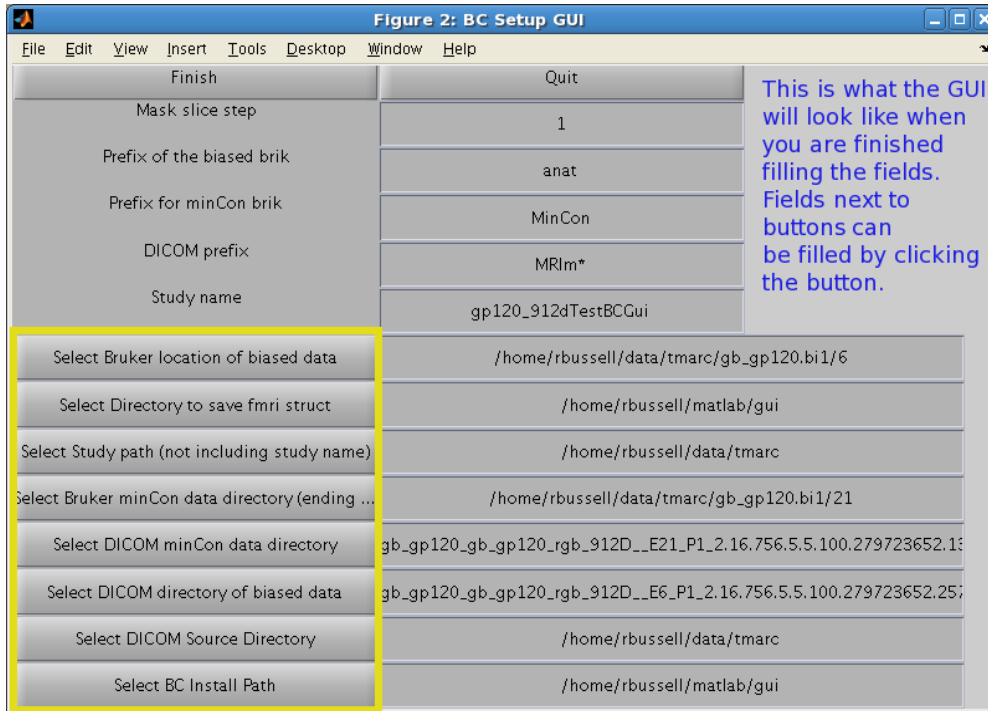
Launch the Graphical User Interface (GUI)

Open MATLAB by typing *matlab* in a terminal (depending on your system). If you have problems launching MATLAB on your system, contact your system administrator. In the MATLAB command window, type *BCGUI*. You should see the startup window below with some fields that require input from you labeled “_required_” and some other fields loaded with reasonable default value. Whether or not you need to change these default values depends on your preferences and your data sets.



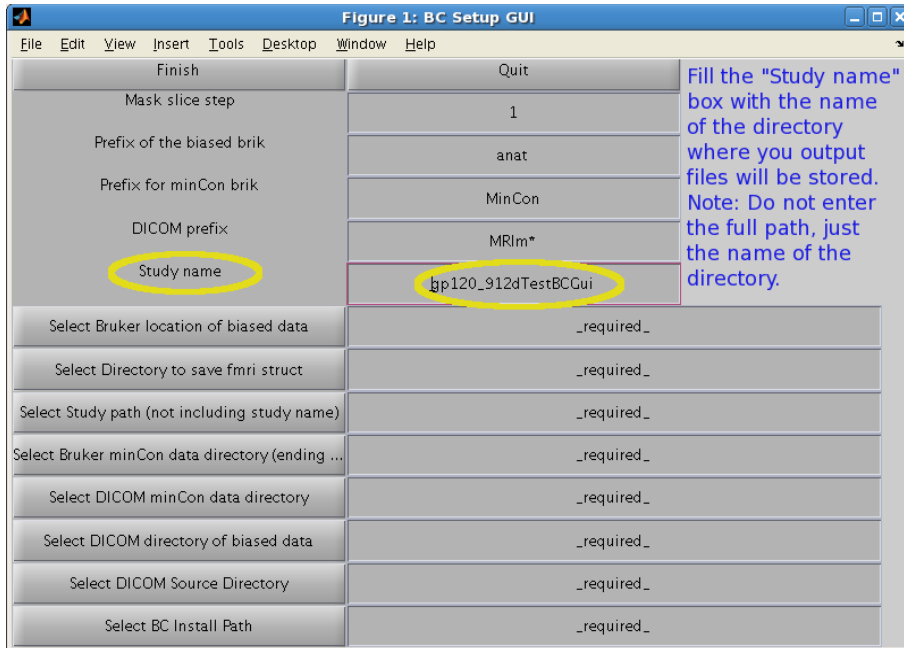
Completing the GUI

An example of what the GUI looks like for my data set names and locations is shown below. The upper text boxes will need to be filled out by typing into them. The lower text windows have buttons to their left.



