Adrien: The following procedure below did not work because of the matlab error

*Error using minmax (line 26): Data is not two-dimensional.*

*Error in mrLoad (line 267)mr.dataRange = minmax(mr.data);*

*Error in mrParse (line 13): if ischar(mr), mr = mrLoad(mr);*

*Error in mrInit2 (line 166): inplane = mrParse(params.inplane);*

I assume this is coming from an incorrect nifit folder and will then try the whole pipeline using another nifti converter. I assumed so because the nifti files don’t have the correct freq\_dim/phase\_dim when read with the readNifti function and because looking at mr.hdir in mrReadNifti when using Kelly’s code, gave incorrect freq\_dim/phase\_Dim.

Will have to retest with old mrReadNifti code too.

-created nifti\_conversion directory with a nifiti\_conversion\_nifti folder full of the converted nii files (not in directory, starting in order with epi01, epi02…) + a nifti\_conversion\_dicom folder with the first epi folder full of dicom files (same name as first epi nii folder). This is used by the motioncorrect.py file to motion correct using the dicom files as a reference volume.

-did not work because motioncorrect save the data in the wrong nifti format and I cannot find where it does it so I cannot change it. It means I should try switching all of the preprocessing to Summer motioncorrect method or another one.

-I actually ended up commenting the error line in mrLoad (line 267): mr.dataRange = minmax(mr.data); and it worked.

-I wonder what do I get if I worked with the new motion not corrected files. Lets see tomorrow after playing a little with mrVista

Eunice: The error you receive is probably this:

Warning: mr.dims has length<4: concatenating a "1" to it

NIFTI header origin is at or outside the image volume- setting it to the image center.

Warning: freq\_dim not set correctly in NIFTI header.

Warning: phase\_dim not set correctly in NIFTI header.

This is the error message that I’ve used to receive using silverlab’s old vistasoft code. The reason you get this is because there is a mrReadNifti.m has always had trouble with coronal slices. specifically line 30 says this in the code: mr.hdr  = niftiApplyCannonicalXform(mr.hdr); %%% does not work for coronal slices (rd)

Rachel D. figured this problem out for me a long time ago and the way to get around it is to change line 30 to:

if sum(mr.hdr.dim>100)==3 % only for mprage

    mr.hdr  = niftiApplyCannonicalXform(mr.hdr); %%% does not work for coronal slices (rd)

end

After that you will only receive the following warning: “Warning: mr.dims has length<4: concatenating a “1” to it” which is perfectly fine.

You will know this is the problem because mrInit2 saves the wrong number of slices under the folder Inplane-> Original-> TSeries-> Scan#s. There should be the same number of mat files as the number of slices in your gems/bold scans. If there are more its because mrReadNifti read the order of the dimensions incorrectly- for example instead of reading 74x74voxels x16slices, it would see 74slices, 74x16voxels and make 74 mat files.

So once you edit the mrReadNifti file in mrvista\_development folder, you should be fine. The error you receive that the matlab version is unsupported is fine and is what i always get since the old vistasoft was made for matlab 2009 or 2010 (i can’t remember which).

You will receive other errors as you go through the pipeline using the old vistasoft primarily because some functions are obsolete (e.g. javafeature) in the newer matlab versions. Attached are the four matlab scripts that I have had to edit so i would not get errors with matlab2012b (includes mrReadNifti). If you put them in the mrvista\_development folder (and this folder is higher in the matlab path directory than vistasoft), you should be fine.

Right now I am using the old vistasoft code that’s in the megavista repo with matlab2012b. Kelly is working on getting the new vistasoft code working. Once we have data analyzed through both versions,  we compare the results between the two since the code edited by other lab members (in the mrvista\_development folder) are modified for data acquired at berkeley and includes fixes/updates and we have no idea how the new version differs from the old version. Kelly, let me know if this is what we decided on or that we were going to just scrap the old version altogether and not even try to compare the results.