Diffusion Imaging Motion Evaluator

Quality control software and visualization for diffusion tensor imaging

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WHY SHOULD I CHECK MY DIFFUSION WEIGHTED IMAGING DATA?

- Head motion can corrupt DWI data, adding both noise and bias as FA is systematically increased with increasing noise in grey matter (Jones & Cercignani, 2010).
- Differences in head motion between groups can drive statistical results (Yendiki et al, 2013).

WHAT ARE THE GENERAL CHALLENGES FOR EVALUATING MOTION IN MAGNETIC RESONANCE IMAGING DATA?

- Increasingly large numbers of MRI acquisitions are being collected for neuroimaging studies and the number of researchers utilizing these data sets is also growing, both within and outside of the academic institution in which data is stored, and from a widening range of research areas.
- This diversity in researcher training and experience, along with the overwhelming working memory demands that traditional quality assurance requires, places a strong emphasis on a systematic approach to the question of inclusion and exclusion criteria.

WHAT ARE THE SPECIFIC CHALLENGES FOR EVALUATING MOTION IN DIFFUSION WEIGHTED IMAGING DATA?

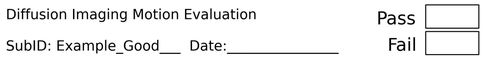
- Diffusion tensor imaging works by acquiring many images of the brain under different magnetic field environments. By definition these will be different to each other and therefore matching each volume in a 4D "timeseries" will always be imperfect.
- In particular, there are large differences between volumes acquired with no diffusion weighting (b0 volumes) and those for which the powerful diffusion gradients have been applied (diffusion weighted volumes).

SO WHAT CAN WE DO?

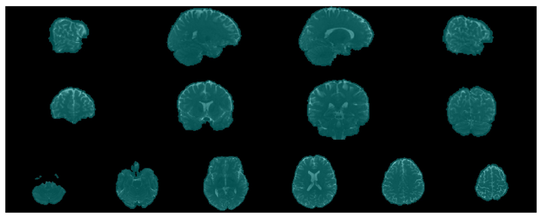
- The first rule of quality control assessment is ***look at your data***.
- The second rule of quality control assessment is ***look at your data***.
- There is a clear working memory challenge of these quality control is applying objective inclusion and exclusion criteria. The diffusion imaging motion evaluator overcomes this problem by creating a one page report for each participant.
- These reports can be easily referred to through out the analysis stream and shared along with data sets.

WHAT INFORMATION DOES THE DIFFUSION IMAGING MOTION EVALUATOR REPORT?

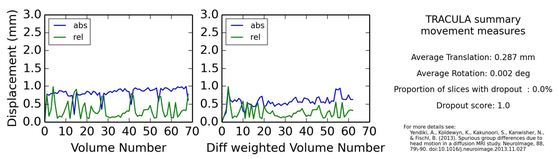
- The DIME report is an A4 sized image, with a header that can be used to keep track of the participant's identification number (SubID) and the date that the researcher evaluated the quality of the data. There is also a checkbox to record whether the participant's data met inclusion criteria.



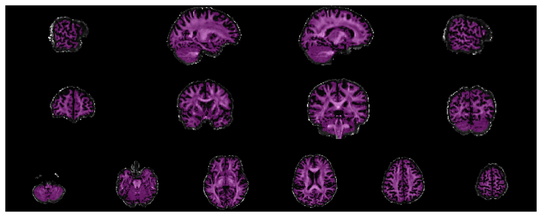
- Next DIME shows sagittal, coronal and axial slices of the first volume in the time series (usually the non-diffusion weighted volume). These images are overlaid with the brain mask created from brain extraction in order to check that this step has not excluded brain regions that should have been included.



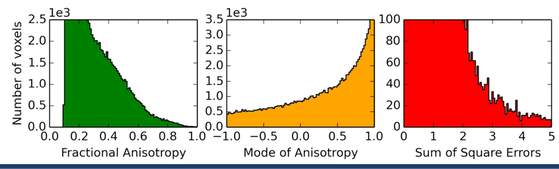
- The following row shows volume to volume displacement values for all volumes (left) and only the diffusion weighted volumes (middle). The two lines represent absolute displacement from the first volume in the series, (blue) and the relative displacement from the previous volume (green). The final panel reports the four summary measures proposed in Yendiki et al 2013 and generated in Freesurfer's TRACULA trac-all processing.



- The next panel shows the FA map with regions of high FA highlighted. There is a beta option to pass your own white matter mask defined from a structural scan.



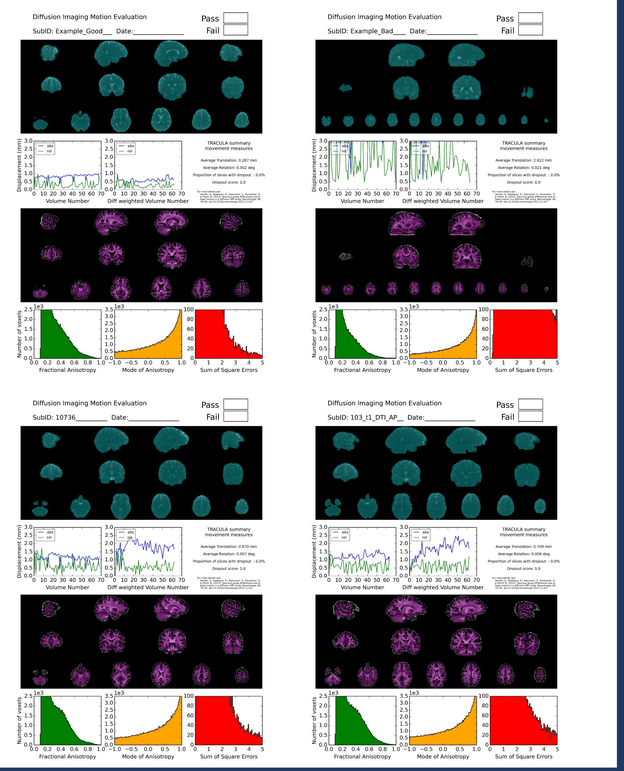
- Finally the lower panel shows histograms of FA, mode (MO) and sum of square errors for values defined as white matter. Importantly the scale is the same across all participants to ensure that these reports are comparable across different scan sessions.



HOW CAN I GET STARTED USING DIME?

- DIME is hosted on GitHub and can be downloaded as a release from: www.github.com/HappyPenguin/DIME/releases
- There are resources on the DIME wiki covering required installation and how to get started www.github.com/HappyPenguin/DIME/wiki

SAMPLE REPORTS



ACKNOWLEDGMENTS

This toolbox is designed to simply wrap around the exceptional tools that are already provided for researchers by the Freesurfer, FSL and Neuroimaging in Python teams. These communities work tirelessly to support neuroimaging researchers such as myself and I am endlessly grateful for the help provided through mailing lists and online resources. DIME was conceived while working with Dr Lara Menzies at University College London, and developed during Code Club events arranged by Jessica Leach and Catherine Breslin for the Cambridge Women in Technology network, although countless others have contributed through their invaluable discussions.