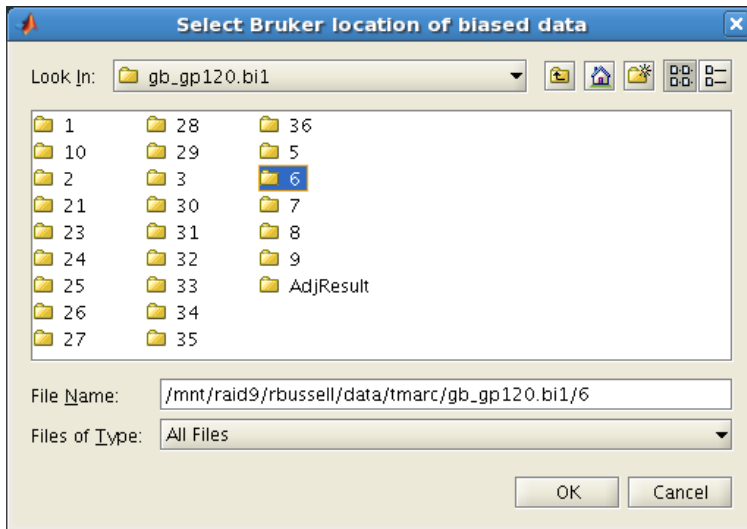
Enter the Study Name

The study name box (circled in the right hand column) must be filled out by hand. Carefully erase any text that is already there and type in the study name. This should match the name of the directory in the study directory that you already created (see the section entitled *Create a Study Directory and Select a Study Name* above).



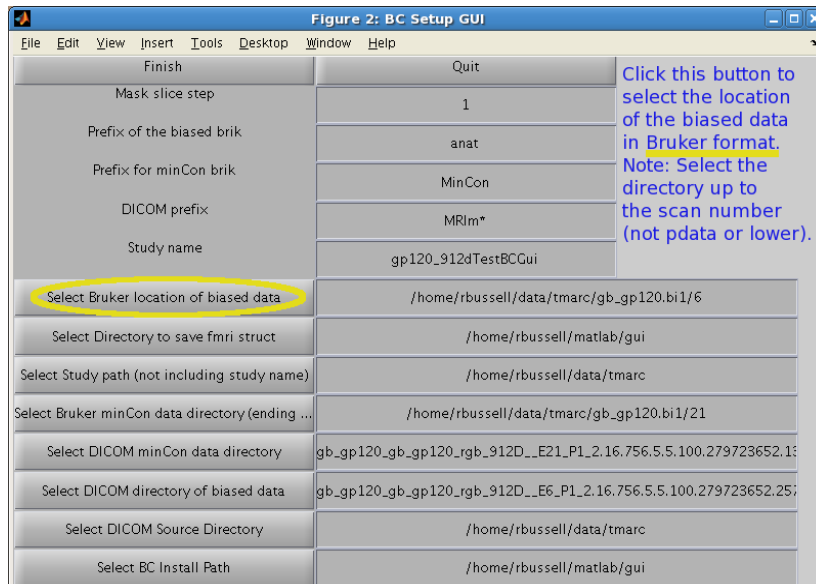
Enter the Location of the Biased Data in Bruker Data Format

Click the button that says “Select Bruker location of biased data” and a dialog box will open up similar to the one shown below.



