

Pre-processing QC

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Important

- 1) Understand your data.**
- 2) What is the quality of your structural image?**
- 3) How do you plan to organize your data naming structure?**
- 4) Understand the origin of the artifacts.**
- 5) Maintain a QC spreadsheet.**

When you have a new study, there are certain steps you can use to quickly go through the data

> Import the data in to TORTOISE using ImportDicom command.

> While this may use the information from header, it is important to understand if this information is being read correctly by the software.

> If you have a small study, then it can be done for a few datasets. If it is a large study, over the course of couple years, it is recommended to do the upcoming QC steps periodically, to make sure scanner/software upgrades have not caused any changes to your protocol or the way acquisition information is being stored in the header.

> Once you import your data, please make sure you fit a tensor in DIFFCALC and check the nonsymm heures map. Examine the colors as on this page:

<https://tortoise.nibib.nih.gov/tortoise/v313/5-check-your-import-results>

BMATRIX QC

- Convert bmtxt to bvals and bvecs to check if your data has been imported correctly.
- You may use the command from diffprep to generate bvals and bvecs from bmtxt file:

TORTOISEBmatrixToFSLBvecs

The command generates bvals and bvecs file. Please check if the numbers in bvals text file are those expected for your data. If not, you may have to use a gradient text file to import your data.

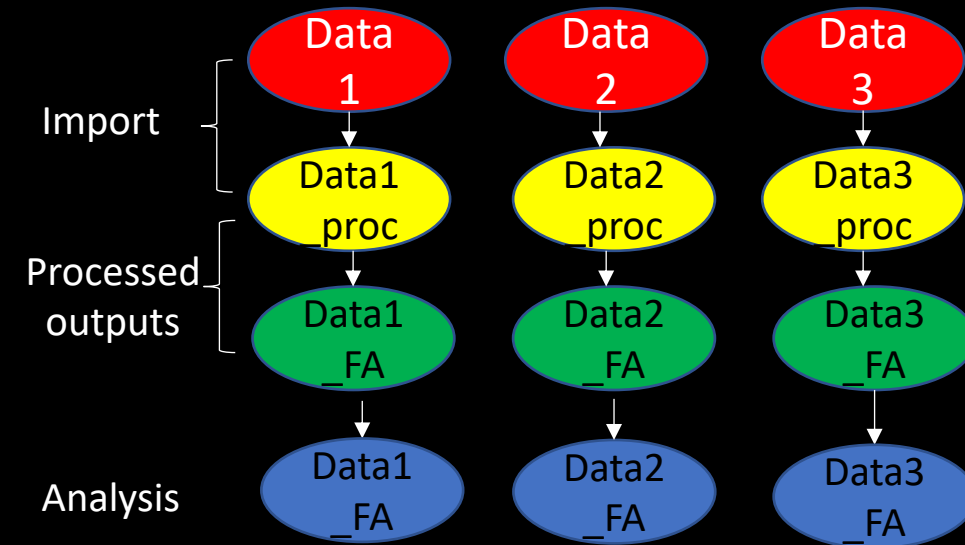
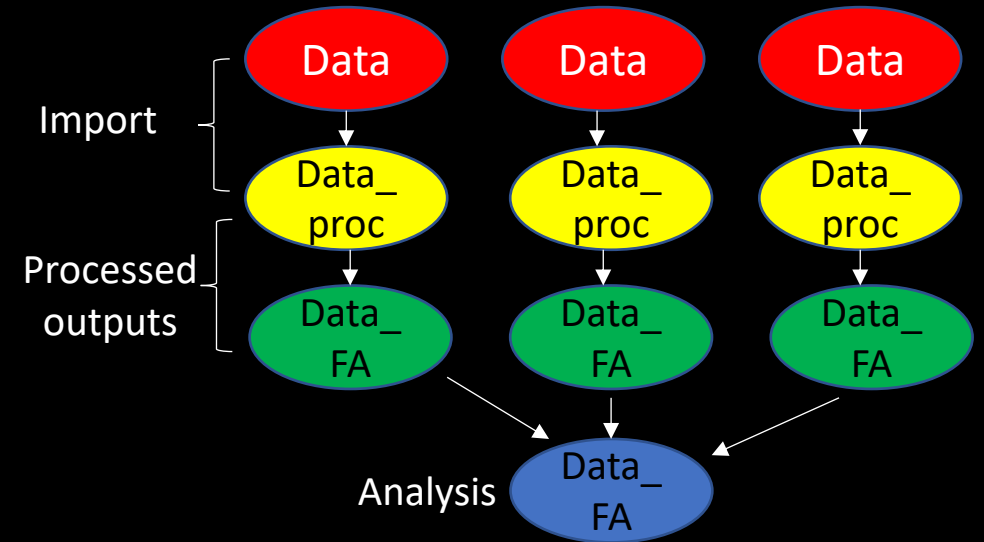
Structural reference quality

A T2w structural data needs to be provided for EPI distortion correction, both in DIFFPREP and in DRBUDDI. It is important that this reference image be free of artifacts and is fat suppressed, so that you are not introducing more artifacts in your DWI data, during registration.

