

Protocol for FA and Skeleton Visual QC analysis for ENIGMA-DTI

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The following steps will allow you to visualize your FA images after registration to the ENIGMA-DTI template, and to see if your extracted skeletons are all projected onto the ENIGMA Skeleton.

These protocols are offered with an unlimited license and without warranty. However, if you find these protocols useful in your research, please provide a link to the ENIGMA website in your work: www.enigma.ini.usc.edu

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.
- Run the ENIGMA DTI processing protocol to project individual skeletons onto the common template: <http://enigma.ini.usc.edu/protocols/dti-protocols/#eDTI>

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_Skel_QC_webpage.sh
- Mac: http://enigma.ini.usc.edu/wp-content/uploads/DTI_Protocols/make_enigmaDTI_FA_Skel_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 registered FA image.
- **Skeleton**: full path to skeletonized FA image.

subjectID	FAimage	Skeleton
USC_01	/path/USC_01_masked_FA.nii.gz	/path/USC_01_masked_FAskel.nii.gz
USC_02	/path/USC_02_masked_FA.nii.gz	/path/USC_02_masked_FAskel.nii.gz
USC_03	/path/USC_03_masked_FA.nii.gz	/path/USC_03_masked_FAskel.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_SKEL/
```

Start Matlab:

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

Next we will run the `func_QC_enigmaDTI_FA_skel.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 overlays from the `Skeleton`.

In the Matlab command window paste and run:

```
TXTfile='/enigmaDTI/QC_ENIGMA/Subject_Path_Info.txt';
output_directory='/enigmaDTI/QC_ENIGMA/QC_FA_SKEL/';

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

for s = 1:length(subjs)
    subj=subjs(s);
    Fa=FAs(s);
    skel=SKElS(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 skel
    [pathstrskel,nameniiskel,gzskel] = fileparts(skel{1,1});
    [naskel,nameskel,niiskel] = fileparts(nameniiskel);
    newnamegzskel=[pathstrskel,'/',nameskel,'_reslice.nii.gz'];
    newnameskel=[pathstrskel,'/',nameskel,'_reslice.nii'];
    copyfile(skel{1,1},newnamegzskel);
    gunzip(newnamegzskel);
    delete(newnamegzskel);
    reslice_nii(newnameskel,newnameskel);

% qc
    func_QC_enigmaDTI_FA_skel(subj,newnamefa,newnameskel,
    output_directory);
```

```

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

% delete
    delete(newnamefa)
    delete(newnameskel)
    end

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

    end

```

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

```

func_QC_enigmaDTI_FA_skel('subjectID', 'FA_image_path',
    'Skel_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_Skel_QC_webpage.sh*** and ensure it is executable:

```

chmod 777 make_enigmaDTI_FA_Skel_QC_webpage.sh

```

or for Mac,

```

chmod 777 make_enigmaDTI_FA_Skel_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_Skel_QC_webpage.sh /enigmaDTI/QC_ENIGMA/QC_FA_SKEL/

```

or for Mac,

```

sh make_enigmaDTI_FA_Skel_QC_webpage_mac.sh /enigmaDTI/QC_ENIGMA/QC_FA_SKEL/

```

This script will create a webpage called **enigmaDTI_FA_Skel_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_SKEL/enigmaDTI_FA_Skel_QC.html

```

Scroll through each set of images to check that the images are all aligned and well registered and all skeletons are composed of the same voxels. 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_SKEL/` 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 skeletons line up!