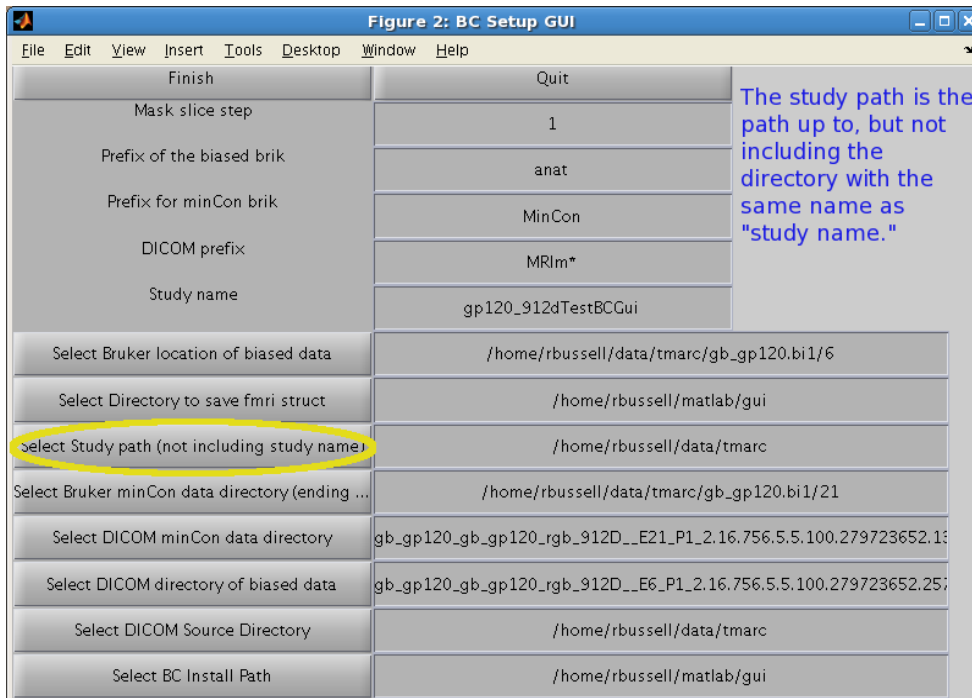
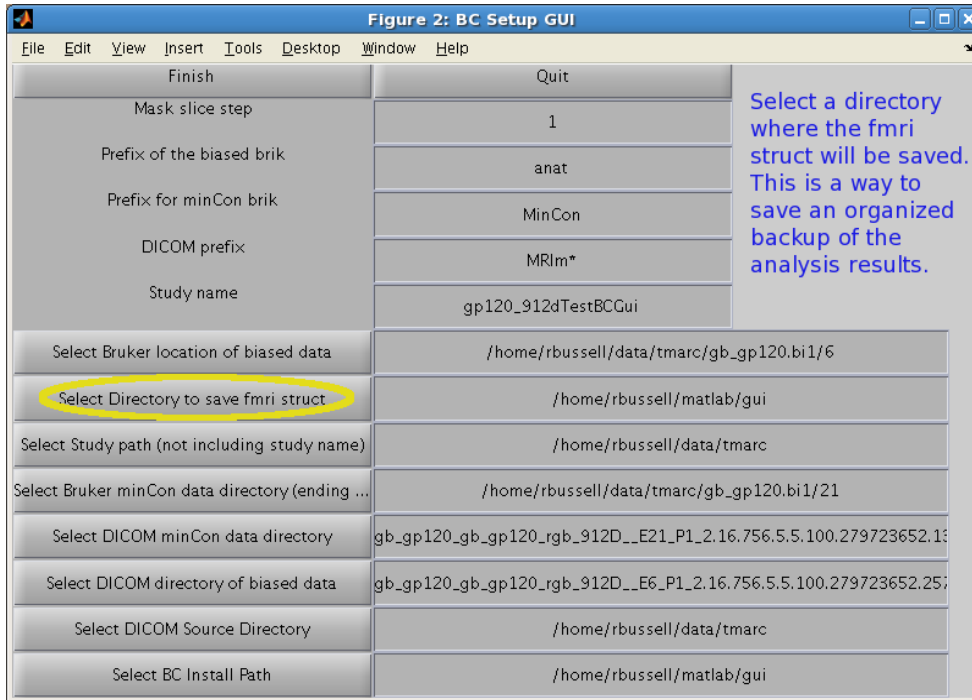
Use the dialog box to select the location of the Bruker scan directory that contains your biased data (the data you want to correct).

