Protocol for FA and vector alignment QC analysis for ENIGMA-DTI
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The following steps will allow you to visualize your raw FA images before registration to the ENIGMA-DTI template, and to see if your principle direction vectors are appropriately aligned to the white matter tracts.

Highlighted portions of the instructions may require you to make changes so that the commands work on your system and data.

INSTRUCTIONS

Prerequisites

- Matlab installed http://www.mathworks.com/products/matlab/
- Diffusion-weighted images preprocessed using FSL's DTIFIT (http://fsl.fmrib.ox.ac.uk/fsl/fsl4.0/fdt/fdt_dtifit.html) or equivalent. This requires the creation of FA maps and eigenvectors comprising of three volumes, the first being the x-component of the eigenvector, the second being the y-component and the third being the z-component.

Step 1 – Download the utility packages

Download the Matlab scripts package for Step 3:
http://enigma.ini.usc.edu/wp-content/uploads/DTI_Protocols/enigmaDTI_QC.zip

Download the script to build the QC webpage for Step 4:

- Linux: http://enigma.ini.usc.edu/wp-content/uploads/DTI_Protocols/make_enigmaDTI_FA_V1_QC_webpage.sh
- Mac:http://enigma.ini.usc.edu/wp-content/uploads/DTI_Protocols/make_enigmaDTI_FA_V1_QC_webpage_mac.sh

Step 2 – Build a text file defining the location of subject files

Create a three column tab-delimited text file (e.g. **Subject_Path_Info.txt**):

- **subjectID**: subject ID
- **FAimage**: full path to original FA image.
- **V1image**: full path to original V1 image. This is a 4D volume that represents the primary eigenvector of the diffusion tensors at every voxel (i.e. x-component of the eigenvector).

subjectID	**FA**image	**V1**image

```
USC_01   /path/to/FA/USC_01_FA.nii.gz  /path/to/V1/USC_01_V1.nii.gz
USC_02   /path/to/FA/USC_02_FA.nii.gz  /path/to/V1/USC_02_V1.nii.gz
USC_03   /path/to/FA/USC_03_FA.nii.gz  /path/to/V1/USC_03_V1.nii.gz
```

Step 3 – Run Matlab script to make QC images

Unzip the Matlab scripts from Step 1 and change directories to that folder with the required Matlab *.m scripts. For simplicity, we assume you are working on a Linux machine with the base directory `/enigmaDTI/QC_ENIGMA/`.

Make a directory to store all of the QC output:

```
mkdir /enigmaDTI/QC_ENIGMA/QC_FA_V1/
```

Start Matlab:

```
/usr/local/matlab/bin/matlab
```

Next we will run the **func_QC_enigmaDTI_FA_V1.m** script that reads the **Subject_Path_Info.txt** file to create subdirectories in a specified **output_directory** for each individual **subjectID**, then create an axial, coronal and sagittal image of the **FA_image** with vectors from the **V1_image** overlaid on top. The **threshold** (0 to ~0.3, default 0.1) overlay the V1 information only on voxels with FA of the specified threshold or greater. Increasing the threshold above 0.1 will run the script faster and is recommended for groups with many subjects.

In the Matlab command window paste and run:

```
      TXTfile='/enigmaDTI/QC_ENIGMA/Subject_Path_Info.txt';
      output_directory='/enigmaDTI/QC_ENIGMA/QC_FA_V1/';
      thresh=0.1;

      [subjs,FAs,VECs]=textread(TXTfile,'%s %s %s','headerlines',1)

      for s = 1:length(subjs)
      subj=subjs(s);
      Fa=FAs(s);
      Vec=VECs(s);
      try
% reslice FA
      [pathstrfa,nameniifa,gzfa] = fileparts(Fa{1,1});
      [nafa,namefa,niifa] = fileparts(nameniifa);
      newnamegzfa=[pathstrfa,'/',namefa,'_reslice.nii.gz'];
      newnamefa=[pathstrfa,'/',namefa,'_reslice.nii'];
      copyfile(Fa{1,1},newnamegzfa);
      gunzip(newnamegzfa);
      delete(newnamegzfa);
      reslice_nii(newnamefa,newnamefa);

% reslice V1
      [pathstrv1,nameniiv1,gzv1] = fileparts(Vec{1,1});
      [nav1,namev1,niiv1] = fileparts(nameniiv1);
```

```
        newnamegzv1=[pathstrv1,'/',namev1,'_reslice.nii.gz'];
        newnamev1=[pathstrv1,'/',namev1,'_reslice.nii'];
        copyfile(Vec{1,1},newnamegzv1);
        gunzip(newnamegzv1);
        delete(newnamegzv1);
        reslice_nii(newnamev1,newnamev1);

% qc
        func_QC_enigmaDTI_FA_V1(subj,newnamefa,newnamev1,
        output_directory);

        close(1)
        close(2)
        close(3)

% delete
        delete(newnamefa)
        delete(newnamev1)
        end

        display(['Done with subject: ', num2str(s), ' of ',
        num2str(length(subjs))]);

        end
```

For troubleshooting individual subjects that **func_QC_enigmaDTI_FA_V1.m** script can be run in the command console with the following parameters:

```
func_QC_enigmaDTI_FA_V1('subjectID', 'FA_image_path',
'V1_image_path','output_directory')
```

Step 4 - Make the QC webpage

Within a terminal session go to the `/enigmaDTI/QC_ENIGMA/` directory where you stored the script ***make_enigmaDTI_FA_V1_QC_webpage.sh*** and ensure it is executable:

```
chmod 777 make_enigmaDTI_FA_V1_QC_webpage.sh
```

or for Mac,

```
chmod 777 make_enigmaDTI_FA_V1_QC_webpage_mac.sh
```

Run the script, specifying the full path to the directory where you stored the Matlab QC output files:

```
./make_enigmaDTI_FA_V1_QC_webpage.sh /enigmaDTI/QC_ENIGMA/QC_FA_V1/
```

or for Mac,

```
sh make_enigmaDTI_FA_V1_QC_webpage_mac.sh
/enigmaDTI/QC_ENIGMA/QC_FA_V1/
```

This script will create a webpage called **enigmaDTI_FA_V1_QC.html** in the same folder as your QC output. To open the webpage in a browser in a Linux environment type:

```
firefox /enigmaDTI/QC_ENIGMA/QC_FA_V1/enigmaDTI_FA_V1_QC.html
```

Scroll through each set of images to check that the vector directions are correct. For closer inspection, clicking on a subject's preview image will provide a larger image. If you want to check the segmentation on another computer, you can just copy over the whole /enigmaDTI/QC_ENIGMA/QC_FA_V1/ output folder to your computer and open the webpage from there.

Congrats! Now you should have all you need to make sure your FA images turned out OK and their vector fields are aligned!