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🌐 DIFFPREP for DTI Processing and Corrections V.2

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Protocol status: In development
We are still developing and optimizing this protocol

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Abstract

This protocol will provide a basic guide to utilizing the DIFFPREP tool in TORTIOSE.

Note: Steps may vary based upon image.

Troubleshooting

Introduction

1   DIFFPREP is a distortion and motion correction module in TORTOISE. When processing MR images you will commonly start with DIFFPREP for corrections.

Beginning Steps

2   Build your directory in the terminal, and make sure to use copied raw data for processing

2.1   In the terminal go to your new directory with the data

Import DTI Data

3   Type the following command in your terminal to read information and options available:

Command

new command name

```
ImportBruker
```

Type the following command to import your blip_up and blip_down data:

Command

new command name

```
ImportBruker -i  directory/file_name_blip_up -c 1
ImportBruker -i  directory/file_name_blip_down -c 1
```

3.1 Blip up is the forward phase encoding of a scan while blip down is the same exact scan but with reversed phase encoding.

You may not always will have both blip up and blip down, but for the purpose of this protocol both will be shown.

3.2 Note:
Sometimes your blip up and blip down data will be split across four scans (two blip up scans and two blip down scans). If that is the case, simply make a new folders and move the all the blip up raw data into one folder, rename the first blip up raw folder as 01, and the second as 02. Do the same for the blip down data.

In other words you should have two folders (one for blip up and down) each with two sub-folders labeled as 01 and 02 corresponding to their scan order.

For the ImportBruker command, you **only need to input UP to the blip up/down folder** containing the subfolders for the path.

3.3 Note:
If you want to control where InputBruker puts the output proc folder, use -o with the desired directory.

Viewing DTI Images

4 Change directories to the containers.

Command

new command name

```
cd /rsgrps/hutchinsone/Singularity_Containers
```

5 Load the singularity containers

Command

new command name

```
module load singularity
singularity run nklab-neurotools-v0.4.sif
```

5.1   You should be able to see the contents of the container.

6   Start by loading ITKSNAP and looking at the orientation of your image

       Note: You can also use MIPAV and MRtrix (mrview) to view your imags

6.1   Type:

Command

new command name

```
singularity run nklab-neurotools-v0.4.sif itksnap
```

6.2   On the ITKSNAP GUI, scroll over to file and import your DTI NIFTI file.

6.3   View the raw data image, and make note of the orientation of the blip down image.

This will become important in step 8.

(Note: The image should naturally be in RPS, and for our purposes of DTI images you want LPS)
Here are a couple sources for understanding orientation.
https://www.slicer.org/wiki/Coordinate_systems
http://www.grahamwideman.com/gw/brain/orientation/orientterms.htm

6.4   If desired, to use MIPAV

Command
new command name
`/rsgrps/hutchinsone/Programming/mipav/mipav`

Or type the following command to access mrview.

Command
new command name
`singularity run nklab-neurotools-v0.4.sif mrview`

Get .bval and .bvec

7   Type the following command to get your bval and bvec files.

> **Command**
>
> ## new command name
>
> ```
> TORTOISEBmatrixToFSLBVecs directory_to_bmatrix_file
> ```

7.1 Note: The blip down and blip up should have matching bmatrix files, so this command only needs to be done once.

ImportNIFTI

8 This step is crucial for obtaining the *.list* file which will be used in DIFFPREP and DRBUDDI

Type the following to get information and options of the command.

> **Command**
>
> ## new command name
>
> ```
> ImportNIFTI
> ```

8.1 The general full command is the following:

> **Command**
>
> **new command name**
>
> ```
> ImportNIFTI -i directory/file_name.nii -p phase_direction -o
> output_folder -b file_name.bval -v file_name.bvec
> ```

Note:
- directory: where your NIFTI file is stored
- phase_direction: can either be vertical or horizontal based upon what your phase encoding direction is
- output_folder: where you want your data to be stored when it's done importing

Reorient DTI Images

9   In the terminal type:

> **Command**
>
> **new command name**
>
> ```
> ReorientImage
> ```

This will give you information about the command, and the different options available.

9.1   Type:

> **Command**
>
> **new command name**
>
> ```
> ReorientImage -i directory_name_DTI/file_name_blip_down.list -r RPS
> ```

9.2   Note: This should be done with the list file in your proc folder.

9.3   Note: You only need to reorient the blip down data. The blip down data is inverse when it is acquired form the scanner, changing the orientation of the image.

Extract DTI Images

10   To check your reoriented image use the following command to extract from 4D image.

> **Command**
>
> **new command name**
>
> ```
> ExtractImage
> ```

This will give you information about the command, and the different options available. Yo

10.1   Type:

Command

new command name

```
ExtractImage -i directory_name_DTI/file_name_blip_down_reoriented.nii
```

11   You can view and edit your extracted image on ITKSNAP.

Edit Settings File

12   Before you run DIFFPREP, you must make sure your settings file is
- Compatible with size and resolution of your data
- In your user's directory
- Will give you the corrections needed in DIFFPREP

13   In your user's directory make a folder titled "DIFF_PREP_WORK". By doing it in the file browser GUI or by navigating in your terminal and typing:

Command

new command name

```
cd /home/u26/cjoy1895

mkdir DIFF_PREP_WORK
```

13.1   Copy the setting templates to YOUR OWN DIFF_PREP_WORK

Command

new command name

```
cp /rsgrps/hutchingsone/Programming/DIFF_PREP_WORK/IVmouse_2D.dmc
/home/u26/cjoy1895/DIFF_PREP_WORK
```

13.2
- Only need to make the directory and copy the settings file if you haven't done it already
- There are multiple settings.dmc templates on the HPC, it would be a good idea to copy all of them to your DIFF_PREP_WORK directory

14   In your home DIFF_PREP_WORK directory, right click on the IVmouse_2D.dmc and select Open With > gedit
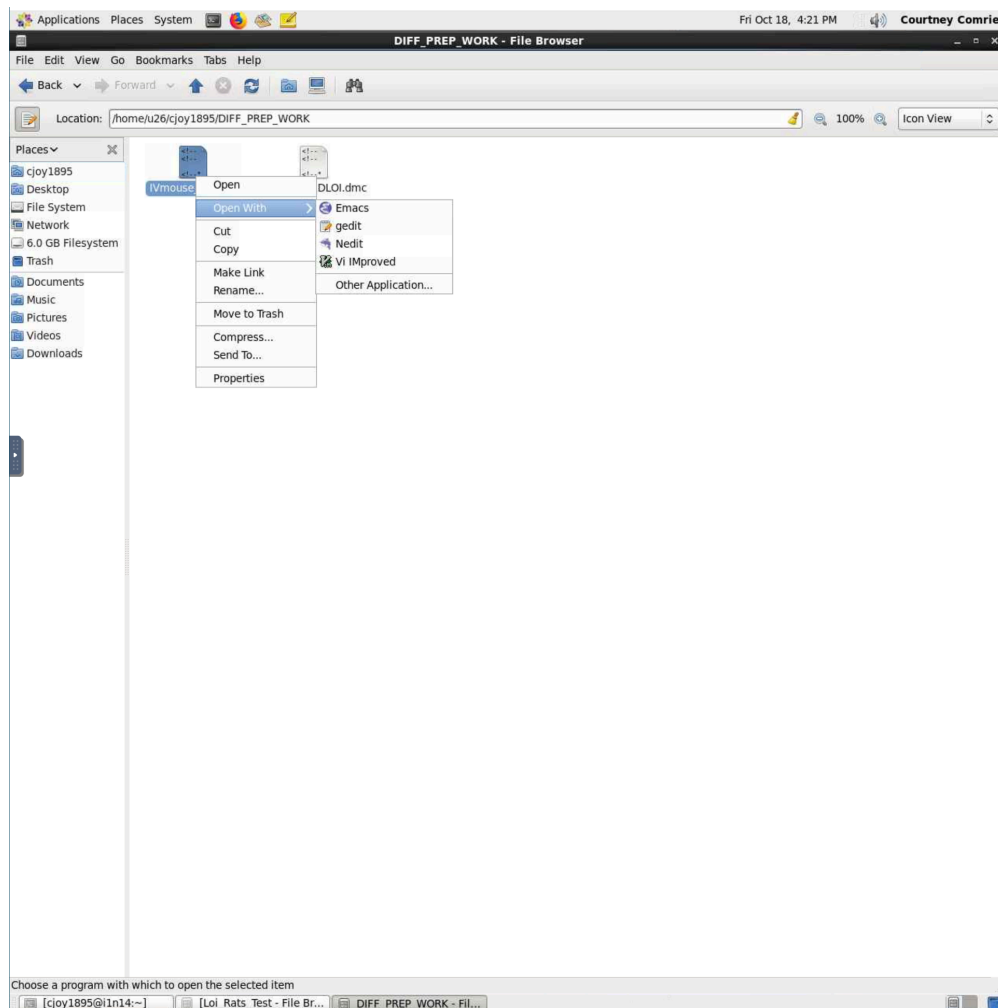
14.1 You should see a bunch of text like the following:

The DARK BLUE text tells you information about the sections and options you can use, the BLACK text is what you can edit.

Correction Mode
- Change to the registration to **rigid**

EPI Correction
- Make sure it is turned off.
- Only turn it on if you don't plan on using DRBUDDI later.

Gibbs Ringing Correction
- on

Denoising
- for_final

Humanity
- 0
- Basically is asking if your brain is human or not

Upsampling
- all

High B-value Registration
- You need to know the 3 values for the scan you are processing. If you don't know it, you can find it in the methods file.

- Enter your three values

Pre-Smoothing
- Turn off!!! Very important!

FOV
- You need to know the 3 values for the scan you are processing. If you don't know it, you can find it in the methods file.

Resolution
- You need to know the 3 values for the scan you are processing. If you don't know it, you can find it in the methods file.

These are the main settings you will need to change on a scan to scan basis, but keep in mind you may change other settings not mentioned here or will need different inputs than what are mentioned above.

DIFFPREP

15   Type in terminal:

Command

new command name

```
DIFFPREP -i directory/file_name_blip_up.list --reg_settings
IVmouse_2D.dmc

DIFFPREP -i directory/file_name_blip_down_reoriented.list --
reg_settings IVmouse_2D.dmc
```

The specific settings.dmc file will change based upon the animal and type of image you are processing. This specific .dmc file is for ferrets, but be aware mice will use a different settings file.