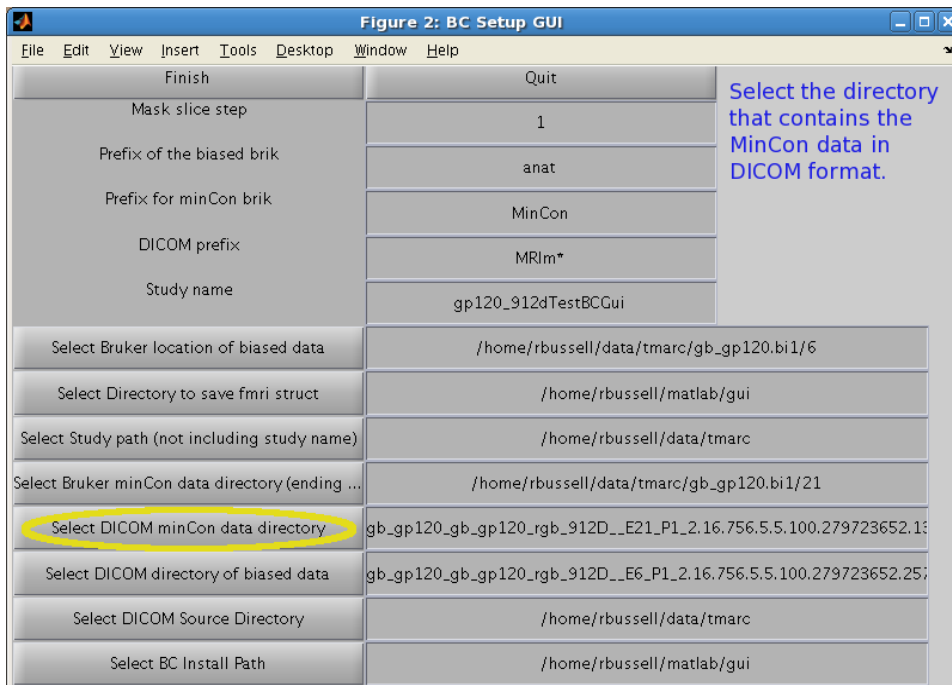
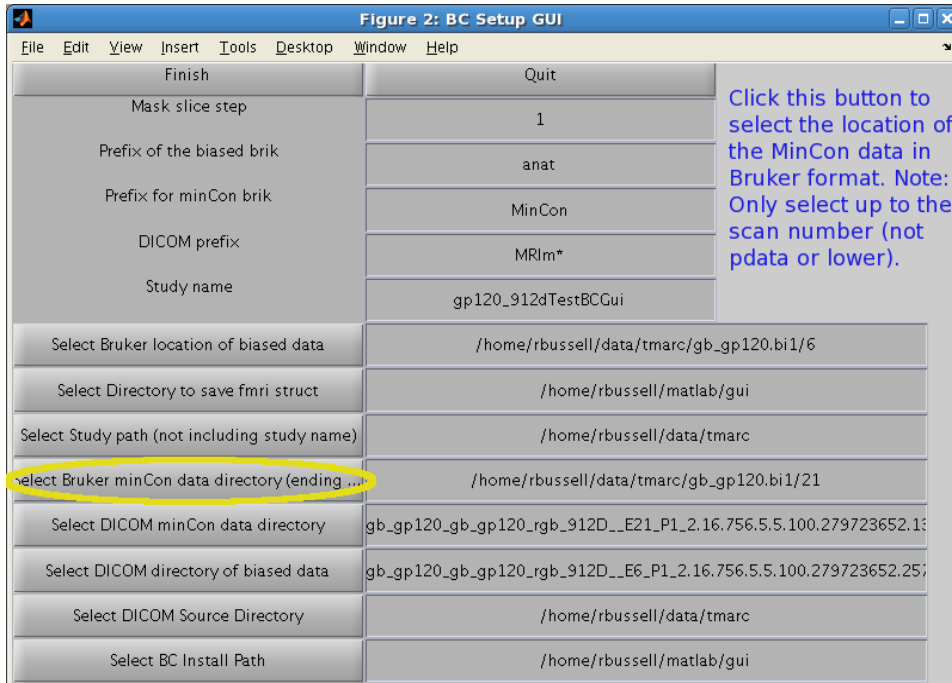
Important Note: You should select the directory up to and including the scan number ('6' in the example below). Neither the 'pdata' directory nor any lower directory should be present in the directory name. For instance, the *pdata* in the following should NOT be present `/home/rbussell/data/tmarc/gb_gp120.bi1/6/pdata/` even though it is a valid directory that exists on the system.