Please ensure that the structural quality is good. This takes a higher priority than DWIs as DWI correction relies on your structural data quality.

Data organizing

- Data naming convention is very important. Maintaining a data tree structure helps in scripting, easy data mining. More importantly, if you are using the diffusion tensors generated or its scalar maps in any analysis, having a unique identifier prevents overwriting and analysis mishaps.
- If your parent folder where you raw image files are named as “data”, please be aware that the folder being named will have “data_proc” as the name, unless you use the `-o` tag during import. Here is your opportunity to decide upon a unique identifier, that may stay throughout the study and into your analysis.

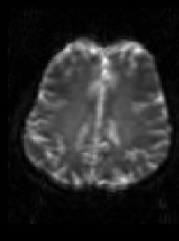
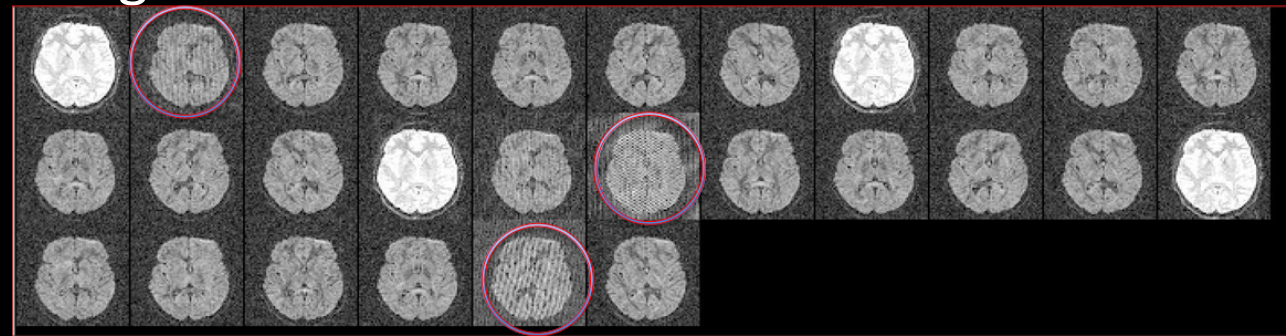


Observe for artifactual patterns in your data

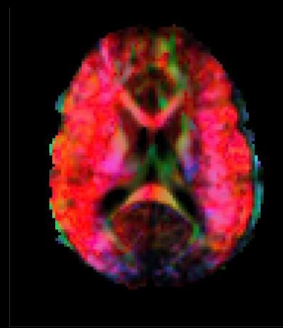
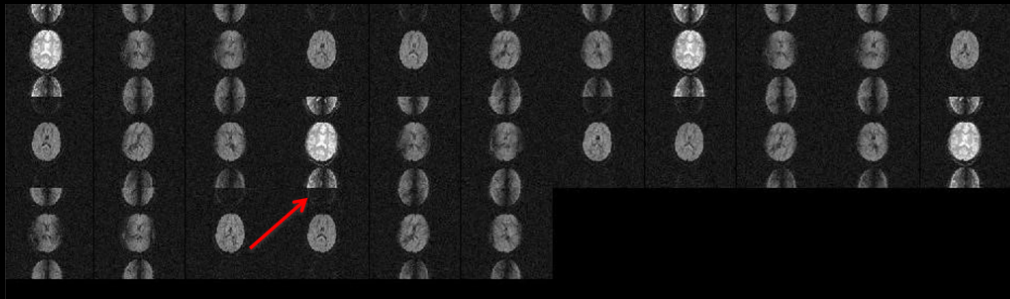
- While consistency in data acquisition is expected in a study, watch out for consistency in the occurrence of artifacts.
- If you see certain artifacts, repeatedly affecting datasets in your study, acquired at a certain scanner, during a time period, please make sure to examine the scanner room and the scanner. These maybe issues that if caught early, can save your study and future datasets from being acquired incorrectly.
- Please remember! Artifacts consistently affecting all volumes of the data cannot be corrected.

