Steps for voxel ROI placement with Gannet
(v2. Jan27-2017)

You will need to have:

1. unix executable called: *print_raw_headers* (from the scanner- I can give that out: sofia.chavez@camhpet.ca), add the location of the executable to your $PATH in your .cshrc or .bashsrc file or just type the entire path to it before it
   > eg. /home/user/scripts/print_raw_headers
2. matlab
3. spm : http://www.fil.ion.ucl.ac.uk/spm/
4. Gannet: http://gabamrs.blogspot.ca/
5. Make sure your paths to spm folder and Gannet folder are set so that matlab can find the functions (use 'addpath' in matlab)

Highlights are used for possible problems/adjustments that may beed to happen when using Gannet. Simple ROIs (i.e., without a lot of obliquing) should not need that... eg. ACC, caudate. DLPFC is one region that may require these extra tweaks, depending on the subject.

Prepare your data:

1. make an MRS folder where you will do all the VoxelCSFCorrection processing, here we will call it 'MRS_VoxelCSFCor'
2. copy directories with dcm images into 'MRS_VoxelCSFCor': (i) Original BRAVO (ii) reformatted images (BRAVO Series#*100+1,2,3... eg. BRAVO Se#=2, reformatted AX=200, Cor=201, Sag=202)
3. copy pfiles from ftp server MRS folder into 'MRS_VoxelCSFCor'and rename to only P#####.7 (I keep a copy with the original name which tells me the location of the voxel)

Steps to make a mask of a single Pfile ROI in the space of dcmdir1:

1. From 'MRS_VoxelCSFCor', run: *print_raw_headers P#####.7 > P#####.7.hdr*
   this will create a text file called P#####.7.hdr with the info needed by Gannet as well as for you to know which series was used to prescribe the voxel
2. Search the text file for the second instance of "Series from which prescribed" and write down the Series#. You can use the following Unix command line or open the P*.7.hdr textfile with a text editor: *grep -A 2 "serrx" Pfile.7.hdr*
   This is the series that was used to get the angulation of the voxel (may be a double oblique) and the entire path to the dcm images for this series will be referred to as dcmdir2.

*** You may need to check which image# was used. It will be listed right below the second instance of "serrx" and can be checked using: *grep -A 2 "imgrx" Pfile.7.hdr* . If the Image# is NOT = 1, you may have a problem (if the series has only a few dcm images in it). If the series has several dcm images, as per newer folders or a BRAVO folder, it is likely a volume of images all taken with same orientation so you should not have any problem. If you see a few images int he series folder and view them and they do not appear to be slices of the same volume, you will have to isolate the dcm file given by "imgrx" by copying it to a "new" fake series folder and using that folder path as dcmdir2. ***

3. Copy dcmdir2 (directory with dcm images for Series# found above) into 'MRS_VoxelCSFCor' if it is not already there (it may be one of the above reformatted Ax, Cor or Sag so series # >100)
4. Choose which folder has images where you will want to overly the ROI. You may choose several for viewing (to match the Screen Saves) and then ultimately use the original BRAVO for the correction.
5. In Matlab, run the following:
   - *MRS_struct=GannetLoad({pname});*
     where pname=<full path to Pfile.7>, when it is done a window/figure will open up, just close it and don't worry about it- not relevant for us.
     eg.
     pname='/ResearchData/mr_research/sofia/MRS_CSFcor/StudyData/034_SERO1MR/TestGannet/2013_0110_TW010/P06144.7'
   - assign dcmdir1 (dcms where you want to create the ROI) and dcmdir2 (dcms for angulation of voxel)
     eg.
     dcmdir1='/ResearchData/mr_research/sofia/MRS_CSFcor/StudyData/034_SERO1MR/TestGannet/2013_0110_TW010/Ex01002Se02/'
     dcmdir2='/ResearchData/mr_research/sofia/MRS_CSFcor/StudyData/034_SERO1MR/TestGannet/2013_0110_TW010/Ex01002Se201/'
   - *MRS_struct=GannetMask_GE(pname,dcmdir1,MRS_struct,dcmdir2,1);*

The result will be two nifti volumes created in the dcmdir1: (1)s<name-#-#-#>-01 .nii is the volume created from the dcms in that directory (2) P*_mask.nii is the mask for corresponding Pfile in that space.

Sometimes, the voxel dimensions will not be assigned correctly to the 3 dimensions and another permutation is necessary. For this, you need to find the following code in GannetMask_GE.m:

```
"
ap_size = MRS_struct.p.voxsize(ii,2);
lr_size = MRS_struct.p.voxsize(ii,1);
cc_size = MRS_struct.p.voxsize(ii,3);
ap_off = MRS_struct.p.voxoff(ii,2); %assume offset is correct
lr_off = MRS_struct.p.voxoff(ii,1); %assume offset is correct
cc_off = MRS_struct.p.voxoff(ii,3); %assume offset is correct
"
```

and simply change the three inputs that are: ap_size, lr_size and cc_size (which now read 2-1-3) to another order of the numbers 1,2,3: eg. 2-3-1 as follows:

```
"
ap_size = MRS_struct.p.voxsize(ii,2); %changed
lr_size = MRS_struct.p.voxsize(ii,3); %changed
cc_size = MRS_struct.p.voxsize(ii,1);%changed
ap_off = MRS_struct.p.voxoff(ii,2); %assume offset is correct
lr_off = MRS_struct.p.voxoff(ii,1); %assume offset is correct
cc_off = MRS_struct.p.voxoff(ii,3); %assume offset is correct
"
```

You may then chose to change the name of the output mask so that you can keep track of which mask was made with which permutation of those values. I add the permutation (eg. 213=default, 231=1st test, 132=2nd test) at the end of the mask name:

I edit:
" fidoutmask = fullfile(dcm_dir,[namespar '_mask.nii'])"
to
"fidoutmask = fullfile(dcm_dir,[namespar '_mask213.nii'])" % for default m-file
to
"fidoutmask = fullfile(dcm_dir,[namespar '_mask231.nii'])" % for 1st test
to
"fidoutmask = fullfile(dcm_dir,[namespar '_mask132.nii'])" % for 2nd test

Verfiy ROI Placement:

Make sure to replicate the placement shown in the Screen Saves taken by technologist by looking at *.dcm images in the 'Screen Save' folder (these can be viewed using 'Mango' by selecting one and then using the Page Up/Down to scroll through all three views) while looking at an overlay of the P*_mask.nii on the anatomical s<name-#-#-#>-01.nii within a directory.