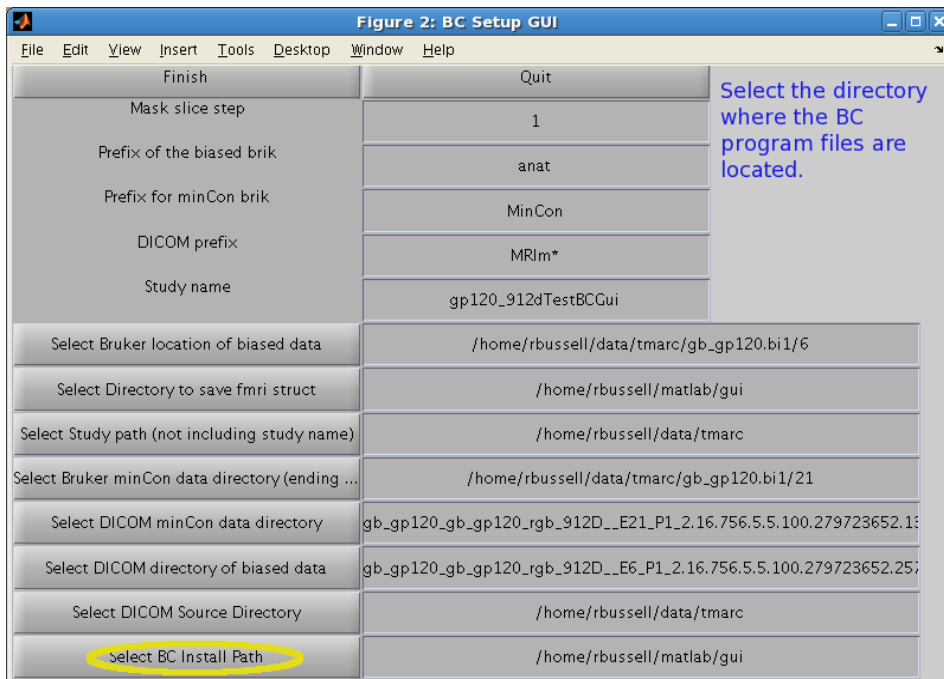
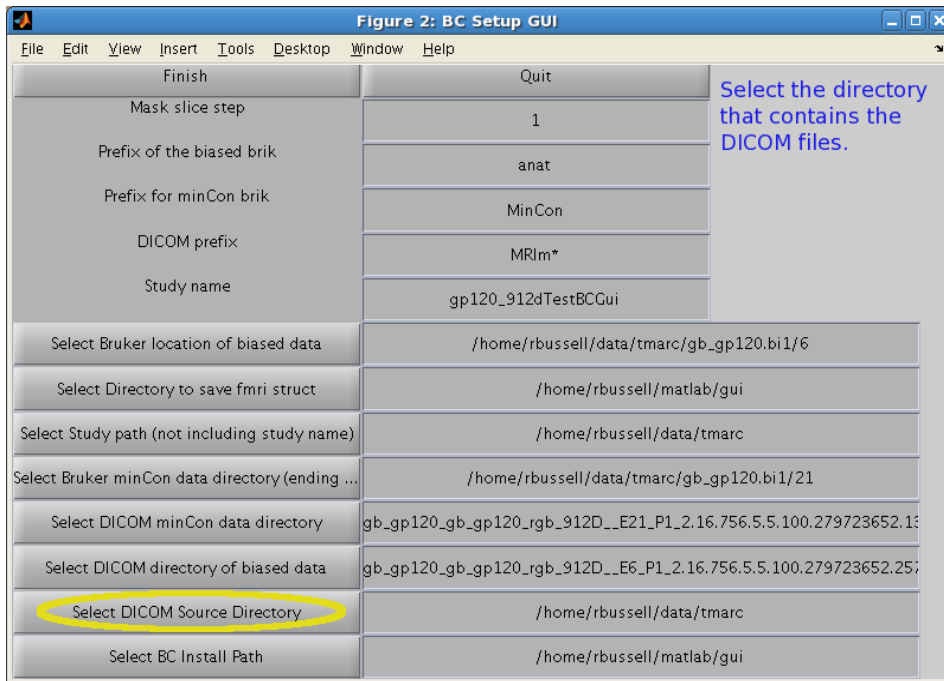


Filling the Other Fields

See the inset text in each figure below for instructions regarding each field.