Examples:

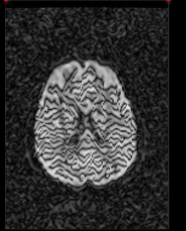
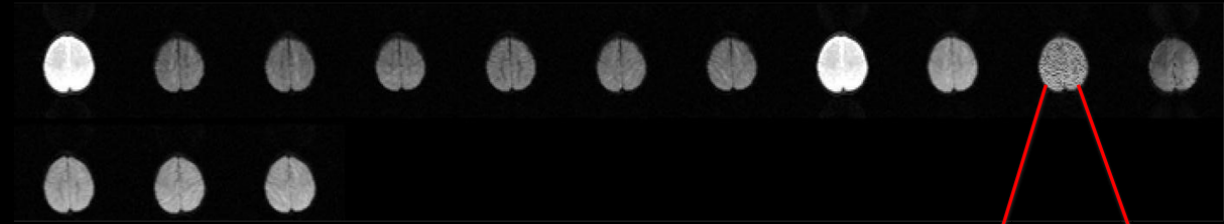
- ✓ prevalent spike artifacts through all volumes in many datasets maybe related to some RF interference in the room.
- ✓ Consistent large eddy distortions through almost all datasets acquired within a time period maybe related to scanner issue.



A few examples of uncorrectable artifacts:



Severe ghosting



Motion artifact present in a dataset through all volumes.

Couple tips on how to check your data

- While a QC folder is generated during processing, some of the initial checks for your data can be done using few commands, easily.
- If you have AFNI installed using commands such as these from the AFNI scripts folder, that is housed inside `./TORTOISE/bin` you can generate movie (gif) and snapshots (png) files, quickly
- Perhaps, an initial QC at a beginning of a study to make sure they have been acquired according to prescribed standard.

Example commands

1) generate 3d image files using the command

```
tcsh fat_tort_qc_viewer_3d.tcsh input_3d_image output_snapshot_image.png
```

Here you can feed any input image and generate slices to open the images.

2) generate 4d image files using the command

```
tcsh fat_tort_qc_viewer_4d.tcsh dwi.nii dwi_img AGIF
```

can generate any movie gifs for you to view. You can load any imported nii file and check if these images have high motion, large eddy distortions etc.

3) check your T2w structural image that you will use in your processing as the quality of this image is important.

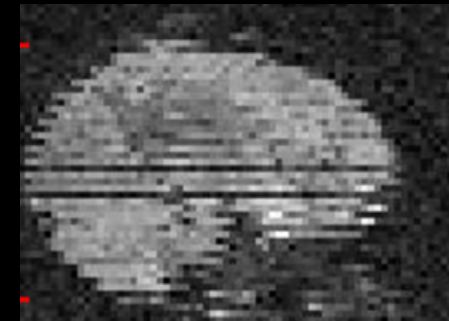
4) 3dZipperZapper script to check for interslice motion.

Increased patient motion in your data, through multiple volumes can be an indication of perhaps patient discomfort and may need to be looked into.

5) Running the generate glyphs and non symm heures command can give information about the data import. As if this is incorrect, then you may have to evaluate the import routine and incorporate additional parameters to ensure that this is not observed late into your analysis.

Alternate steps, If the AFNI scripts do not work on your machine for any reason:

- Open any nifti image visualizer software to open the imported DWI.nii file
- Quickly go through the volumes to ensure that the ordering of the b0's and DWI's are in order.
- You may also assess the quality of the structural image similarly.
- The motion within a volume can be assessed better by looking at the sagittal view of the volumes. In the presence of interleave slice motion, you will notice a zipper pattern at the edge of the brain.
- This motion in diffusion images can be handled by removing the volumes but for structural data, it can be problematic. You will then have to consider using another reference image.



Conclusion

- Once you have dotted all your 'i's and crossed all your 't's, you can proceed towards DIFFPREP to do the magic.
- Please remember, YES, TORTOISE can do wonders on your data in terms of data correction, but it is important to remember that there is a certain standard that is expected for all the correction to work smoothly. If all of the data points are artifactual, there is no good data points to perform correction with.
- pre processing QC can be sometimes time consuming, but VERY important part of your processing pipeline.
- If you use any other software, other than TORTOISE or AFNI to do QC and save data, please make sure the images are saved with the correct image orientation information.