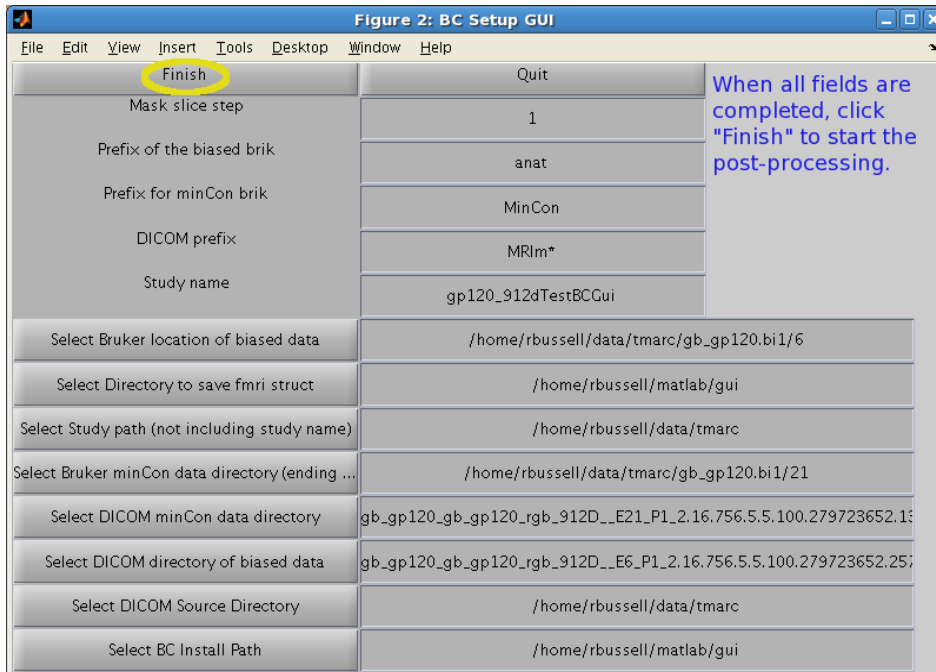






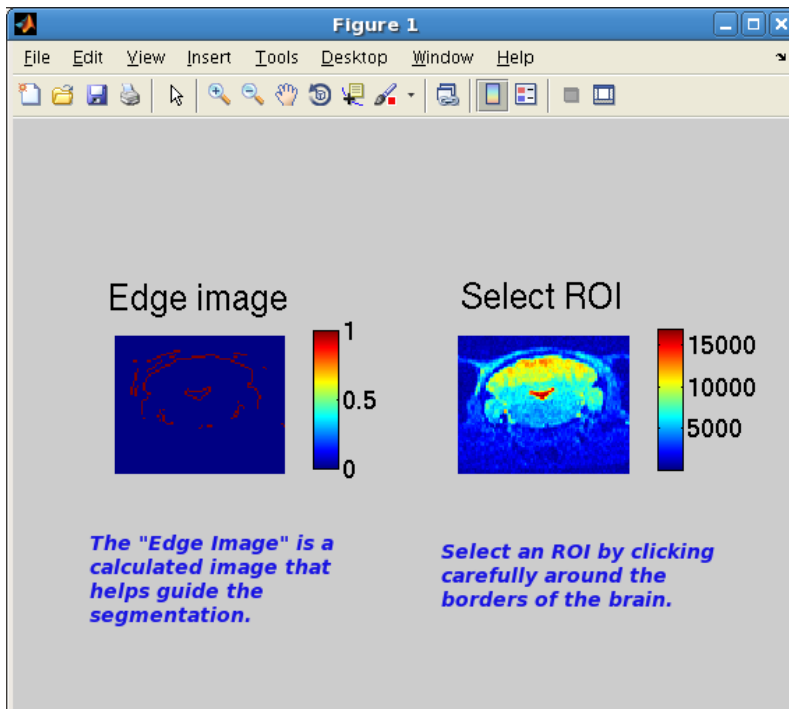
Running the Post-Processing Correction

When you are finished filling all the fields click the “Finish” button. The *BC* program will launch using the values that you entered into the GUI. To exit without running the code, click “Quit.”

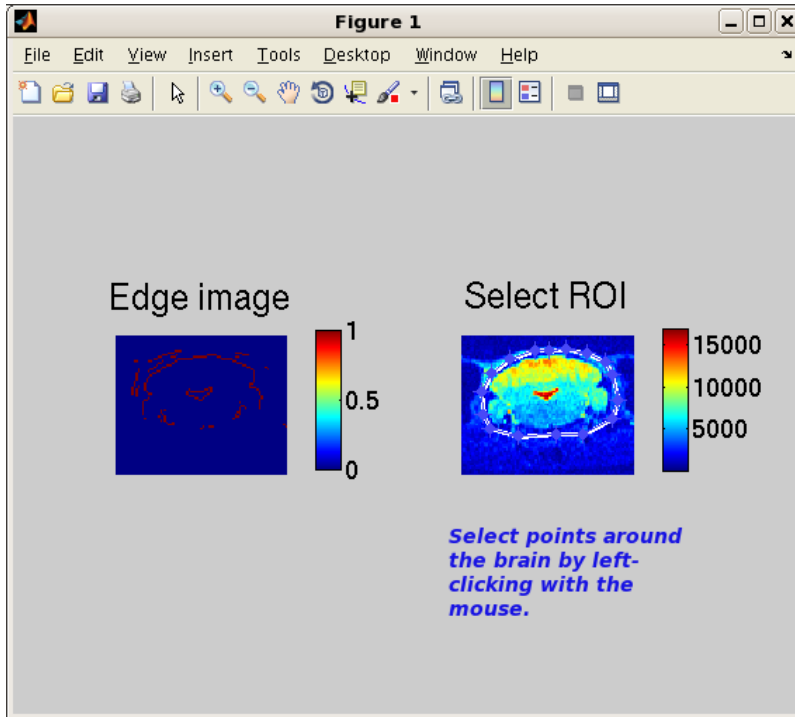


Segmentation

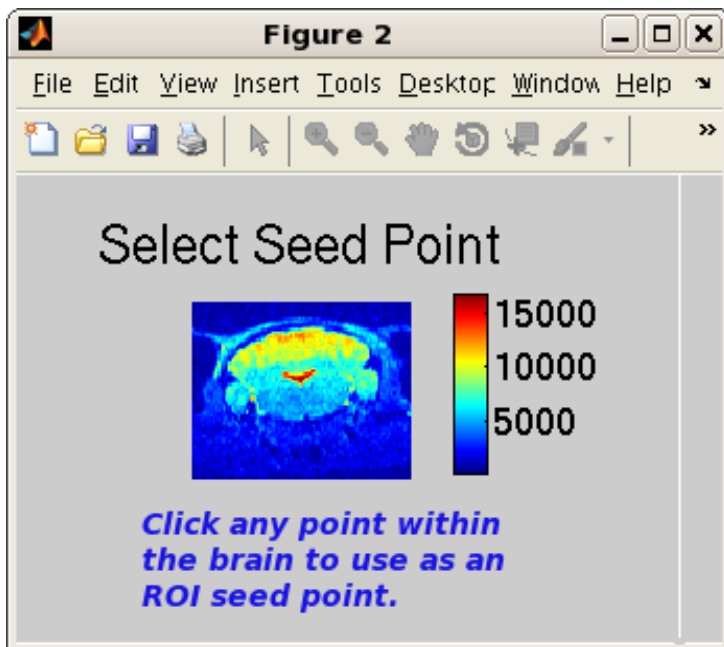
The BC program requires a brain mask. The segmentation is manual with some assistance from an edge detection algorithm. Images of each slice will appear one after another.



You will provide input to the segmentation routine by manually clicking on points just outside of the brain to trace a polygon. When you are finished tracing all the way around the brain click once on the "open" end of the polygon, which is the first point that you clicked on the brain image.



To finish selection around the slice double click inside the selected polygon. Another image of the same slice will appear, as shown below.



Click any point within the brain to select a seed point to grow an ROI. The next slice should then appear for segmentation and you will repeat the process. The *BC* program should now run without additional user input.

Viewing the Output Files

Open a terminal and change into the directory with the name “study name.” Execute the following command to view the corrected data:

```
afni anatCorrAnatRes+orig
```

Troubleshooting

If the BC program does not run through completely check that the DICOM and Bruker formatted versions of the biased data and the mincon data are present and in the locations you entered into the gui.

If the afni command *afni anatCorrAnatRes+orig* does not show you a data set, check that you are in the directory named “study name” and that the files *anatCorrAnatRes+orig.BRIK* and *anatCorrAnatRes+orig.BRIK* are present. If they are not, BC did not run completely. Check that it is not currently running by looking at the MATLAB command window.

Bug Reports

Send bug report to Robert Bussell at the Center for fMRI, rbussell@ucsd.edu.